International Conference on Emerging Infectious Diseases

ICEID

1998
2018

AUGUST
26-29
2018

Program and Abstracts Book

Omni Atlanta Hotel at CNN Center | Atlanta, GA

U.S. Department of
Health and Human Services
Centers for Disease
Control and Prevention

THE TASK FORCE FOR GLOBAL HEALTH

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ICEID 2018:

Sunday, August 26, 2018	Monday, August 27, 2018
	Registration: 7:30 AM – 4:30 PM
	Poster set-up: 7:00 AM – 8:00 AM
	Concurrent Plenary Sessions: 8:00 AM – 9:00 AM A1. Healthcare-Associated Infections in Europe and the United States A2. Zika: Human Neurological Outcomes A3. Challenges for Disease Elimination and Eradication A4. Lessons Learned from the West Africa Ebola Outbreak
	Concurrent Plenary Sessions: 9:10 AM – 10:10 AM B1. Genomic Epidemiology B2. Infectious Diseases in Humanitarian/ Disaster Settings B3. Vaccines for Dengue, A Major *Aedes*-Transmitted Arbovirus B4. IHR and Global Health Security
	Break: 10:10 AM – 10:30 AM
	Concurrent Panel Sessions: 10:30 AM – 12:00 PM C1. Emerging Vector-Borne Diseases and New Control Strategies C2. Bioinformatics and Big Data in Public Health C3. Respiratory Diseases: Focus on *Legionella*, MERS, and Plague C4. Emerging Issues in Sexually Transmitted Diseases
	Lunch (*on your own*): 12:00 PM – 12:30 PM
	Lunchtime Panel Session: 12:15 PM – 1:30 PM* Emerging and Re-emerging Infectious Diseases in the WHO Eastern Mediterranean Region
	Poster Sessions with Authors: 12:30 PM – 1:45 PM
Registration: 1:00 PM – 6:00 PM	**Concurrent Panel Sessions: 1:45 PM – 3:15 PM** D1. New Data Systems and Platforms for Disease Surveillance D2. Bugs from Drugs: Emerging Infections in People Who Use Opioids D3. Emerging Fungal Infections in Healthcare Settings D4. Environmental/Ecological Factors and Emerging Infectious Diseases: A Multi-Continental Approach
	Break: 3:15 PM – 3:30 PM
Opening Keynote Session **5:30–7:30 PM** **Opening Reception** **7:30–9:30 PM**	**Oral Presentation Abstracts: 3:30 PM – 5:00 PM** E1. Novel Surveillance Strategies E2. Emerging Threats in Healthcare E3. Vector-Borne Diseases E4. Frontline Public Health

**Limited sandwiches & salads available for purchase outside meeting room*

Schedule-at-a-Glance

Tuesday, August 28, 2018	Wednesday, August 29, 2018
Registration: 7:30 AM – 4:30 PM	**Registration: 8:00 AM – 2:00 PM**
Poster set-up: 7:00 AM – 8:00 AM	**Poster set-up: 7:00 AM – 8:00 AM**
Concurrent Plenary Sessions: 8:00 AM – 9:00 AM	**Concurrent Plenary Sessions: 8:00 AM – 9:00 AM**
F1. The Microbiome and Human Health	K1. Forecasting Emerging Infections
F2. Public Health Preparedness and Outbreak Response	K2. 100 Years After the 1918 Influenza Pandemic
F3. Reemergence of Vaccine-Preventable Diseases: Focus on Diphtheria	K3. Addressing Neglected Tropical Diseases: Focus on Guinea Worm
F4. Cholera: The Beginning of the End?	K4. Globalization of People and Disease
Concurrent Plenary Sessions: 9:10 AM – 10:10 AM	**Concurrent Plenary Sessions: 9:10 AM – 10:10 AM**
G1. National Control of Carbapenem-Resistant Enterobacteriaceae	L1. Infectious Causes of Child Mortality
G2. Advanced Molecular Detection of Infectious Diseases	L2. Novel Surveillance Strategies
G3. Africa CDC	L3. Emerging Tickborne Diseases
G4. One Health	L4. Foodborne Disease Surveillance and Culture-Independent Diagnostic Tests
Break: 10:10 AM – 10:30 AM	**Break: 10:10 AM – 10:30 AM**
Concurrent Panel Sessions: 10:30 AM – 12:00 PM	**Concurrent Panel Sessions: 10:30 AM – 12:00 PM**
H1. Emerging Scientific Issues for Global Immunization Programs	M1. Emerging Paths to Publishing Your Work: The Good, the Fast, and the Ugly
H2. Viral Hemorrhagic Fevers	M2. Rodent-Borne Zoonoses
H3. More Answers, More Questions: Whole-Genome Sequencing in Foodborne Disease Epidemiology	M3. Mathematical Modeling to Better Understand the Emergence and Transmission of Multidrug-Resistant Organisms
H4. Emerging Infections Associated with Life-Saving Medical Devices	M4. Make History: End TB
Lunch (*on your own*): 12:00 PM – 12:30 PM	**Lunch (*on your own*): 12:00 PM – 12:30 PM**
Lunchtime Panel Session: 12:15 PM – 1:30 PM* Building a GHS Implementation Evidence Base: Demonstrating Impact of GHS/IHR Investments	**Lunchtime Panel Session: 12:15 PM – 1:30 PM*** Measuring Progress and Impact of Global Health Security Capacity-Building Implementation in Partner Countries
Poster Sessions with Authors: 12:30 PM – 1:45 PM	**Poster Sessions with Authors: 12:30 PM – 1:45 PM**
Concurrent Panel Sessions: 1:45 PM – 3:15 PM	**Concurrent Panel Sessions: 1:45 PM – 3:15 PM**
I1. Rising Above the Noise to Communicate Sound Science and Public Health Advice	N1. Prevention and Control of Viral Hepatitis
I2. Detecting and Preventing Novel Transplant-Associated Infections	N2. Microbiome: Pathology, Ecology, Epidemiology
I3. Genomic Epidemiology: From the Lab to the Street	N3. Epidemic Prediction Initiative: Moving from Research to Decisions
I4. Monitoring for the Next Pandemic Threat: Emerging Influenza Viruses (H7N9)	N4. Pathogen Discovery and Investigation of New Syndromes
Break: 3:15 PM – 3:30 PM	**Break: 3:15 PM – 3:30 PM**
Oral Presentation Abstracts: 3:30 PM – 5:00 PM	**Oral Presentation Abstracts: 3:30 PM – 5:00 PM**
J1. Molecular Epidemiology	O1. Detection and Diagnosis
J2. Preparedness and Response	O2. Seasonal Influenza and RSV
J3. Viral Zoonoses	O3. Evolving Challenges
J4. Late Breakers I	O4. Late Breakers II

Conference Organizers

ICEID Steering Committee

Robin Moseley, Chair
Office of Infectious Diseases, CDC

Planning and Resources

Andréa Berlin
Amanda Bradica
Samantha Kluglein
Center for Vaccine Equity
Task Force for Global Health, Inc.

Doug Browne
Office of Infectious Diseases, CDC

Scientific Program

Co-chairs

Alexandra Levitt
Michael Shaw
Office of Infectious Diseases, CDC

Marta Gwinn
CFOL

Inger Damon
Todd Weber
National Center for Emerging and Zoonotic Infectious Diseases, CDC

Brian Edlin
National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, CDC

Alicia Fry
National Center for Immunization and Respiratory Diseases, CDC

Vikas Kapil
Center for Global Health, CDC

Joanne Andreadis
Office of Public Health Preparedness and Response, CDC

Partner Representatives

Meredith Allen
Association of State and Territorial Health Officials

Evan Anderson
Pediatric Infectious Diseases Society

Hayley Ashbaugh
US Department of Defense

Joanne Bartkus
Association of Public Health Laboratories

Mike Catchpole
European Centre for Disease Prevention and Control

Kendra Chittenden
US Agency for International Development

Richard Danila
Council of State and Territorial Epidemiologists

Karen Ehnert
American Veterinary Medical Association

François Elvinger
Association of American Veterinary Medical Colleges

Michael Feldgarden
US National Institutes of Health, National Center for Biotechnology Information

Paul Freeman
American Public Health Association

Paula Fujiwara
International Union Against Tuberculosis and Lung Disease

Kathleen Gensheimer
US Food and Drug Administration, Center for Food Safety and Applied Nutrition

Stefan Hagmann
International Society of Travel Medicine

Elizabeth Hilborn
US Environmental Protection Agency

Rosemary Humes
US Department of Health and Human Services, Biomedical Advanced Research and Development Authority

April Johnson
Food and Agriculture Organization of the United Nations

John Johnston
US Department of Agriculture, Food Safety and Inspection Service

Patrick Joseph
National Foundation for Infectious Diseases

Lilly Kan
National Association of County and City Health Officials

Julianna Lenoch
US Department of Agriculture, Animal and Plant Health Inspection Service

Larry Madoff
International Society for Infectious Diseases

Yvonne Maldonado
American Academy of Pediatrics

Maja Maric
US National Institutes of Health, National Institute of Allergy and Infectious Diseases

Patrick McDermott
US Food and Drug Administration, Center for Veterinary Medicine

Mark McKinlay
Task Force for Global Health

Stefano Messori
World Organisation for Animal Health

Pascal Michel
Public Health Agency of Canada

Palmer Orlandi
US Food and Drug Administration, Office of Foods and Veterinary Medicine

Freddy Perez
Pan American Health Organization

Philip Polgreen
Infectious Diseases Society of America

Katie Richgels
US Geological Survey, National Wildlife Health Center

John Sanders
American Society for Tropical Medicine and Hygiene

Nahoko Shindo
World Health Organization

Steven Specter
American Society for Microbiology

Mary Grace Stobierski
National Association of State Public Health Veterinarians

Jay Varma
Africa CDC

Marc-Oliver Wright
Association for Professionals in Infection Control and Epidemiology

CDC Representatives

Kashef Ijaz
Barbara Marston
Eric Mast
Susan Wang
Center for Global Health

Greg Armstrong
Cristina Carias
Ardath Grills
Joseph Igietseme
Jeremy Sobel
Steve Waterman
National Center for Emerging and Zoonotic Infectious Diseases

Walid Heneine
Robert Kirkcaldy
Phil Spradling
Taraz Samandari
Carla Winston
National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention

Susan Gerber
Aron Hall
Andrew Kroger
Brian Raphael
Tim Uyeki
National Center for Immunization and Respiratory Diseases

Editorial

Laurie Dieterich
Cathy Young
National Center for Emerging and Zoonotic Infectious Diseases, CDC

Kim Distel
Office of Infectious Diseases, CDC

Graphics

Laura Ribas
Northrop Grumman

Communications and Media

Jennifer Mitchell, Lead
Katie Fowlie
Candice Hoffmann
Christine Pearson
Tom Skinner
National Center for Emerging and Zoonotic Infectious Diseases, CDC

Scott Bryan
Paul Fulton
National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, CDC

Kristen Nordlund
National Center for Immunization and Respiratory Diseases, CDC

Bert Kelly
Office of the Associate Director for Communication, CDC

Laura Bellinger
Amy Rowland
Center for Global Health

ICEID 2018 Leaders Program

The ICEID Leaders Program was created over a decade ago (as a component of ICEID 2008) to promote global health partnerships and collaboration in the area of infectious disease prevention by increasing ICEID participation by public health leaders from resource-limited countries. Selected through a competitive process and representing ministries of health, other health and research institutions, and nongovernmental organizations, the following individuals are welcomed as the ICEID 2018 Leaders:

Maiwand Ayoub Ahmadzai
National Emergency Operations Center for Polio Eradication in Afghanistan
Kabul, Afghanistan

William K. Ampofo
Noguchi Memorial Institute for Medical Research
Accra, Ghana

Paritosh K. Biswas
Chittagong Veterinary and Animal Sciences University (CVASU)
Chittagong, Bangladesh

Jean Marc Feussom Kameni
Ministry of Livestock, Fisheries and Animal Industries
Yaounde, Cameroon

Sandra Gomez Ventura
Universidad Tecnológica Centroamericana (UNITEC)
Laureate International Universities
Tegucigalpa, Honduras

Elsie Ilori
Nigeria Centre for Disease Control
Abuja, Nigeria

Thérèse Samdapawindé Kagoné
Ministry of Health
Bobo-Dioulasso, Burkina Faso

Jean Felix Kinani Sangwa
One Health Approach for Conservation (OHAC)
Kigali, Rwanda

Portia Manangazira
Ministry of Health
Harare, Zimbabwe

Awa Ndir
Infection Control Africa Network (ICAN)
Dakar, Senegal

Syed Moinuddin Satter
icddr,b
Dhaka, Bangladesh

Ngoc Le Van Truong
Ministry of Health
Hanoi, Vietnam

Ork Vichit
Ministry of Health
Phnom Penh, Cambodia

General Information

Americans with Disabilities Act Compliance

The Omni Hotel at CNN Center is in compliance with the Americans with Disabilities Act to the extent of the law. If special accommodations would enhance your enjoyment of the conference, please visit the ICEID Program Planner's Office in the Cypress Room on the International Ballroom Level. We will make reasonable accommodations to ensure your comfort at the meeting.

Business Center

The Omni Hotel business center is located on the lobby level of the South Tower to the right of Hotel Registration.

Hours:

- Monday—Sunday . . . . . 7:00 AM – 7:00 PM

Concierge

The Omni Hotel Concierge will be available from 7:00 AM to 8:00 PM throughout the conference to assist with everything ranging from local area information to making restaurant reservations. The Concierge Desk is located at the entrance to the North Tower just before Conference Registration.

Charging Stations

The Task Force for Global Health is providing tabletop charging stations throughout the common areas for recharging your mobile devices.

Continuing Education

Continuing education for physicians, nurses, veterinarians, health educators, and public health professionals for this activity will be offered. Please visit the ICEID website or mobile app for details.

Exhibits

Exhibits will be on display in Grand Ballroom E.

Hours:

- Sunday, August 26 . . . . . 4:30 PM – 9:30 PM
- Monday, August 27 . . . . . .10:00 AM – 4:30 PM
- Tuesday, August 28 . . . . . .10:00 AM – 4:30 PM
- Wednesday, August 29. . . . . .10:00 AM – 2:00 PM

A complete list of Exhibitors is available on the mobile app.

Food and Beverage

There are dining options in the hotel, in the CNN Center Atrium, and within walking distance outside of the hotel. A list of some of the local restaurant options is available on the mobile app.

Mobile App/Information

ICEID 2018 has a mobile conference app for meeting attendees to download and use on iOS and Android devices. The app can be used to connect with other participants, build a personalized schedule, and share information with colleagues. You will also find conference information, local area attractions, and maps.

Opening Reception

Be sure to attend the Opening Reception with food, drink, and camaraderie on Sunday, August 26, from 7:30 PM – 9:30 PM. *Pre-purchased tickets are required*.

Poster Presentations

The posters will be on display in Grand Ballroom C/D, adjacent to the Exhibit Hall and available for viewing from 10:00 AM – 4:30 PM.

Poster Set up is from 7:00 AM – 8:00 AM each day. Presenters should have their posters in place by 8:00 AM on the day of their presentations. *Poster Sessions with Authors* are scheduled each day, Monday–Wednesday, August 27-29, from 12:30 PM – 1:45 PM. Authors should plan to be present and available to answer questions about their posters during the designated presentation sessions.

Press Room

CDC Media Staff will be at the conference. The Press Room is located in the Willow Room, on the North Tower's M4 Grand Ballroom Level.

Registration

Registration is located on the Grand Ballroom Level.

Hours:

- Sunday, August 26 . . . . . 1:00 PM – 6:00 PM
- Monday, August 27 . . . . . 7:30 AM – 4:30 PM
- Tuesday, August 28 . . . . . 7:30 AM – 4:30 PM
- Wednesday, August 29. . . . . 8:00 AM – 2:00 PM

Social Media

Please join the social media conversation by using the conference hashtag, #ICEID2018, and following @CDC_NCEZID. Along with Twitter, other social media channels include Facebook, LinkedIn, and Instagram.

Speaker Ready Room

The Speaker Ready Room is located in the Willow Room, on the North Tower's M4 Grand Ballroom Level. Technical staff will be available for assistance throughout conference hours.

WiFi

Complimentary WiFi is available in all conference rooms and throughout the commons areas.

Please use the following to log on to our free conference WiFi:

Network: **ICEID**

Password: **publichealth**

Sunday, August 26

Keynote Session

5:30 PM – 7:30 PM
Grand Ballroom A/B/C/D1

Moderator

Michael Iademarco
Acting Deputy Director for Infectious Diseases
Acting Director, Office of Infectious Diseases
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Welcome and Opening Remarks
Robert Redfield
Director, Centers for Disease Control and Prevention, and Administrator, Agency for Toxic Substances and Disease Registry; Atlanta, Georgia

ICEID 1998: Back to the Beginning
James Hughes
Professor of Medicine and Public Health
Emory University; Atlanta, Georgia

Learning While Doing: Tackling Emerging Infections since SARS
Anne Schuchat
Principal Deputy Director
Centers for Disease Control and Prevention; Atlanta, Georgia

Data Analytics for Optimising Outbreak Response
Neil Ferguson
Director, MRC Centre for Global Infectious Disease Analysis
School of Public Health
Imperial College London; London, United Kingdom

Opening Reception

7:30 PM – 9:30 PM
Grand Ballroom D2/E

Pre-purchased tickets are required

Monday, August 27

Poster Set-up for the Day

7:00 AM – 8:00 AM

All posters presented on Monday will be available for viewing in Grand Ballroom C/D from 10:00 AM to 4:30 PM. Authors will be present at posters from 12:30—1:45 PM each day.

Scientific Sessions

A. Concurrent Plenary Sessions

8:00 AM – 9:00 AM

A1. Healthcare-Associated Infections in Europe and the United States

International Ballroom D

Moderator

Denise Cardo: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Continental Divide: Healthcare-Associated Infections in Europe and the United States
Stephan Harbarth: Geneva University Hospitals; Geneva, Switzerland

A2. Zika: Human Neurological Outcomes

Grand Ballroom A/B

Moderator

Margaret Honein: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Congenital Zika Syndrome: Beyond Microcephaly
Vanessa van der Linden: Association for Assistance of Disabled Children; Recife, Pernambuco, Brazil

A3. Challenges for Disease Elimination and Eradication

International Ballroom E

Moderator

Nancy Messonnier: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Joy and Agony on the Road to Polio, Measles, and Rubella Eradication
Steve Cochi: Centers for Disease Control and Prevention, Atlanta, Georgia

A4. Lessons Learned from the West Africa Ebola Outbreak

International Ballroom A/B/C

Moderator

Beth Bell: Department of Global Health, University of Washington; Seattle, Washington

Speaker

What We Learned from the Ebola Response in 2014-2016
David Heymann: London School of Hygiene and Tropical Medicine; London, United Kingdom

B. Concurrent Plenary Sessions

9:10 AM - 10:10 AM

B1. Genomic Epidemiology

International Ballroom A/B/C

Moderator

Duncan MacCannell: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Real-time Genomic Surveillance of Pathogen Evolution and Spread
Trevor Bedford: Fred Hutchinson Cancer Research Center; Seattle, Washington

B2. Infectious Diseases in Humanitarian / Disaster Settings

International Ballroom D

Moderator

Mark Anderson: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Effects of Conflict on Diseases of Epidemic Potential
Paul Spiegel: Johns Hopkins Bloomberg School of Public Health; Baltimore, Maryland

B3. Vaccines for Dengue, A Major Aedes-Transmitted Arbovirus

International Ballroom E

Moderator

Neil Ferguson: Imperial College London; London, United Kingdom

Speaker

Live Attenuated Vaccines for Dengue Virus: A Long and Adventurous Journey
Steve Whitehead: National Institutes of Health; Bethesda, Maryland

B4. IHR and Global Health Security

Grand Ballroom A/B

Moderator

Rima Khabbaz: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Preparedness: Half Full or Empty?
Keiji Fukuda: The University of Hong Kong, Hong Kong, China

Break

10:10 AM – 10:30 AM
Grand Ballroom and International Ballroom Levels

C. Concurrent Panel Sessions

10:30 AM - 12:00 PM

C1. Emerging Vector-Borne Diseases and New Control Strategies

International Ballroom A/B/C

Moderators

Neil Ferguson: Imperial College London; London, United Kingdom
Ben Beard: Centers for Disease Control and Prevention; Fort Collins, Colorado

Speakers

Borrelia miyamotoi: An Emerging Tick-Borne Disease
Peter Krause: Yale School of Public Health; New Haven, Connecticut

Alpha-gal Red Meat Allergy: An Emerging Tick-Borne Epidemic of Anaphylaxis
Scott Commins: University of North Carolina; Chapel Hill, North Carolina

World Mosquito Program: Using Wolbachia to Stop Arboviral Disease Transmission
Cameron Simmons: Monash University; Clayton, Victoria, Australia

The Application of Gene Drive Technology for the Elimination of Malaria in sub-Saharan Africa
Greg Lanzaro: University of California, Davis; Davis, California

C2. Bioinformatics and Big Data in Public Health

International Ballroom D

Moderators

Greg Armstrong
Nancy Chow
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Building a Real-Time Global Pathogen Surveillance System Integrated with Clinical Diagnostics
Zamin Iqbal: EMBL-EBI, Wellcome Trust Genome Campus; Cambridge, United Kingdom

The European Union's COMPARE Project
Marion Koopmans: The Erasmus University Medical Center; Rotterdam, The Netherlands

From Ebola to Zika—Tracking Outbreaks Using Genomics
Kristian Andersen: The Scripps Research Institute; La Jolla, California

C3. Respiratory Diseases: Focus on Legionella, MERS, and Plague

Grand Ballroom A/B

Moderator

Cynthia Whitney: Centers for Disease Control and Prevention (retired); Atlanta, Georgia

Speakers

Laboratory Diagnosis of Legionnaires' Disease
Paul Edelstein: University of Pennsylvania; Philadelphia, Pennsylvania

Public Health Response to MERS CoV: Six Years' Experience of Saudi Arabia
Ahmed Hakawi: Ministry of Health; Riyadh, Saudi Arabia

Panic in the Streets: Pneumonic Plague in Madagascar and Beyond
Paul Mead: Centers for Disease Control and Prevention; Fort Collins, Colorado

C4. Emerging Issues in Sexually Transmitted Diseases

International Ballroom E

Moderators

Alex de Voux
Robert Kirkcaldy: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Public Health STD Programs Successfully Engaging Primary Care Providers to Improve Chlamydia Screening
Gale Burstein: Erie County Department of Health; Buffalo, New York

Emerging Issues in STI Diagnostics: How to Plan for STI Self-Testing
Charlotte Gaydos: Johns Hopkins University; Baltimore, Maryland

Emerging Issues in Antibiotic-Resistant Gonorrhea and Beyond
Emily Weston: Centers for Disease Control and Prevention; Atlanta, Georgia

Lunch

12:00 PM – 12:30 PM

On your own

Lunchtime Panel I

12:15 PM – 1:30 PM

Emerging and Re-emerging Infectious Diseases in the WHO Eastern Mediterranean Region

International Ballroom F

Limited sandwiches & salads available for purchase outside meeting room

Moderators

Mamunur Malik: WHO Regional Office for the Eastern Mediterranean; Cairo, Egypt
Kashef Ijaz: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Emerging Health Threats in the Eastern Mediterranean Region: Current, Past, and Future and Key Challenges for Control
Mamunur Malik

Hospital Outbreaks of MERS: What We Have Learned So Far to Prevent a Major Catastrophe
Ahmad Hakawi: Ministry of Health, Riyadh, Saudi Arabia

Insights from Epidemiological Studies Conducted in Countries with Hospital Outbreaks of MERS: Do We See Any Alarming Trend?
Susan Gerber: Centers for Disease Control and Prevention; Atlanta, Georgia

MERS as the Next Global Pandemic: What We Currently Know and What WHO Is Doing to Prevent a Global Health Emergency
Maria Van Kerkhove: World Health Organization; Geneva, Switzerland

Global Health Security and Accelerating Progress for Better Preparedness and Response for Epidemic and Pandemic Threats in the Eastern Mediterranean Region
Kashef Ijaz
Mamunur Malik

Poster Session with Authors – I

12:30 PM - 1:45 PM
Grand Ballroom C/D

One Health I

Board 1. Themes from One Health Zoonotic Disease Prioritization Workshops in 18 Countries, 2014–2017

Board 2. Extending the Reach of Public Health: The Public Health Talk Expansion to Animal Care Providers

Board 3. Prevalence of Zoonotic Enteropathogens in Domestic Animals and Associated Household Risk Factors in Kisumu, Kenya

Board 4. Surveillance for Respiratory and Diarrheal Pathogens at the Human-Pig Interface in Sarawak, Malaysia

Board 5. Expression of Genes Associated with Enterotoxin YstA Production by *Yersinia enterocolitica* Strains Isolated from Humans and Pigs

Board 6. Fecal Virome Diversity of Healthy and Diarrheic Pigs in the Philippines

Board 7. Minnesota One Health Antibiotic Stewardship Collaborative: Improving Public and Professional Awareness of Antibiotic Use and Resistance

Board 8. Longitudinal Field Study in Evaluating the Spillover of Antibiotic-Resistant *Escherichia coli* from Poultry to Humans in Rural Ecuador

Board 9. Outbreak of *E. coli* O157:H7 Infections in a Community: Utah and Arizona—June 2017

Board 10. Glanders Disease in Equines: Re-Emerging or Endemic? A Report from India

Board 11. Field-Portable, Rapid and Specific Test for Probable Identification of *Burkholderia pseudomallei* and *Burkholderia mallei*

Board 12. Establishment and Utility of a Brucellosis Surveillance System—Bamyan Province, Afghanistan, 2011-2015

Board 13. Septicemic Pasteurellosis: A One-Health Framework Case Study

Board 14. Two Cases of Cutaneous Anthrax in Italy, 2017

Board 15. Outbreak of Cutaneous Anthrax Associated with Handling Livestock Meat after Natural Death: Arua District, Uganda, 2015-2017

Board 16. The Determinants of Diagnosis Establishment of an Anthrax Outbreak in Yogyakarta, Indonesia

Board 17. Blastomycosis in Minnesota, 1999-2016: Descriptive Epidemiology and Evidence of Delayed Diagnosis

Board 18. Genomic Characterization of Viruses Identified in Upper Respiratory Samples in Dromedary Camels from United Arab Emirates (UAE)

Board 19. Drivers for MERS-CoV Emergence in Qatar

Board 20. Avian Influenza A-H9 Virus Causing Mortality in Common Geese and Ducks in Rawalpindi, Pakistan

Board 21. Pattern of Highly Pathogenic Avian Influenza Virus Circulation among Domestic Poultry in Bangladesh: 2007-2017

Board 22. Exploring the Acceptability and Feasibility of Portable Workstation for Handwashing with Soapy Water in a Bangladeshi Live Bird Market

Board 23. Emerging Pet-Rodent-Transmitted Infectious Diseases

Healthcare-Associated Infections

Board 24. Large Numbers of Occupational Blood Exposure Accidents Outside the Hospital (2006-2014, Netherlands) Requires Turning to Profile-Based Preventive Actions

Board 25. Establishing a National Standardized Surveillance System for Healthcare-Associated Infections in Vietnam

Board 26. The Beijing Healthcare-Associated Infections Surveillance System: Identifying Strengths and Limitations through an Evaluation of Central Line Association Blood Stream Infection (CLABSI) Case Reporting, Beijing, China, 2015

Board 27. Methicillin-Resistant *Staphylococcus aureus* (MRSA) Nasal Carrier among Healthcare Workers as Compared to Community

Board 28. Characteristics of Infection Control Practices at North American Veterinary Teaching Hospitals – Promoting a Safety Culture in Veterinary Medicine

Board 29. Surgical Site Infection Prevention Program: Wisconsin Division of Public Health Initiative

Board 30. Hospital-Associated, Multicenter Outbreak of *Ralstonia pickettii* in Colombia, 2017

Board 31. Finding the Pathogen in the Haystack: Outbreak Investigation of *E. coli* K1 Neonatal Meningitis Using Culture and Culture-Independent Methods—Kansas, 2017-2018

Board 32. Characteristics of Invasive *Candida* Bloodstream Infections among People Who Inject Drugs, Oregon and New Mexico, 2011-2017

Board 33. Hepatitis C Outbreak in a Respiratory Care Ward Associated with Frequent Unsafe Injections—Taiwan, 2017

Board 34. Molecular Epidemiology of an Outbreak of Human Parainfluenza Virus 3 in Transplant Patients

Board 35. Burden and Risk Factors of Nosocomial Urinary Tract Infection in Renal Transplant Recipients in Nepal

Board 36. Evaluation of Colonization and Infection by Multi-Resistant Bacteria in Renal Transplant Patients

Board 37. Computational Modeling for Comparison of Prophylaxis for Cytomegalovírus in Renal Transplants

Foodborne Infections

Board 38. The Trend of Foodborne Disease Outbreaks in Taiwan (1991–2016)

Board 39. Multi-City Viral Diarrheal Disease Outbreaks Associated with Raw Shellfish Consumption in Taiwan in 2012 and 2015

Board 40. Understanding the Incubation Period Distribution of *Salmonella* Typhi

Board 41. Salmonellosis Outbreaks by Food Vehicle, Serotype, Seasonal and Geographical Variation, United States, 1998–2015

Board 42. *Salmonella* Infections and Socioeconomic Status, Georgia, 2011-2015

Board 43. Utility of Whole Genome Sequencing in a Multi-State Outbreak of Salmonellosis Associated with Papayas

Board 44. Are Culture-Independent Diagnostic Tests Decreasing Capacity to Detect Outbreaks?

Board 45. Changing Epidemiology of *Yersinia enterocolitica* Infections and the Rapid Adoption of Culture-Independent Diagnostic Tests—Foodborne Diseases Active Surveillance Network (FoodNet), 2010–2017

Board 46. Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Soy Nut Butter—United States, 2017

Board 47. Comparative Epidemiology of O157 Versus Non-O157 Shiga Toxin-Producing *E. coli* in Georgia, 2011-2017

Board 48. Laboratory Investigations of Botulism Outbreaks Associated with Consumption of Pruno – United States, 2011-2016

Board 49. Cyclosporiasis among Patrons of Restaurant A—Houston Metropolitan Area, Texas, May-August 2017

Board 50. Contaminated Powdered Infant Formula from Opened Containers as a Vehicle for Transmission of *Cronobacter sakazakii*—United States, 2002–2017

Board 51. Using Peer Support to Strengthen Foodborne Illness Surveillance and Outbreak Response Capacity

Board 52. Restaurant Characteristics as Predictors of Cross-Contamination Behavior

Board 53. Restaurant Characteristics Associated with Food Cooling Practices

Board 54. Restaurant Characteristics Associated with Good Hot Holding Practices

Influenza Surveillance

Board 55. A Visual Approach to Influenza Surveillance in the Department of the Navy

Board 56. Comparison of Three Data Collection Systems in the Detection of Influenza during the Season 2017/2018 in Abu Dhabi, United Arab Emirates

Board 57. Setting Up an Indian Network of Population-Based Surveillance Platform for Influenza and Other Respiratory Viruses among Elderly (INSPIRE)

Board 58. Influenza Seasonality in Kathmandu: Seven-Year Trends and Lessons Learned

Board 59. Defining Influenza Baselines and Intensity Threshold Values Using 3 Indicators in Iran

Board 60. The Results of Influenza Sentinel Surveillance in Ukraine in 2017-2018 Season

Board 61. Descriptive Analysis of National Sentinel Surveillance System Data for Influenza Virus Subtypes Circulating among Children under 15 Years of Age in Pakistan

Board 62. Withdrawn

Board 63. A Surge in Influenza Illness in Pregnant Women during the 2017-2018 Season: A Brief Report from Active Surveillance for Influenza-Associated Respiratory Illness in Suzhou, China

Board 64. Epidemiology of Seasonal Influenza in Afghanistan, a Chronic Conflict Setting: Evidence from the National Disease Surveillance and Response System

Board 65. Influenza Trends and Risk Factors Associated with Influenza-Like Illness in Damanhour District, Egypt, 2011–2016

Board 66. Influenza Trends in Morocco: An Overview of Surveillance Data

Board 67. National Surveillance for Influenza-Like Illness in Lao PDR, 2013-2017

Board 68. Seasonal Influenza among Unvaccinated Children in Khartoum State during February 2017–February 2018

Board 69. Epidemiological and Molecular Description of an Outbreak of Influenza A (H1N1) pdm09 in Tunisia during 2017-2018 Season

Board 70. Viral Acute Lower Respiratory Infections among Elderly in a Community Cohort in North India

Board 71. Severe Acute Respiratory Infection (SARI) in Qatar, January-December 2017

Board 72. Analysis of SES of SARI in the Republic of Kazakhstan, 2014/2015 & 2015/2016

Board 73. Withdrawn

Board 74. Respiratory Disease Surveillance on the United States-Mexico Border, 2016–2017

Board 75. Influenza-Associated Hospitalization among Children Less Than Five Years of Age in Suzhou, China, 2011-2016

Board 76. Trends of Viruses Causing Respiratory Illness in Qatar, January-December 2017

Board 77. Epidemiology and Assessment of a SARI Sentinel Site in Egypt

Board 78. Seasonal Influenza and Severe Acute Respiratory Infection Surveillance, Lebanon, 2015-2018

Board 79. Results of Sentinel Epidemiological Surveillance of Severe Acute Respiratory Infections (SARI) in the Republic of Kazakhstan during Epidemiological Seasons 2012/2013-2016/2017

Preparedness and Global Health Security

Board 80. Challenges and Opportunities for Building Zoonotic Disease Surveillance Systems through GHSA Efforts in Sierra Leone

Board 81. A Survey on Implementation of the One Health Approach for Preparedness and Control of MERS-CoV in the Gulf Cooperation Council (GCC) and Middle East Countries

Board 82. Standardized Quantitative and Qualitative Analysis of Software Solution Decisions for the Task Force for Global Health

Board 83. Using Rapid Diagnostic Tests in a Public Health Response: A Framework Approach for Thinking Beyond Test Accuracy

Board 84. Global Emergency Vaccine Stockpiles: Progress and Persistent Challenges

Board 85. Prevention of Infectious Diseases Associated with Mass Gatherings through Use of Vaccines: International Perspectives and Outstanding Questions

Board 86. Finding Outbreaks Faster: A Framework for Measuring the Public Health Response to Infectious Disease Outbreaks

Board 87. Successful Pilot of Event-Based Surveillance in Viet Nam

Board 88. Assessing Applied Epidemiology Competencies in the South Carolina Department of Health and Environmental Control (SC DHEC) Workforce

Board 89. Reestablishment of Diagnostic and Surveillance Laboratory Activities at the Puerto Rico Department of Health after Hurricane Maria

Board 90. Improving Medical Preparedness for Highly Infectious Diseases in Taiwan from 2015 to 2017

Board 91. Beyond Ebola: Are We Ready?

Board 92. Political Corruption and State Failure: How Macro Level Pathologies Increase the Risks of Emerging Infectious Disease

Board 93. Towards Early Detection, Assessment, and Response to Acute Public Health Events: Tunisian Experience

Board 94. The Joint Mobile Emerging Disease Intervention Clinical Capability (JMEDICC): A Mobile Clinical Trials Capability for Rare and Highly Infectious Pathogens

Board 95. Role of Private Sector Extractive Industries during the Ebola Virus Disease Crisis in West Africa

Board 96. Improving International Health Regulations Capacity through Point of Entry Public Health Preparedness and Response, Tanzania

Board 97. Strengthening Public Health Emergency Preparedness Systems and Capacities through the Development of Point of Entry Specific Public Health Emergency Contingency Plans (PHECP) in Nigeria

Board 98. Integration of International Health Regulations into National Health System: A Case for Fostering Their Implementation in the Eastern Mediterranean Region

Vector-Borne Diseases I

Board 99. Epidemic Arboviral Diseases in the Eastern Mediterranean Region: Findings from a Systematic Review

Board 100. Risk of Epidemic Arboviral Diseases in the Eastern Mediterranean Region: Current Information Gaps

Board 101. Human West Nile Virus Infection in Tunisia: Three Outbreaks in the Past 20 Years

Board 102. Epidemiological Profile, Incidence, and Trends of West Nile Virus in Tunisia during Five Years

Board 103. Clinical Parameters and Lethality of West Nile Virus Infections in Humans: Tunisia, 2012-2016

Board 104. Severe Disease Presentations Are Correlated with Previous Exposure of Multiple Members of the *Flaviviridae* Family in the Caribbean Island of Sint Maarten

Board 105. Enhanced Surveillance for Heartland Virus in Tennessee

Board 106. Increase in Reported Rocky Mountain Spotted Fever Cases—Indiana, 2017

Board 107. Bioclimatic Indicators of Rift Valley Fever Activity

Board 108. Epidemiology and Cost of Lyme Disease-Related Hospitalizations—United States, 2005-2014

Board 109. Targeted Metagenomics as a High-Throughput Tool for Surveillance and Discovery of Tickborne Agents in Clinical Specimens

Board 110. Validating Targeted Metagenomic Identification of Bacterial Species in Specimens from Patients Suspected of Tickborne Illness

Board 111. Geographic Information for Vector Surveillance (GIVeS): Collaboration for GIS Capacity Building for Vector Surveillance

Board 112. Molecular Prevalence of Selected Canine Vector-Borne Pathogens in the United States (2008-2015)

Board 113. Prioritization of Vector-Borne Diseases in Canada under Current Climate and Projected Climate Change

Surveillance I

Board 114. Can Wearable Sensors Detect Influenza Epidemics? Correlation of Anomalous Fitbit Data with Influenza Surveillance Data

Board 115. Estimating Weekly Call Volume to a National Nurse Telephone Triage Line in an Influenza Pandemic

Board 116. Enhancing Surveillance for Emerging Respiratory Infectious Diseases through Clinician Participation: An Assessment of Pneumonia of Unknown Etiology Surveillance in China, 2016

Board 117. Establishing Influenza Surveillance Thresholds for India

Board 118. Performance of a Large-Scale Implementation of a Participatory Influenza-Like-Illness Surveillance System in Guatemala

Board 119. Establishing an Online Platform for Influenza Data Sharing and Analysis – Experience from the Eastern Mediterranean Region of WHO

Board 120. Comparing the 2016-17 and 2017-18 Influenza Season with Participant-Reported Symptoms from Flu Near You

Board 121. A Real-Time Automated SMS Tool for Monitoring Persons Potentially Exposed to Avian Influenza Twice Daily

Board 122. Identification of Unplanned Closure of K-12 Schools via Twitter and Online Systematic Search: A Pilot Study of Public Schools in Michigan, September 2015-June 2016

Board 123. Using Legal Epidemiology to Assess Electronic Disease Reporting Laws to Overcome Issues with Manual Disease Reporting and to Improve Surveillance of Emerging Diseases

Board 124. A Rapid Communication Protocol for Sharing Infectious Disease Risk Alerts with Cross-Border Partners in the Euregion of Germany, Belgium, and the Netherlands

Board 125. Baseline Measurement of Invasive Mold Infections before Hurricane Harvey—Hospitals A and B, Houston, Texas, 2016–2017

Board 126. Evaluation of a Case Definition for Surveillance of Invasive Mold Infections: Hurricane Harvey—Houston, October 2017

Board 127. Hurricane-Associated Mold Exposures among Patients at Risk of Invasive Mold Infections—Houston, TX, 2017

Board 128. Developing and Pilot Testing an Early Warning System for Epidemic-Prone Events Based on Syndromic Surveillance System (SSS) in Iran: Initial Results

Board 129. Improving Cross-Border Public Health Surveillance and Response through a Participatory Approach to Population Movement Mapping, Togo and Benin

Board 130. Tools for Monitoring and Evaluation of Event-Based Surveillance in Vietnam

Board 131. Daily Surveillance of Laboratory Records: Enhanced Outbreak Response for Military Readiness

Laboratory: Detection and Diagnosis

Board 132. Rabies Surveillance: Training and Implementation of Next Gen Sequencing

Board 133. The Recovery of Nontyphoidal *Salmonella* from CIDT-Positive Stool Specimens

Board 134. Comparison of the Cepheid GeneXpert Carba-R and Streck ARM-D Kit, β-Lactamase for the Detection of Carbapenem-Resistant Enterobacteriaceae

Board 135. Development of a Targeted Sequencing Panel to Detect Antimicrobial Resistance Determinants in Human Stool

Board 136. Replication of Human Norovirus in Human Intestinal Enteroids as a Model to Measure Virus Inactivation

Board 137. Eukaryotyping: A Novel Typing Method Developed for Sexual Eukaryotes and Its First Application to *Cyclospora cayetanensis*

Board 138. Improved Differentiation of *Streptococcus pneumoniae* from Other Streptococcal Species Using Pyrosequencing and *comC* PCR in Respiratory Autopsy Tissues

Board 139. Real-Time PCR for Diagnosis and Differentiation of Relapsing Fever *Borrelia*

Board 140. Utilization of High-Throughput Multi-Locus Sequence Typing for Strain Characterization of *Borrelia* Directly from Patient Samples

Board 141. Unexpected Viruses Detected in Patients Presenting with Lyme-like Symptoms

Board 142. Development and Use of In Vitro RNA Transcript as a Positive Control for Detection of Dengue Serotypes by RT-PCR

Board 143. LeDantec Rhabdovirus Human Infection in Uganda: Identification of the Transmitted/Founder Virus

Board 144. Molecular Diagnosis of Hemorrhagic Fever with Renal Syndrome

Board 145. An Evaluation of Four Molecular Assays Used for the Diagnosis of Zika

Board 146. Multiplex Arbovirus IgM and IgG Serology Assay Evaluation for Rapid Presumptive Diagnosis of Zika Virus Infection

Board 147. Comparison of Zika Virus Inactivation Methods for Reagent Production

Board 148. Development and Characterization of Mouse Monoclonal Antibodies against Zika Virus Non-Structural Glycoprotein 1 (NS1)

Board 149. A Systematic Review of Environmental Survival across 27 Viral Families

Late Breakers

Board LB-01. Changes to the Federal Policy for the Protection of Human Research Subjects and Why They Matter for Public Health Surveillance

Board LB-02. Training in Applied Epidemiology: A Strategic Impact to Respond to Emergent Infectious Diseases

Board LB-03. Tanzania GHSA Program: Meeting IHR Core Capacities One Milestone at a Time

Board LB-04. Strengthening Public Health in Colombia through National Public Health Institutes Partnerships

Board LB-05. Building Public Health Workforce Capacity in 12 Countries over 15 Months: The Establishment of FETP Frontline across the Americas as a Rapid Response Strategy to the Zika Epidemic

Board LB-06. Successes and Lessons Learned from CDC's Employee Monitoring Program during the Ebola and Zika Emergency Responses

Board LB-07. Assessing the Role of Built Environment Improvements on Doffing High-Level Personal Protective Equipment in Biocontainment Units

Board LB-08. Developing Influenza Vaccine Supply Hubs in Low- and Middle-Income Countries

Board LB-09. Pandemic Influenza Severity Assessment — Modelling Canadian Influenza Epidemic Activity and Severity Thresholds Using the Moving Epidemic Method

Board LB-10. Applying Machine Learning Models with an Ensemble Approach to Make Accurate Real-Time Influenza Forecasts in Taiwan

Board LB-11. Active Surveillance for Avian Influenza Virus in Poultry in Vietnam, 2016 – 2018

Board LB-12. Features of the Influenza Epidemic Season in Azerbaijan (2016 – 2017).

Board LB-13. Epidemiological Characterization of Acute Respiratory Viral Infections and Influenza Dynamics in the Republic of Kazakhstan in 2015-2017

Board LB-14. School Closures and Mitigation of Influenza B, Hong Kong, 2018

Board LB-15. The Curious Case of Influenza Twice: Case Presentation of Two Sequential, In-Season Infections with Influenza A(H3N2) in a Usually Healthy, Vaccinated Child

Board LB-16. Influenza Prevalence and Self-Medication Practices among Patients with Self-Reported ILI Presenting to Community Pharmacies—Guatemala, 2018

Board LB-17. The Host-Targeted Iminosugar UV-4B Inhibits Influenza Virus without Selecting for Resistance

Board LB-18. A Universal Influenza Vaccine against Multi-Strain Flu Viruses

Board LB-19. Unraveling the Evolutionary Origin of Low Vaccine Efficacy in the H3N2 Influenza Virus

Board LB-20. Efficacy of Live Attenuated and Inactivated Influenza Vaccines against Laboratory-Confirmed Influenza Infection among Children in Rural Ballabgarh, India: A Randomized, Triple-Blinded, Placebo-Controlled Trial

Board LB-21. Utilization of Antisera Generated in Immunized Chickens for Antigenic Characterization of A(H5N1) Viruses in Vietnam

Board LB-22. Relative Effectiveness of Cell-Based Influenza Vaccines Compared with Egg-Based Influenza Vaccines, Active Component U.S. Service Members, 2017–18 Season

Board LB-23. High Mortality by Severe Acute Respiratory Syndrome among Patients in Long-Term Hospital Care, Goias, Brazil, 2018

Board LB-24. Probable Diphtheria's Death Case in Nan Bosquets, Fond-Parisien, Croix-des-Bouquets, Haiti, April 2018

Board LB-25. Measles Outbreak in a Daycare Related to Overseas Travel--Johnson County, KS

Board LB-26. Locking Down a Bad Bug—*N. meningitidis* Serogroup Y Outbreak in a Transitional Correctional Facility, Georgia, 2017-2018

Board LB-27. Phylogenetic Diversity of Environmental Isolates *Legionella pneumophila* Serogroup 5 and 6 by *rpoB* Gene in Korea

D. Concurrent Panel Sessions

1:45 PM - 3:15 PM

D1. New Data Systems and Platforms for Disease Surveillance

International Ballroom A/B/C

Moderator

Julianna Lenoch: US Department of Agriculture, Animal and Plant Health Inspection Service; Fort Collins, Colorado
Larry Madoff: International Society for Infectious Diseases; Brookline, Massachusetts

Speakers

The One Health Approach to Disease Surveillance
Neo Joel Mapitse: World Organisation for Animal Health (OIE); Paris, France

Use of Geospatial Data in Disease Surveillance
Amy Wesolowski: Johns Hopkins Bloomberg School of Public Health; Baltimore, Maryland

Use of Social Media in Disease Surveillance
John Brownstein: Harvard Medical School; Boston, Massachusetts

D2. Bugs from Drugs: Emerging Infections in People Who Use Opioids

International Ballroom D

Moderators

Lilly Kan: National Association of County and City Health Officials; Washington, DC
Jono Mermin: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

The Opioid Crisis: An Epidemic without a Pathogen
Mark Tyndall: British Columbia Centre for Disease Control; Vancouver, BC, Canada

Kentucky Responds to the Opioid Crisis: Law Enforcement and Public Health as Partners
Van Ingram: Kentucky Office of Drug Control Policy; Frankfort, Kentucky

Drug Use in Public Health: Practical Solutions to Complex Problems
Alice Asher: Centers for Disease Control and Prevention; Atlanta, Georgia

D3. Emerging Fungal Infections in Healthcare Settings

International Ballroom E

Moderator

Tom Chiller: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

The Fight to Control the Spread of *Candida auris* in a Large Hospital in Spain
Ana Alastruey-Izquierdo: Instituto de Salud Carlos III; Madrid, Spain

The Emergence and Spread of *Candida auris* in South Africa
Nelesh Govender: National Institute for Communicable Diseases; Johannesburg, South Africa

Aspergillus in Holland and Beyond: Emerging as an Important Cause of Death in Severe Flu and Becoming Resistant to First-Line Therapy
Jacques Meis: Canisius-Wilhelmina Ziekenhuis; Nijmegen, Netherlands

D4. Environmental / Ecological Factors and Emerging Infectious Diseases: A Multi-Continental Approach

Grand Ballroom A/B

Moderators

Karen Ehnert: Los Angeles County Department of Public Health; Los Angeles, California
Elizabeth Hilborn: US Environmental Protection Agency; Chapel Hill, North Carolina

Speakers

Global Environmental Change as a Driver of Infectious Disease Threat Events in Europe
Jan Semenza: European Centre for Disease Prevention and Control; Stockholm, Sweden

Transforming Landscapes and the Ecology of Scale: Understanding Disease Emergence at the Human-Wildlife-Environmental Interface
Kathleen Alexander: Virginia Polytechnic Institute and State University; Blacksburg, Virginia

Factors Driving Honey Bee Colony Losses
Dennis VanEngelsdorp: University of Maryland; College Park, Maryland

Break

3:15 PM – 3:30 PM
Grand Ballroom and International Ballroom Levels

E. Oral Presentations

3:30 PM – 5:00 PM

E1. Novel Surveillance Strategies

Grand Ballroom A/B

Moderators

Mark Smolinkski: Ending Pandemics; San Francisco, California
Michael Iademarco: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Strengthening Global Event-Based Surveillance Capacity—Epidemic Intelligence from Open Sources (EIOS) Project
C. Hercik: CDC Foundation; Atlanta, Georgia

2. EpiHack™—An Innovative Process for Developing Local Solutions to Infectious Disease Surveillance Challenges
A. Crawley: Ending Pandemics; San Francisco, California

3. Lessons Learned from Community Event-Based Surveillance Implementation in Ghana
S. Merali: Synergy America, Inc.; Atlanta, Georgia

4. Leveraging Community Health Worker Engagement for Early Detection and Reporting of Emerging Infectious Diseases
S. Kanga: Medic Mobile; Nairobi, Kenya

5. Association between Community-Level Ethnic and Linguistic Distributions and the Spatiotemporal Spread of Ebola Virus Disease—Liberia, 2014
L. Zabrano: Centers for Disease Control and Prevention; Atlanta, Georgia

6. Use of SaTScan to Identify Clusters of HIV Diagnoses to Guide Public Health Investigation
A. Board: Oak Ridge Institute for Science and Education; Oak Ridge, Tennessee

E2. Emerging Threats in Healthcare

International Ballroom D

Moderators

Phil Polgreen: University of Iowa; Iowa City, Iowa
Awa Ndir: Infection Control Africa Network; Dakar, Senegal

Speakers

1. Council for Outbreak Response: Healthcare-Associated Infections and Antibiotic Resistance (CORHA)
M. Anderson: Iowa Department of Public Health; Des Moines, Iowa

2. Epidemiologic Approach for an Outbreak Investigation by *Ralstonia mannitolilytica* in Dialysis Units, Colombia, 2017–2018
S. Rivera Vargas: The National Institute of Health; Bogata, Columbia

3. Estimating the Attributable Disease Burden and Effects of Inter-Hospital Patient Sharing on *Clostridium difficile* Infections
D. Sewell: University of Iowa; Iowa City, Iowa

4. Healthcare-Associated Infections Related to Medical Devices—United States, 2017
I. Benowitz: Centers for Disease Control and Prevention; Atlanta, GA

5. High Prevalence of Metallo-β-Lactamase Carbapenemase-Producing *Acinetobacter baumannii* in Tripoli, Libya: Dominance of OXA-23 and NDM-1
A. Zorgani: Faculty of Medicine; Tripoli, Libya

6. Successful Control of a Multi-Patient Use Equipment Driven *Candida auris* Outbreak in a UK Intensive Care Unit
D. Eyre: University of Oxford; Oxford, United Kingdom

E3. Vector-Borne Diseases

International Ballroom A/B/C

Moderators

Tyler Sharp
Steve Waterman
Centers for Disease Control and Prevention; San Juan, Puerto Rico

Speakers

1. Yellow Fever Outbreak Response in Kebbi State, Northwestern Nigeria—January 2018
A. Hassan: Nigeria Field Epidemiology and Laboratory Training Program; Abuja, Nigeria

2. CDC's International Vector Response to the Zika Virus Outbreak: Strengthening Regional Public Health Entomology Networks
R. Levine: Centers for Disease Control and Prevention; Atlanta, GA

3. Environmental Suitability and Predicted Distribution of *Aedes albopictus* and *Aedes aegypti* Mosquitoes in Canada and the United States: Assessing Arboviral Risks in North America
S. Khan: University of Guelph; Guelph, ON, Canada

4. Tracking the Spread of Insecticide Resistance in *Aedes aegypti* and *Ae. albopictus* for Informed Vector Control of Arboviral Diseases
M. Hadi: Vestergaard; Nairobi, Kenya

5. Changing Trends in Age and Sex Distributions of Human Lyme Disease—United States, 1992–2016
K. Kugeler: Centers for Disease Control and Prevention; Fort Collins, Colorado

6. Evaluating the Risk of Tick-Borne Relapsing Fever Among Occupational Cavers—Austin, TX, 2017
S. Campbell: Centers for Disease Control and Prevention; Fort Collins, Colorado

E4. Frontline Public Health

International Ballroom E

Moderators

Kathleen Gensheimer: US Food and Drug Administration, Center for Food Safety and Applied Nutrition; College Park, Maryland
Phil Spradling: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Missed Opportunities to Diagnose Infections Related to Injection Drug Use Are Common: A Population-Based Investigation
A. Miller: University of Iowa; Iowa City, Iowa

2. Hepatitis C Testing among Health Department Clients in Tennessee
L. Sizemore: Tennessee Department of Health; Nashville, Tennessee

3. Repeat Chlamydial Infections among Women Aged 15 to 34 Years—Louisiana, 2000–2015
S. Cha: Centers for Disease Control and Prevention; Atlanta, Georgia

4. Sexual Activity, Abstinence, and Condom Use among Pregnant Women During the Zika Virus Outbreak—Puerto Rico
K. Turay: Centers for Disease Control and Prevention; Atlanta, Georgia

5. Level and Factors Influencing Uptake of Human Papilloma Virus Vaccine among Female Adolescents in Lira District, Uganda, 2016
E. Kisaakye: Makerere University; Kampala, Uganda

6. Measles Outbreak in an Underimmunized Community—Minnesota, 2017
J. Griffith: Minnesota Department of Health; St. Paul, Minnesota

Tuesday, August 28

Poster Set-up for the Day

7:00 AM – 8:00 AM

All posters presented on Tuesday will be available for viewing in Grand Ballroom C/D from 10:00 AM to 4:30 PM. Authors will be present at posters from 12:30—1:45 PM each day.

Scientific Sessions

F. Concurrent Plenary Sessions

8:00 AM – 9:00 AM

F1. The Microbiome and Human Health

Grand Ballroom A/B

Moderator

Scott Sammons: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Invisible Influence: The Microbiome and Human Health
Jack Gilbert: University of Chicago; Chicago, Illinois

F2. Public Health Preparedness and Outbreak Response

International Ballroom A/B/C

Moderator

Stephen Redd: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Changing Landscape of US Preparedness
Tom Inglesby: Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland

F3. Reemergence of Vaccine-Preventable Diseases: Focus on Diphtheria

International Ballroom D

Moderator

Laura Conklin: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Diphtheria: A Re-Emerging Threat in Countries Affected by Conflict, Migration, and Economic Disruption
Stephen Hadler: Centers for Disease Control and Prevention (retired), Atlanta, Georgia

F4. Cholera: The Beginning of the End?

International Ballroom E

Moderator

Chris Braden: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Ending Cholera: A Global Roadmap to 2030
Dominique Legros: World Health Organization; Geneva, Switzerland

G. Concurrent Plenary Sessions

9:10 AM - 10:10 AM

G1. National Control of Carbapenem-Resistant Enterobacteriaceae

International Ballroom E

Moderator

Mike Catchpole: European Centre for Disease Prevention and Control; Solna, Sweden

Speaker

Control of Carbapenem-Resistant Enterobacteriaceae at the National Level
Mitchell Schwaber: Israel Ministry of Health; Tel Aviv, Israel

G2. Advanced Molecular Detection of Infectious Diseases

International Ballroom A/B/C

Moderator

Joanne Bartkus: Minnesota Department of Health; St. Paul, Minnesota

Speaker

Making of a Pathogen
Ashlee Earl: The Broad Institute of MIT and Harvard; Cambridge, Massachusetts

G3. Africa CDC

International Ballroom D

Moderator

Vik Kapil: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Africa CDC: A New Public Health Order for Africa's Health Security
John Nkengasong: Africa Centres for Disease Control and Prevention, African Union; Addis Ababa, Ethiopia

G4. One Health

Grand Ballroom A/B

Moderator

Stefano Messori: World Organisation for Animal Health; Paris, France

Speaker

Infectious Disease Emergence: A One Health Perspective
William Karesh: EcoHealth Alliance; New York, New York

Break

10:10 AM – 10:30 AM
Grand Ballroom and International Ballroom Levels

H. Concurrent Panel Sessions

10:30 AM - 12:00 PM

H1. Emerging Scientific Issues for Global Immunization Programs

International Ballroom D

Moderator

Kimberley Fox: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Addressing Vaccine Hesitancy as an Obstacle to Global Immunization
Robb Butler: World Health Organization Regional Office for Europe; Copenhagen, Denmark

Progress Towards a Comprehensive Maternal Immunization Platform
Saad Omer: Emory University; Atlanta, Georgia

New Vaccines on the Horizon for Global Immunization Programs
Jon Abramson: Wake Forest University School of Medicine; Winston-Salem, North Carolina

H2. Viral Hemorrhagic Fevers

International Ballroom A/B/C

Moderators

Evan Anderson: Emory University School of Medicine; Atlanta, Georgia
Inger Damon: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Hantaviruses in the Americas
Greg Mertz: University of New Mexico; Albuquerque, New Mexico

Lassa Fever—West African Experience
Stephan Guenther: Bernhard Nocht Institute for Tropical Medicine; Hamburg, Germany

What We Have Learned About VHF Disease Pathogenesis
Anita McElroy: University of Pittsburgh; Pittsburgh, Pennsylvania

H3. More Answers, More Questions: Whole-Genome Sequencing in Foodborne Disease Epidemiology

Grand Ballroom A/B

Moderators

Tim Jones: Tennessee Department of Health; Nashville, Tennessee
Heather Carlton: Centers for Disease Control and Prevention; Atlanta, GA

Speakers

Routine Genomic Surveillance of Enteric Disease in England
Tim Dallman: Public Health England; London, United Kingdom

U.S. Foodborne Disease Surveillance in the Genomics and Metagenomics Era
John Besser: Centers for Disease Control and Prevention; Atlanta, Georgia

Sources of Infection of *Campylobacter* Approached by Whole Genome Sequencing and Classical Epidemiology—A Perspective from Denmark
Steen Ethelberg: Statens Serum Institute; Copenhagen, Denmark

H4. Emerging Infections Associated with Life-Saving Medical Devices

International Ballroom E

Moderator

Joe Perz: Centers for Disease Control and Prevention; Atlanta, GA

Speakers

Ineffective Endoscope Reprocessing and the Use of Prophylactic Antimicrobials: Opening the Door to Efficient Pathogen Transmission
Cori Ofstead: Ofstead & Associates; St. Paul, Minnesota

Cardiac Surgery-Associated *Mycobacterium chimaera* Infections
Peter Werner Schreiber: University Hospital Zurich; Zurich, Switzerland

Regulatory Perspectives on Ensuring the Safety of Cleared or Approved Medical Devices
Suzanne Schwartz: U.S. Food and Drug Administration; Silver Spring, Maryland

Lunch

12:00 PM – 12:30 PM

On your own

Lunchtime Panel II

12:15 PM – 1:30 PM

Building a Global Health Security Implementation Evidence Base: Demonstrating Impact of GHS/IHR Investments

International Ballroom F

Limited sandwiches & salads available for purchase outside meeting room

Moderators

Rebecca Bunnell
Kashef Ijaz
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Contributions and Impact of FETP in Advancing Global Health Security
Dionisio Herrera: Task Force for Global Health, Inc.; Decatur, Georgia

Strengthening Global Health Security through the Establishment of Africa's First Post-Master's Field Epidemiology Fellowship Program in Uganda
Bao Ping Zhu: Centers for Disease Control and Prevention; Kampala, Uganda

The Viral Research & Diagnostic Laboratory Network in India and Its Linkages with GHS Platform
Nivedita Gupta: Indian Council of Medical Research; New Delhi, India

Indian EIS
SK Jain: National Centre for Disease Control; New Delhi, India

Poster Session with Authors – II

12:30 PM - 1:45 PM
Grand Ballroom C/D

One Health II

Board 150. Wildlife Disease Surveillance as an Early Warning System for High Consequence Zoonotic and Animal Diseases

Board 151. Improving Response Time through Private Sector Contributions and One Health Approach in Guinea

Board 152. One Health Approach Involving Rabies Control and Prevention in Thailand

Board 153. Determining the Minimum Level of Vaccination Needed to Prevent Re-introduction of Dog Rabies Once It Has Been Eliminated

Board 154. A Comparative Study of Enumeration Techniques for Free-Roaming Dogs in Rural Baramati, District Pune, India

Board 155. Deaths from Clinically Identifiable Human Rabies in Bangladesh: A Survey through Verbal Autopsy

Board 156. Dynamics of and Factors Affecting the Occurrence of Rabies in Humans and Animals in South America

Board 157. A Case of Mistaken Identity: HSV Encephalitis Confirmed in a Patient Highly Suspect for Rabies Infection

Board 158. Genome Sequence of Akhmeta Virus, an Early Divergent Old World Orthopoxvirus

Board 159. Behaviors of High-Risk Individuals in the Bushmeat Value Chain in the Democratic Republic of the Congo: Suggestions for Behavioral Interventions

Board 160. Outbreak of Monkeypox in the Likouala Department, Republic of Congo, 2017

Board 161. Epidemiology and Molecular Characterization of Group A Rotavirus from Rhesus Macaques (*Macaca mulatta)* at Wildlife-Human Interfaces in Bangladesh

Board 162. Establishing New Protocol for Field Collection of Rodents for Disease Surveillance in the Country of Georgia

Board 163. Study of Tularemia Prevalence in Commensal Rats from the Country of Georgia

Board 164. Assessing Viral Diversity in Rodents and Shrews in Bangladesh

Board 165. Two Case Examples Illustrating the One Health Approach to Identify Emerging Tick-Borne Diseases

Board 166. Characterization of Multiple Rift Valley Fever Virus Re-emergence Events in Uganda, 2017-8

Board 167. Molecular Characterization of Ulceroglandular Tularemia Cases in Slovenia

Board 168. Bat Hunting: Risk of Disease Emergence at Thriving Ecosystem Interface in Bangladesh

Board 169. Serological Detection of *Pteropine orthoreovirus* in Singapore

Board 170. Aquatic Animal-Inflicted Envenoming Injuries: Common Culprits and Emerging Pathogens

Waterborne Infections

Board 171. Characterizing Multiple Spatial Waves of the 1991-1997 Cholera Epidemic in Peru

Board 172. Assessing the Knowledge, Attitudes, and Practices Regarding Cholera Preparedness and Prevention in Owerri, South East Nigeria

Board 173. Case Management and Clinical Outcomes during an Outbreak of Typhoid Fever—Harare, Zimbabwe, October-December, 2017

Board 174. Etiologic Agents of Diarrhea in Vientiane Capital, Lao People's Democratic Republic

Board 175. Acute Gastroenteritis Outbreak in Union Council Neemargh, District Kalat, Pakistan 2017

Board 176. Antibiotic Resistance Detected in *Escherichia coli* and *Klebsiella* spp. Isolates from Household Water, Food Preparation Surfaces, and Soil in Compounds in Maputo, Mozambique: Implications for Environmental Transmission Outside the Clinic

Board 177. Incidence Trend and Epidemiology of Legionnaires' Disease, Delaware, 2006-2017

Board 178. WGS Analysis of *Legionella pneumophila* Reveal Diversity Within and Across Water Samples Over Time in a Hospital Premise Plumbing System

Board 179. Epidemiology of Nontuberculosis Mycobacteria Notifications and Association with Drinking Water Disinfectant in Queensland, Australia

Board 180. Evolving Epidemiology of Reported Giardiasis Cases in the United States, 1995–2016

Board 181. Molecular Surveillance of *Cryptosporidium* Infection in Children in Kuwait

Board 182. *Acanthamoeba* Disease Associated with the Practice of Nasal Rinsing in Immunocompromised Patients

Antimicrobial Resistance

Board 183. Assessment of HAI/AR Outbreak Detection Data, Tools, and Barriers

Board 184. Year One of the Antimicrobial Resistance Laboratory Network (ARLN): A New Laboratory Network That Allows Early Identification of Emerging Resistance in Healthcare-Associated Infections—United States, 2017

Board 185. Architecture of an Extensively Drug-Resistant Organism (XDRO) Registry Utilizing the Existing Infrastructure of the State of Tennessee's NEDSS Base System (NBS)

Board 186. External Validation of Surveillance and Reporting of Carbapenem-Resistant Enterobacteriaceae to the National Healthcare Safety Network—Wisconsin

Board 187. Impact of Ertapenem on Detection of Carbapenemase-Producing Enterobacteriaceae in Tennessee, United States

Board 188. Impact of Human and Food Animal Wastes on Antimicrobial Gene Abundance and *E. coli* Susceptibility Patterns

Board 189. Characterization of Multidrug-Resistant Gram-Negative Bacilli from Human Infections, Nicaragua

Board 190. The Epidemiology of Antibiotic Resistance in Clinical Non-Typhoidal *Salmonella* (NTS) Isolates in Michigan

Board 191. Decreased Susceptibility to Azithromycin among Nontyphoidal *Salmonella* Isolates in the United States, 2011–2017

Board 192. Antimicrobial Resistance of *Salmonella* & *Staphylococcus* Species Isolated from Free-Ranging Rhesus Macaques (*Macaca mulatta*): Eco-epidemiological Assessment at a Human-Animal Interface in Bangladesh

Board 193. Etiology and Antimicrobial Resistance Patterns of *Salmonella* Bacteremia in Hospitalized Children with Acute Febrile Illness—Uganda, 2016-2017

Board 194. Evolution of Antimicrobial Resistance among *Shigella* Isolates in Argentina from 2007-2016

Board 195. Emerging Quinolone Resistance Mechanisms among *Shigella* in the United States

Board 196. Characterizing *Shigella* Species Distribution and Antimicrobial Susceptibility to Ciprofloxacin and Nalidixic Acid in Latin America between 2000-2015, Using Data from the Latin American Antimicrobial Resistance Surveillance Network (ReLAVRA)

Board 197. Colistin-Resistant *Klebsiella pneumoniae* Bloodstream Infection: Old Drug, Bad Bug

Board 198. In Vitro Antimicrobial Activity of Fosfomycin Tromethamine against Urinary Extended Spectrum Beta-Lactamase-Producing *Escherichia coli* and *Klebsiella pneumoniae*

Board 199. KPC Carbapenemase is Common among Carbapenem-Resistant Enterobacteriaceae in Connecticut, but Other Mechanisms Have Been Detected, 2017

Board 200. Molecular Characterization of Carbapenem-Resistant *Acinetobacter baumannii* in the United States, 2013-2015

Board 201. Pharmacoeconomic Evaluation of Meropenem Versus Imipenem/Cilastatin in Hospital-and Ventilator-Acquired Pneumonia (HAP/VAP), Alexandria, Egypt, 2017

Board 202. Identifying the Misidentified: Detecting *Candida auris* through the Antibiotic Resistance Laboratory Network, United States, 2017

Board 203. Characterizing *Candida* Species Identification Isolate Submission to the Southeast Regional Laboratory for the US Antibiotic Resistance Laboratory Network (ARLN)

Board 204. Antibiotic Use and Drug-Resistant Late-Onset Infections among Neonates Admitted to Neonatal Intensive Care Units in Pune, India

Board 205. Predicting Bacteria Detection in Pediatric Acute Gastroenteritis to Encourage Appropriate Treatment

Board 206. Parental Knowledge, Attitude and Practices Regarding Antibiotic Usage among Children under Five in Pakistan

Board 207. Developing and Implementing Antibiotic Stewardship in ICU Setting: Prospective Interventional Pilot Study, Cairo, Egypt, 2016

Board 208. Implementation of Antimicrobial Stewardship and Infection Control and Prevention Practices in Long-Term Care Facilities—Pennsylvania, 2017

Board 209. Policy Writing Tools and Workshops as a Way to Advance Antibiotic Stewardship in Long-Term Care

Board 210. Using Web-based Seminars for Healthcare and Public Health Professionals to Increase Knowledge on Emerging Antimicrobial Resistance in Latin America

Hepatitis / HIV / STDs / TB

Board 211. Assessment of Risk Behaviors and Sex-Seeking Practices among Male Active Duty Sailors and Marines Infected with HIV, 2010-2016

Board 212. Co-Occurrence of HIV, HBV, and HCV Infections in Tennessee by Region

Board 213. Building HIV/HCV Outbreak Response Capacity in Tennessee

Board 214. Hepatitis C Infection in Pregnant American Indian and Alaska Native Women, 2003-2015

Board 215. Withdrawn

Board 216. National Prevalence Survey of Viral Hepatitis B and C in Tunisia, 2015

Board 217. Next Generation Sequencing of the Hepatitis A Virus Outbreak in San Diego County

Board 218. Withdrawn

Board 219. Prevalence of Anal and Oral HPV DNA and HPV Seroprevalence among Transgender Women in Two Cities, United States, 2012–2014

Board 220. Surveillance for Disseminated Gonococcal Infections, Active Bacterial Core Surveillance (ABCs)—United States, 2015-2017

Board 221. Characterizing *Neisseria gonorrhoeae* Susceptibilities for Isolates Submitted to the Southeast Regional Laboratory for the US Antibiotic Resistance Laboratory Network (ARLN)

Board 222. Testing and Utilization of Preventive Services for Sexually Transmitted Infections (STIs) among Men Who Have Sex with Men (MSM) in the Boston National HIV Behavioral Surveillance (NHBS) Survey

Board 223. Developing Messaging to Prevent Multidrug-Resistant *Shigella* Infections among Men Who Have Sex with Men

Board 224. Determinants of Health Care-Seeking Delay among Tuberculosis Patients in a Rural Area of Central China: A Multicenter Study

Board 225. Risk Factors of Multidrug-Resistant Tuberculosis among Pediatric Patients: A Retrospective Cohort Study

Board 226. Cerebral and Cerebellar Toxoplasmosis Presenting with Disseminated Mycobacterium Co-infection in a Patient with HIV/AIDS: A Case Report

Influenza Burden

Board 227. Comparison of Incidence and Cost of Influenza in Healthy and High-Risk Children <5 Years Old in Thailand, 2011-2015

Board 228. Estimating Annual Direct Medical Costs from Seasonal Influenza in China

Board 229. Withdrawn

Board 230. Burden of Hospitalized Influenza in Vietnam: Hospitalization Admission Survey in Quang Ninh Province

Board 231. Heterogeneity in Rates of Influenza-Associated Hospitalizations: A Systematic Review, 2007-2016

Board 232. Evaluation of Hospital Discharge Diagnoses as a Surrogate for the World Health Organization Severe Acute Respiratory Illness Case Definition for Influenza Surveillance

Board 233. Estimating the National Burden of Hospitalized Influenza in Lao People's Democratic Republic, 2016

Board 234. Active Surveillance of Influenza-Associated Hospitalizations among Persons Aged 16 Years and Older in Shanghai, China, April 2017-March 2018

Board 235. Incidence of Hospitalization Due to Influenza-Associated Acute Respiratory Infection in Bangladesh, 2009-2016

Board 236. Estimation of Influenza-Associated Hospitalization in the United States Using a Rate Method, 2011 to 2015

Board 237. Regional Estimates of Influenza-Associated Mortality in India, 2007-2013

Board 238. Characterization of Influenza-Related Lethal Cases in Georgia, 2014-2017 Seasons

Board 239. Mortality-Associated Risk Factors among Patients with Influenza A(H1N1)pdm09 Infections, Pakistan, 2009-2016

Board 240. Genomic Variability and Neuraminidase Inhibitor Drug Susceptibility Profile of Influenza A/H1N1pdm09 Strains Circulating in Morocco during 2015-2016 Season

Board 241. Efficacy of FLU-IGIV in Ferrets and Mice Infected with H1N1pdm09 Influenza Virus

Board 242. Cytokine Profile in Pregnant Ferrets Infected with 2009 Pandemic Influenza A(H1N1) Virus

Board 243. Obesity Increases the Duration of Influenza A Shedding in Adults

Board 244. Absolute Humidity and Influenza Transmissibility in Subtropical Hong Kong

Board 245. Withdrawn

Board 246. Laboratory-Confirmed Influenza among Family Caregivers in District Hospitals in Bangladesh, 2015-2017

Respiratory Infections

Board 247. Differences in Legionnaires' Disease Incidence among Large Counties—United States, 2012-2016

Board 248. Cases of Legionnaires' Disease with Travel Exposures—United States, 2015-2016

Board 249. Outbreak of *Kingella kingae* Infections in a North Dakota Child-Care Facility

Board 250. Severe Acute Respiratory Infection (SARI) Surveillance: Building on an Existing Influenza Platform to Test for Non-Influenza Respiratory Viruses

Board 251. Adenoviruses Associated with Influenza-Like Illness among College Students—Pennsylvania, 2016–2017

Board 252. Viral Growth Characteristics of Clinical Isolates Identified as Human Adenovirus Type 1 (HAdV-1) with Molecular Homology to Feline Adenovirus

Board 253. A Retrospective Examination of a Human Rhinovirus-Associated Pneumonia Outbreak at a Long-Term Care Facility in Georgia Using McGreer's Criteria

Board 254. Whole Genomes of Rhinovirus C47 and a Newly Discovered Genotype, C56, Characterized Using Advanced Molecular Detection

Board 255. Development of a Duplex Real-Time RT-PCR Assay for Detection and Subgroup-Specific Identification of Human Respiratory Syncytial Virus (HRSV)

Board 256. Estimating Age- and Region-Specific Excess Mortality Caused by Influenza and Respiratory Syncytial Viruses in Japan, 2006-2014

Board 257. Surveillance for Respiratory Syncytial Virus and Parainfluenza Virus among Patients Hospitalized with Pneumonia in Sarawak, Malaysia

Board 258. Increased Burden of Respiratory Syncytial Virus in Southern California, 2016-18

Board 259. Respiratory Syncytial Virus among Children Hospitalized with Acute Lower Respiratory Infection in Kashmir, a Temperate Region in Northern India

Board 260. Respiratory Viruses Associated with Severe Acute Respiratory Infection (SARI) among Children under Five Years Old in Morocco, during Two Seasons 2014-16

Board 261. Middle East Respiratory Syndrome in Humans: Current Knowledge Gaps for Effective Public Health Response

Board 262. Genomic Sequence and Growth Characterization of Novel MERS Coronaviruses from Saudi Arabia

Board 263. Withdrawn

Board 264. Morbidities & Mortalities of (MERS-COV) Epidemic Threatens Opportunities and Containment Strategies

Board 265. MERS-CoV Outbreak at Domat Al-Jandal Hospital

Board 266. Contemporaneous Outbreaks of Middle East Respiratory Syndrome in Two Hospitals in Riyadh, Saudi Arabia, May-June 2017

Board 267. Evaluating the Potential Impact of Targeted Vaccination Strategies against Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Outbreaks in the Healthcare Setting

Tropical Infections

Board 268. Epidemiology of Imported Malaria among Travelers and Expatriates in the State of Qatar, 2016

Board 269. Crimean-Congo Hemorrhagic Fever Outbreak in Central Uganda—August 2017

Board 270. When There Is a Will, There Is a Way: Evolution of Ebola Diagnostics during the 2014-2016 West African Outbreak

Board 271. Stillbirths and Neonatal Deaths during the Ebola Outbreak, Sierra Leone, 2014–2015

Board 272. Comparative Survival of Two Ebola Surrogate Viruses

Board 273. Detection and Characterization of Environmental Strains of *Mycobacterium ulcerans* from the Southwest Region of Cameroon

Board 274. Spatial Distribution and Temporal Trends of Leprosy, Uganda, 2012-2016

Board 275. The Prevalence of *Trypanosoma cruzi* in Mexican Free-Tailed Bats (*Tadarida brasiliensis*) at Three Maternity Roosts in Oklahoma

Board 276. Outbreak Investigation of Cutaneous Leishmaniasis in District Kilasaifullah, Pakistan, November 2017-February 2018

Board 277. Assessment of Challenges and Proposed Activities to Strengthen the Management of Patients with Cutaneous Leishmaniasis in Alta Verapaz, Guatemala, 2017

Board 278. Investigation of Suspected Cutaneous Leishmaniasis at Village Gulderi, District Nowshera, Pakistan, January 2016

Board 279. Evaluation of the Risk of Reintroduction of Onchocerciasis to Guatemala by Military Peacekeeper Missions to Onchocerciasis—Endemic Democratic Republic of Congo

Laboratory: Sequencing

Board 280. Evaluation of Illumina's MiniSeq Sequencing Platform

Board 281. An Evaluation and Comparison between Ion Torrent S5 and Illumina MiSeq Sequencing Platforms for Whole Genome Sequencing of *Escherichia coli*

Board 282. Evaluation of the Oxford Nanopore MinION Sequencer for Virus Discovery, Identification, and Characterization

Board 283. Evaluation of the Oxford Nanopore MinION for Low-Cost Rabies Virus Sequence Typing

Board 284. A Comparison of Next Generation Sequencing Library Preparation Using Illumina Nextera XT and New England Biolabs NEBNext Ultra II Kits

Board 285. A Whole Genome Multi-Locus Sequence Typing Workflow for Reference Characterization, Surveillance and Outbreak Detection of Shiga Toxin-Producing *Escherichia coli* (STEC)

Board 286. Bioinformatic Pipeline for the Analyses of Whole Genome Sequencing Data for Legionnaire's Disease Outbreak Investigations

Board 287. Data Management, Workflows, and Communication for Whole-Genome Sequencing-Based Surveillance of Foodborne Pathogens in a Large State Public Health Laboratory

Board 288. Amplicon Prediction Pipeline for an Extended MLST Approach to Culture-Independent Pathogen Subtyping

Board 289. Development of Strain Nomenclature Based on Core Genome MLST for Surveillance of Shiga Toxin-Producing *Escherichia coli*

Board 290. Whole Genome MLST-Based Typing and Strain Nomenclature for *Clostridium difficile* Isolates

Board 291. Targeted Metagenomics through Marker Creation—T-MArC

Board 292. Evaluation of Fecal Nucleic Acid Stabilization Methods for Culture-Independent Pathogen Subtyping

Board 293. Sequencing *Salmonella* on an Illumina NextSeq, the New York State Experience: Impact on Cost, Quality, and Turn-Around Time

Board 294. Comparison of Shotgun and Amplicon Sequencing for Antimicrobial Resistance Determinant Detection in Stool and Isolate Samples

Board 295. Optimization of Predictive Antimicrobial Resistance Analytics for State Public Health Laboratories

Board 296. *De novo* Prediction of Pyrazinamide Resistance in *Mycobacterium tuberculosis* from Structural and Evolutionary Information

Late Breakers

Board LB-28. Level of Awareness of Disease Transmission between Humans and Wild Animals at the Interface of Queen Elizabeth National Park, Uganda

Board LB-29. Implementation of Q Fever Diagnostics in Georgia

Board LB-30. Improvement of Brucellosis Laboratory Diagnostics in Animals in Georgia

Board LB-31. Characterizing Human Target Cell Infection by Three Geographically Distinct Isolates of Mayaro Virus

Board LB-32. First Serologic Evidence of Emerging Zoonotic Alphaviruses in Humans from a Remote Indigenous Community in the Peruvian Amazon

Board LB-33. Novel G4P[49] Rotavirus Strains Identified in a Diarrheal Outbreak in Piglets in Bangladesh, February, 2014

Board LB-34. Risk Assessment of Human Behaviors that May Impact the Health of the Mountain Gorillas around Bwindi Impenetrable National Park, Western Uganda

Board LB-35. Investigation of Three Geographically-Distinct Anthrax Outbreaks in Uganda, 2018

Board LB-36. Anthrax Laboratory Studies and GIS Analyses in Georgia, 2015-2017

Board LB-37. Clinical and Epidemiological Features of Human Rabies Cases in Bangladesh, 2011-2015

Board LB-38. Development of a Glycoprotein-Based ELISA for Diagnosis of Rabies Virus-Neutralizing Antibody

Board LB-39. Combining Culture with Real-Time PCR for Improved Detection of Spotted Fever Group *Rickettsia*

Board LB-40. Risk of Yellow Fever Virus Introduction in the United States from Brazil during 2016-2018

Board LB-41. Identification of Yellow Fever Vaccine Deserts in the United States, 2017

Board LB-42. Wild Yellow Fever: Public Health Emergency: Study of Cases in Emílio Ribas Institute of Infectology - IIER, Sao Paulo, Brazil, January to March 2018

Board LB-43. Chikungunya: Strategic Plans for Public Health in a Local Community in Honduras

Board LB-44. Spatio-Temporal and Socio-Demographic Patterns of Chikungunya, Dengue, and Zika Infections in Mexico in 2016-2017

Board LB-45. TEPHINET's Management Response to the Zika Emergency in the Americas (2016-2018)

Board LB-46. Obstetric Ultrasound Service Delivery: Assessment Tools Used in the Context of the Zika Virus Epidemic in Five USAID Priority Countries

Board LB-47. Zika Virus Testing of Amniotic Fluid in Colombia

Board LB-48. Confirmed Urological Sequela in the Settings of Congenital Zika Syndrome

Board LB-49. Performance Evaluation of InBios ZIKV Detect 2.0 IgM Capture ELISA for Detection of Zika Virus Exposure

Board LB-50. Barriers to Zika Virus-Related Counseling and Use of Public Health Alerts among NYC Healthcare Providers

Board LB-51. Zika Virus Knowledge, Attitudes, and Practices among Medical Students in North Carolina, United States

Board LB-52. Community Support for Novel *Aedes aegypti* Control Methods after the Zika Outbreak in Puerto Rico

Board LB-53. Persistent Zika Virus Infection of HUVECs Regulates Endothelial Permeability, Matrix Metalloproteases, and Cytokines Activation

Board LB-54. Stability of Ebola and Rift Valley Fever Viruses in Semen and Blood Matrices during Typical Field Laboratory Storage Conditions

Board LB-55. Prevalence *Y. enterocolitica* among People for 2012-2017 in Azerbaijan

Board LB-56. Evaluating Fluticasone Propionate as a Treatment for Late Stage Pneumonic Plague

Board LB-57. An Ex Vivo Human Tissue Platform Reveals the Role of Pla in Initial Interactions of *Yersinia pestis* with the Human Lung Environment

Board LB-58. Investigation of Falciparum Malaria Outbreak in Laghman Province, September 2017-January 2018: Descriptive Epidemiology

Board LB-59. *Plasmodium falciparum* Reduction in Transfusable Whole Blood Products Treated with Riboflavin and Ultraviolet Light

I. Concurrent Panel Sessions

1:45 PM - 3:15 PM

I1. Rising Above the Noise to Communicate Sound Science and Public Health Advice

International Ballroom A/B/C

Moderators

Lilly Kan: National Association of County and City Health Officials; Washington, DC
Michelle Bonds: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Call Me, Maybe
Helen Branswell: STAT; Boston, Massachusetts

Building Communications Capacity to Counter Infectious Disease Threats
Jennifer Gardy: British Columbia Centre for Disease Control; Vancouver, BC, Canada

Emergency Risk Communication in a Changing Media Environment
Katherine Lyon Daniel: Centers for Disease Control and Prevention; Atlanta, Georgia

I2. Detecting and Preventing Novel Transplant-Associated Infections

International Ballroom D

Moderator

Jefferson Jones: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Histopathological Recognition of Donor-Derived Transmission of Emerging Pathogens in the United States
Sherif Zaki: Centers for Disease Control and Prevention; Atlanta, Georgia

Fungi, Multi-Drug Resistant Bacteria, and Arboviral Disease Transmission through Solid Organ Transplantation in Europe
Paolo Antonio Grossi: University of Insubria; Varese, Italy

HIV-to-HIV Transplantation in Africa: Drug Resistance, Opportunistic Infections, and a New Lease on Life
Elmi Muller: Groote Schuur Hospital; Cape Town, South Africa

I3. Genomic Epidemiology: From the Lab to the Street

International Ballroom E

Moderators

Christin Hanigan: Association of Public Health Laboratories; Silver Spring, Maryland
Duncan MacCannell: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Linking Whole-Genome Sequencing to Epidemiology and Delivery for Decision-Making
David Aanensen: University of Oxford; Oxford, United Kingdom

Reconstructing Transmission Patterns from Sequence Information: Examples from Influenza and Dengue
Derek Cummings: University of Florida; Gainesville, Florida

Data Integration and Visualization for Tuberculosis Outbreak Investigations
Ben Silk: Centers for Disease Control and Prevention; Atlanta, Georgia

I4. Monitoring for the Next Pandemic Threat: Emerging Influenza Viruses (H7N9)

Grand Ballroom A/B

Moderators

Hayley Ashbaugh: US Department of Defense, Armed Forces Health Surveillance Branch; Silver Spring, Maryland
Tim Uyeki: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

From Human Infection with Avian Influenza Viruses to Pandemic Preparedness in China
Lei Zhou: Chinese Center for Disease Control and Prevention; Beijing, China

The Pathogenesis of Asian H7N9 Avian Influenza in Poultry
David Suarez: U.S. Department of Agriculture; Athens, Georgia

Virologic Characteristics of Avian Influenza A(H7N9) Viruses Detected in Humans
Todd Davis: Centers for Disease Control and Prevention; Atlanta, Georgia

Break

3:15 PM – 3:30 PM
Grand Ballroom and International Ballroom Levels

J. Oral Presentations

3:30 PM – 5:00 PM

J1. Molecular Epidemiology

International Ballroom D

Moderators

Jill Taylor: Wadsworth Center, New York State Department of Health; Albany, New York
Alison Halpin: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Distributed Cloud-Based Bioinformatics for Microbial Characterization and Outbreak Surveillance
J. Sevinsky: Colorado Department of Public Health and Environment; Denver, Colorado

2. Norovirus Outbreaks in China During 2014–2017
L. Ran: Chinese Center for Disease Control and Prevention; Beijing, China

3. Large-Scale Surveillance of Wild Bird Populations for Emergent Influenza Viruses
S. Bevins: National Wildlife Research Center; Fort Collins, Colorado

4. Linked Whole Genome Sequencing and Epidemiological Analysis Reveals Nationally Distributed Clusters of *M. abscessus* which Cross Disease Boundaries and Are Unlikely To Be Spread Through Person-to-Person Transmission
S. Lipworth: University of Oxford; Oxford, United Kingdom

5. Antibiotic Resistance Among Group B Streptococcal Isolates from Invasive Early- and Late-Onset Disease in the United States, 2006–2015
S. Nanduri: Centers for Disease Control and Prevention; Atlanta, Georgia

6. Can Social Media Advance Science? A Case Study from the 2016 *Elizabethkingia anophelis* Outbreak
A. Guinn: Centers for Disease Control and Prevention; Atlanta, Georgia

J2. Preparedness and Response

International Ballroom E

Moderators

Erin Kennedy
Sam Posner
Centers for Disease Control and Prevention; Atlanta, GA

Speakers

1. Early Warning Alert and Response Network in Emergencies: An Evaluation Protocol to Guide Better Emergency Response to Outbreaks
M. Malik: World Health Organization Office for the Eastern Mediterranean Region; Cairo, Egypt

2. Establishing and Sustaining National Multisectoral One Health Coordination Mechanisms to Prevent, Prepare for, Detect, and Respond to Public Health Threats
M. Rasmuson: DAI Global Health; Bethesda, Maryland

3. Connecting Organizations for Regional Disease Surveillance (CORDS): Building a Safer World for Communities in Underserved Regions
C. Longuet: Connecting Organisations for Regional Disease Surveillance; Lyon, France

4. OIE Laboratory Twinning Projects: A Global Tool to Strengthen Laboratory Capacity for Control of Terrestrial and Aquatic Animal Diseases
G. Pavade: World Organisation for Animal Health (OIE); Paris, France

5. Building a Foundation in Surveillance and Laboratory Capacity to Rapidly Detect Public Health Threats—Uganda, 2016–2017
K. Kugeler: Centers for Disease Control and Prevention; Fort Collins, Colorado

6. Assessing Capacities for Pandemic Influenza Preparedness and Response Through IHR Joint External Evaluation in Low and Middle-Income Countries
W. Zhou: World Health Organization; Geneva, Switzerland

J3. Viral Zoonoses

International Ballroom A/B/C

Moderators

Inger Damon
Pierre Rollin
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Marburg Virus Disease Outbreak—Kween District: Uganda, September–November, 2017
I. Nkonwa: Uganda Public Health Fellowship Program; Kampala, Uganda

2. Trend and Epidemiology of Crimean-Congo Hemorrhagic Fever (CCHF) in Afghanistan (2011–2017)
M. Rasooly: Ministry of Health; Kabul, Afghanistan

3. The Rabies Puzzle in India: A One Health Approach to Understanding a Multi-Faceted Problem
A. Vanak: Wellcome Trust/DBT India Alliance; Bangalore, India

4. The Cost of Rabies Post-Exposure Prophylaxis in Minnesota, 2017-2018
S. Johnson: Minnesota Department of Health; St. Paul, Minnesota

5. Fifteen Years of Enhanced Rabies Related Lyssavirus Surveillance in South Africa
W. Markotter: University of Pretoria; Pretoria, South Africa

6. Exposures Among Middle East Respiratory Syndrome Coronavirus Patients—Saudi Arabia, July–October 2017
E. Rose: Ministry of Health; Riyadh, Saudi Arabia

J4. Late Breakers I

Grand Ballroom A/B

Moderators

RL Sarita: Director of Health Services; State of Kerala, India
Kayla Laserson: Centers for Disease Control and Prevention; New Delhi, India
Vikas Kapil: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Outbreak of Nipah Virus in Kerala, India, 2018.
G. Arunkumar: Manipal Centre for Virus Research, Manipal Academy of Higher Education; Manipal, India

2. Multi-Sectoral Emergency Response to the Nipah Outbreak, Kerala, India, May, 2018.
S. Singh: National Centre for Disease Control; Delhi, India

3. *Pteropus* Bats Positivity For Nipah Virus From Kozhikode, Kerala, India: Possible Link of Infection To Human.
D. Mourya: ICMR-National Institute of Virology; Pune, India

4. Near Real-Time Risk Assessment of Ebola Spillover: An Open-Source, Publicly Available Platform for Satellite-Based Change Detection.
S. Malloy: The Ohio State University; Columbus, Ohio

5. Habitat Fragmentation and Land-Use Change as Drivers of Yellow Fever Outbreaks in South America.
A. Hamlet: Imperial College London; London, United Kingdom

6. A Scoping Review of Chikungunya Virus and Its Vectors from Global Evidence.
M. Mascarenhas: National Microbiology Laboratory, Public Health Agency of Canada; Guelph, OH, Canada

Wednesday, August 29

Poster Set-up for the Day

7:00 AM – 8:00 AM

All posters presented on Wednesday will be available for viewing in Grand Ballroom C/D from 10:00 AM to 4:30 PM. Authors will be present at posters from 12:30—1:45 PM each day.

Scientific Sessions

K. Concurrent Plenary Sessions

8:00 AM – 9:00 AM

K1. Forecasting Emerging Infections

International Ballroom A/B/C

Moderator

Michael Johansson: Centers for Disease Control and Prevention; San Juan, Puerto Rico

Speaker

The Present is Pregnant with the Future: Lessons Learned from Forecasting
Rebecca Grais: Médecins Sans Frontières; Paris, France

K2. 100 Years after the 1918 Influenza Pandemic

Grand Ballroom A/B

Moderator

Steve Redd: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

100 Years since 1918: Are We Ready for the Next Severe Influenza Pandemic?
Dan Jernigan: Centers for Disease Control and Prevention; Atlanta, Georgia

K3. Addressing Neglected Tropical Diseases: Focus on Guinea Worm

International Ballroom D

Moderator

Barbara Marston: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Wrapping Up the Final Inch: Achievements and Challenges in Reaching Guinea Worm Eradication
Sharon Roy: Centers for Disease Control and Prevention; Atlanta, Georgia

K4. Globalization of People and Disease

International Ballroom E

Moderator

Marty Cetron: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Travelers as Sentinels of Disease Outbreaks: The GeoSentinel Experience
David Hamer: Boston University Schools of Public Health and Medicine; Boston, Massachusetts

L. Concurrent Plenary Sessions

9:10 AM - 10:10 AM

L1. Infectious Causes of Child Mortality

International Ballroom E

Moderator

Pratima Raghunathan: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Focusing on Targets for Reducing Childhood Mortality Through the Child Health and Mortality Prevention Surveillance (CHAMPS) Network
Robert Breiman: Emory University; Atlanta, Georgia

L2. Novel Surveillance Strategies

International Ballroom A/B/C

Moderator

Oliver Morgan: World Health Organization; Geneva, Switzerland

Speaker

Towards Digital Pathogen Surveillance
Jennifer Gardy: British Columbia Centre for Disease Control; Vancouver, BC, Canada

L3. Emerging Tick-borne Diseases

International Ballroom D

Moderator

Gil Kersh: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

The Changing Climate for Lyme Disease and Other Tick-Borne Zoonoses
Alan Barbour: University of California, Irvine; Irvine, California

L4. Foodborne Disease Surveillance and Culture-Independent Diagnostic Tests

Grand Ballroom A/B

Moderator

Patricia Griffin: Centers for Disease Control and Prevention; Atlanta, Georgia

Speaker

Public Health Response to Foodborne Diseases in the Era of Culture-Independent Diagnostic Testing
Timothy Jones: Tennessee Department of Public Health; Nashville, Tennessee

Break

10:10 AM – 10:30 AM
Grand Ballroom and International Ballroom Levels

M. Concurrent Panel Sessions

10:30 AM - 12:00 PM

M1. Emerging Paths to Publishing Your Work: The Good, the Fast, and the Ugly

Grand Ballroom A/B

Moderators

Marta Gwinn
Todd Weber
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Doing Science Is Not Enough: The Importance of Communicating Your Work in Any Way That You Can
Chris Gunter: Children's Healthcare of Atlanta; Atlanta, Georgia

Publication Options for Research Authors: Cascading Peer Review, Public Access, and Open Access
Annette Flanagin: JAMA and The JAMA Network; Chicago, IL

Tips for Avoiding Questionable Infectious Diseases Journals and Conferences
Sharon Bloom: Centers for Disease Control and Prevention; Atlanta, Georgia

M2. Rodent-Borne Zoonoses

International Ballroom D

Moderators

Ilana Schafer: Centers for Disease Control and Prevention; Atlanta, Georgia
Mary Grace Stobierski: Michigan Department of Health and Human Services; Lansing, Michigan

Speakers

Eco-Epidemiology of Urban Leptospirosis in Brazil
Federico Costa: Federal University of Bahia; Salvador, Brazil

Mighty Rodents: Recent Zoonotic Outbreaks in Feeder Mice and Pet Rats
Barbara Knust: Centers for Disease Control and Prevention; Atlanta, Georgia

National Park Service Ecological and Prevention Initiatives
Danielle Buttke: National Park Service; Fort Collins, Colorado

M3. Mathematical Modeling to Better Understand the Emergence and Transmission of Multidrug-Resistant Organisms

International Ballroom A/B/C

Moderators

Richard Danila: Minnesota Department of Health; St. Paul, Minnesota
Rachel Slaton: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Enhancing Multidrug Resistant Organism Prevention Strategies with Mathematical Modeling
Prabasaj Paul: Centers for Disease Control and Prevention; Atlanta, Georgia

Regional Transmission of Healthcare-Associated Infections: How Mathematical Modeling Can Inform Prevention
Karim Khader: University of Utah; Salt Lake City, Utah

Estimating the Magnitude and Effects of Bystander Selection for Antibiotic Resistance in the United States
Christine Tedijanto: Harvard T.H. Chan School of Public Health; Boston, Massachusetts

M4. Make History: End TB

International Ballroom E

Moderators

Paula Fujiwara: International Union Against Tuberculosis and Lung Disease; Paris, France
Carla Winston: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Tuberculosis Outbreaks in the United States: A National Perspective
Jonathan Wortham: Centers for Disease Control and Prevention; Atlanta, Georgia

TB Outbreak in Perry County, Alabama, and the Implementation of Interventions to Contain
Pam Barrett Scanlon: Alabama Department of Public Health; Montgomery, Alabama

Using Models of Transmission to Prioritize Action in the Fight to End Tuberculosis
David Dowdy: Johns Hopkins University; Baltimore, Maryland

New and Repurposed Drugs for Drug-Resistant Tuberculosis
Payam Nahid: University of California, San Francisco; San Francisco, California

Lunch

12:00 PM – 12:30 PM

On your own

Lunchtime Panel III

12:15 PM – 1:30 PM

Measuring Progress and Impact of Global Health Security Capacity-Building Implementation in Partner Countries

International Ballroom F

Limited sandwiches & salads available for purchase outside meeting room

Moderators

Rebecca Bunnell
Kashef Ijaz
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Using Minimal and Optimal Objectives to Advance Progress on Building IHR Capabilities
Mike Mahar: Centers for Disease Control and Prevention; Atlanta, Georgia

Development of Metrics to Measure Progress: From 270 to 20 Indicators
Cynthia Cassell: Centers for Disease Control and Prevention; Atlanta, Georgia

Progress in Respiratory Laboratory Capacity Building in 17 Phase I Countries
Susan Hiers: Centers for Disease Control and Prevention; Atlanta, Georgia

Monitoring IHR Compliance in India
Meera Dhuria: National Centre for Disease Control; New Delhi, India

Poster Session with Authors – III

12:30 PM - 1:45 PM
Grand Ballroom C/D

Infections in Infants and Pregnant Women

Board 297. Seroprevalence of Selected Congenital Infections among Pregnant Women in Coatepeque, Guatemala

Board 298. Early-Onset Neonatal Sepsis by Group B *Streptococcus agalactiae* and *Escherichia coli*

Board 299. Invasive Group A Streptococcal Postpartum Infections in Minnesota, 2000-2016

Board 300. Trends in Incidence of Invasive Early- and Late-Onset Group B Streptococcal Disease, United States, 2006-2015

Board 301. Group B *Streptococcal* Bacteremia Burden and Trends over Time, 2007-15, Thailand

Board 302. Respiratory Illness and Birth Weight in Infants with Prenatal Exposure to Maternal Influenza Infection during 2013-2017 in Bangladesh

Board 303. Changing Estimates of Incidence of Congenital Zika Syndrome with Changing Case Definitions

Board 304. Overview of Zika en Embarazadas y Niños en Colombia (ZEN): A Prospective Cohort Study Examining Zika Virus Infection during Pregnancy and Risk of Adverse Pregnancy, Birth, and Infant Outcomes

Board 305. Surveillance of Microcephaly and Other Congenital Central Nervous System Malformations: The Colombian Experience during the 2015-2016 Zika Virus Epidemic

Board 306. The Zika Virus Infection in Pregnant Women in Honduras (ZIPH) Cohort Study

Board 307. Prevalence of Small for Gestational Age among Live Births with Confirmed and Possible Prenatal Exposure to Zika Virus Infection, United States Zika Pregnancy and Infant Registry, 2015-2017

Board 308. Stopping the Next Zika: Lessons Learned to Help Protect Mothers and Babies from Emerging and Existing Threats

Board 309. Health System Preparedness and Response to the Emergence of Zika in Iquitos and Piura, Peru: A Qualitative Comparative Case Study

Board 310. Local Response to an Emerging Infectious Disease: Results and Lessons from a Urosurvey to Investigate Local Zika Virus Transmission

Influenza Vaccines, Preparedness, and Response

Board 311. Dose Effect of Influenza Vaccine on Protection against Laboratory-Confirmed Influenza Illness among Children 6 months to 8 years of Age in Southern China, 2013-2016 Seasons: A Matched Case-Control Study

Board 312. Demographic Differences in Flu Vaccination among Florida's High School Students: Evidence from 2017 Florida Youth Risk Behavior Survey

Board 313. Do Thai Physicians Recommend Seasonal Influenza Vaccines to Pregnant Women? A Cross-Sectional Survey of Physicians' Perspectives and Practices in Thailand

Board 314. Predictors of Seasonal Influenza Vaccination among Older Adults in Thailand

Board 315. Immunogenicity Following Influenza Vaccination among Thai Older Adults with and without Prior Vaccination

Board 316. Effectiveness of Trivalent Inactivated Influenza Vaccine among Community-Dwelling Older Adults in Thailand: A Two-year Prospective Cohort Study

Board 317. Seasonal Influenza Vaccine Effectiveness among Persons with Chronic Obstructive Pulmonary Disease in Thailand, 2011-2013: A Retrospective Cohort Analysis

Board 318. Blunting of Serum Hemagglutinin Inhibition Antibody Response to 2010-11 Trivalent Influenza Vaccines Is Associated with Receipt of Specific Prior Inactivated Influenza Vaccines and Mediated by Antibodies to These Vaccine Strains

Board 319. Analysis of Impact of Flu Vaccination on Acute Respiratory Viral Infections (ARVI) Morbidity among Population in South Kazakhstan Region, 2010-2015

Board 320. Post-Licensure Surveillance of Trivalent Adjuvanted Influenza Vaccine (Fluad®) in Adults Aged >65 years, United States, Vaccine Adverse Event Reporting System (VAERS), July 2016-June 2018

Board 321. Public Awareness Status against Influenza A H1N1: A Comparative Case Study at District Lahore and Multan, Punjab, Pakistan

Board 322. Molecular Characterization of Influenza Viruses Circulating in Casablanca, Morocco from 2013 to 2018

Board 323. Pandemic Influenza Surveillance: Learning from the Past to Improve Future Responses

Board 324. Tool for Influenza Pandemic Risk Assessment (TIPRA)

Board 325. Pandemic Influenza Risk and Impact Management: Building Sustainable and Resilient Capacities for Pandemic Response—the WHO's Approaches

Board 326. WHO Guidance for Surveillance during an Influenza Pandemic: 2017 Update

Board 327. Reinforcing Response to an Influenza Pandemic under the Pandemic Influenza Preparedness Program—Experience from a Country in the Eastern Mediterranean Region of WHO

Board 328. One Hundred Years of Influenza Since the 1918 Pandemic—Is China Prepared Today?

Board 329. WHO Public Health Research Agenda for Influenza—2017 Update: Advance Science to Address Unmet Public Health Needs

Board 330. A Data-Driven Tool for Local Influenza Response Policy

Board 331. Workplace Attendance with Acute Respiratory Illness or Influenza: Effect of Access to Telework

Board 332. Pandemic Influenza Severity Assessment (PISA)

Societal Challenges and Solutions

Board 333. Evaluation of the Surveillance System in Adjumani District Refugee Settlements, Uganda, April 2017

Board 334. A Comparative Cost Analysis of the Vaccination Program for US-Bound Refugees

Board 335. Etiology of Upper Respiratory Tract Infections among Displaced Rohingya Population in Bangladesh

Board 336. CDC Migration Health Data Management and Notification of Newly Arrived Persons with Overseas Tuberculosis Classification: eMedical to EDN

Board 337. Cholera Outbreaks within Humanitarian Context: A Challenge between Disaster Management, Health Systems, and Environmental Conditions

Board 338. Oral Cholera Vaccination Coverage in a Complex Humanitarian Setting: Lessons from Somalia, 2017

Board 339. *Shigella* Infections in the United States Are Associated with Poverty and Crowding, FoodNet, USA, 2004–2014

Board 340. Addressing a Culture of Health Inequity in Ohio's Appalachian Region during Outbreak Investigations

Board 341. A Survey of Open Defecation Sites in Atlanta

Board 342. Invasive Pneumococcal Disease among Adults Living with HIV/AIDS in NYC, 2008-2016

Board 343. Health Disparity and Invasive Group A Streptococcal Infections: A Multilevel Analysis Using Census-Derived Area-Based Socioeconomic Measures

Board 344. Awareness and Knowledge of Coccidioidomycosis in Arizona: Findings from the 2016 Behavioral Risk Factor Surveillance System

Board 345. Communicating Clinical Guidance during an Emergency Response: Zika Virus Clinical Tools

Board 346. Risk Communication in Health Emergencies: The Experience of Local Journalists during the 2014-15 Ebola Outbreak in Sierra Leone

Board 347. Emerging Infectious Diseases and Risk Communication: Lessons from the GCC's Experience during MERS Epidemic

Board 348. Examining the *Emerging Infectious Diseases* Journal's Reach and Influence through Metrics

Vector-Borne Infections II

Board 349. Sylvatic Yellow Fever: Public Health Emergence

Board 350. Descriptive Epidemiology of CCHF in Afghanistan: Reported Cases to National Surveillance System, 2007-2017

Board 351. Spatial Distribution and Temporal Variation of the Risk by Zika Virus Disease in the Colombian Regions during the 2015-2016 Epidemic: A Bayesian Approach

Board 352. Exposure and Effects of Four Zika Prevention Interventions during the Zika Epidemic in Puerto Rico, 2016-2017

Board 353. Increased Incidence of Guillain-Barré Syndrome following the Zika Virus Epidemic in Rio de Janeiro, 2015-2016

Board 354. Understanding Zika Knowledge and Risk Perception at the Community Level: The Role of Gender Hierarchy and Reproductive Decision Making in Piura, Peru

Board 355. Development of a Novel Inactivated, Vero-Cell Culture-Derived Zika Virus Vaccine Candidate

Board 356. Climate Conditions Prior to 2013 Chikungunya Outbreaks in the Americas

Board 357. Epidemiological and Entomological Investigation of Chikungunya and Dengue Fever-like Suspected Cases in Burao District, Somaliland, 2017

Board 358. Chikungunya: Recent Outbreak in Dhaka City, 2017

Board 359. Local Transmission of Chikungunya in Rome and the Lazio Region, Italy: The First Outbreak in a Metropolitan Area in a Western Country

Board 360. Differences in Transmission and Disease Severity between Two Successive Waves of Chikungunya

Board 361. Chikungunya – A Reemerged Tropical Disease: Development of a Live-Attenuated Vaccine

Board 362. Field Epidemiological Investigation Report of Chikungunya Outbreak in Gwadar District of Pakistan in the Month of July 2017

Board 363. From Data to Decisions: Utilizing Machine Learning and Monte Carlo Simulations to Map Epidemic Potential

Board 364. High Prevalence of Dengue among Pregnant Women in India

Board 365. Prolonged Detection of Dengue Virus in the Semen of a Man Returning from Thailand to Italy, January 2018

Board 366. Evolving Spectrum of Dengue in India

Vaccine-Preventable Diseases

Board 367. Imported *Corynebacterium diphtheriae* in Minnesota, 2014-2017

Board 368. Invasive *Haemophilus influenzae* and *Haemophilus influenzae* Serotype A Cases in Minnesota, 2006-2017

Board 369. Epidemiology of *Haemophilus influenzae* Serotype A in Alaska, 2000-2017

Board 370. Study on the Prevalence of *N. meningitidis* Serogroups and Features of Meningitis Cases in Beijing, China, 2007-2016

Board 371. Outbreak of Bacterial Meningitis in Mali Associated with a New Sequence Type of *Neisseria meningitidis* Serogroup C Clonal Complex 10217

Board 372. Investigation of Suspected Pertussis Outbreak in Kunar Province, Afghanistan, March 2016

Board 373. Geographic Variation in Invasive Pneumococcal Disease (IPD) Following Six Years of 13-Valent Pneumococcal Conjugate Vaccine (PCV13) Use in the United States

Board 374. Impact of 13-Valent Pneumococcal Conjugate Vaccine (PCV13) on Invasive Pneumococcal Disease in Connecticut

Board 375. Long-Term Impact of 10-valent Pneumococcal Conjugate Vaccine (PCV10) Introduction on Carriage of Vaccine Serotype and Antimicrobial-Resistant Pneumococci among Children Less Than 5 Years Old in Mozambique, 2012-2016

Board 376. Effectiveness of Pneumococcal Vaccines against Invasive Pneumococcal Disease among US Medicare Beneficiaries Aged 65 Years and Older

Board 377. Come and Take it: Why Vaccine Advocates Are Losing the Battle in Texas

Board 378. Analysis of Measles Immunity Level in Permanent Population in Beijing, 2017

Board 379. A Coverage Survey of Measles-Containing Vaccination among Healthcare Workers in Beijing

Board 380. Impact of Exclusion on Measles Transmission in Childcare Settings, Minnesota, 2017

Board 381. Measles Outbreak Investigation in Killi-Qadirabad District, Noshki, Baluchistan (15 September to 21 October 2017)

Board 382. Measles Outbreak Investigation of Union Council, Taimoorabad District, Quetta, Pakistan, 2017

Board 383. Circulating Vaccine-Derived Poliovirus Type1 Outbreak Response in Lao People's Democratic Republic, 2015-2017

Board 384. Enhanced Surveillance in the Context of Poliovirus Importation Risk in Lebanon, 2013-2017

Board 385. An Update from Hospital-Based Surveillance for Rotavirus Gastroenteritis among Young Children in Bangladesh, July 2012 to June 2017

Board 386. Whole Genome Sequencing of Rotavirus Strains Causing Outbreaks in California, USA, in the Post-Licensure Vaccine Era

Board 387. Rubella Infection in an Unvaccinated Pregnant Woman—Johnson County, Kansas

Board 388. Withdrawn

Board 389. Epidemiological Study of Herpes Zoster (Shingles) in Qatar, 2012-2016

Surveillance II

Board 390. Strengthening Local and Regional Infectious Disease Control in the South of the Netherlands Using a Secure Web-based Dashboard for Real-time Data Exchange

Board 391. Surveillance Outbreak Response Management and Analysis System (SORMAS®-open)— mHealth-Implementation for Integrated Disease Surveillance and Response in 15 Federal States of Nigeria, 2017/18

Board 392. I-Lab: Countrywide Implementation of an Automated Platform for the Collection and Reporting of Laboratory Data for Improved Preparedness and Response to Outbreaks in Senegal

Board 393. The Epi Info™ Mobile Vector Surveillance System

Board 394. Improving Infectious Disease Surveillance in West Africa through Standardized Platforms Permitting Molecular Epidemiologic Investigations and Reporting Disease Emergence

Board 395. EpiCore: Crowdsourcing Epidemic Intelligence across the Globe to Verify Outbreaks Faster

Board 396. Participatory One Health Disease Detection (PODD) – Community-Based Reporting for Emerging Infectious Diseases in Thailand

Board 397. A Novel Syndromic Surveillance System for Travelers' Health in the Caribbean Region

Board 398. Assessing Event-Based Surveillance of Zoonotic Disease Reports for Impacts on Human Health

Board 399. Real-Time Surveillance of a Canine Rabies Outbreak in a Large Indian Metropolis

Board 400. Chagas Disease Surveillance Activities—7 US States, 2017

Board 401. CHIKRISK: Mapping and Assessment of Chikungunya Risk

Board 402. Examining Foodborne Illness Complaints Online Using the Twitter platform *(Will be displayed with Foodborne Infections posters on Monday)*

Board 403. Multisite Active Surveillance for Acute Gastroenteritis in Veterans Affairs Hospitals, 2016–17

Board 404. Surveillance for Acute Gastroenteritis Outbreaks through the National Outbreak Reporting System (NORS), United States, 2009–2016

Board 405. Geospatial Open Data Platforms to Tackle Hospital-Associated Infections

Board 406. Identification of Facilities at Risk of Receiving Patients Colonized with Emerging Multidrug-Resistant Organisms

Board 407. Interactive Visualizations of Carbapenem-Resistant Enterobacteriaceae (CRE) Surveillance Data in Tennessee, United States

Board 408. Development and Implementation of a Cloud-Based Meningitis Surveillance and Specimen Tracking System in Burkina Faso

Board 409. Death Certificate Review to Ascertain Additional Deaths among Patients Hospitalized with Invasive Bacterial Infections 90 Days Post-Discharge, Minnesota, 2012-2016

Board 410. Z-POINT: An Adaptable Data System for Outbreak-Related Case Review Designed for the Zika Emergency Response

Board 411. Integrated Monitoring for Zika-Exposed Persons: Georgia, 2016-2017

Genomic and Molecular Epidemiology

Board 412. Genomic Epidemiology of *Salmonella* Mississippi in Australia

Board 413. The Emergence of *Salmonella* Typhimurium DT 160 in Australia among Humans and Sparrows

Board 414. Impact of Population-Based Prospective Whole-Genome Sequencing on *Salmonella* Outbreaks in British Columbia (BC), Canada

Board 415. Whole Genome Sequencing-Based Analysis of a Child Care-Associated *Salmonella* Infantis Cluster with Conflicting Pulsed-Field Gel Electrophoresis Patterns

Board 416. Application of Whole Genome Sequencing Analytics to Aid Local Salmonellosis Outbreak Investigation in the Commonwealth of Virginia

Board 417. Evidence of Long-Term *Salmonella* Contamination Linked to a Single Restaurant in Michigan

Board 418. Are Georgia's Non-Typhoidal *Salmonella* Isolates Joining the (Antimicrobial) Resistance?

Board 419. Use of Whole Genome Sequencing during a Multistate Outbreak of Multidrug-Resistant *Campylobacter jejuni* Linked to Pet Store Puppies

Board 420. Genetic Diversity in Non-O157 Shiga Toxin-Producing *Escherichia coli* (STEC) and Clustered Regularly Interspaced Palindromic Repeat (CRISPR) Spacer Variation

Board 421. Genomic Concordance of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Clinical and Colonization Isolates from US Army Trainees with Skin and Soft Tissue Infection

Board 422. The European Survey of Carbapenemase-Producing Enterobacteriaceae (EuSCAPE) Reveals Widespread Emergence of Carbapenem Resistance in Diverse Genomic Backgrounds of *Klebsiella pneumoniae*

Board 423. A Longitudinal Birth-Cohort Study for Norovirus Infections in Children ≤2 Years of Age from Resource-Constrained Communities in Peru

Board 424. Outbreaks of Acute Gastroenteritis Associated with a Re-emerging GII.P16/GII.2 Norovirus in the 2016/17 Season in China

Board 425. Emerging Norovirus Recombinant Strains Causing Outbreaks in the United States

Board 426. Distinguishing Circulating Type 2 Vaccine-Derived Polioviruses (VDPVs) from Immunodeficiency-Associated VDPVs

Board 427. Genetic Characterization of Parapoxviruses (PPVs) Circulating in Sheep, Goats, and Dromedary Camels in Eastern Sudan, 2016

Laboratory Capacity

Board 428. Clinical Diagnostic "Lab-in-a-Pack" for Disease Surveillance and Outbreak Response in LMICs

Board 429. Establishment and Use of Field Forward Diagnostic Laboratories and Assays for Viral Pathogens during Outbreaks

Board 430. Utilizing Local Collaborations to Gain Capacity in Bioinformatics

Board 431. Building Next-Generation Sequencing Capacity in Ghana—Successes, Challenges, and Future Directions

Board 432. FoodCORE Centers Demonstrate Improvements in Isolate Testing during a Shift in Laboratory Techniques for Enteric Disease Surveillance

Board 433. Withdrawn

Board 434. Performance of NIC, Afghanistan, for Isolating and Sharing Influenza Virus Isolates during 2015-17

Board 435. Lebanese NIC Roadmap: Achievement and Future Improvement Plan

Board 436. Expanding a Trans-Atlantic Quality Assurance Laboratory Mentor Program

Board 437. The US Centers for Disease Control and Prevention-Supported National Laboratory Strengthening Initiative in India

Board 438. Laboratory Mapping in India: A Joint Initiative of the US Centers for Disease Control and Prevention and Indian Association of Medical Microbiologists

Late Breakers

Board LB-60. Estimating the Burden of Waterborne Disease in the United States

Board LB-61. Responding to a Large Norovirus Outbreak at a University Complicated by a Water Main Break, Connecticut 2018

Board LB-62. Viral Metagenomic Analysis of Stool Specimens from Undiagnosed Cases Acute Gastroenteritis in Children

Board LB-63. Outbreak of Acute Diarrheal Disease by *E. coli* Pathogen in Mass Event in Brazil, a Case-Control Study, Brasília, 2018

Board LB-64. First National Conference on Health Surveillance in Brazil, Monitoring of Medical Care in Real Time-New Strategies and Experiences in Mass Event.

Board LB-65. Natural History of Astrovirus- and Sapovirus-associated Gastroenteritis in Children Visiting the Emergency Department

Board LB-66. Use of Digital Channels Facilitates Active Case Finding Following a Foodborne Botulism Exposure Event—Alaska, 2018

Board LB-67. ClinEpiDB: The Clinical Epidemiology Database Resource

Board LB-68. Carbapenem-Resistant *Enterobacteriaceae* Surveillance in Wisconsin: The First Eleven Months of the Antibiotic Resistance Lab Network (ARLN)

Board LB-69. Epidemiology of Bloodstream Infections and Antimicrobial Resistance in Adult, Pediatric, and Neonatal Intensive Care Units in a Regional Referral Hospital, Guatemala, 2016-2018

Board LB-70. Point Prevalence and Epidemiology of Antimicrobial Use in Nursing Homes, New Haven and Hartford Counties, Connecticut, 2017

Board LB-71. Recent Increase in Colistin-Resistant Acinetobacter Infections at a Tertiary Care Center in Pakistan

Board LB-72. Evaluation of The Impact Of Antimicrobial Hand Towels On Hand Contamination With *Escherichia coli* Among Mothers in Nyanza Province, Kenya, 2011-2012

Board LB-73. Combating Antimicrobial Resistance: Utility of Antimicrobial Combination Therapy and / or β–Lactamase Inhibitors

Board LB-74. Medicine Quality and Antimicrobial Resistance

Board LB-75. Evaluation of Candidate Diagnostic Culture Media for ESBL *E. coli* in Environmental Samples as a One Health Indicator System for Global Antimicrobial Resistance Surveillance

Board LB-76. Combating Antimicrobial Resistance by Utilizing Novel Antibiotics from Soil and Marine Microorganisms in Lebanon

Board LB-77. The Emerging Fungal Pathogen *Candida auris* Contains Cell Wall Mannans That Exhibit Unique Structural Features Not Found in Other Fungi

Board LB-78. Efficacy of Dettol Antiseptic Liquid for Inactivation of Ebola-Makona Virus Suspended in an Organic Load – a Targeted Hygiene Intervention for Reducing Virus Spread

Board LB-79. Investigation of Zika Virus Transmission in a Laboratory Setting

Board LB-80. Implementation of Next Generation Sequencing Technology for HIV Resistance Determination and Genotyping

Board LB-81. Utilizing TaqMan Array Card (TAC) to Study the Etiology of Community-acquired Pneumonia among Hospitalized Adults in Hunan Province, China

Board LB-82. One Thousand Bacterial Genomes in One Week: Microfluidics for Molecular Epidemiology

Board LB-83. A Thousand Assays in One Night: Detecting Over >150 Genotypes of Picornaviruses from 11 Divergent Genera through Microfluidic Real-time RT-PCR

Board LB-84. A Reference-Free, Alignment-Free Approach for Epidemiological Outbreak Investigations and Clinical Microbiology of Fungal Pathogens

Board LB-85. Developing Capacity for Whole Genome Sequencing in PulseNet International Laboratories

Board LB-86. Contribution of HIV Molecular Data to Understanding an HIV Epidemiologic Investigation – West Virginia, 2017

Board LB-87. PA-Led Implementation of a Co-Located HIV/HCV/MAT Program in an FQHC in Rural Idaho: A Proactive Approach to Reduce Infectious Disease Outbreaks in the Context of the Opioid Crisis

Board LB-88. Deaths with Possible Infectious Etiologies among Persons with Reported Alcohol, Opioid, or Illicit Drug Use, 2016-2018

Board LB-89. Development of Shigellosis-Related Health Communication Materials: Results of a Qualitative Study among Gay, Bisexual, and Other Men Who Have Sex with Men (MSM)

Board LB-90. Assays for the Detection of Bacteria and Viruses Involved in Urinary Tract Infections and Profiling their Antibiotic Resistance

N. Concurrent Panel Sessions

1:45 PM - 3:15 PM

N1. Prevention and Control of Viral Hepatitis

International Ballroom D

Moderator

Paul Weidle: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Hepatitis A Outbreaks—United States, 2016-2018
Monique Foster: Centers for Disease Control and Prevention; Atlanta, Georgia

The Cherokee Nation HCV Elimination Program: Overcoming Barriers to Move Forward
Jorge Mera: Cherokee National Health Service; Tahlequah, Oklahoma

The HCV Epidemic in People Who Use Drugs in the United States: Emerging or Resurging?
Kimberly Page: University of New Mexico; Albuquerque, New Mexico

N2. Microbiome: Pathology, Ecology, Epidemiology

Grand Ballroom A/B

Moderators

Claressa Lucas
Cliff McDonald
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Exploiting the Microbiome to Reduce Intestinal Colonization with Antibiotic-Resistant Bacteria
Eric Pamer: Memorial Sloan Kettering Cancer Center; New York, New York

A Microbiome Perspective on Antibiotic Resistance and Pathogens in Water Systems
Amy Pruden: Virginia Polytechnic Institute and State University; Blacksburg, Virginia

Establishing Causality in Microbiota Research
Volker Mai: University of Florida; Gainesville, Florida

N3. Epidemic Prediction Initiative: Moving from Research to Decisions

International Ballroom E

Moderator

Matt Biggerstaff: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

Real-Time Epidemic Forecasting: Advancing the Science and Public Health Utility of Forecasting
Michael Johansson: Centers for Disease Control and Prevention; San Juan, Puerto Rico

Forecasting Infectious Disease Incidence
Steven Riley: Imperial College London; London, United Kingdom

Epidemic Prediction and Outbreak Decision-Making
Jean-Paul Chretien: National Center for Medical Intelligence, Defense Intelligence Agency; Ft. Detrick, Maryland

N4. Pathogen Discovery and Investigation of New Syndromes

International Ballroom A/B/C

Moderators

Michael Shaw
Sue Tong
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

The Ecology of MERS-CoV: From Host Reservoir to Disease
Vincent Munster: National Institutes of Health; Hamilton, Montana

Metagenomic Sequencing for Pathogen Surveillance and Discovery
Charles Chiu: University of California, San Francisco, School of Medicine; San Francisco, California

Development of Rapid Response Platforms for Highly Pathogenic Emerging Respiratory Viruses
Ralph Baric: University of North Carolina; Chapel Hill, North Carolina

Break

3:15 PM – 3:30 PM
Grand Ballroom and International Ballroom Levels

O. Oral Presentations

3:30 PM – 5:00 PM

O1. Detection and Diagnosis

Grand Ballroom A/B

Moderators

Rosemary Humes: US Department of Health and Human Services, Office of the Assistant Secretary for Preparedness and Response, Biomedical Advanced Research and Development Authority; Washington, DC
Maureen Diaz: Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. The Association between Precipitation, Temperature, and the Detection of Viruses in Six Community Groundwater Supplies in Minnesota
S. Gretsch: Minnesota Department of Health; St. Paul, Minnesota

2. A Comparison of Reference-Based and Reference-Free Binning Tools for *Salmonella enterica* Subtyping Directly from Stool
J. Shay: Association of Public Health Laboratories; Silver Spring, Maryland

3. Development of a Human Pathogen-Specific Sequencing Assay for the Detection of Unknown Infection
J. Chen: Alaska State Public Health Virology Laboratory; Fairbanks, Alaska

4. Antimicrobial Resistance Genotypes Are Consistent with AMR Phenotypes in NARMS Isolates
M. Feldgarden: National Institutes of Health; Bethesda, Maryland

5. Prevalence and Assessment of Risk Factors Associated with Antibiotic Resistance Genes (ARGs) among Children Under 5 in Informal Urban Maputo, Mozambique
A. Wood: Georgia Institute of Technology; Atlanta, Georgia

6. Rapid, Specific, and Cost-Effective Identification of Zika Virus from Fixed Tissues of Congenital and Pregnancy-Associated Infections using a Novel Pyrosequencing-Based Assay
J. Bhatnagar: Centers for Disease Control and Prevention; Atlanta, Georgia

O2. Seasonal Influenza and RSV

International Ballroom A/B/C

Moderators

Angela Campbell
Gayle Langley
Centers for Disease Control and Prevention; Atlanta, GA

Speakers

1. Assessing the Burden of Respiratory Syncytial Virus (RSV) within a Community-Based Prospective Birth Cohort
J. Kubale: University of Michigan; Ann Arbor, Michigan

2. Respiratory Syncytial Virus Deaths in Minnesota, 2006–2017
E. Bye: Minnesota Department of Health; St. Paul, Minnesota

3. The Economic Impact of Influenza Hospitalizations on Families in Lao PDR
V. Khanthamaly: National Immunization Program; Vientiane, Lao People's Democratic Republic

4. Effect of 9- to 16-day Holiday Breaks on the Time Courses of Seasonal Influenza Outbreaks in a School Population: ORCHARDS—Wisconsin, 2014–2018
J. Temte: University of Wisconsin School of Medicine and Public Health; Madison, Wisconsin

5. Correlation between Hospitalized Influenza and Invasive Methicillin-Resistant *Staphylococcus aureus* Infections in Minnesota, 2010–2017
C. Bernu: Minnesota Department of Health; St. Paul, Minnesota

6. Homotypic and Heterotypic Protection from Influenza Infection in Children
A. Gordon: University of Michigan; Ann Arbor, Michigan

O3. Evolving Challenges

International Ballroom D

Moderators

Eduardo Azziz-Baumgartner
Susan Gerber
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Increasing Incidence of Invasive Nontyphoidal *Salmonella* Disease in Queensland, Australia, 2007–2016
A. Parisi: Australian National University; Canberra, Australia

2. Medical Examiner Investigated Fungal Deaths, Minnesota, 2012-2017
S. Holzbauer: Centers for Disease Control and Prevention; St. Paul, Minnesota

3. A Cause for Concern: *Candida auris* Fungemia in Critically Ill Patients
R. Petrossian: Flushing Hospital Medical Center; New York, New York

4. Antibody Responses among MERS-CoV Infected Patients in Saudi Arabia
C. Midgley: Ministry of Health; Riyadh, Saudi Arabia

5. Enhanced Environmental Surveillance for Avian Influenza A(H7N9), A(H5), and A(H9) Viruses in Guangxi, China, 2017–2018
D. Wang: Chinese Center for Disease Control and Prevention; Beijing, China

6. Nationwide Prevalence of the Chagas Disease Parasite, *Trypanosoma cruzi*, in Government Working Dogs and Associated Cardiac Health Abnormalities
A. Meyers: Texas A&M University; College Station, Texas

O4. Late Breakers II

International Ballroom E

Moderators

Alexandra Levitt
Bob Pinner
Centers for Disease Control and Prevention; Atlanta, Georgia

Speakers

1. Nationwide Outbreak of Listeriosis Associated with Ready-to-Eat Processed Meat Products, South Africa.
J. Thomas: National Institute for Communicable Diseases; Johannesburg, South Africa

2. Post-Hurricane Leptospirosis Case Increase in Puerto Rico, October – December 2017.
I. Schafer: Centers for Disease Control and Prevention; Atlanta, Georgia

3. Active Surveillance for Rabies in Animals in Vietnam, 2016 – 2017.
L. Nguyen: Department of Animal Health of Viet Nam; Hanoi, Viet Nam

4. High Tetanus Burden among Men—Uganda, 2017.
R. Casey: Centers for Disease Control and Prevention; Atlanta, Georgia

5. Novel Use of Syndromic Surveillance Data to Identify when *Candida auris* Carriers Present to Emergency Departments—New York City, 2018.
D. Bloch: New York City Department of Health and Mental Hygiene; Queens, New York

6. A Mathematical Model of the Transmission of Middle East Respiratory Syndrome Coronavirus in Dromedary Camels (*Camelus dromadarius*).
A. Dighe: MRC Centre for Outbreak Analysis and Modelling, Imperial College London; London, United Kingdom

Conference Abstracts

Monday, August 27

Poster Abstracts

Poster / Exhibit Hall

One Health I

Board 1. Themes from One Health Zoonotic Disease Prioritization Workshops in 18 Countries, 2014–2017

C. Barton Behravesh, R. Ghai, V. Krishnasamy, G. Goryoka, K. Varela, N. Oussayef, S. Salyer
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Zoonotic diseases continue to have adverse global impacts on both human and animal health. A One Health approach that recognizes the need for multisectoral collaboration can mitigate this impact, and is critical to advance global health security. CDC developed a One Health Zoonotic Disease Prioritization (OHZDP) process that uses a One Health approach to enhance multisectoral selection of priority zoonoses. During a multi-day workshop, representatives from human, animal, and environmental health sectors develop criteria and questions to rank zoonoses; the semi-quantitative methods allow for outcomes in the absence of complete country-level data. The typical workshop goal is to use a multi-sectoral, One Health approach to prioritize emerging and endemic zoonotic diseases that should be jointly addressed by human, animal, and environmental health ministries within a country. **Methods:** OHZDP data from workshops conducted globally from 2014–2017 were compiled and analyzed to identify themes in workshop disease criteria, prioritized zoonoses lists, and future actionable items discussed during the workshop. **Results:** From 2014 to 2017, CDC and partners facilitated OHZDP workshops in 18 countries in Africa (n=13), Asia (n = 4), and North America (n =1). All countries selected criteria that captured the epidemic or pandemic potential and the disease severity of each zoonosis. Other common criteria included ability to prevent or control the zoonosis (n = 17), economic impacts associated with losses in production, trade, or travel (n = 16), and the bioterrorism potential of the zoonosis (n = 6). Frequently prioritized zoonotic diseases were rabies (n=17); zoonotic influenza viruses (n=16); anthrax (n=12); brucellosis (n=12); and Ebola or Marburg (n=10). Finally, the most common future action noted was the need to strengthen multi-sectoral, One Health coordination (n =14; 78%). **Conclusions:** The CDC OHZDP process provides a method for prioritizing zoonotic diseases of national concern while fostering collaboration and developing One Health-based recommendations. Assessing workshop themes not only strengthens One Health at the national level but also supports the development of One Health guidance, tools, and resources to strengthen One Health at the regional and global levels.

Board 2. Extending the Reach of Public Health: The Public Health Talk Expansion to Animal Care Providers

D. Crosby
Cobb & Douglas Public Health, Marietta, GA, USA

Background: The Public Health Talk (PH Talk) initiative was initiated in 2014 to "bridge the gap" between Cobb & Douglas Public Health (CDPH), a local public health district agency, and the Cobb & Douglas counties' health care community. A total of 31 PH Talks were conducted, including 2 at veterinarian offices. Due to rabies being a heightened concern, the initiative is being expanded to other animal care providers. Targeted animal care providers are projected to include, but not limited to, groomers, rescue organizations, animal daycares, and pet shops. Between 01/01/2012-12/31/16, 3,756 animal bite incidences were reported to Cobb & Douglas Public Health, with 28 specimens testing positive for rabies. This project is a continuation of a quality improvement project that was done in 2016 to address a gap in the audience to cover animal care providers. **Methods:** Using the general PH Talk format, a new survey was created to target animal care providers. This survey is used to assess the base knowledge of the attendees and the knowledge that is gained upon completion. The presentation given to animal care staff was modified to include detailed information concerning reporting notifiable zoonotic diseases and to provide updated data for animal bite incidences at the national and local level. The presentation was also updated to detail the process for reporting animal bite incidences to Public Health and/or Animal Control due to the risk of rabies exposure and follow up procedures by CDPH Epidemiology. **Results:** Local animal care providers will be educated by Public Health and knowledge of animal care providers will be increased (anticipated). **Conclusions:** The knowledge of attendees at PH Talks will be increased concerning public health practices with regards to reducing the incidence of rabies exposure in the community and advising post-exposure prophylaxis to those who are at risk in Cobb & Douglas counties in the state of Georgia.

Board 3. Prevalence of Zoonotic Enteropathogens in Domestic Animals and Associated Household Risk Factors in Kisumu, Kenya

A. Barnes[1], J. Mumma[2], F. Ade[3], O. Cumming[4]
[1]Duke University, Durham, NC, USA, [2]Great Lakes University Kisumu, Kisumu, Kenya, [3]KEMRI, Kisumu, Kenya, [4]London School of Hygiene and Tropical Medicine, London, United Kingdom

Background: The presence of domestic animals and animal waste at a household can expose residents to zoonotic enteropathogens through contact with an infected animal or their feces. Within peri-urban communities of Kisumu, Kenya, free-roaming domestic animals present a zoonotic risk for households that is exacerbated by a lack of improved water, sanitation, and hygiene (WASH). The purpose of this study was to detect zoonotic enteropathogens in animal waste from the household living space and to identify WASH risk factors that could contribute to disease exposure for household members. **Methods:** Multiplex PCR was used to detect the presence of zoonotic enteropathogens from composite animal waste samples collected from household compounds. The results were compared to household sur-

vey data on WASH factors. **Results:** Household surveys were conducted in Nyalenda A, Nyalenda B, and Kanyakwar communities (n=800). When present, animal waste was collected from inside the compound boundaries of each household and tested for zoonotic enteropathogens (n=320). Over forty percent (n=97) were positive for at least one of the following pathogens: enterotoxigenic *Escherichia coli* [ETEC] n= 67, enteropathogenic *E. coli* [EPEC] n= 81, enteroaggregative *E. coli* [EAEC] n=20, Shiga-toxigenic *E. coli* [STEC] n=18, enteroinvasive *E. coli* [EIEC] n=2*, Cryptosporidium spp.* n= 3, and *Giardia spp.* n=5. Of the households with contaminated animal waste in their compound, 32% reported animal ownership (n=31), 47% sometimes or frequently treat their drinking water before use (n=46), 63% reported washing their hands before cooking (n=61), and a single household reported washing their hands after animal contact. **Conclusions:** Zoonotic enteric pathogens are present in the living space of many peri-urban households due to indiscriminate animal waste. Household WASH risk factors put residents at risk for exposure to zoonotic disease through contact with infected animal waste. More research is needed on the contribution of proximal animal waste to diarrheal disease.

Board 4. Surveillance for Respiratory and Diarrheal Pathogens at the Human-Pig Interface in Sarawak, Malaysia

L. Borkenhagen[1], K. Mallinson[1], R. Tsao[1], S. Ha[2], W. Lim[2], T. Toh[2], B. Anderson[1], J. Fieldhouse[1], S. Philo[1], K. Chong[3], A. Ramirez[4], J. Lowe[5], K. Coleman[6], G. Gray[1]
[1]Duke University, Durham, NC, USA, [2]Sibu Hospital, Sibu, Malaysia, [3]Divisional Health Office, Sibu, Malaysia, [4]Iowa State University, Ames, IA, USA, [5]University of Illinois at Urbana-Champaign, Champaign, IL, USA, [6]Duke-NUS Medical School, Singapore, Singapore

Background: The large livestock operations and dense human population of Southeast Asia are considered a hot-spot for emerging viruses. The primary objective of this study was to determine if a panel of pathogens with known or suspected transmission between pigs and humans, including adenovirus (ADV), coronavirus (CoV), encephalomyocarditis virus (EMCV), enterovirus (EV), influenza A-D (IAV, IBV, ICV, and IDV), porcine circovirus 2 (PVC2), and porcine rotaviruses A and C (RVA and RVC), are aerosolized at the animal-interface, and if humans working in these environments are carrying these viruses in their nasal airways. **Methods:** This cross-sectional study took place in Sarawak, Malaysia among 11 pig farms, 2 abattoirs, and 3 animal markets in June and July of 2017. Pig feces, pig oral secretions, bioaerosols, and worker nasal wash samples were collected and analyzed via rPCR and rRT-PCR for respiratory and diarrheal viruses. **Results:** In all, 55 pig fecal, 49 pig oral or water, 45 bioaerosol, and 78 worker nasal wash samples were collected across 16 sites. PCV2 was detected in 21 pig fecal, 43 pig oral or water, 3 bioaerosol, and 4 worker nasal wash samples. In addition, one or more samples (all types) were positive for ADV, CoV, EV, IAV, IBV, IDV, and RVC. **Conclusions:** This study demonstrates that nucleic acids from a number of targeted viruses were present in pig oral secretions and pig fecal samples, and that several viruses were detected in bioaerosol samples or in the nasal passages of humans with occupational exposure to pigs. These results suggest pathways for future research in strengthening viral surveillance at the human-animal interface. Ultimately, this information will help to improve biosecurity as farms rapidly increase in size and assist in protecting the health of humans, animals, and the environment.

Board 5. Expression of Genes Associated with Enterotoxin YstA Production by *Yersinia enterocolitica* Strains Isolated from Humans and Pigs

A. Bancerz-Kisiel, M. Pieczywek, K. Lipczńska-Ilczuk, W. Szweda
University of Warmia and Mazury, Olsztyn, Poland

Background: *Yersinia enterocolitica* is one of the main causative agents of human diarrhea which poses a growing threat for public health. Various authors have postulated a correlation between strains isolated from clinically healthy pigs and yersiniosis in humans. Aim of this study was to verify the hypothesis that the *ymoA* gene decreases the expression of the *ystA* gene in *in vitro* cultures and eliminates the enterotoxic properties of selected *Y. enterocolitica* strains. **Methods:** The experiment involved two groups of *Y. enterocolitica* strains, producing and not producing enterotoxin YstA, which were isolated from humans and pigs. Selected genes were analyzed by quantitative real-time PCR (qPCR) with the Rotor-Gene6000™ real-time analyzer. The expression of *ystA* and *ymoA* was normalized to that of the *gapA* and *polA* reference genes. Amplification curves were generated from real-time qPCR data, and the cycle threshold (CT) was calculated based on a fluorescence threshold of 0.01. **Results:** The relative expression level of the *ystA* gene was significantly higher than the expression level of the *ymoA* gene in *Y. enterocolitica* strains isolated from humans with clinical yersiniosis and diarrhea. In *Y. enterocolitica* strains isolated from humans with asymptomatic yersiniosis, a significant decrease in *ystA* gene transcription was observed, and the relative expression level of the *ymoA* gene was significantly higher than the expression level of the *ystA* gene. Statistically significant differences were not observed in either group of strains isolated from pigs. **Conclusions:** Our results support the hypothesis that YmoA could inhibits the expression of the *ystA* gene, but further research involving a larger number of *Y. enterocolitica* strains is required to validate this observation. Studies were funded by KNOW (Leading National Research Centre) Scientific Consortium "Healthy Animal - Safe Food", decision of Ministry of Science and Higher Education No. 05-1/KNOW2/2015.

Board 6. Fecal Virome Diversity of Healthy and Diarrheic Pigs in the Philippines

C. Pangilinan[1], T. Collantes[2], R. Cena[1]
[1]University of the Philippines Manila- NIH Institute of Molecular Biology and Biotechnology, Manila City, Philippines, [2]University of the Philippines Los Banos- College of Veterinary Medicine, Los Banos, Philippines

Background: Pigs frequently act as reservoirs for zoonotic viruses and novel viruses which have zoonotic potential. In the Philippines, the community of enteric viruses in pigs is largely unknown. This study investigated the viral composition of the fecal flora of healthy and diarrheic pigs and correlated it with the potential of the virome to cause diarrhea. **Methods:** We performed high-throughput viral metagenomic sequencing on pools of RNA extracted from 25 healthy and 25 diarrheic pigs from a commercial farm in the Philippines. Contigs were assembled using de novo and reference-based assembly tools and the scaffold identities were determined by comparison with sequences from the NCBI Genbank database. The full-genome sequences were further validated by performing the Sanger method using virus-specific primers. **Results:** The RNA viruses identified in the samples belonged to the viral genera Rotavirus, Mamastrovirus, Sapelovirus, Enterovirus, and Kobuvirus. Pairwise identity comparison of the nucleotide and amino acid sequences of the samples and Genbank references

also indicated the presence of novel viral genotypes. Differentiation of the viral abundance based on sequencing depth showed that there was a higher prevalence rate for the viruses in the diarrheic pigs. A higher co-infection mean was also observed in the diseased pigs as compared to the healthy ones. **Conclusions:** The results provide the first description of the diversity of viral communities present in the fecal samples of healthy and diarrheic pigs in the Philippines. These provide knowledge on the viral population in pigs and can serve as baseline levels in case of outbreaks. As the data may also be relevant to human health, the potential of the viruses to be pathogenic and cause diarrhea must be further established.

Board 7. Minnesota One Health Antibiotic Stewardship Collaborative: Improving Public and Professional Awareness of Antibiotic Use and Resistance

A. Beaudoin[1], K. Boeser[2], A. Rashid[3], B. Thompson[4], S. Vetter[1], E. Leof[1], J. Walters[1], R. Lynfield[1]
[1]Minnesota Department of Health, Saint Paul, MN, USA, [2]Fairview Health Services, Minneapolis, MN, USA, [3]Saint Paul Infectious Disease Associates, Saint Paul, MN, USA, [4]Minnesota Board of Animal Health, Saint Paul, MN, USA

Background: Antibiotic resistance (AR) is a local, national, and global problem with considerable implications for human health. Antibiotic use, a chief driver of AR, is a major component of healthcare and animal health and contributes to contamination of the natural environment. "One Health" (OH) is the recognition that human, animal, and environmental health are interconnected. The United Nations General Assembly and US government have advocated for a OH approach to AR and antibiotic stewardship (improving how antibiotics are used, AS). **Methods:** In 2016, Minnesota leaders in public health, healthcare, veterinary medicine, agriculture, academia, and industry met at a One Health Antibiotic Stewardship Summit. This led to strategic planning and formation of the Minnesota OH AS Collaborative (MOHASC). Since MOHASC activities began in August 2016, progress has been made by hiring a One Health Antibiotic Stewardship Director at Minnesota Department of Health, establishing four OHASC work groups with designated chair persons, and using quarterly calls and annual meetings to set goals and review progress. Work groups are aligned with strategic plan goals: promote OH AS, improve AS in healthcare, improve AS in animal health, and understand the environmental "footprint" of antibiotic use. Interdisciplinary site visits and AS knowledge, attitudes, and practices surveys have been used to exchange knowledge and learn about AS needs, respectively. Social media, an OH AS website, and public events have been used to interface with the community. **Results:** Qualitative data collected in 2016 show similar AR and AS "wants" and "fears" among human, animal, and environmental professionals. Cross-professional engagement has improved AR and AS knowledge among MOHASC members. By using surveys and engagement at professional meetings, state agencies and professional groups have improved understanding of AS barriers and facilitators in healthcare and animal health. MOHASC cross-disciplinary research has been recognized by legislators for state financial support. **Conclusions:** Communication and understanding can improve transparency, trust, and cooperation among disciplines, assets which are essential to impact AU and AR. All or parts of the Minnesota approach might be replicable in other states and countries.

Board 8. Longitudinal Field Study in Evaluating the Spillover of Antibiotic-Resistant *Escherichia coli* from Poultry to Humans in Rural Ecuador

H. Hedman[1], J. Eisenberg[1], G. Trueba[2], R. Zurita Herrera[2], D. Vinueza[2], J. Villacís[2], S. Megha[3], E. Krawczyk[1], L. Zhang[3]
[1]University of Michigan, Ann Arbor, MI, USA, [2]Universidad San Francisco de Quito, Quito, Ecuador, [3]Michigan State University, East Lancing, MI, USA

Background: Small-scale farming operations in rural communities often prescribe high amounts of antibiotics for industrial meat production breeds of chickens (e.g. broilers). In contrast, free-ranging local varieties of backyard chickens receive almost no antibiotics. Recent evidence suggests that backyard chickens in proximity to broiler chickens have increased levels of phenotype and genotype antibiotic resistance. **Methods:** We conducted a seven-month longitudinal study aimed to examine whether backyard chickens and children serve as sentinels for detecting antibiotic resistance spread into the environment from broiler chickens in northwestern Ecuador. *Escherichia coli* isolates were identified from children (n = 1144), backyard chickens (n = 1323), and 1-day-old broiler chickens purchased from vendor sources (n = 253). Isolates were examined for their resistance phenotypes to 12 antibiotics and selected resistance genes. **Results:** Phenotype resistance profiles fluctuated over time for human and backyard chicken samples. In contrast, broiler chicken resistance profiles remained high for all antibiotics tested. We also detected that households closest to households raising broiler chickens yielded significantly greater phenotype resistance levels among avian and human samples (general additive model; $p < 0.005$). The same *bla*CTX-M gene was detected in both human and chickens. **Conclusions:** These results likely suggest that small-scale broiler farming operations may function as sources of environmental antimicrobial exposure for the surrounding human and animal populations. Our results indicate that industrial meat-producing animals may introduce antibiotic resistance into other animal breeds, likely through horizontal gene transfer spillover events into backyard breeds and humans.

Board 9. Outbreak of *E. coli* O157:H7 Infections in a Community: Utah and Arizona—June 2017

C. Basler[1], S. Luna[1], V. Krishnasamy[1], R. Hassan[1], L. Saw[2], L. Smith[3], J. Wagner[3], J. Weigand[4], M. Tewell[5], M. Kellis[5], R. Penev[5], L. McCullough[2], J. Eason[2], K. McCaffrey[2], D. Barlow[6], A. Scherzer[6], M. Sarino[7], M. Wise[1], L. Gieraltowski[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Utah Department of Health, Salt Lake City, UT, USA, [3]Utah Public Health Laboratory, Salt Lake City, UT, USA, [4]Southwest Utah Public Health Department, St. George, UT, USA, [5]Arizona Department of Health Services, Phoenix, AZ, USA, [6]Mohave County Department of Public Health, Kingman, AZ, USA, [7]La Paz County Health Department, Parker, AZ, USA

Background: On July 7, 2017, officials from the Utah Department of Health notified CDC of a cluster of *Escherichia coli* O157:H7 (O157) infections in a community near the Utah and Arizona border. Infection with O157 can cause severe diarrhea leading to hemolytic uremic syndrome (HUS) and death. We investigated to identify the source and prevent additional illnesses. **Methods:** Cases were defined as follows: onset of diarrhea in a resident of the border community after June 1, with either (i) infection with an O157 isolate indistinguishable from the outbreak strain, or (ii) post-diarrheal HUS. We conducted a fo-

cus group to generate hypotheses, an age-matched case-control study of cases to identify illness-associated exposures, and environmental sampling. We also performed contact tracing for all case-patients to identify secondary cases resulting from person-to-person transmission. **Results:** Twelve case-patients met the case definition; eight were primary. Nine patients were hospitalized, four diagnosed with HUS, and two died. Ten (83%) of 12 patients were under five years old. We enrolled six primary case-patients and 16 controls in the case-control study. Sixty-seven percent of cases versus 19% of controls reported playing in an area that had manure (matched odds ratio, 7.7; 95% confidence interval, 0.8-71.3). Horse and cow manure samples collected from a case-patient's household yielded the outbreak strain. We did not identify a common food or water source for the outbreak. Contact tracing identified epidemiologic links between primary and secondary cases that supported person-to-person transmission. **Conclusions:** The source of the outbreak was not confirmed, but evidence supported O157 infection spread via animal contact and person-to-person transmission. Consequently, investigators disseminated guidelines on animal and manure contact to promote infection prevention. This investigation highlights difficulties in solving outbreaks of enteric pathogens when both foodborne and zoonotic transmission modes are possible.

Board 10. Glanders Disease in Equines: Re-Emerging or Endemic? A Report from India

S. Nath, R. Perumal
Donkey Sanctuary India, New Delhi, India

Background: Glanders is a notifiable highly contagious zoonotic disease caused by *Burkholderia mallei*. The disease primarily affects equids (horses, donkeys, mules and ponies). In humans *B. mallei* causes a febrile illness with characteristic clinical signs (localized, pulmonary, septicaemia, and chronic). Incidence of human infections has been related to close contact with infected equids. The aim of the study is to share incidence of glanders disease outbreak in equines working in a pilgrimage site in mountains of J&K, India. Glanders is a contagious bacterial disease, incidence of this infections can be life threatening. **Methods:** The reports are collected by working in mountainous field conditions with local agencies. **Results:** The 1st positive case of glanders confirmed in a mule in April 2015 based on clinical signs, symptoms and microbiological and serological investigations. The last glanders outbreak reported in India in 2006-2007. In this mountainous location at any time of the year there are 2500-3000 equines working together carrying loads or pilgrimage uphill of 12kms track. Total equine population in this area would be above 7000-7500. A total of 7051 samples have been collected from equines so far. A total of 53 samples were found positive by complement fixation test. Among infected were mostly mules, then horses, and ponies respectively. All 53 positive equines had nasal form of glanders of which 32 animals were culled, the rest were isolated until culling. Our paper explains about migration of equines from neighboring states and transmission of the disease in equines. **Conclusions:** The positive results indicate that Glanders disease is remerging in India. The recent incidence of the disease is an evidence of prevalence of glanders in mountainous equines of J & K, India. Since 2006, this is second time glanders disease was diagnosed in equines in India. Though cases in humans are rare, 53 positive cases of glanders disease can be a reason for concern to human lives of the area. The big question remains is the disease limited to equines or there has been transmission to humans.

Board 11. Field-Portable, Rapid and Specific Test for Probable Identification of *Burkholderia pseudomallei* and *Burkholderia mallei*

K. Venkateswaran[1], N. Parameswaran[1], J. Sarwar[1], A. Plummer[2], A. Santos[2], S. Bowen[3], M. Granville[3], S. Selvan[1], P. Babu[1], P. Mullasseril[4], N. Thirunavukkarasu[4], S. Sharma[4], N. Venkateswaran[2], S. Morse[5], D. Hodge[3], S. Pillai[6]
[1]Omni Array Biotechnology, Rockville, MD, USA, [2]Tetracore, Inc., Rockville, MD, USA, [3]Department of Homeland Security, Washington, DC, USA, [4]Center for Food Safety and Applied Nutrition, College Park, MD, USA, [5]IHRC, Inc., Atlanta, GA, USA, [6]Food and Drug Administration, Silver Spring, MD, USA

Background: *Burkholderia pseudomallei* and *Burkholderia mallei* are biothreat bacterial agents affecting humans and animals. *B. mallei* produces glanders predominantly in horses with the potential to transmit to humans. *B. pseudomallei* is the causative bacterium for the human disease melioidosis. Early detection of *Burkholderia* infection is quintessential for initiating proper treatment and undertaking measures to reduce the spread of the disease. We carried out a multi-phase laboratory evaluation to assess the performance of a simple, rapid lateral flow immunoassay with a smart phone reader as additional enhancement. **Methods:** *Active Glanders and Melioidosis Detect*™ Rapid Test (AGMD) is an immunochromatographic test (ICT) produced by *InBios* International Inc. for detection of presence of the *Burkholderia* bacterial antigens in the sample. In our study, we also used a field portable smart-phone reader (Omni Array Reader, OAR) for digitizing the ICT results. This study was conducted at two sites. Sensitivity of the test was evaluated with an inclusivity panel consisting of 35 *Burkholderia* strains. Inclusivity panel testing was done in a BSL3 laboratory following necessary biosafety procedures. Specificity of the test was assessed using 64 stains of clinical background panel. Multiple replicates of each samples were tested and a total of 520 tests were performed in this study. **Results:** Performance of the AGMD test was measured by testing the bacterial colonies resuspended in the assay buffer. Color development in the AGMD test cassette was noted visually to determine the positivity of the sample. In addition to qualitative visual measurement, OAR was also used to digitize the test result and to get an objective reading from the cassette. AGMD correctly detected 92.31% of *B. mallei* and 95.55% of *B. pseudomallei* samples both visually and using the OAR. AGMD did not show cross-reactivity to any of the sixty-four clinical background strains. AGMD test seems to be a sensitive, specific and reliable test for presumptive identification of *Burkholderia*. **Conclusions:** Our performance evaluation showed AGMD can be used as a qualitative, field portable test for presumptive identification of *B. mallei* and *B. pseudomallei* in a clinical setting.

Board 12. Establishment and Utility of a Brucellosis Surveillance System—Bamyan Province, Afghanistan, 2011-2015

H. Bakhshi
Ministry of Public Health, Kabul, Afghanistan

Background: Brucellosis is a globally widespread zoonosis. Humans become infected through contact with tissues or secretions/blood of infected animals or eating infected products. A 16-Province study in Afghanistan of human rates and a sero-survey of animals identified Bamyan Province as having a high prevalence of brucellosis among animals (7%). Accordingly, a sentinel site surveillance system for human cases was constructed. We report results of this system, 2011-2015.

Methods: A case was defined as anyone who suffered from ≥ fever, general body pain, anorexia, back pain, arthralgia, sweating, tremor or chills. The Rose Bengal test was used to confirm cases. **Results:** Outbreaks were reported from May 2011 to December 2015, particularly from Panjab, Yakowlang and Waras districts. The number of cases increased gradually from 597 in 2011 to 1750 in 2014 before declining to 830 in 2015 (total, 4,487 cases of whom 2,015, 44.9%, were male and 2,472, 55.1%, were female). The principal source of infection was attending abortion in animals and, in Afghanistan, women have primary responsibility for birthing among animals. The mean age of cases was 31 years. A total of 4,241 cases (94.5%) were tested serologically of which 1,425 (33.6%) were positive. Special investigations of suspected cases to determine causes of unusual illness found 27 of 28 samples (96.4%) were serologically positive for Q-fever and 12 (42.9%) were positive for toxoplasmosis. Based on surveillance data, important actions resulted in decreasing numbers of cases related to abortion, introducing behavioral change regarding animal husbandry, improved precaution measures when dealing with animal tissues/secretions, introduction of vaccination of all small ruminants and establishment of a Provincial Zoonotic Committee. **Conclusions:** The establishment of a surveillance system and using data from it led to recognition of highly endemic areas and to important prevention measures, and to recognition that Q-fever and toxoplasmosis may occur commonly.

Board 13. Septicemic Pasteurellosis: A One-Health Framework Case Study

N. Hull[1], K. Sondgeroth[2], K. LeCount[3], D. O'Toole[2], W. Manley[1], T. Stuber[4], N. Blouin[5], S. Buss[1]
[1]Wyoming Public Health Laboratory, Cheyenne, WY, USA, [2]Wyoming State Veterinary Laboratory, Laramie, WY, USA, [3]United States Department of Agriculture - National Veterinary Services Laboratories, Ames, IA, USA, [4]Diagnostic Bacteriology and Pathology Laboratory, National Veterinary Services Laboratories (NVSL), USDA, Ames, IA, USA, [5]University of Wyoming, Laramie, WY, USA

Background: *Pasteurella multocida* a Gram-negative coccobacillus, is an etiologic agent of pasteurellosis. It is well known as a zoonotic agent that can cause lymphadenopathy, bacteremia, and in rare cases can cause endocarditis and osteomyelitis in human populations. There are five serogroups identified (A-F) based on polysaccharide capsule composition. Two cases (five-month old domesticated American bison [*Bison bison*]) presented at the Wyoming State Veterinary Laboratory for investigation. **Methods:** A gross necropsy was performed and samples were submitted for histopathology, parasitology, toxicology, virology, and bacteriology testing. Whole genome sequencing was completed on an Illumina MiSeq at the Wyoming Public Health Laboratory. Bioinformatic assembly was completed at the University of Wyoming, INBRE Bioinformatics Core using the Mount Moran high performance computer. Assembled sequence was comparatively assessed with GenBank for most similar identities. **Results:** Gross findings consisted of fibrinous pleuritic with pericarditis. Histopathology noted intralesional bacteria and appreciated bacterial septicemia. Diagnostic bacteriology yielded *Pasteurella multocida* subspecies *multocida* via aerobic culture with confirmation on the Biolog microbial identification system and MALDI-TOF (log score value = 2.45; high confidence identification). Gel diffusion precipitin test was conducted at the USDA-National Veterinary Services Laboratories and grouped the isolate as a serogroup A:3, implicated in fowl cholera outbreaks. The isolate was compared in GenBank and was most similar to domestic turkeys (*Meleagris gallopavo*) from California. **Conclusions:** Utilizing a One-Health framework with collaborations with the Wyoming State Veterinary Laboratory, Wyoming Public Health Laboratory, and the University of Wyoming INBRE Bioinformatics Core, early detection of novel spillover events can be realized and preparedness measures can be undertaken to conduct bio-surveillance in susceptible populations. In this case, novel *Pasteurella multocida* serogroup A:3 was identified and could be used to compare any human infections that presented to the state public health laboratory.

Board 14. Two Cases of Cutaneous Anthrax in Italy, 2017

E. Nicastri[1], N. Petrosillo[1], C. Agrati[1], A. Battisti[2], A. Donatiello[3], A. Caprioli[2], R. Adone[4], E. Cimini[1], M. Sigismondi[5], S. Carrara[1], S. D'Arezzo[1], A. Franco[2], M. Iannetta[1], C. Aiello[5], A. Mazzarelli[1], P. Mencarini[1], C. Nisii[1], M. Paglia[1], P. Scognamiglio[1], L. Serrecchia[3], C. Venditti[1], D. Di Lallo[6], A. Vulcano[1], R. Marcianò[6], A. Fasanella[3], G. Ippolito[1], F. Vairo[1], A. Di Caro[1]
[1]National Institute for Infectious Diseases "Lazzaro Spallanzani" IRCCS, Rome, Italy, [2]Istituto Zooprofilattico Sperimentale del Lazio e della Toscana "M. Aleandri", Rome, Italy, [3]Istituto Zooprofilattico Sperimentale di Puglia e Basilicata, Foggia, Italy, [4]Istituto Superiore di Sanità, Rome, Italy, [5]Local Health Authority Roma 6, Albano Laziale, Italy, [6]Direzione Regionale Salute e Politiche Sociali, Regione Lazio, Rome, Italy

Background: On August 25, 2017, in the rural municipality of Rocca di Papa, a city 30 km apart from Rome, five bovines were found dead and considered clinically as suspect cases of anthrax. They were positive for *Bacillus anthracis* vegetative forms and confirmed by culture and PCR (chromosomal target, pXO1 and pXO2 plasmidic targets). Here we describe the clinical and laboratory features of two cases of cutaneous anthrax exposed to animals during the outbreak. **Methods:** Review of medical records. T cell specific immunity was evaluated by flow cytometry and Elispot assay after simulation with *B. anthracis* secretome. Results were expressed as Spot forming cells (SCF)/million of PBMC. Ig production has been evaluated by Complement Fixation assay. Identification and typing has been performed by molecular methods. **Results:** On August 31, a male veterinarian was admitted to emergency room (ER) of the Spallanzani Institute in Rome, for the recent onset of skin lesions. On August 22, in the Rocca di Papa municipality, he had inspected a cow dead of digestive hemorrhage. At admission, he was in good clinical conditions, with no fever. On the left hand a black depressed eschar (1.5 cm) on the index finger with a satellite lesion was present. Eschar fragment was positive at PCR for *B. anthracis* DNA. Specific T cells were observed (136 SCF/million), increased overtime (346 SCF/million) on month 1 reaching a stable level on month 3 (333 SCF/million). Flow cytometry analysis identified CD4 T cells as specific IFN-γ producing cells. On the same day a male, 42-year-old worker in a farm involved in the bovine outbreak was referred to the Spallanzani Institute for the clinical suspicion of necrotizing fasciitis with septic syndrome with extensive erythema and edema of the upper limbs. Only few days later, he revealed exposure to the animal products of the same dead bovine inspected by the veterinary. Eschar fragment was positive at PCR for *B. anthracis* DNA Both patients were discharged in good clinical conditions. **Conclusions:** Molecular biology test was proven successful for diagnosis in both cases even after initiation of antibiotic treatment and molecular typing confirmed the identity of strains that affected both animals and humans. One Health strategy to integrate

human and animal zoonosis surveillance is needed to detect rare infectious diseases such as anthrax in Italy.

Board 15. Outbreak of Cutaneous Anthrax Associated with Handling Livestock Meat after Natural Death: Arua District, Uganda, 2015-2017

F. Aceng, P. Alitubeera, A. Ario, D. Kadobera, B. Zhu
Uganda Public Health Fellowship Program, Kampala, Uganda

Background: During May–June 2017, Arua District, Uganda reported three suspected cutaneous anthrax patients; one died. All had recently handled meat from livestock that spontaneously died. A skin lesion from the deceased person and a blood sample from a bull that spontaneously died tested positive for *Bacillus anthracis.* We investigated the outbreak to confirm the etiology, determine the scope, establish risk factors, and recommend control measures. **Methods:** We defined a suspected cutaneous anthrax case as acute onset of a papulo-vesicular skin lesion subsequently forming an eschar in an Arua District resident during January 2015–August 2017. A confirmed case was a suspected case that tested positive for *B. anthracis* by PCR. We reviewed medical records and conducted active community case-finding. We conducted a case–control study to compared exposures between case-patients and frequency-matched asymptomatic village controls. **Results:** We identified 68 cases (67 suspected; one confirmed); two (2.9%) died. All cases occurred following spontaneous livestock deaths. Men (attack rate[AR]=17/100,000) were 22 times more affected than women (AR=0.78/100,000). Persons aged 30-39y (AR=63/100,000) were the most affected. All cases were from two neighboring sub–counties: Rigbo (n=63, AR=201/100,000) and Rhino Camp (n=5, AR=21/100,000). Cases occurred throughout the three-year period, peaking during dry seasons. Of 68 case-persons and 136 controls, 65 (96%) case-persons and 76 (56%) controls butchered livestock that spontaneously died (OR_{M-H}=22, 95%CI=5.5–89); 61 (90%) case-persons and 74 (54%) controls carried the meat (OR_{M-H}=6.9, 95%CI=3.0–16); 57 (84%) case-persons and 72 (53%) controls skinned the livestock (OR_{M-H}=5.0, 95%CI=2.3–11). **Conclusions:** An anthrax outbreak probably occurred among livestock in Arua District since 2015; humans contracted cutaneous anthrax by contact with livestock. At our recommendation, the district is improving surveillance and response in animals and humans. We recommended eating meat from slaughtered healthy livestock only, safe disposal of animal carcasses, and livestock vaccination.

Board 16. The Determinants of Diagnosis Establishment of an Anthrax Outbreak in Yogyakarta, Indonesia

A. Aman[1], Y. Mawarti[2], R. Asdie[3], C. Indriani[4], R. Ahmad[4], D. Lokida[5], M. Karyana[5], T. Wibawa[1]
[1]Department of Microbiology, Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada, Yogyakarta, Indonesia, [2]INA-RESPOND site 580 Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada, Yogyakarta, Indonesia, [3]Department of Internal Medicine, Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada, Yogyakarta, Indonesia, [4]Department of Biostatistics, Epidemiology and Population Health, Faculty of Medicine, Public Health and Nursing, Universitas Gadjah Mada, Yogyakarta, Indonesia, [5]INA-RESPOND, NIHRD of The Ministry of Health of Indonesia, Jakarta, Indonesia

Background: Anthrax is an infectious disease with distinctive clinical appearance, however its diagnosis establishment was challenging in the setting of remote mountainous region of Yogyakarta. Although the nearby primary health-care facilities provided symptom-based treatment, the diagnosis were undetermined. It was until 2 local farmers died, the disease diagnosis establishment was never questioned. **Methods:** This is a case study to elucidate the determinants of diagnosis establishment of the anthrax outbreak that affected farmers of remote mountainous region in Yogyakarta during 2016- 2017. Data of the subjects' disease history and physical examination, as well as social-economy status were collected. Laboratory (culture, PCR and serology) tests were conducted by Indonesia research partnership on infectious disease (INA-RESPOND) for a local government request. Deep interviews were conducted to analyze the determinants of diagnosis establishment. **Results:** After 10 months of the first suspected anthrax case, their etiological diagnosis was established in reference laboratory of INA-RESPOND. Of 30 subjects with suspected anthrax, 9 subjects serology tests were positive for anthrax. *Bacillus anthracis* was isolated form a subject with cutaneous anthrax. Challenging geographical setting, the low social-economy status, and low laboratory capacity of primary health care facility were associated with the outbreak emerging, and the failure of establishing etiology diagnosis promptly. **Conclusions:** Etiology identification that required reference laboratory, challenging geographical setting, and low social-economy status were the determinants of the delay of diagnosis establishment of the anthrax outbreak in Yogyakarta.

Board 17. Blastomycosis in Minnesota, 1999-2016: Descriptive Epidemiology and Evidence of Delayed Diagnosis

M. Ireland, C. Klumb, T. Whitten, J. Scheftel
Minnesota Deparment of Health, St. Paul, MN, USA

Background: Blastomycosis, a systemic fungal disease caused by *Blastomyces dermatiditis* or *B. gilchristii*, is endemic in Minnesota. Infection usually occurs via inhalation of fungal spores and results in pneumonia which can progress to disseminated illness. We summarized 17 years of blastomycosis cases reported to the Minnesota Department of Health (MDH). **Methods:** MDH performs statewide surveillance for blastomycosis. A confirmed case was defined as a patient with either: 1) a positive *Blastomyces* culture; 2) *Blastomyces* visualized in tissue or bodily fluid; or 3) a positive *Blastomyces* antigen test with compatible symptoms. Medical records were reviewed and confirmed cases interviewed to assess clinical course, outcomes, and potential exposures in the 3 months prior to illness. **Results:** During 1999-2016, 569 confirmed blastomycosis cases were reported to MDH, (median, 33 cases/year). Median age was 45 years; 70% were male. Most cases (72%) had only pulmonary disease; 21% had disseminated disease. Case fatality rate was 8.7%. Fatal cases were 5.3 times more likely to have co-morbidities than non-fatal cases (70% vs 31%; OR 5.3; $p<0.001$). The majority (69%) of cases were hospitalized; 60% had no blastomycosis diagnostics until after hospital admission. The median number of days from illness onset to first diagnostic test was lower for fatal cases compared to non-fatal cases (35 days vs. 60 days; $p=0.001$). Prior to diagnosis, 65% of cases were diagnosed with bacterial pneumonia. Of the cases who recalled antibiotic history, 82% were prescribed antibiotics prior to diagnosis, 71% were prescribed ≥2, and 37% were prescribed ≥3 antibiotics. Forty-three percent of cases were diagnosed by culture alone, of which 50% were diagnosed using invasive sampling such as bronchoalveolar lavage. **Conclusions:** Blastomycosis cases are often misdiagnosed as bacterial pneumonia, resulting in delayed antifungal therapy and unnecessary antibiotic therapy. Even in an endemic state, *Blastomyces* appears to

be low on providers' differential list considering the large number of cases diagnosed following hospitalization. Providers in endemic states should consider blastomycosis for any patient with pneumonia who does not respond to initial antibiotic therapy or who has co-morbidities, and pursue blastomycosis diagnostics earlier.

Board 18. Genomic Characterization of Viruses Identified in Upper Respiratory Samples in Dromedary Camels from United Arab Emirates (UAE)

Y. Li[1], A. Khalafalla[2], C. Paden[1], M. Yusof[2], Y. Eltahir[2], Z. Al Hammadi[2], F. Hosani[3], A. Hall[1], S. Gerber[1], S. Muhairi[2], S. Tong[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Abu Dhabi Food Control Authority, Abu Dhabi, United Arab Emirates, [3]Health Authority Abu Dhabi, Abu Dhabi, United Arab Emirates

Background: Because of the role played by camels in the emergence and transmission of MERS-CoV, it has become increasingly clear that camels can potentially serve as a source for zoonotic transmission of viruses to humans. Thus, it is important to understand the viruses that camels harbor and their zoonotic potential. Our recent metagenomic study of nasopharyngeal swab samples from dromedary camels in Abu Dhabi, UAE identified partial genomic sequences of five potentially novel virus species or strains using next generation sequencing (NGS). In this study we performed full genome sequencing to further characterize these viruses. **Methods:** To fill the gaps in the sequences generated by NGS for generating their full genome sequences, PCR primers were designed based on the sequences obtained from NGS or designed from the conserved regions among closely related, previously known viruses. The amplicons obtained from RT-PCR or PCR were sequenced by Sanger sequencing. Genome annotation and phylogenetic analysis were done to further characterize the virus genomes. **Results:** We obtained full or close-to-full genome sequences of five recently discovered camel viruses: camel polyomavirus (PyV) Abu Dhabi, camel Crimean-Congo hemorrhagic fever virus (CCHFV) Abu Dhabi, camel parainfluenza virus 3 (PIV3) Abu Dhabi, camel parainfluenza virus 4 (PIV4) Abu Dhabi and camel bocavirus 3 (BoV3) Abu Dhabi. The nucleotide identities of camel PyV, camel CCHFV, camel PIV3, camel PIV4 and camel BoV3 to the closest relatives are about 63% (to sheep polyomavirus), 87% (to CCHFV strain SPU103/87), 85% (to bovine PIV3 isolate TVMDL20, 80% (to human PIV4b strain 04-13) and 85% (to canine BoV3 isolate UCD), respectively. Annotation and characterization of the genomes predict similar ORFs and genomic features shared by the other viruses in the same taxonomical group. **Conclusions:** These genomic sequences provide data for a more accurate taxonomical classification of the novel camel viruses. We propose that the camel PyV be classified as a novel virus species, and the other four camel viruses as novel strains. Because we observe viruses in camels which are related to those that are known to cause disease in humans, we expect that camels may pose a risk as an intermediate species for transmitting viruses to humans.

Board 19. Drivers for MERS-CoV Emergence in Qatar

E. Farag[1], R. Sikkema[2], T. Vinks[2], M. Islam[3], M. Nour[1], H. Al-Romaihi1[1], M. Atta[3], M. Al-Hajri[1], M. Al-Thani[1], S. Al-Marri[1], C. Reusken[2], M. Koopmans[2]
[1]Ministry of Public Health, Doha, Qatar, [2]Erasmus Medical Center, Roterdam, Netherlands, [3]Ministry of Environment, Doha, Qatar

Background: The recent discovery of MERS CoV as a zoonotic disease endemic in dromedary camels raised questions about the possible origin of this infection. In addition, it remains unclear why and how MERS-CoV transmission occurs exactly and many questions remain concerning the ecology of this virus in relation to human exposure. Therefore, we set out to review the history and statistics of camel farming in Qatar, in order to generate hypotheses about the drivers for MERS CoV emergence and human infection. **Methods:** Based on initial interviews and brainstorming within the joint Qatar-NL MERS CoV outbreak investigation team, a list of possible determinants and contributing factors of MERS CoV emergence was drafted. Available statistics and literature was reviewed. The available data was used to generate hypotheses about the factors leading to emergence of MERS CoV as a human health threat. **Results:** Over the past 40 years, the practices of animal ownership, herding and farming have changed considerably. With the discovery of oil in 1940, major changes occurred in lifestyle and wealth. The increased wealth led to huge increase in ownership of camels, mainly for racing activities. The total camel population increased from 4300 in 1992 to over 84000 in 2015. As a precious animal, camels are being kissed, hugged, and greeted. Consistent with the disease seasonality, contact with animals intensifies during winter time where camel-related activities flourish through race and beauty competitions, trade, and breeding. These activities imply extensive camel movement and mixing along with their owners and workers from all over the Gulf region. Moreover, camel products are used for a variety of domestic purposes. Camel workers live inside camel barns while owners pay regular visits to their barns. Nevertheless, they all strongly deny that MERS-CoV can be transmitted from camels to humans. **Conclusions:** The rapid increase in GDP in the past two decades has been paralleled with rapid growth of the camel trade and racing industry. Current practices of people around camels involve frequent contact with camels, which might provide an opportunity for the infection transmission. More in-depth studies were needed to understand the role of social practices in the virus transmission.

Board 20. Avian Influenza A-H9 Virus Causing Mortality in Common Geese and Ducks in Rawalpindi, Pakistan

S. Dil[1], Z. Hayat[2]
[1]FELTP/Livestock Department, Punjab, Rawalpindi, Pakistan, [2]Federal Medical & Dental College, Islamabad, Pakistan

Background: Respiratory infections in avian species are mainly due to Influenza A viruses, these viruses have potential to infect human and many other mammalian species. Among Influenza A viruses, subtypes *H5* and *H7* are of particular importance for poultry because of their highly pathogenic nature. Avian influenza virus (*AIV) H9* usually causing low bird mortality can become virulent inducing heavy losses. On 22nd January, 2018 high mortality was reported in common geese and ducks in New Lalazar colony, Rawalpindi. This study was carried out to investigate cause of mortality in common geese and ducks. **Methods:** A cross-sectional study was conducted. Bird keeper was interviewed and epidemiological information was recorded on structured

questionnaire. Samples including sera (from sick birds), oral/cloacal swabs (from sick and dead birds) and tissue (from dead birds) were collected for laboratory testing. **Results:** A total of 152 birds were affected. Overall attack rate was 94.4%. Attack rate was highest in flamingo, pelican, Muscovy duck, macaw, black swan (100%) followed by common duck 95% and common geese (93%).Overall mortality rate was 18.2%. Flu-like symptoms, torticollis, and lameness were observed in affected birds. Postmortem findings showed involvement of lungs, trachea, and intestines. Laboratory testing indicated presence of *AIV-H9* and *New castle disease virus* in samples submitted for analysis. No symptoms of respiratory infection were noted in family members and workers of birds keeper. **Conclusions:** Mortality in birds was due to respiratory illness caused by *AIV H9* and *New castle disease virus*. Morbidity was high among flamingo, pelican, Muscovy duck, macaw, black swan as compared to common duck and common geese.

Board 21. Pattern of Highly Pathogenic Avian Influenza Virus Circulation among Domestic Poultry in Bangladesh: 2007-2017

S. Chowdhury[1], S. Khan[2], M. Rahman[1], M. Hossain[1], S. Ghosh[1], P. Ghosh[1], N. Gerloff[3], N. Zanders[3], E. Hodges[3], P. Yang[3], Y. Jang[3], J. Jones[3], S. Thor[3], H. Di[3], E. Gurley[4], S. Luby[5], K. Sturm-Ramirez[3], T. Davis[3], E. Kennedy[3]
[1]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Department of Population Medicine, University of Guelph, Canada, Toronto, ON, Canada, [3]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [4]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, USA, Baltimore, MD, USA, [5]Center for Innovation in Global Health, Stanford University, USA, Stanford, CA, USA

Background: Highly pathogenic avian influenza (HPAI) viruses are deadly zoonotic pathogens that can uncommonly be transmitted from poultry to humans. Since 2003, 860 human cases have been reported globally with 53% case fatality. In Bangladesh, 558 H5N1 outbreaks in poultry and 8 human cases have been reported from 2007 to present. This report describes the pattern of HPAI virus circulation among domestic poultry from August 2007 to December 2017. **Methods:** We visited selected live bird markets (LBMs) across the country on a monthly basis to collect cloacal swabs from healthy or sick poultry. We also collected pooled environmental specimens from poultry droppings, cages, feed, water, slaughtering sites, market floors and drains of each LBM. We tested samples to detect AI viruses using rRT-PCR. A subset of AI positive samples were further tested for full genome sequencing. We calculated prevalence and trends over the past decade. To identify the association of AI with poultry species and sampling season, we calculated the odds ratio using logistic regression. **Results:** We collected 16,757 poultry and 2,040 LBM environment samples. AI/H5 virus was detected in 814 (5%) poultry and 212 (10%) environmental samples. The prevalence of AI/H5 virus was <3% during 2007-2009, 6-9% during 2011-2012 and <3% during 2013-2017. We detected 6 clades of H5N1 viruses; clade 2.2.2, 2.2.2.1, 2.3.2, 2.3.4.2, 2.3.2.1 and 2.3.2.1a. Among the detected clades, clade 2.3.2.1a was predominant, circulating since 2011. Waterfowl were more likely to be positive for H5 subtype viruses than chickens (OR 2.9, 95% CI: 1.8-4.6). Circulation of AI/H5 was year-round. However, samples collected during colder months (Nov-Feb) were more likely to be positive than warmer months (OR 1.2, 95% CI: 1.04-1.6). In 2017, we detected another HPAI virus (clade 2.3.4.4 H5N6) for the first time in Bangladesh. **Conclusions:** HPAI viruses continue to circulate in poultry. We detected more AI/H5 during 2011-2012. This peak circulation could be due to the introduction of new clade 2.3.2.1a in 2011. This surveillance is crucial for both animal health and public health authorities to respond to epidemics by providing interventions at LBMs to mitigate AI transmission from poultry to human. Genetic data obtained from this surveillance can facilitate the testing and selection of pre-pandemic vaccine viruses for humans.

Board 22. Exploring the Acceptability and Feasibility of Portable Workstation for Handwashing with Soapy Water in a Bangladeshi Live Bird Market

M. Hassan[1], N. Rimi[1], M. Fahad[1], R. Sultana[1], S. Mortaza[1], A. Mahmud[1], N. Amin[1], M. Ziaur Rahman[1], K. Sturm-Ramirez[2]
[1]icddr,b, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA

Background: In Bangladesh, influenza A/H5N1 is endemic in poultry. Live bird markets (LBMs) are implicated as a source of A/H5N1 transmission and often lack minimum infrastructure, such as hand washing facility to limit the spread of the virus. We designed portable workstations for poultry workers and explored its acceptability and feasibility for hand washing with soapy water to remove influenza viruses from worker's hands after selling, slaughtering, and processing poultry. **Methods:** During June-November 2015, we provided workstations with a handwashing facility and refillable bottles with soapy water (20 gm detergent per liter water) to 13 shops in one LBM. We recommended that workers wash hands with soapy water after handling birds. We collected pre- and post-wash hand swabs. The swabs were tested for influenza A viral RNA by rRT-PCR and subtyped (H1N1pdm09, H3, H5, H7, H9) if positive. Only post-wash swabs whose paired pre-wash swab had detectable influenza viral RNA were tested and the proportion of post wash-swabs with undetectable viral RNA was calculated. We also conducted eight in-depth interviews with workers for feedback on the use of soapy water. **Results:** We collected pre-wash hand swabs from 100 of 135 market workers; 27 tested positive for influenza A virus (19 H9, 3 H5+H9, 5 A/unsubtypable). Influenza A viruses were undetectable in 18 (67%, 95% CI 46-83%) of the paired swabs collected after hand washing. Before the intervention, 5 shops had either soap or detergent (average cost US$ 0.02/shop/day) but workers from 2 of these shops did not report using either for handwashing. Although workers reported the handwashing acceptable, they did not continue using it after the intervention. Major barriers reported were inability to wash hands during busy hours and additional expenses to purchase detergent. When asked about benefits, workers mentioned that slaughtering equipment and hands could be washed more easily and better compared to their usual practice of rinsing only, and soapy water removed poultry odor from hands. **Conclusions:** Soapy water was effective in removing influenza viruses from poultry workers' hands. However, workers were reluctant to use it after the study due to additional cost and inconvenience. Provision of soapy water by market authorities and promoting handwashing as a habit might improve hand washing among workers and may limit the spread of viruses.

Board 23. Emerging Pet-Rodent-Transmitted Infectious Diseases

J. Diaz.
Louisiana State University Health Sciences Center, New Orleans, LA, USA

Background: Internet purchasing and globalization of the exotic animal trade have accelerated the popularity of adopting wild, non-native animals as pets. As pet rodent ownership in the United States (US) grew, so did the potential for the introduction of rodent-borne zoonoses into naive animal and human populations. In 2003, a multistate outbreak of monkeypox infected 81 people when imported monkeypox-infected Gambian giant pouched rats infected prairie dogs later sold as pets. France and Germany reported outbreaks of cowpox in pet rodent owners in 2009. In 2017, 17 cases of the rodent-borne Seoul hantavirus infection with hemorrhagic fever and renal failure were reported in rat breeders and owners in three US states. **Methods:** The objectives of this study were to describe the epidemiology and clinical manifestations of pet rodent-borne infectious diseases and to recommend new strategies for their management, prevention, and control. To meet these objectives, Internet search engines were queried with these key words: animal importation, exotic animal trade, poxvirus, zoonoses, monkeypox, cowpox, hantavirus, tularemia, lymphocytic choriomeningitis virus, and rat-bite fever. **Results:** With the eradication of smallpox by vaccinia vaccination in the 20th Century, waning immunity to zoonotic orthopoxviruses will result in an increased potential for rodent-to-human transmission of domestic and imported orthopoxviruses. Like the poxviruses, hantaviruses can propagate in imported rodent colonies and will increase infection risks in pet breeders and owners. **Conclusions:** The most effective prevention and control strategies for pet rodent-borne infectious diseases will include educational, importation, and retail sale interventions. Educational interventions should discourage demand for exotic and wild pet ownership; and regulatory interventions should prohibit importation of reservoir species harboring zoonotic infections transmissible to native animals and man. The medical history should always include questions regarding pet ownership and any pet-inflicted injuries.

Healthcare-Associated Infections

Board 24. Large Numbers of Occupational Blood Exposure Accidents Outside the Hospital (2006-2014, Netherlands) Requires Turning to Profile-Based Preventive Actions

H. ter Waarbeek[1], C. Somers[1], J. Frantzen[1], N. Dukers-Muijrers[1], C. Hoebe[2]
[1]Public Health Service South Limburg, Heerlen, Netherlands, [2]Caphri Maastricht University, Maastricht, Netherlands

Background: This study assess the profiles of victims of occupational blood exposure accidents outside the hospital and their management by Public Health Service (PHS) South Limburg, 2006-2014. **Methods:** We conducted a retrospective cohort study including all non-hospital employees with this type of accident in our region, using univariate and multinomial regression analysis. A standardized case report form collected data on sex, age, occupation, location, time of reporting and occurrence, vaccination status, type of injury, source information and serostatus (hepatitis B (HBV), hepatitis C (HCV), HIV), risk assessment, action taken, and outcome of victim testing. **Results:** A total of 975 accidents were reported, mostly occurring in nursing homes (49%) and during home care (17%). HBV vaccination coverage ranged from 18% (household workers) to 91% (policemen, nurses, and nursing-assistants). Among nurses, assistants, students and household-workers, injuries were mostly caused by subcutaneous needles (51-67%) and lancets (25%); whereas biting (26%), scratching or spitting (70%) were the causal acts for policemen. Older workers (>50 years) reported accidents later and were less often vaccinated against hepatitis B (76%) ($p < 0.05$). Late reporting was also noted in police, home care, and ambulance settings. For 419 accidents (43%), there was a risk on both HBV and HCV/HIV transmission; mostly (>50%) in ambulance, medical sterilization, police, and dental practice settings. For 52% of all accidents, post exposition measures were necessary (mostly HBV immunization). Source serostatus testing was done for 356 people (37%): 5 people tested HbsAg-positive (prevalence 1.4%), 7 HCV-positive (2%), and 10 HIV-positive (2.8%). None of the employees seroconverted. **Conclusions:** Custom-made prevention guidance and measures are necessary based on HBV vaccination coverage and blood exposure accidents' profile. These should separately target each occupational risk group and setting. For example: improve vaccination for household and older workers, decrease reporting time for police, homecare, ambulance or older workers, and reduce unnecessary testing of sources.

Board 25. Establishing a National Standardized Surveillance System for Healthcare-Associated Infections in Vietnam

D. Coker[1], P. Malpiedi[1], N. Tran[2], L. Nguyen[3], H. Tran[4], U. Hogan[4], T. Nguyen[4], A. Vasquez[1], Q. Nguyen[4], H. Bui[3], N. Gupta[1], P. Ha[2], T. Hoang[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Vietnam Administration for Medical Services, Hanoi, Viet Nam, [3]Centers for Disease Control and Prevention, Hanoi, Viet Nam, [4]PATH, Hanoi, Viet Nam

Background: surveillance for healthcare-associated infections (HAI) is critical to understand HAI burden and inform prevention strategies at a national level. In 2017, the Vietnam Administration for Medical Services (VAMS) under the Ministry of Health, with the support of partners, began to establish Vietnam's national, standardized HAI surveillance system for bloodstream infections (BSI) and urinary tract infections (UTI) among six pilot hospitals. We evaluated the system to assess acceptability and adherence to surveillance protocols. **Methods:** Standardized surveillance began in 11 intensive care units (ICUs) in six hospitals in Jan 2017. Uniform protocols for healthcare-associated BSI, including central line-associated BSI (CLABSI), and UTI, including catheter-associated UTI (CAUTI), surveillance were adapted from CDC's National Healthcare Safety Network. Cases were identified among patients hospitalized in ICUs >2 calendar days and reported to VAMS through a newly established, national web-based reporting platform. To evaluate the system, we conducted stakeholder interviews and reviewed microbiology and clinical data from 94 blood and 70 urine positive cultures isolated from Jul–Sep 2017. **Results:** As of Dec 1, 2017, 152 ICU-onset BSIs were reported to the system, including 117 (77%) CLABSIs; 148 ICU-onset UTIs were reported, including 142 (96%) CAUTIs. Rates varied by ICU type; CLABSI rates (per 1,000 central line days) were 3.7, 9.0, and 2.0 in general adult ICUs (n=5), specialty adult ICUs (n=4), and general pediatric ICUs (n=2) respectively; CAUTI rates (per 1,000 urinary catheter

days) were 2.8, 4.5, and 3.3 respectively. Among 45 BSIs and 33 UTIs that met the case definition, 30 (67%) BSIs and 24 (73%) UTIs were reported to the system. Stakeholders found the standardized approach to HAI surveillance to be efficient, useful, and timely. Inadequate sharing and review of microbiology data negatively impacted case finding and inconsistent culturing practices affected overall sensitivity of the system. **Conclusions:** Vietnam has established an important foundation for a national, standardized HAI surveillance system. Efforts to improve culturing practices, enhance communication between lab and surveillance staff, and conduct regular surveillance audits are warranted.

Board 26. The Beijing Healthcare-Associated Infections Surveillance System: Identifying Strengths and Limitations through an Evaluation of Central Line Association Blood Stream Infection (CLABSI) Case Reporting, Beijing, China, 2015

W. Yinghong[1], L. Juyuan[2]
[1]Renmin Hospital, Beijing, China, [2]Beijing Hospital, Beijing, Christmas Island

Background: In 2004, the Beijing Center for Quality Control and Improvement on Patient Safety established the HAIs Surveillance System in Beijing. In 2014, we evaluated the strengths and limitations of the Beijing HAI surveillance system for accurately identifying and reporting central line associated blood stream infections (CLABSI) among Intensive Care Unit patients. **Methods:** We selected five of the 148 hospitals in the HAI surveillance network for the evaluation. At each hospital, we verified the accuracy (sensitivity and positive predictive value [PPV]) of CLABSI case reporting from available medical charts and the electronic HAI database for patients admitted to an ICU during 2013 to 2014. We defined sensitivity as the percent of medical records indicating a CLABSI diagnosis that were reported to the electronic HAI surveillance database and PPV as the percent of CLABSI cases reported to the electronic surveillance system with a positive blood culture. We interviewed ICU staff on CLABSI case definitions and diagnostic criteria in the ICUs at the selected hospitals. **Results:** During the medical chart review, we identified 114 CLABSI cases admitted to ICUs during the project period from four of the five selected hospitals. The estimated sensitivity of CLABSI case reporting to the electronic HAI surveillance system was 94%, and among the CLABSI cases reported to the system, the positive predictive value (PPV) was approximately 90%. Of the 42 (50% of those recruited) ICU staff interviewed, 91% could state the definition of CLABSI and 85% understood CLABSI diagnostic criteria. **Conclusions:** The majority of CLABSI cases were accurately reported to the HAI surveillance system. Additional training on the use of case definition and diagnostic criteria for CLABSI would likely enhance the utility of the Beijing HAI surveillance system and further improve CLABSI reporting accuracy. Routine evaluations can help identify gaps in reporting and strengthen the quality of the surveillance data.

Board 27. Methicillin-Resistant *Staphylococcus aureus* (MRSA) Nasal Carrier Among Healthcare Workers as Compared to Community

R. Manzoor[1], M. Abbasi[2]
[1]Kulsum International Hospital, Islamabad, Pakistan, [2]Federal General Hospital, Islamabad, Pakistan

Background: MRSA is an organism commonly found in hospital settings. It leads to a serious infection and is difficult to treat. MRSA nasal carriage is also a common condition. They are usually asymptomatic but this a risk factor for the spread of MRSA and possible subsequent development of an active infection. MRSA nasal carriage is present in hospital as well as community settings. **Methods:** A cross-sectional study was done at Kulsum International Hospital (KIH), Islamabad, Pakistan, from September to December 2017. A total of 423 subjects (322 healthy subjects and 101 healthcare workers) were screened for MRSA after obtaining verbal consent from subjects. Using premoistened, sterile cotton swabs, specimens were collected from the anterior nares of patients and healthcare workers. A standardized questionnaire was used to collect information including age, sex, and department. Statistical analysis was done with SPSS 20.The risk factor and association with MRSA colonization was calculated using the Chi-square test. **Results:** MRSA screening for nasal carriage was positive in 20 (19.8%) healthcare workers. Screening in community showed 18 (5.6%) individuals were positive for MRSA nasal carriage. The following results showed high prevalence of MRSA in healthcare workers as compared to the community (the p-value is .000004 which is significant). Among healthcare workers, the highest prevalence of MRSA was in surgical ICU workers 8 (53%) followed by Medical ICU 6 (20%), while CCU, private ward, and emergency department all were negative. **Conclusions:** MRSA nasal carriage is highly prevalent in healthcare workers, with those who work in intensive care units being at high risk. Based on these results, it is recommended that all healthcare workers, especially those working in ICUs, be screened for presence of MRSA carriage. Early detection and proper treatment for decolonization will reduce risk of MRSA infection in the patients.

Board 28. Characteristics of Infection Control Practices at North American Veterinary Teaching Hospitals – Promoting a Safety Culture in Veterinary Medicine

C. De La Hoz Ulloa[1], P. Morley[2], B. Burgess[3]
[1]Virginia Polytechnic and State University, Blacksburg, VA, USA, [2]Colorado State University, Fort Collins, CT, USA, [3]Univesity of Georgia, Athens, GA, USA

Background: Infection control is critical to the operation of veterinary hospitals not only to protect the patients and hospital but also to protect personnel (which have an increased occupational risk for developing a zoonotic infection). The objective of this study was to characterize current infection control practices in place for the prevention of healthcare-associated infections (HAIs), including zoonotic infections, in North American veterinary teaching hospitals (VTHs). **Methods:** A cross-sectional study was conducted in all North American VTHs that had been operational for at least one year (n=32). A phone survey was conducted of biosecurity experts at each institution that addressed infection control policies for hygiene, surveillance, patient contact, education and awareness, and enteric infectious disease control. **Results:** Most participating VTHs recognized zoonotic disease among personnel (63.2%), yet only 57% required training on infection control policies and procedures. During the interviews, several themes emerged

that likely impact policy compliance. First, the majority of infection control programs were deemed to be a 'work-in-progress' with incomplete written policies. Second, many study participants felt that for a program to be successful there had to be support at the leadership level and demonstrable cost-benefit relationship, features that were uncommonly reported. **Conclusions:** Results of this study indicate that we need to continue to develop evidence-based, cost-effective strategies for preventing HAIs, including zoonotic infections, among patients and personnel in veterinary medicine. It also identified a general lack of education to promote protocol compliance and demonstrates the need for targeted educational tools to promote a safety culture in veterinary medicine.

Board 29. Surgical Site Infection Prevention Program: Wisconsin Division of Public Health Initiative

G. Borlaug[1], C. Edmiston[2], A. Dowdell[1], J. Tans-Kersten[1], N. Shrivastwa[1]
[1]Wisconsin Divison of Public Health, Madison, WI, USA, [2]Medical College of Wisconsin, Milwaukee, WI, USA

Background: Surgical site infections (SSI) are the most frequently reported healthcare-associated infection (HAI) in Wisconsin, with approximately 900 SSIs reported annually to the Wisconsin Division of Public Health (WDPH) during 2013 through 2015. WDPH launched a statewide SSI prevention initiative based on a current evidence-based surgical care bundle. This initiative was targeted toward surgeons and surgical teams, with the goals of promoting interdisciplinary team approaches to SSI prevention, and fostering collaboration among surgical colleagues across the state. **Methods:** In Wisconsin, SSIs are reportable through the National Healthcare Safety Network (NHSN), a web based HAI surveillance system maintained by Centers for Disease Control and Prevention (CDC). During 2015, 106 hospitals reported SSI data into NHSN. During May 2015, WDPH launched the SSI prevention initiative using an SSI subject matter expert to serve as the state surgical care champion (SCC). The WDPH SSI team visited healthcare facilities, presented evidence-based SSI prevention guidelines to surgical teams and helped to develop facility-specific SSI prevention action plans. These onsite visits were voluntary, non-regulatory, and confidential. Periodic email and telephone consultations were provided to the facilities who participated in the SSI prevention initiative. **Results:** Hospitals that participated in the SSI prevention initiative and received a visit reported decreased SSIs. The ten hospitals visited by the WDPH SSI team during August through December 2015 reported an overall decrease of 36 SSIs in a one year time period. The overall SSI standardized infection ratio (SIR) decreased by 45% from 1.61 to 0.88 ($p = 0.002$) in the ten participating facilities. On the other hand, facilities that did not participate in this project (96 hospitals) did not observe any improvement in their SSI prevention data. The overall SSI SIR for these non-participating facilities was 0.96 in 2015 and 1.02 in 2016 ($p = 0.19$). **Conclusions:** The findings of this project suggest that a statewide SSI prevention initiative that presents facility-specific data and evidence-based guidelines directly to hospital management and surgical teams using subject matter experts may result in practice improvements and better surgical patient outcomes.

Board 30. Hospital–Associated, Multicenter Outbreak of *Ralstonia pickettii* in Colombia, 2017

S. Rivera Vargas[1], M. Pardo Bayona[2], M. Ovalle[1], M. Campos[3], L. Castro[1], Y. Arias[1], M. Rodriguez[1], P. Diaz[1], G. Zabaleta[1], F. Prieto[1]
[1]National Health Institute, Bogotá, Colombia, [2]The Andes University, Bogota, Colombia, [3]Deparment Health of Bogotá, Bogotá, Colombia

Background: The National Surveillance System for Healthcare Infections detected an unusual increase in *Ralstonia spp* cases starting September 2017 in Colombia. Fifteen hospitals reported *Ralstonia spp* outbreaks and eight detected outbreaks by *R. pickettii* between September and December 2017. We conducted an epidemiologic investigation for characterization of the outbreak and for control action implementation. **Methods:** We conducted a cross-sectional study in eight hospitals in three cities in Colombia between October and December 2017. Cases were defined as patients with bloodstream infection (BSI) for *R. picketti* confirmed by using mass spectrometry (MALDI-TOF MS). Medical records were collected by using a standard data form, and all intravenous medications administered seven days previous to those with a positive blood culture were characterized. Sterility tests were performed in medications common to all patients, and ten isolates recovered from patients and three from fluconazole batches were analyzed by pulsed-field gel electrophoresis (PFGE) for clonality. **Results:** 23 cases of BSI by *R. picketti* were confirmed. The epidemic curve showed a common, intermittent source. 52% of the infected patients were male, and the median age was 34 years old. 63.6% had immunosuppressive comorbidities, and 77.8% had exposure to a central catheter. Intravenous medication characterization showed all patients had been exposed to intravenous fluconazole from a common pharmaceutical and *R. pickettii* was recovered in sterility tests from the two fluconazole common batches. The main cluster grouped consisted of eight isolates from patients and three from fluconazole samples with 100% genetic similarity. No new cases appeared after fluconazole batches were removed. **Conclusions:** *R. picketti* caused a systemic infection mainly in immunosuppressed patients and those with a central catheter. Specific fluconazole batches were the source, as all cases were exposed, sterility tests were positive for *R. picketti*, and isolates in fluconazole were genetically identical to isolates recovered from blood samples. Control measures were adequate and prevented new cases from appearing. The overall increase in *Ralstonia* spp in Colombia indicates further studies are required.

Board 31. Finding the Pathogen in the Haystack: Outbreak Investigation of *E. coli* K1 Neonatal Meningitis Using Culture and Culture-Independent Methods — Kansas, 2017-2018

T. de Man[1], J. Blanding[2], R. Link-Gelles[1], B. Stacey[2], S. Cunningham[3], K. Perry[1], G. McAllister[1], P. Jeraldo[3], R. Geist[2], R. Patel[3], C. Elkins[1], K. Mayi Perkins[1], A. Laufer Halpin[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Kansas Department of Health and Environment, Topeka, KS, USA, [3]Mayo Clinic, Rochester, MN, USA

Background: In November 2017, the Kansas Department of Health and Environment notified CDC of three infants with *E. coli* K1 meningitis in a neonatal intensive care unit (NICU). These infants were cohorted as part of the infection control response. A fourth infant with *E. coli* K1 conjunctivitis was identified one month later, raising concern that unrecognized infants with *E.coli* K1 meningitis were a source of ongoing transmission. Identifying colonized infants is challenging

since *E. coli* is common in NICU infant gut microbiomes, and identifying a specific strain through traditional culture methods is laborious. Therefore, a novel sequencing strategy was initiated to rapidly identify asymptomatic, colonized infants. **Methods:** Whole genome sequencing (WGS) of samples from *E. coli* K1-infected infants was performed. Analyses included conventional multilocus sequence typing (MLST), core genome MLST (cgMLST), and single nucleotide polymorphism (SNP) identification. Lastly, assembled WGS data were annotated with protein coding genes including antimicrobial resistance mechanisms, K1 gene cluster, and serotype marker genes. Stool samples from seven high-risk, non-infected infants underwent culture-independent metagenomic sequencing for microbiome analysis. Using the outbreak strain as reference, Bowtie2, SAMtools, and Picard were applied to the metagenomic data to detect whether the outbreak strain was present in these infants' gut microbiomes. **Results:** Five outbreak-related isolates from *E. coli* K1-infected babies were sequenced; all were identical by MLST (ST1193), cgMLST, and serotype (O75:H5). These isolates also harbored the same bla_{CMY-2} beta-lactamase gene and had identical plasmid type profiles. Finally, the genetic diversity among all five isolates was 0-1 SNPs over a large core genome (89%). Of the seven non-infected infants' stools that underwent metagenomic sequencing, our approach identified one infant's gut microbiome that contained the outbreak strain (*E. coli* O75:K1:H5 with bla_{CMY-2} and identical plasmid type profile). **Conclusions:** We employed a novel approach combining single isolate and metagenomic sequencing to identify colonized infants that could serve as reservoir for *E. coli* K1 during an outbreak. This approach demonstrated potential for future clinical surveillance to aid in outbreak response and infection control efforts.

Board 32. Characteristics of Invasive *Candida* Bloodstream Infections among People Who Inject Drugs, Oregon and New Mexico, 2011-2017.

A. Zhang[1], S. Shrum[2], R. Pierce[1], E. Phipps[3], S. Vallabhaneni[4], S. Williams[4]
[1]Acute and Communicable Disease Prevention-Oregon Public Health Division, Portland, OR, USA, [2]New Mexico Department of Health, Santa Fe, NM, USA, [3]University of New Mexico, Albuquerque, NM, USA, [4]Mycotic Diseases Branch-Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Candidemia is usually a healthcare-associated infection and risk factors include prolonged hospitalization, surgery, antibiotic use, and presence of a central line. Injection drug use is not a well-recognized risk factor for candidemia, but is important to assess given the ongoing opioid epidemic and its recognized infectious disease sequelae. Using data from CDC Emerging Infections Program's active population-based surveillance for candidemia, we examined prevalence and characteristics of candidemia cases associated with injection drug use. **Methods:** A case was defined as a positive blood culture for any species of *Candida* in a surveillance area resident. A standardized case report form was used to collect demographic, clinical, and laboratory information. Cases identified from initiation of surveillance (2011 in OR; 2017 in NM), December 2017, were included. We compared candidemia cases found among people who inject drugs (PWID) and non-PWID. **Results:** Of a total of 547 candidemia cases, 104 (19%) were identified in PWID (19% PWID in OR and 29% PWID in NM). The proportion of cases associated in PWID increased from 24% to 31% in OR during 2014–2016. Mean age for PWID (37 years) was lower than for non-PWID (55 years, $p<0.0001$). PWID were more likely to have liver disease (54% vs 42%; $p<0.001$), particularly hepatitis C (66% vs 35%, $p< 0.0001$). PWID were less likely to have had recent surgery (14% vs 25%, $p=0.01$) or have a central line (47 vs 65%, $p=0.005$). PWID were more likely to have infections with non-*albicans Candida* species than non-PWID (65%% vs 40%, $p< 0.0001$). PWID were more likely to have community-onset candidemia (blood culture positive <4 days after admission) (75% vs 56%, $p=0.0005$). Mortality was lower among PWID (4% vs 27%, $p<0.0001$). **Conclusions:** One-fifth of candidemia cases were among PWID. More information is needed to assess whether and how the increasing proportion of PWID cases in OR may be related to the ongoing expansion of the opioid epidemic. Candidemia cases associated with PWID are demographically and clinically distinct from non-PWID candidemia cases, suggesting that exposures and source of candidemia are different from infections that occur in the healthcare setting. Clinicians should be aware of the risk of candidemia in PWID, and research is needed to identify specific injection factors that increase the risk.

Board 33. Hepatitis C Outbreak in a Respiratory Care Ward Associated with Frequent Unsafe Injections — Taiwan, 2017

P. Wu[1], M. Hung[2], H. Lin[2], C. Su[1]
[1]Centers for Disease Control, Taipei, Taiwan, [2]Centers for Disease Control, Kaohsiung, Taiwan

Background: Healthcare-associated outbreaks of hepatitis C virus (HCV) infection has been identified in Taiwan and poses serious risks of harm to patients. During May–July 2017, Taiwan Field Epidemiology Training Program (FETP) was notified of four patients with acute HCV infection in a respiratory care ward (RCW). We conducted an investigation to identify the transmission route and risk factors for infection to prevent further transmission. **Methods:** We performed HCV testing for patients and staff in July 2017; all HCV-positive sera underwent phylogenetic analysis to examine genetic relatedness. We defined cases as patients who were hospitalized from November 2016 to April 2017 (6 months to 2 weeks before the first case was diagnosed) and had HCV seroconversion during hospital stay. We selected controls from patients who were hospitalized during the same period and had a negative HCV test. We reviewed medical records to collect types and times of parenteral medications and invasive procedures. We used Wilcoxon rank-sum test to compare the number of injections between cases and controls, and calculated hazard ratios to identify factors associated with infection by Cox proportional hazards model. We evaluated infection control via on-site observations of injection practice. **Results:** Of 19 staff and 29 RCW patients, we identified four case-patients and a chronic hepatitis C patient with >99% genetic similarity. Compared to 12 control-patients, case-patients received a higher number of injections per day (3.86 vs 0.02, p =0.01). The hazard ratio of 100 injections for HCV infection was 1.6 (95% confidence interval 1.04–2.59). We found the RCW lacked a designated area and standardized workflow for injection preparation, which could possibly cause blood contamination of environment and medication vials. **Conclusions:** We identified that the patient-to-patient transmission of HCV was associated with frequent injections and infection control lapses. Healthcare personnel should follow safe injection practices and reduce injection frequency to prevent HCV transmission.

Board 34. Molecular Epidemiology of an Outbreak of Human Parainfluenza Virus 3 in Transplant Patients

E. Bailey, E. Lobaugh-Jin, B. Smith, N. Henshaw, G. Gray
Duke University, Durham, NC, USA

Background: Respiratory viruses, such as human parainfluenza virus type 3 (hPIV3) are an important cause of morbidity and mortality in immunocompromised patients. As the early diagnosis and treatment of respiratory pathogens is key to the control the spread of infection in hospitals, the focus of this study was to epidemiologically investigate a cluster of 12 oncology (leukemia and lymphoma) patients with possible related hPIV3 infection. **Methods:** Bronchoalveolar lavage (BAL) samples were taken from patients diagnosed with leukemia or lymphoma in a single hospital ward presenting with respiratory illness on admission or during hospitalization. Cases confirmed as hPIV3 by hospital diagnostic techniques (GenMark Dx) were further analyzed by reverse transcriptase polymerase chain reaction (RT-PCR) and partial genome sequencing. Partial genome sequencing methods were used to examine both the HN and Fusion genes of hPIV3; Sequences were aligned with MegAlign 15 software (DNASTAR, Madison, WI) using the Clustal W method. Phylogenetic analysis was carried out using the MegAlign 15 software maximum likelihood method with a bootstrap value of 1,000. Fusion gene sequencing was used to differentiate the epidemiological links between an equivocal cluster identified during HN gene sequencing. **Results:** From the 15 originally identified hPIV3 isolates from 12 oncology patients, 12 were confirmed by RT-PCR and by partial genome sequencing methods. Phylogenetic analysis of the partial genome sequences revealed a cluster of 10 cases related to the outbreak. Further analysis of the F gene within the cluster was performed because the HN gene had low discriminate power. The F gene analysis revealed four sub-clusters of 2 identical hPIV3 strains. **Conclusions:** The major findings of this study indicate that this outbreak of hPIV3 was likely from a single source, and it seems likely that hPIV3 transmission occurred from patient-to-patient. This study demonstrates that despite an outbreak scenario in immunocompromised oncology patients, infection control was able to identify, prevent further spread, and eradicate hPIV3 in a ward of the hospital using early intervention strategies.

Board 35. Burden and Risk Factors of Nosocomial Urinary Tract Infection in Renal Transplant Recipients in Nepal

R. Shrestha[1], P. Shrestha[2], K. Shrestha[2], B. Awal[2]
[1]Bhaktapur Hospital, Bhaktapur, Nepal, [2]Human Organ Transplant Center, Bhaktapru, Nepal

Background: Nosocomial urinary tract infections (UTIs) are major threats of renal transplant recipients. Its burden and risks are unmeasured in Nepal. **Methods:** A retrospective study was conducted to assess burden and risk factors of nosocomial UTIs among consecutive live related renal transplant recipients (LRTR) transplanted during 2014 to 2017 at Human Organ Transplant Center in Nepal. Only microbiologically confirmed, physician diagnosed UTIs within a month of renal transplantation requiring hospitalization were included. **Results:** Nosocomial UTIs were diagnosed in 21.4% of 229 patients at the mean of 13.48 days after transplantation. Urinary isolates were *Escherichia coli* (42.86%), *Pseudomonas aeruginosa* (36.73 %), and *Klebsiella pneumoniae* (20.41%). Antibiotic resistance observed against imipenem was 36.73%, amikacin- 40.82%, and ciprofloxacin- 95.92%. Urosepsis occurred in 14.29% and graft loss due to UTI in one case. Infections were treated with carbapenem alone or in combination in 67.34% and polymixin B in 10.2%. Risk factors associated with infection were prolonged transplant hospitalization (p=0.0023) and re-operation (p=0.042). **Conclusions:** There was high burden of nosocomial UTIs among LRTR resulting into escalating use of carbapenems. Prolonged transplant hospitalization and re-operation were risk factors associated with these infections.

Board 36. Evaluation of Colonization and Infection by Multi Resistant Bacteria in Renal Transplant Patients

M. Taminato[1], T. Resende[1], C. Grothe[1], D. Fram[1], S. Manfredi[1], R. Pereira[2], A. Pignatari[1], D. Barbosa[1]
[1]UNIFESP, São Paulo, Brazil, [2]USP, Sao Paulo, Brazil

Background: Infection is the major cause of morbidity and the second most frequent cause of mortality in patients with chronic renal failure. The *Staphylococcus aureus*, coagulase negative *Staphylococcus* and *Enterococcus spp* are the main colonizing agents and causing infections in this population, as well as producing *Klebsiella pneumoniae* carbapenemase (KPC). *S. aureus* with intermediate resistance to vancomycin (VISA), vancomycin-resistant *Enterococcus* (VRE) and KPC. To determine the prevalence of colonization or infection, morbidity and mortality and identify the risk factors. **Methods:** Cohort study in the Department of Transplantation of University of São Paulo – UNIFESP was included 200 patients. The prevalence of colonization was conducted by surveillance of microorganisms: MRSA and VISA through collection of nasal samples from all patients. Surveillance of VRE and KPC through stool samples or rectal swab. Patients were followed by a period of six months to record the morbid complications such as infection and causes of hospitalization and death. **Results:** Of 200 patients included, 76 (38%) patients included in our sample were colonized, corresponding to 8% *S. aureus*, 11% *Enterococcus*, and 19% *Klebsiella pneumonia*. The most prevalent colonization concomitant identified in our population was *E. coli* and *Klebsiella pneumoniae*. Outcomes related to transplantation were post-transplant stay (RR 5.61 CI 2.91-10.8), need for post-transplant dialysis (RR 2.85 CI 4.00-15.39), and postoperative ICU (RR 2.80 CI 11.4-78.09). After 6 months, we identified that prior colonization by *Enterococcus* is a risk factor for UTI. **Conclusions:** Failure to identify and isolate colonized patients contribute to increased rates of nasocomial infection by MRSA and increased colonization by VRE and KPC. These results are fundamental for health professionals in the characterization of bacteria, transmission, and mechanisms of resistance and mainly instruments for the prevention and control of the multiresistant bacteria of patients colonized pretransplant, with the purpose of reducing morbimortality.

Board 37. Computational Modeling for Comparison of Prophylaxis for Cytomegalovírus in Renal Transplants

R. Pereira[1], M. Taminato[2], D. Barbosa[2], E. Tuesta[3]
[1]University of São Paulo- USP, São Paulo, Brazil, [2]UNIFESP, São Paulo, Brazil, [3]USP, São Paulo, Brazil

Background: The increase in health costs is a relevant issue both for its economic and political aspects, and one of its main causes is the adoption of new health technologies. This also applies to kidney transplantation, where maintenance of the transplanted organ may depend on different prophylactic treatments against cytomegalovirus infection, or CMV (major cause of graft loss), for the post-transplant period. In Brazil, more than 5000 kidney transplants are performed annually

and the adoption of a specific prophylaxis method should be analyzed objectively and effectively with the aid of computational simulations using data imputation and Markov chains. **Methods:** Data were collected from 96 adult renal transplant patients at Hospital do Rim in São Paulo, the largest in the country, where more than 2000 transplants were performed in 2014. All patients are adults and no prophylaxis has been adopted in these cases. These records served as a basis for the construction of transition matrices for the Markov chains, together with imputation methods for completing the database. Literature reports have contributed to the adaptations of the probabilities for cases where two prophylaxis are compared: ganciclovir versus valganciclovir. Microstimulation was performed to obtain data for both survival and cost-effectiveness analysis. **Results:** It has been observed that as the population increases cost-effectiveness for alternative therapy it becomes more attractive, within the desired range of around 1000 to 10000 patients. It has been observed that eventually the change in the cost effectiveness ratio may follow a power law, information that may be relevant to the resource manager. **Conclusions:** Computational modeling, imputation methods and survival and cost-effectiveness analyzes are methods that can be used to adopt new health technologies at a low cost without risk to patients.

Foodborne Infections

Board 38. The Trend of Foodborne Disease Outbreaks in Taiwan (1991–2016)

L. Lin, Y. Huang, W. Cheng, H. Lin
Food and Drug Administration, Ministry of Welfare and Health, Executive Yuan, Taipei, Taiwan

Background: For food safety management, foodborne disease outbreaks (FBDO) are an important issue. Conducting outbreak surveillance can provide information so that the government can identify the key problems and give administrative guidance to control and prevent them. **Methods:** FBDO investigations were initiated by local health departments. Suspicious residual food, stool, vomit, or environmental samples were collected and analyzed by the Taiwan Food and Drug Administration (TFDA) and Centers for Disease Control (TCDC) of the Ministry of Welfare and Health. **Results:** Among the results of 26 years (1991–2016) of investigation on FBDOs, 7,244 FBDOs (113,752 cases) were reported. The most common bacterial etiology agent was *Vibrio parahaemolyticus* (20.5%), followed by *Staphylococcus aureus* (6.6%), and *Bacillus cereus* (4.9%). The average annual number during 2001–2016 was substantially greater than that during 1991–2000 (363 and 143 outbreaks reported, respectively), while the average cases per outbreak in 2001–2016 was much lower than that in 1991–2000 (12.9 cases and 28.5 cases per outbreak, respectively). Small-scale FBDOs increased during 2001–2016 compared to that during 1991-2000. During 2001–2016, FBDOs resulting from *B. cereus* and *Salmonella* spp. exhibited an increasing trend, whereas that from *V. parahaemolyticus* showed a decreasing trend. **Conclusions:** Policies were made to reduce possible FBDOs. Food business operators shall implement the sanitary management by carrying out GHP. Moreover, the schools and certain meal box providers shall perform HACCP to eliminate the possible hazards by controlling the critical points. No *Clostridium botulism* cases resulting from packaged foods were reported since the registration of vacuum-packed ready-to-eat soybean food was enforced in 2010. No cases from imported shellfish were detected in 2016 after policy intervention in the border. Natural toxins of wild plants and unsafe seafood such as pufferfish caused FBODs had been effectively reduced with risk communication with the public by booklets, posters, flyers, and press conferences.

Board 39. Multi-City Viral Diarrheal Disease Outbreaks Associated with Raw Shellfish Consumption in Taiwan in 2012 and 2015

L. Lin, Y. Huang, W. Cheng, H. Lin
Food and Drug Administration, Ministry of Welfare and Health, Executive Yuan, Taipei, Taiwan

Background: Sapovirus and norovirus cause disease in human and can be found in shellfish from contaminated water. The infection in humans can cause diarrhea, throwing up, nausea, and stomach pain. In May-June 2012 and 2015, excess number of viral gastroenteritis cases in multiple cities were reported to competent authority. The samples were examined and investigations were conducted to find the potential risk factors. **Methods:** Suspicious residual food, stool, vomit, or environmental samples were collected and analyzed. Meanwhile, product management distribution system, medical records, and laboratory records were reviewed. Person-to-person interviews with a structured questionnaire were implemented and case-control study was performed to identify possible risk factors in the 2012 outbreak. Food supply chains, including marine harvest area that were related to the cases, were surveyed to examine the existence of the pathogen in both outbreaks. **Results:** In 2012, there were 77 reported cases from May to June in Taipei and Taichung. Consuming raw shellfish imported from certain harvest area was significantly associated with sapovirus infection (OR = 20.5). In 2015, 136 cases were reported from May to June in Taitung, and norovirus GI and GII were detected in the imported shellfish from a certain country. No cases were reported in 2012 and 2015 after the policy intervention such as batch-by-batch inspection in the border. **Conclusions:** Consuming raw products, especially shellfish from contaminated water, could attribute risk to gastroenteritis outbreak. Health education should be emphasized and awareness of disease severity should be raised to the public continuously. Meanwhile, collaboration between the border inspection sector and the food safety sector is needed. The policy that shellfish imported for human consumption shall be accompanied with a health certificate, including the information of the harvest area, and issued by the competent authority of exporting country came into effect on January 1, 2018, in Taiwan to safeguard the health of the consumers.

Board 40. Understanding the Incubation Period Distribution of *Salmonella* Typhi

A. Awofisayo-Okuyelu[1], I. Hall[2], A. Pratt[3], N. McCarthy[4]
[1]University of Oxford, Oxford, United Kingdom, [2]University of Manchester, Manchester, United Kingdom, [3]Public Health England, Porton Down, United Kingdom, [4]University of Warwick, Warwick, United Kingdom

Background: *Salmonella* Typhi is a human pathogen that causes typhoid fever. It is a major cause of morbidity and mortality in developing countries and is responsible for several outbreaks in developed countries. Studying certain parameters of the pathogen, such as the incubation period, provides a better understanding of its pathophysiology. **Methods:** In order to understand the incubation period distribution of *S.* Typhi, we carried out a systematic review and developed a mathematical model. Published literature on outbreaks and human experimental studies reporting incubation period were reviewed. Studies

with limited evidence of heterogeneity between them were identified using hierarchical clustering analysis and grouped for further analysis. Factors contributing to the distribution of incubation period were also identified by applying a generalized linear model. Separately, a biological compartmental model describing the process of *S.* Typhi infection from ingestion to onset of clinical illness was described using evidence from in vitro and in vivo literature and formalized as mathematical equations. Parameter values were derived from the literature and model was solved using Berkeley Madonna software. **Results:** Analyzing extracted data from the systematic review showed previous vaccination and attack rates as factors that may lengthen and shorten the incubation period respectively. Five subgroups with limited evidence of heterogeneity were identified, and the mean incubation period of the subgroups ranged from 9.7 days to 21.2 days. Outbreaks with reported cases with vaccination history were clustered in a single subgroup and had the longest incubation period. The mathematical model was developed using two possible scenarios of *Salmonella* invasion. The output of both scenarios was similar, showing the onset of clinical symptoms around 3.3 days and 5.4 days. **Conclusions:** The incubation period distribution of *S.* Typhi is influenced by some host and pathophysiological factors. Clinical onset takes longer than predicted by our current mathematical model based on biological experimental data.

Board 41. Salmonellosis Outbreaks by Food Vehicle, Serotype, Seasonal and Geographical Variation, United States, 1998–2015

T. Snyder[1], N. M'ikanatha[2]
[1]Pennsylvania State University College of Medicine, Hershey, PA, USA, [2]Pennsylvania Department of Health, Harrisburg, PA, USA

Background: *Salmonella* remains a major cause of foodborne illnesses in the United States. Although salmonellosis outbreaks are relatively common, implicated food vehicles and other characteristics are not well understood. **Methods:** Data collected by state and local public health departments on non–typhoidal salmonellosis outbreaks during 1998–2015 were requested from CDC's Foodborne Disease Outbreak Surveillance System. SAS and Excel were used to analyze the surveillance system data to describe food vehicle attribution, serotypes, geographic distribution, and trends over time. **Results:** A total of 2,447 outbreaks (yearly average: 136, range: 112 in 2005 – 165 in 2015) with a confirmed or suspected etiology of non–typhoidal *Salmonella* were identified. A total of 65,916 individual cases were associated with these outbreaks (mean 30 cases/outbreak, range 2 – 1,939). A likely food vehicle was identified in 49% of outbreaks. Among outbreaks for which a vehicle was known, frequently implicated foods included eggs (12.5%), chicken (12.4%), and pork (6.5%). 55 (2.2%) of outbreaks had associated fatalities; 87 (0.1%) individual cases died. Serotypes associated with the most deaths were Typhimurium (23% of deaths, n = 20), Enteritidis (18% of deaths, n = 16), and Newport (14% of deaths, n = 12). Outbreaks associated with S. Javiana increased from 2 in 1998 to 9 in 2013; S. I4, [5],12: i- increased from 0 in 1998 to 18 in 2015. Other serotypes that increased over time included S. Infantis, Braenderup, and Oranienburg. Outbreaks occurred most frequently in summer months (June–August). States with the highest incidence of outbreak-associated cases (infections per 100,000 population) were observed in Alaska (0.137), Minnesota (0.121), and Hawaii (0.118); the states with the lowest incidence were Delaware (< 0.001), Wyoming (< 0.001), and Texas (0.006). **Conclusions:** This study identified commonly consumed foods (eggs, chicken, and pork) as frequent vehicles for salmonellosis outbreaks. Deaths were infrequent among outbreak-associated cases. Geographic variations in outbreak incidence may reflect differences in outbreak detection and investigation, as well as differences in risk. Federal and state agencies should continue efforts to control food contamination from production to preparation.

Board 42. *Salmonella* Infections and Socioeconomic Status, Georgia, 2011-2015

N. Oosmanally[1], L. Jones[2], K. Parada[3], M. Tobin-D'Angelo[1]
[1]Georgia Department of Public Health, Georgia Emerging Infections Program, Atlanta, GA, USA, [2]Georgia Department of Public Health, Atlanta, GA, USA, [3]Georgia Emerging Infections Program, Atlanta, GA, USA

Background: Annually, *Salmonella* is estimated to cause over 1 million illnesses in the United States. Georgia (GA) has one of the highest burdens of *Salmonella* infections with more than 2000 cases reported to the Georgia Department of Public Health (DPH) annually. Regional variation in numbers of reported *Salmonella* infections occur nationally and within GA. However, the role of socioeconomic status as a risk factor for *Salmonella* infections in GA has not been characterized, and this relationship has not been consistently described in the global literature. **Methods:** *Salmonella* infections are identified through active population-based surveillance in GA. *Salmonella* demographic and laboratory data for cases reported to DPH from 2011 to 2015 along with economic data from the American Community Survey were analyzed. Associations between household incomes per county and different age groups were examined using SAS version 9.3. **Results:** From 2011 to 2015, 12,536 *Salmonella* infections were reported to DPH. Almost half of the cases were among adults 18 years and older (46%), while 36 percent were among children between 1 and 17 years, and 18 percent were among infants under one year. Most cases (73%) resided in a non-rural county and were White (71%). Five serotypes - Javiana, Newport, Enteriditis, Typhimurium, and S. I 13,23:b:- - accounted for 64 percent of all reported cases. A significant association between the likelihood of patients being infected with these common serotypes in each county and median household income was found among cases of all ages. When age group was evaluated, a significant association with one of the five common *Salmonella* infections and increased median household income was observed in adults ($p<0.001$) and in children ($p<0.001$). Household income was not significantly associated with illnesses in infants. **Conclusions:** The association between socioeconomic status and *Salmonella* illness varies by age among those infected with the most common serotypes. This association should be further explored and characterized to target policies and interventions to reduce disparities in *Salmonella* illness.

Board 43. Utility of Whole Genome Sequencing in a Multi-State Outbreak of Salmonellosis Associated with Papayas

A. Adediran, M. Leeper, D. Wagner, L. Gladney, Y. Joung, T. Griswold
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: PulseNet is the national foodborne disease surveillance network that rapidly detects foodborne outbreaks. Pulsed-field gel electrophoresis (PFGE) and whole genome sequencing (WGS) are used by PulseNet to detect Salmonellosis outbreaks. Between May and October 2017, we investigated an outbreak of 220 cases that included five different *Salmonella* serotypes (Agona, Gaminara, Kiambu, Senftenberg, Thompson) associated with consumption of papayas. Whole

genome multi-locus sequence typing (wgMLST) and high quality single nucleotide polymorphism (hqSNP) analysis were used to determine the relatedness between isolates. **Methods:** PFGE was performed on 285 isolates using the PulseNet *Salmonella* protocol and PFGE patterns were uploaded to the PulseNet *Salmonella* National Database (BioNumerics v.6.610). Representative isolates were sequenced using the Illumina MiSeq. Sequences were compared by hqSNP analysis generated using the Lyve-SET pipeline (github.com/lskatz/lyve-SET) and by wgMLST using version 1 of the *Salmonella* allele database (BioNumerics v7.6). **Results:** In this investigation, WGS provided more differentiation of isolates than PFGE alone. For *Salmonella* serotypes Kiambu, Thompson, and Senftenberg, background cases with indistinguishable PFGE patterns were found to be unrelated by WGS and were excluded from the investigation. For *Salmonella* serotypes Agona, Senftenberg, and Thompson, multiple PFGE patterns were found to be related by WGS, which linked cases with variant patterns to the investigation. WGS was more useful than PFGE alone in determining the relatedness between isolates for all serotypes except for Gaminara, where PFGE alone would have been sufficient given the rarity of the serotype and PFGE pattern. For all serotypes, WGS showed that clinical and food isolates were closely related, which contributed to identifying the source of the outbreak. **Conclusions:** This investigation showed that WGS is useful in differentiating *Salmonella* isolates of various serotypes that are indistinguishable by PFGE and in linking isolates with variant PFGE patterns. WGS analysis can be used to support epidemiologic investigations, and to link food and clinical cases with confidence which is desirable for regulatory actions.

Board 44. Are Culture-Independent Diagnostic Tests Decreasing Capacity to Detect Outbreaks?

E. Marder[1], P. Sundararaman[1], M. Boyle[2], K. Burzlaff[3], P. Cieslak[4], J. Dunn[5], D. Eikmeier[6], L. Jones[7], S. Lathrop[8], T. Libby[9], Q. Phan[10], E. Wilson[11], A. Geissler[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Maryland Department of Health, Baltimore, MD, USA, [3]New York State Department of Health, Albany, NY, USA, [4]Oregon Health Authority, Portland, OR, USA, [5]Tennessee Department of Health, Nashville, TN, USA, [6]Minnesota Department of Health, St. Paul, MN, USA, [7]Georgia Department of Public Health, Atlanta, GA, USA, [8]University of New Mexico, Santa Fe, NM, USA, [9]California Emerging Infections Program, Oakland, CA, USA, [10]Connecticut Emerging Infections Program, Hartford, CT, USA, [11]Colorado Department of Public Health and Environment, Denver, CO, USA

Background: Molecular subtyping is a critical tool for the identification of clusters, outbreaks (OB), and OB-associated cases. However, increasing use of culture-independent diagnostic tests (CIDTs) without reflex culture decreases the number of isolates available. This could decrease detection of clusters, OBs, and OB-associated cases. **Methods:** We analyzed data from the Foodborne Diseases Active Surveillance Network (FoodNet), the National Outbreak Reporting System (NORS), and PulseNet to describe changes in OB-associated cases, OBs, and clusters of Shiga toxin-producing *E. coli* (STEC), *Salmonella*, and *Campylobacter*. Only clusters and outbreaks reported in FoodNet states were included. **Results:** During 2012–2013, 8% (n=191) of STEC, 1% (n=193) of *Salmonella*, and 13% (n=1,958) of *Campylobacter* cases were CIDT-positive only and 10% (n=238) of STEC, 6% (n=908) of *Salmonella*, and 0.5% (n=72) of *Campylobacter* cases were OB-associated. During 2015–2016, the percentage of CIDT-positive only cases increased to 20% (n=660) of STEC, 6% (n=1,052) of *Salmonella*, and 29% (n=5,035) of *Campylobacter.* The percentage of OB-associated cases significantly decreased to 7% (n=228; p=0.03) for STEC, and did not change significantly for *Salmonella* (n=1,052, 6%) or *Campylobacter* (n=53, 0.3%). The average number of single etiology OBs reported to NORS decreased from 29 to 23 for STEC, 80 to 74 for *Salmonella*, and 18 to 13 for *Campylobacter* whereas the average number of PulseNet clusters decreased from 44 to 41 for STEC, 173 to 156 for *Salmonella*, and 9 to 6 for *Campylobacter*. **Conclusions:** The number of CIDT-only cases increased whereas the percentage of OB-associated STEC cases decreased, and number of clusters and OBs reported for all three pathogens decreased slightly. Other factors, such as differences in food contamination or states' capacity to perform subtyping, may influence the occurrence and recognition of clusters and outbreaks. These limited data are of concern; continued monitoring of clusters and outbreak reports is needed to monitor the impact of CIDTs on outbreak detection. Reflex culture is critical to obtain isolates for molecular subtyping needed to identify OBs and OB-associated cases.

Board 45. Changing Epidemiology of *Yersinia enterocolitica* Infections and the Rapid Adoption of Culture-Independent Diagnostic Tests—Foodborne Diseases Active Surveillance Network (FoodNet), 2010–2017

L. Ray[1], K. Barrett[1], K. Burzlaff[2], M. Boyle[3], K. Garman[4], E. Marder[1], J. Rounds[5], B. Shiferaw[6], E. Wilson[7], S. Wilson[8], A. Geissler[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]New York State Department of Health, Albany, NY, USA, [3]Maryland Department of Health, Baltimore, MD, USA, [4]Tennessee Department of Health, Nashville, TN, USA, [5]Minnesota Department of Health, Saint Paul, MN, USA, [6]Oregon Public Health Division, Portland, OR, USA, [7]Colorado Department of Public Health and Environment, Denver, CO, USA, [8]Georgia Department of Public Health, Atlanta, GA, USA

Background: *Yersinia enterocolitica* (YE) causes an estimated 117,000 illnesses annually in the United States. The incidence of YE infections has declined since 1996, partly due to targeted educational efforts directed at the historically highest incidence group, black children under 5 years. In 2016, YE incidence increased in the Foodborne Disease Active Surveillance Network (FoodNet), likely driven by the adoption of more sensitive syndrome panel culture-independent diagnostic tests (CIDTs) that can simultaneously detect multiple pathogens, including YE, from a single specimen. YE is not typically included in routine stool culture testing because it requires specialized laboratory media. **Methods:** We summarized laboratory-diagnosed YE infections reported to the 10 FoodNet sites during 2010–2017. Average annual incidence rates per 100,000 persons (IRs) were calculated. Statistical significance was defined as $\alpha < 0.05$. **Results:** During 2010–17, 1,488 YE infections were reported to FoodNet. The IR was 0.38 cases/100,000 persons (range per year, 0.22–0.87). IRs were highest among infants (children <1 year old) (3.51) and children aged 1–5 years (0.87). Annual IRs increased markedly from 0.27 during 2010–15 to 0.70 during 2016–17 with the greatest increases among white persons aged ≥65 (360%). Compared with 2010–15, IRs significantly increased during 2016-17 among all races, sexes, ethnicities, and age groups, except that IRs decreased among Asian infants (9.11 to 4.61) and black children aged 1–5 years (2.29 to 0.88). The seasons with the highest percentage of cases was winter 2010–15 (29%) and summer 2016–17 (33%). The percentage of infections with any

CIDT-positive result increased markedly (3% vs 71%) comparing 2016–17 with 2010–15. **Conclusions:** The incidence of YE infections reported to FoodNet has markedly increased since 2010-15, as use of CIDTs increased. Demographic differences underscore the need for focused prevention efforts, particularly among older adults. Use of panel CIDTs might increase identification, and thus, improve incidence estimates of YE across broader population subgroups for which testing was previously limited. Continued surveillance, a better understanding of risk factors, and targeted public health action are needed.

Board 46. Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Soy Nut Butter—United States, 2017

R. Hassan[1], S. Seelman[2], V. Peralta[3], H. Booth[4], M. Tewell[5], B. Melius[6], B. Whitney[2], R. Sexton[2], A. Dwarka[2], J. Vidanes[7], D. Kiang[7], E. Gonzales[8], N. Dowell[1], S. Olson[1], L. Gladney[1]
[1]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [2]United States Food and Drug Administration (FDA), College Park, MD, USA, [3]California Department of Public Health, Richmond, CA, USA, [4]Oregon Health Authority, Portland, OR, USA, [5]Arizona Department of Health Services, Phoenix, AZ, USA, [6]Washington State Department of Health, Shoreline, WA, USA, [7]California Department of Public Health, Sacramento, CA, USA, [8]Public Health - Seattle & King County, Seattle, WA, USA

Background: Shiga toxin-producing *Escherichia coli* (STEC) O157 causes an estimated 63,000 foodborne illnesses and 2,000 hospitalizations annually in the United States. In February 2017, PulseNet, the national laboratory network for foodborne disease surveillance, detected seven indistinguishable STEC O157:H7 infections with a novel pulsed-field gel electrophoresis pattern combination. We launched a multistate investigation to determine the outbreak source and identify prevention measures. **Methods:** A case was an infection with an outbreak strain of STEC O157:H7 in a person with illness onset from January 4–April 18, 2017. Patients were interviewed to find common exposures. Investigators conducted environmental inspections and tested product for STEC. Select clinical and food isolates were characterized by whole-genome sequencing (WGS). **Results:** We identified 32 cases from 12 states. The median patient age was 9 years (range 1–70); 41% were female. Twelve (38%) patients were hospitalized, nine (28%) developed hemolytic uremic syndrome, and none died. Twenty-five (78%) patients reported eating Brand A soy nut butter at home (n=19) or attending a facility (n=2) or daycare (n=4) that served Brand A soy nut butter in the week before illness. The outbreak strain was isolated from nine opened packages of Brand A soy nut butter collected from patient homes in California, Oregon, and Washington, and two unopened retail packages collected in California. FDA identified multiple food safety concerns at Brand A's contract manufacturing facility and subsequently suspended its food facility registration to sell or distribute food. Selected clinical and food isolates were highly related genetically by WGS. **Conclusions:** Investigational evidence implicated a novel food product, soy nut butter, as the source of an STEC outbreak mainly affecting children. Rapid identification of the outbreak vehicle and subsequent voluntary recalls of Brand A soy nut butter products likely prevented additional illnesses linked to this shelf stable product.

Board 47. Comparative Epidemiology of O157 Versus Non-O157 Shiga Toxin-Producing *E. coli* in Georgia, 2011-2017

S. Wilson, B. LaClair, M. Tobin-D'Angelo, C. Drenzek
Georgia Department of Public Health, Atlanta, GA, USA

Background: Nationally, non-O157 Shiga toxin-producing *E. coli* (STEC) infections have increased relative to O157 STEC. During 2011-2017, this was also true in Georgia, but these infections and exposures have not been characterized. This study assessed the epidemiology of non-O157 STEC compared to O157 in Georgia. **Methods:** Georgia Department of Public Health (DPH) conducts laboratory-based surveillance through the Foodborne Disease Active Surveillance Network (FoodNet). STEC surveillance data between 2011 and 2017 were queried from our notifiable disease surveillance system. Differences among age, race, ethnicity, hospitalization, and travel were compared between case-patients with O157 and non-O157 serotypes using Pearson's chi-square and descriptive analyses of non-O157 serotypes were conducted using SAS 9.3. **Results:** During 2011-2017, 824 confirmed STEC infections were identified. Of these, 603 were non-O157 STEC (73.2%). The top five non-O157 serotypes were O103 (22.4.9%), O26 (17.9%), O111 (14.3%), O118 (9.0%), and O186 (6.6%). Among non-O157 reports, children less than five years old accounted for the highest percentage (35.2%) while ages 10-19 accounted for the highest percentage among O157 (25.3%; p: 0.009). Both O157 (70.6%) and non-O157 (73.0%) case-patients were more likely to be White, but more non-O157 case-patients were Hispanic (16.6%) compared to O157 (5.0%; p< 0.001). Hospitalization was more common among O157 case-patients (35.3%) than non-O157 (11.3%). Non-O157 case-patients reported more international travel (16.3%) than O157 (0.9%; p<0.001) with the highest percent travel among O186-infected patients (31.6%). Among the top 5 non-O157 serotypes, 35.6% reported international travel to Mexico. **Conclusions:** Non-O157 STEC infections in Georgia were more commonly reported than O157 and less likely to result in hospitalization. Young children, Hispanics, and international travelers were disproportionately affected. While serotype O186 accounted for the smallest percentage of non-O157 serotypes, it represented the highest percentage of international-travel associated infections. Further analysis should focus on the epidemiologic characteristics of specific non-O157 serotypes. Prevention messages should be targeted to families with children, as well as travelers.

Board 48. Laboratory Investigations of Botulism Outbreaks Associated with Consumption of Pruno—United States, 2011-2016

J. Dykes, L. Joseph, J. Halpin, G. Gomez, C. Luquez
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Botulism is a severe illness caused by botulinum neurotoxin (BoNT). Foodborne botulism is a public health emergency. Suspected cases are confirmed by identifying BoNT in clinical specimens or in foods, or by isolating *Clostridium botulinum* from stool specimens. From 2011 to 2016, CDC's National Botulism and Enteric Toxins Laboratory received specimens associated with four botulism outbreaks in US prisons. All four outbreaks were associated with the consumption of pruno, an illicit alcoholic beverage brewed by prisoners. This is a summary of the laboratory investigations. **Methods:** We received 133 clinical specimens from 46 inmates from all four outbreaks, and pruno samples from three outbreaks. Sera, stool, and gastric aspirate samples were tested for the presence of BoNT.

Stool, gastric aspirate, and rectal swabs were cultured for presence of BoNT-producing clostridia using standard anaerobic methods. Isolates from three outbreaks were subtyped by PFGE, using *Sma*I and *Xho*I enzymes. **Results:** All four outbreaks were laboratory confirmed. BoNT type A and/or *C. botulinum* type A were identified in clinical specimens. *C. botulinum* type B was also isolated from stool samples in one of the outbreaks. BoNT type A was identified in one of the pruno specimens, the first and only laboratory identification of BoNT in pruno. *C. botulinum* type A was isolated from two pruno samples. Clinical isolates within each outbreak were indistinguishable by PFGE. In addition, isolates from pruno and clinical samples were also indistinguishable by PFGE. **Conclusions:** We received 143 specimens related to four botulism outbreaks that occurred in US prisons. Of particular note, one of the outbreaks was the largest botulism outbreak in the United States since 1978. BoNT and/or *C. botulinum* was identified in clinical specimens from all four outbreaks, confirming the diagnosis of botulism. In one outbreak, pruno was laboratory-confirmed as the source of contamination by identification of pre-formed BoNT in the sample. In another outbreak, *C. botulinum* type A was isolated from pruno, but the sample was not laboratory-confirmed as the contamination source because BoNT was not detected. Still, additional information was provided through PFGE, as the patterns of clinical isolates and pruno isolates from this outbreak were indistinguishable.

Board 49. Cyclosporiasis among Patrons of Restaurant A — Houston Metropolitan Area, Texas, May–August 2017

R. Chancey[1], N. Hall[2], A. Keaton[1], V. Heines[3], V. Cantu[3], V. Vakil[4], S. Long[4], K. Short[4], E. Franciscus[5], N. Wahab[5], A. Haynie[5], L. Gieraltowski[1], A. Straily[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, Austin, TX, USA, [3]Texas Department of State Health Services, Austin, TX, USA, [4]Houston Health Department, Houston, TX, USA, [5]Harris County Health Department, Houston, TX, USA

Background: Cyclosporiasis is an intestinal illness caused by the parasite *Cyclospora cayetanensis*. During July 21–August 8, 2017, CDC was notified of 20 confirmed or probable cases of cyclosporiasis in persons who dined at one of four Restaurant A locations in the Houston metropolitan area. The Texas Department of State Health Services and local health departments requested assistance in an epidemiologic investigation to identify the vehicle(s) of infection among restaurant patrons. **Methods:** A case-control study was conducted using a Restaurant A-specific questionnaire. A confirmed case was defined as laboratory-confirmed infection in a person with clinically compatible illness that began within two weeks of eating at a Restaurant A location on or after May 28 and who had not traveled internationally in the two weeks before symptom onset. A probable case was defined similarly, but without laboratory confirmation of infection. Case-patients and controls were matched on dining date and location. Using bivariate logistic regression, associations between food exposures and cyclosporiasis were examined and matched odds ratios (mORs) and 95% confidence intervals (CIs) were calculated. **Results:** Overall, 24 case-patients (16 confirmed; 8 probable) and 70 controls completed the questionnaire; 22 case-patients were matched with 66 controls. In menu-item analyses, consumption of tabouli was associated with cyclosporiasis (mOR = 8.0; 95% CI 2.1–44.5). In ingredient-level analyses of menu items containing fresh produce, green onions—eaten by 18 case-patients (81.8%), including 15 who reported eating tabouli (which contained green onions)—were associated with cyclosporiasis (mOR = 11.3; 95% CI 2.6–104.7). Traceback investigations conducted by state and federal officials to determine the source(s) of the green onions were inconclusive. **Conclusions:** We present an outbreak of cyclosporiasis epidemiologically linked to green onions, and broaden the range of fresh produce items that have been implicated as vehicles for this infection.

Board 50. Contaminated Powdered Infant Formula from Opened Containers as a Vehicle for Transmission of *Cronobacter sakazakii*—United States, 2002–2017

J. Strysko, J. Cope, H. Moulton-Meissner, J. Noble-Wang, H. Martin, C. Tarr, K. Hise, M. Freeman, A. Bowen
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: *Cronobacter* spp. cause meningitis and bacteremia in infants; clinical outcomes include seizures, brain abscesses, developmental delay, and death in about 40% of cases. Contaminated powdered infant formula (PIF) has been identified as the vehicle in nearly all *Cronobacter* infections for which a source is found, prompting guidance for safer preparation (WHO, 2007) and new regulations on production (FDA, 2014) of PIF. To inform further prevention efforts, we reviewed recent cases where *Cronobacter* was isolated from PIF. **Methods:** We reviewed *Cronobacter* cases voluntarily reported to CDC from 2002 – 2017 and describe cases where *Cronobacter* was isolated from PIF. State health departments detecting a *Cronobacter* case may ask CDC to test clinical isolates, PIF from opened containers, and environmental samples. CDC records epidemiologic information about each case. FDA tests PIF from lot-matched sealed containers to assess whether contamination occurred during production. We compared PIF and clinical isolates using pulsed-field gel electrophoresis (PFGE). **Results:** Among 69 *Cronobacter* cases with known feeding histories, PIF consumption within 7 days before illness onset was reported for 54 (78%) cases. We tested PIF samples from opened containers associated with 23 cases; 11 (48%) yielded *C. sakazakii*. PFGE patterns from all PIF isolates closely matched those of corresponding clinical isolates but not those of other cases. FDA did not detect *Cronobacter* in PIF from sealed containers associated with these cases. Among these 11 patients, 5 had meningitis (+/- bacteremia), 2 had bacteremia only, 3 had gastroenteritis, and 1 had *C. sakazakii* cultured from blood after unexplained sudden infant death. Median age at symptom onset was 14 days (range: 0 days – 13 months). Among 9 families disclosing PIF preparation practices, all reported proper hand hygiene; none reported reconstituting PIF using the WHO-recommended method. **Conclusions:** We document 11 *C. sakazakii* infections associated with contaminated PIF from opened containers from 2002 – 2017, affirming the need for continued efforts to prevent PIF contamination, including re-engineering PIF packaging to minimize product contamination after opening. Additional education and support for parents about proper PIF preparation and handling, and use of PIF alternatives may help prevent illnesses.

Board 51. Using Peer Support to Strengthen Foodborne Illness Surveillance and Outbreak Response Capacity

E. Sillence, D. Morse, D. Sharp
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Foodborne diseases cause approximately 48 million illnesses, 128,000 hospitalizations, and 3,000 deaths in the United States annually. Limited resources can diminish the ability of state and lo-

cal health departments to respond to foodborne disease outbreaks. To help address this concern, the Food Safety Modernization Act (FSMA) required that the Centers for Disease Control and Prevention (CDC) designate at least 5 state health departments in partnership with academic institutions as the Integrated Food Safety Centers of Excellence (CoEs) to assist public health professionals in jurisdictions other than their own with investigations of foodborne illness outbreaks. **Methods:** Through a competitive application process, CDC designated Colorado, Florida, Minnesota, New York, Oregon, and Tennessee as the CoEs. The CoEs provide peer support by developing educational materials, delivering trainings, and providing outbreak consultations. Support provided by the CoEs ranges from services that are tailored to the particular needs of a health department to general online products that were developed to address gaps identified through needs assessments conducted by CoEs in multiple jurisdictions. **Results:** The CoEs have developed over 150 online products that are available for immediate use or download free of charge for anyone at CoEFoodSafetyTools.org. These include outbreak case studies, whole genome sequencing training videos, and foodborne illness complaint system resources. CoEs have also provided one-on-one assistance to state and local health department staff in all 50 states and several US territories. CoEs have the capacity to provide assistance in the form of consultation for long-term projects (e.g., data system improvements) or more urgent consultations during outbreaks. **Conclusions:** The guidance, tools, and assistance provided by the CoEs have helped many jurisdictions implement strategies to improve their foodborne illness surveillance and response programs. The CoE website allows local, state, and federal public health professionals immediate access to tools for a variety of topics from questionnaire templates to just-in-time trainings. The CoEs have strengthened the ability of local and state public health agencies to respond to threats of foodborne illness.

Board 52. Restaurant Characteristics as Predictors of Cross-Contamination Behavior

M. Masters, L. Brown, E. Hoover
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: During food preparation, pathogens can be transferred among hands, preparation surfaces, and food. Cross-contamination of pathogens is a major cause of foodborne illness in the United States. Understanding restaurant characteristics and policies that may be associated with cross-contamination behaviors can potentially help reduce foodborne illness. **Methods:** The study was designed and conducted by CDC's Environmental Health Specialists Network (EHS-Net), a collaborative program of federal, state, and local environmental health programs. Six state and local programs were funded by CDC to participate in the study. The sample comprises 396 randomly selected restaurants in these six sites. EHS-Net data collectors interviewed a manager about restaurant characteristics and then observed workers preparing food and recorded the incidence of five behaviors that could lead to cross contamination. We conducted Poisson regression analysis to examine potential associations between restaurant characteristics and cross-contamination behaviors. **Results:** In the 307 restaurants included in these analyses, data collectors noted no cross-contamination behavior in 139 (45%) restaurants, dirty cloths touching clean equipment in 91 (30%) restaurants, bare hand contact with ready-to-eat (RTE) food in 83 (27%) restaurants, dirty cloths touching clean hands in 64 (21%) restaurants, dirty hands touching clean equipment in 61 (20%) restaurants, and RTE food touching dirty equipment in 40 (13%) restaurants. A complete-case Poisson regression of cross-contamination counts identified four restaurant characteristics that were significantly associated with the total number of cross-contamination behaviors observed: not having a policy against bare hand contact with RTE foods, independent ownership, on-site cooking of raw produce or meat, and a higher number of previous inspection critical violations. **Conclusions:** Cross-contamination in restaurants continues to be prevalent. Instituting policies limiting bare hand contact with RTE food may help reduce the incidence of cross-contamination. Independent restaurants and restaurants with multiple critical violations in their last inspection may benefit from focusing additional efforts on cross-contamination prevention.

Board 53. Restaurant Characteristics Associated with Food Cooling Practices

K. Reed, L. Brown
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Pathogen growth caused by improper cooling of hot food led to 504 outbreaks in restaurants and delis from 1998 to 2008, yet little is known about restaurant cooling practices. To fill this gap, the Centers for Disease Control and Prevention's (CDC) Environmental Health Specialists Network (EHS-Net) conducted a study on restaurant adherence to the US Food and Drug Administration (FDA) guidelines on reducing pathogen growth during cooling. The guidelines state that, during cooling, food should be stored at or in: ≤ 41°F shallow depths ventilated containers with space around them unstacked containers. **Methods:** EHS-Net, a network of federal and state environmental health programs that studies causes of foodborne outbreaks conducted this study. Nine programs were funded by CDC to participate in EHS-Net at the time of the study (2009-2010): CA, CT, GA, IA, MN, NY, OR, RI, and TN. The study sample comprises 352 randomly selected restaurants that cool food in the EHS-Net sites. Data collectors visited each restaurant to conduct a manager interview about restaurant characteristics and an observation of cooling processes. We conducted descriptive statistics on restaurant and cooling practice variables and multiple regressions to examine associations between restaurant characteristics and FDA cooling guideline adherence. **Results:** Restaurants most frequently met the FDA guidelines of unstacked containers (82%), followed by storing food at ≤ 41°F (81%), in containers with space around them (73%), in ventilated containers (62%), and at shallow depths (57%). Regression analyses showed that chain restaurants were more likely to cool food at ≤ 41°F. Restaurants with food safety certified managers on site were more likely to ventilate food. Restaurants only cooling one food and with food safety trained managers were less likely to stack containers. Restaurants cooling one food, with a high worker-to-manager ratio (> 4), and food safety trained managers were more likely to leave space around containers. Restaurants serving more meals a day (> 300) with food safety trained managers had greater overall cooling guideline adherence. **Conclusions:** Results of this study suggest that food safety programs may wish to consider providing manager food safety training, and focusing intervention efforts on independent restaurants serving ≤ 300 meals a day.

Board 54. Restaurant Characteristics Associated with Good Hot Holding Practices

S. Onyeabor, MD, MPH[1], E. Hoover, PhD[2], L. Brown, PhD[2]
[1]Morehouse School of Medicine, Atlanta, GA, USA, [2]Center for Disease Control and Prevention, Atlanta, GA, USA

Background: The majority of foodborne disease outbreaks occur in restaurants; 9% of these restaurant outbreaks are the result of improper hot holding of potentially hazardous food. State and local food safety regulations require restaurants to hot hold food at or above to prevent pathogen growth. To examine associations between restaurant and worker characteristics and hot holding practices, the Centers for Disease Control and Prevention's (CDC) Environmental Health Specialists Network (EHS-Net) conducted this study. **Methods:** EHS-Net, a collaborative program of federal, state, and local environmental health programs, designed and conducted this study. Nine state and local programs were funded by CDC to participate in the study. The sample comprises 388 randomly selected restaurants in these nine sites. Data collectors visited each restaurant to conduct a manager interview about restaurant (e.g., ownership type, food preparation) and worker (e.g., certification, experience) characteristics, and temperature control practices (e.g., thermometer use). Data collectors also took the temperatures of cooked foods, and hot held potentially hazardous foods. We calculated descriptive statistics on hot holding practice variables and adjusted odds ratios, stratified by site, to identify ($p < .05$) significant associations between restaurant and worker characteristics and hot holding practices. **Results:** Of the 279 restaurants in which hot holding temperatures were taken, 55 (19.7%) had foods held above the regulation temperature of 135°F (57°C). Restaurants whose workers received training on food temperature control were more likely to meet hot holding regulations. Restaurants in which food was at appropriate final cook temperatures were more likely to meet hot holding regulations. Restaurants in which workers used devices (e.g., thermometer, timer) to ensure hot holding temperatures were appropriate, compared to those that used other methods (e.g., visual inspection), were more likely to meet hot holding regulations. **Conclusions:** A fifth of hot holding restaurants were holding food improperly, contributing to foodborne illness risk. Our data suggest that targeted training for workers and use of appropriate temperature control tools, such as thermometers, may improve restaurants' hot holding practices.

Influenza Surveillance

Board 55. A Visual Approach to Influenza Surveillance in the Department of the Navy

R. Payne[1], V. Paul[2], S. Rossi[3], G. Nowak[3]
[1]Battelle Memorial Institute, Hampton, VA, USA, [2]Booz Allen Hamilton, Norfolk, VA, USA, [3]Navy and Marine Corps Public Health Center, Portsmouth, VA, USA

Background: The EpiData Center (EDC) at the Navy and Marine Corps Public Health Center monitors influenza activity in the Department of the Navy (DON) and provides surveillance updates through a weekly Influenza Situation Report (SITREP). The SITREP, which began in 2008, is used by the DON's preventive medicine community and operational forces for surveillance, policy, planning, and intervention efforts. The report and indicators are reviewed and updated annually. **Methods:** The 2017-2018 SITREP revision's goal was to create a visually enhanced report that provides a concise summary of key indicators, as well as streamlined illustrations of individual indicators and their accompanying text. Best practices and examples of influenza surveillance nationally and internationally were considered during review. Each element of the report was evaluated and designed to reduce unnecessary text, increase process efficiencies, simplify the graphical display, and improve the interpretability of each indicator. **Results:** The new layout consists of a front page that serves as an executive summary, followed by detailed indicators for customers desiring an in-depth view. The primary front page visual is a dashboard overview of nine key influenza indicators, which include laboratory-positive cases, dispensed influenza antivirals, the percent of influenza-like-illness (ILI) from an outpatient setting, severity indicators, and indicators for active duty and recruit service members. The dashboard contains the indicator's name, the numeric count of cases or percent of ILI, a sparkline showing the seasonal trend, arrows indicating an absolute trend, and an activity indicator (low, normal, or elevated) showing the relationship to baselines/surveillance thresholds. Additional graphs and text for individual indicators were streamlined and, as appropriate, include baselines and thresholds to provide perspective on the volume and timing of influenza activity. Supporting surveillance from other military agencies is also highlighted. **Conclusions:** By approaching the DON's influenza SITREP with a visual, customer-focused perspective, the EDC created a report that balances the goals of providing a comprehensive picture of influenza activity and ensuring that the report is easy to follow and interpret for its DON customers.

Board 56. Comparison of Three Data Collection Systems in the Detection of Influenza during the Season 2017/2018 in Abu Dhabi, United Arab Emirates

S. Weber[1], H. Imambaccus[1], J. Lacanaria[1], S. Abdulmajeed[1], K. Encelan[1], E. Al Zaabi[2], M. Al Mullah[3], F. Al Hosany[3]
[1]Reference Laboratory for Infectious Diseases and National Influenza Reference Center (proposed), Abu Dhabi, United Arab Emirates, [2]Pathology and Laboratory Medicine Institute SKMC, Abu Dhabi, United Arab Emirates, [3]Department of Health, Abu Dhabi, United Arab Emirates

Background: It is important for public health officials to accurately detect the rising in numbers of influenza viruses during the season. In January 2017, the Department of Health (DOH) Abu Dhabi in collaboration with the laboratory at Sheikh Khalifa Medical City (SKMC) established an influenza-like-illness (ILI) sentinel system with 7 Health Care Centers participating in the surveillance. Every tenth patient presenting with an ILI was subsequently screened with a naso-pharyngeal swab. We here present a comparison of the data from this sentinel and the data of the mandatory e-notification system and the data of influenza assays performed as part of the clinical diagnostic. **Methods:** Data from the e-notification system, the sentinel and diagnostic influenza assays were collected and extracted into Excel (Microsoft, Redmont, USA). Data were then cleaned regarding redundancies and entry errors, transformed into a standardized format, and then transported into Stata14 (Stata Inc., Austin, Texas, USA) for statistical analysis. **Results:** Data of all three collection systems indicated a steep rise in influenza A virus infections early in October 2017. Data from the Sentinel and the laboratory assays showed that this was due to the H1N1 subtype. All three data systems correctly identified the increase in cases. Due to these data, public education was intensified and high numbers of residents were subsequently vaccinated. Newly detected influenza virus infections, therefore, fell below the expected numbers in the months of January and February 2018 indicating improved pro-

tection within the community. **Conclusions:** In Abu Dhabi, all three available data collection systems are able to detect a significant rise in influenza infections. However, only laboratory and sentinel data were able to provide information about the influenza subtype. Further typing of the isolated strains by the Centers of Disease Control confirmed that the H1N1 virus strains were mostly of the H1N1 Michigan subtype, which is included in the vaccine. Our data show that the new Sentinel system as it was introduced in Abu Dhabi in January 2017 is able to support Public Health professionals in their decision making.

Board 57. Setting Up an Indian Network of Population-Based Surveillance Platform for Influenza and Other Respiratory Viruses among Elderly (INSPIRE)

R. Kumar[1], R. Amarchand[1], S. Saha[2], A. Prabhakaran[3], K. Lafond[2], G. P[1], R. Kumar[1], S. Kanungo[4], A. Chakrabortty[4], P. Rajkumar[5], G. CP[5], V. Potdar[6], S. Bhardwaj[6], L. Dar[1], A. Krishnan[1]
[1]All India Institute of Medical Sciences, New Delhi, India, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Centers for Disease Control and Prevention, New Delhi, India, [4]National Institute of Cholera and Enteric Diseases, Kolkata, India, [5]National Institute of Epidemiology, Chennai, India, [6]National Institute of Virology, Pune, India

Background: Elderly are at high risk of complications from respiratory disease but may not seek care in formal health facilities because of socioeconomic and accessibility issues. We established a community-based surveillance network to estimate the burden of influenza and respiratory syncytial virus (RSV) associated acute respiratory illness to guide prevention and control policy for elderly. **Methods:** We set up a network of community-based acute respiratory infection (ARI) surveillance sites at four locations in India, attached to national institutes with good research and laboratory capacity. One of the sites was rural, while rests were urban. Trained project staff mapped the surveillance sites, listed all households and collected baseline demographic data using standard protocols developed for the surveillance platform from August to December 2017. We enrolled all consenting persons aged 60 years or more in the household for weekly home-visits to assess ARI by trained nurses. We defined an ARI case as new onset or worsening of one of the four symptoms: cough, difficulty in breathing, sore throat and nasal discharge in past 7 days. The nurses are using Open Data Kit™ based tools on mobile tablets for faster collation and transmission of data. Nasal and oropharyngeal swabs are being collected from 20% of randomly selected ARI cases daily for laboratory testing for influenza and RSV viruses by reverse transcriptase-polymerase chain reaction (RT-PCR). An external quality control process was established in all site laboratories. **Results:** Out of total 4309 persons approached, 4157 (96.5%) comprising 56.6% females consented for weekly ARI surveillance. Median age of participants was 65 years (IQR: 62-70 years) and 9.8% had history of chronic respiratory disease. Mock surveillance using mobile tablets allowed identification and resolution of issues in the interface and data management system. All four sites have successfully completed the laboratory quality control process. The network began ARI surveillance from 1st January 2018. **Conclusions:** A network of community based ARI surveillance sites was set up in India, which may be used for estimating the morbidity of influenza and RSV-associated illness. The platform can also be used for vaccine studies and to evaluate and inform the marginal value of investing in influenza prevention and control measures.

Board 58. Influenza Seasonality in Kathmandu: Seven Years Trends and Lessons Learned

K. Baral[1], S. Upadhyay[1], B. Upadhyay[2], B. Acharya[3]
[1]Patan Academy of Health Sciences, Kathmandu, Nepal, [2]National Influenza Center, Kathmandu, Nepal, [3]Epidemiology and Disease Control Division, Kathmandu, Nepal

Background: In 2006, Nepal prepared the National Avian Influenza and Influenza Pandemic Preparedness and Response Plan. Since then the program has been implemented as part of the national health activities. In 2009, Patan Academy of Health Sciences in collaboration with the Ministry was awarded a grant from US CDC, which led to the implementation of influenza surveillance that aimed at identifying influenza seasonality and circulating types of viruses including novel ones. In 2013, surveillance of Severe Acute Respiratory Illness was added to the program. **Methods:** Nepal has established several influenza surveillance sentinel sites, Patan Hospital, a Tertiary Care, being one among them. In 2011, influenza-like illness (ILI) Surveillance started among general outpatient visitors and continues to date. The site collects year-round data using WHO case definition. A sampling frame was developed and used to collect data and specimens with PCR tests carried out at the National Influenza Center. **Results:** Data showed, out of the total outpatient visitors ILI comprised less than 1%, between 0.42 to 0.99% in different years. Reasons for low reporting may be -for minor illnesses' like ILI patients' preferred over the counter medications to visiting Hospitals. Patients' complex health-seeking behavior could be another reason. Therefore, it reflects seasonality and circulating types of viruses instead of prevalence. Data showed that influenza winter season usually starts mid-January ending in March or beginning April depending on the duration of winter that year. The summer season normally begins late June and lasts until September, depending on the duration of monsoon. The data from 2011 to 2017 year-round surveillance shows a Bi-model seasonality. An average influenza positive rate in samples is found between 18 to 40%, the highest in 2016 and lowest in 2014. Predominantly influenza A (A H3 and A H1N1 pdm09) viruses are found during winter and both A group and B in summer. Influenza Activity levels in both seasons different year to year. **Conclusions:** This sentinel site has generated longitudinal ILI data since 2011 and is the only year-round data from the program. The information is used for policy dialogue for vaccine introduction as well as program planning which uses knowledge of seasonality and circulating type of viruses.

Board 59. Defining Influenza Baselines and Intensity Threshold Values Using 3 Indicators in Iran

P. Hemmati[1], M. Gouya[1], A. Haghdoost[2], K. Seif Farahi[3], D. Eibach[4], N. Schwartz[4], J. May[4], P. Parchami[5], J. Ahmadi Gasem Kheili[6]
[1]Iranian Center for Communicable Diseases Control (CDC), Ministry of Health & Medical Education, Tehran, Islamic Republic of Iran, [2]Dept. of Epidemiology, Kerman University of Medical Sciences & Health Services, Kerman, Islamic Republic of Iran, [3]Independent Researcher, Toronto, ON, Canada, [4]Bernhard Nocht Institute for Tropical Medicine (BNITM), Hamburg, Germany, [5]Iran University of Medical Sciences & Health Services, Tehran, Islamic Republic of Iran, [6]Independent Software Analyzer, Tehran, Islamic Republic of Iran

Background: A significant proportion of the global burden of acute lower respiratory infections is attributable to influenza and respiratory syncytial virus. There are few estimates of seasonal epidemic thresh-

old for influenza and acute respiratory infections in the WHO Eastern Mediterranean region. The objectives of this study were estimations of the epidemic, intensity and post-epidemic thresholds using three indicators i.e. severe acute respiratory infection (SARI), flu-associated SARI (F-SARI) and ILI (influenza-like illness) data. **Methods:** Countrywide data on these 3 indicators for the last 5 years were extracted from the electronic platform of the Iranian Influenza Surveillance System (IISS). By applying the open-source R-based application called Moving Epidemic Method (MEM) the epidemic, intensity and post-epidemic thresholds for the 3 indicators were estimated in the past 5 seasons. And the thresholds for the coming 2017-18 flu season were estimated. **Results:** Based on calculations with MEM in September 2017, the average epidemic start week were estimated as weeks 49, 48 and 41 for SARI, F-SARI and ILI indicators respectively. The sensitivity and specificity of those indicators were calculated as 0.86 & 0.92, 0.88 & 0.94, 0.79 & 0.76 respectively. In the 2017-18 season, epidemic thresholds for SARI and F-SARI were in fact trespassed in week 42 and 44, showing a timeliness of 6 and 7 weeks respectively (EWAR capacity). **Conclusions:** Knowing that the coming epidemic would start in November 2017, we could start preparedness measures since September well before the epidemic. Indeed, by the intensity thresholds, CDC could provide weekly feedbacks to provinces and labs for a better response according to the epidemic dynamics. It was realized that in case of a good recording of ILI syndrome by sentinel sites, it could even predict the seasonal flu 2 to 4 weeks sooner than the other two indicators.

Board 60. The Results of Influenza Sentinel Surveillance in Ukraine in 2017-2018 Season

A. Mironenko, O. Smutko, L. Radchenko, O. Holubka, O. Onyschenko, A. Fesenko, L. Leibenko
L.V. Gromashevsky Institute of Epidemiology & Infectious Diseases NAMS of Ukraine, Kyiv, Ukraine

Background: During the 10 last years the influenza sentinel surveillance system is functioning in Ukraine. The clinical and epidemiological information were collected from 18 adult and pediatric clinics in four cities located in different geographical regions of the country (Kyiv, Dnepropetrovsk, Odessa, and Khmelnitsky). The epidemiological and virological information were collected during the whole year. **Methods:** Throat swabs from patients of sentinel sites in different regions of Ukraine were collected. The specimens were tested for influenza by real-time polymerase chain reaction (RT-PCR) and viruses were isolated in MDCK and MDCK-SIAT cell culture from PCR-positive samples. The epidemiological and virological data of SARI cases are submitted to TESSy system on a weekly basis with the number of samples tested, number of influenza virus detections by (subtype) and population denominators. The sequencing some Ukrainian isolates were performed in WHO CC (CDC, Atlanta, USA) and WHO CC (London). **Results:** The 2017/18 influenza season in Ukraine was lower than three previous seasons. Besides reported influenza activity was lower than in the previous seasons. Up to week 08 2017/18, 173 ILI samples had been tested and 59 (34%) were positive; 377 SARI samples had been tested and 148 (39 %) were positive. Of the 59 ILI positive samples, 95% were influenza B; of the 149 SARI positive samples, 88% were influenza B. Most number of B viruses was belonged to B/Victoria linage strain B/Brisbane/60/2008, especially in the start of season. Among all A viruses 2/3 were subtyped as A(H3N2) and 1/3 – as A(H1N1)pdm09 subtype. Some specific mutations were found in Ukrainian isolates. One of them is associated with antiviral resistance and another – with increasing virulence. **Conclusions:** During the 2017/18 season the predominant circulating strain was the seasonal influenza virus B/Brisbane/60/2008 – B/Victoria lineage. Influenza viruses B/Yamagata lineage, virus A(H3N2), and A(H1N1) pdm09 were also circulated. The proportion of types and subtypes in Ukraine was different than in neighboring countries.

Board 61. Descriptive Analysis of National Sentinel Surveillance System Data for Influenza Virus Subtypes Circulating among Children Under 15 Years of Age in Pakistan

M. Malik[1], N. Badar[2], M. Salman[2], M. Ranjha[2], A. Ikram[2]
[1]Field Epidemiology & Laboratory Training Program, National Institute of Health, Islamabad, Pakistan, [2]National Institute of Health, Islamabad, Pakistan

Background: In Pakistan, there is a dearth of evidence for influenza disease burden and its circulating subtypes. This study was aimed to describe epidemiological characteristics and seasonal trends of influenza virus subtypes among children ≤15 years age. **Methods:** A retrospective laboratory record review of influenza samples received from sentinel sites from 2014-2016 was carried out at National Institute of Health, Islamabad. Respiratory samples of children ≤15 years along with epidemiological information were reviewed. Samples were tested by PCR assay for detection and typing of influenza virus. Descriptive analysis was carried out and seasonal trends were determined by Epi-Info and R software. **Results:** A total of 2,327 samples were tested and 315 (14%) were found positive. Among positive samples, predominant viral-subtype was influenza A(H1N1)pdm09 (n=129; 40%), followed by influenza B virus (n=93; 30%) and influenza A(H3) (n=93; 30%). Median age was 4 years (range <01 month-15 years). Maximum number of cases were found from age groups 1-5 years (n=104; 33%) followed by <1 years (n=96; 30%), 6-10 years (n=75; 24%), and 11-15 years (n=40; 13%). Male to female ratio was 2:1. Most prevalent viral subtype in children <5 years was influenza A(H1N1)pdm09 (n=85; 43%) followed by influenza A(H3) (n=61; 30%) and influenza B (n=54; 27%). Seasonal trends revealed high number of cases for these viral subtypes during January-March each year while maximum cases of influenza A(H1N1)pdm09 (n=125; 97%) and influenza-B (n=73;79%) were found during November-April, and influenza A(H3) (n=89; 95%) during December-February. Maximum cases were reported from Federal areas (n=220; 70%) followed by Gillgit-Baltistan (n=39; 12%), Punjab (n=29; 09%), AJK (n=24; 08%), and Balochistan (n=03; 01%). **Conclusions:** The most prevalent viral subtype was influenza A(H1N1)pdm09 and maximum number of cases were found in children under 5 years age. A high incidence of cases was seen during January-March. Effective surveillance for observing changing trends, dissemination of health advisories and vaccination is need of the time.

Board 62. Withdrawn

Board 63. A Surge in Influenza Illness in Pregnant Women during the 2017-2018 Season: A Brief Report From Active Surveillance for Influenza-Associated Respiratory Illness in Suzhou, China

L. Chen[1], S. Zhou[2], L. Bao[1], Y. Pang[1], Y. Tan[1], Y. Song[2], R. Zhang[2], D. Iuliano[2], M. Thompson[2], C. Greene[2], J. Zhang[1]
[1]Suzhou Center for Disease Control and Prevention, Suzhou, China, [2]United States Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: We conducted active surveillance among pregnant women in Suzhou to assess incidence of influenza associated acute respiratory illness (ARI). **Methods:** From 2015-2018, we enrolled cohorts of pregnant women from prenatal care (PNC) facilities, each year beginning in Oct. Women planning to deliver in Suzhou visiting selected PNC facilities for routine care were eligible. Nurses conducted twice weekly follow-up to capture ARI, defined as >1 respiratory symptom (cough, sore throat, stuffy nose, chest pain, difficulty breathing) and >1 systemic symptom (feverish, temperature ≥38°C, chills, headache) or >2 respiratory symptoms. For reported ARIs, combined nasal/throat swabs were collected. **Results:** As of Jan 31, 2018, we approached 17,670 pregnant women and enrolled 15,468 (88%). Of 5,622 ARIs reported within 10 days of onset, 94% had samples collected. Among the enrolled, zero (upper 95% CI: 0.02%) reported influenza vaccination during pregnancy. During 2015-2016, influenza circulated in Dec-April and July 2016; in the Jan 2016 peak, 37 lab-confirmed influenza illnesses were detected in 2873 person-months observed, or 1.3/100 person-months (95% confidence interval [CI]: 0.9-1.8), and A(H1N1) pdm09 predominated. During 2016-2017, influenza circulated in Oct-April, July 2017 and onward; in the Dec 2016 peak, 55 influenza illnesses were detected in 3547 person-months observed for an incidence of 1.6/100 person-months (95%CI: 1.2-2.0), and A(H3N2) predominated; a late summer peak occurred in Sep 2017, with 7 influenza illnesses detected in 645 person-months observed, for an incidence of 1.1/100 person-months (95%CI: 0.5-2.1). During 2017-2018, influenza illness surged in Jan 2018, with 104 influenza illnesses in 3823 person-months observed, for an incidence of 2.7/100 person-months (95%CI: 2.2-3.3), with B Yamagata predominating. Among influenza ARIs in the first two years, 3 in 67 (4.5%) and 8 in 178 (4.5%) required hospitalization. For both years, ARI incidence was highest in 1st trimester pregnancy (14.5-24.8 person-months), while influenza incidence was highest in 3rd trimester (0.4-0.6 person-months). **Conclusions:** Influenza virus illnesses among pregnant women in Suzhou were common, particularly during the winter season of 2017-2018. Nearly 5% of influenza ARI episodes in pregnant women resulted in hospitalization.

Board 64. Epidemiology of Seasonal Influenza in Afghanistan, a Chronic Conflict Setting: Evidence from the National Disease Surveillance and Response System

M. Rasooly
Ministry of Public Health, Kabul, Afghanistan

Background: Acute respiratory infections (ARIs) is the major cause of mortality among under five children in Afghanistan. Influenza contributes substantially to the burden of ARI. There is little information about the circulating influenza virus among Afghan population. The national influenza surveillance system has been resumed its capacity to detect and confirm the circulating influenza virus since 2016. The aim of this paper is to describe the epidemiology of influenza circulating viruses in Afghanistan during 2017. **Methods:** Data was collected using the WHO standard case definition for severe acute respiratory infections (SARI) and influenza like illness (ILI) under the national influenza surveillance from nine surveillance sites across the country. Demographic and clinical data were collected along with nasopharyngeal swabs tested for influenza using real-time reverse transcription polymerase chain reaction and typed as influenza A or B, with influenza A further subtyped. **Results:** A total of 2699 SARI and ILI cases were tested for influenza, and 109 (4.4%) were positive. While 71% of all tested cases were under 5 years of age, only 55% of influenza-positive cases were under 5 years of age. The proportion of influenza A H3N2 was higher (68.8%) followed by influenza A H1N1 pandemic 2009 (15.6 %) and influenza B (15.6%). The proportion of influenza-positive cases peaked during November–December (11.5–22%) in 2017. **Conclusions:** Evidence from this study shows that despite conflict situation, the system is able to detect and confirm the circulating influenza viruses in Afghanistan. The findings indicates to focus on continuation and comprehensive influenza surveillance in the country. Further studies required to determine the burden of influenza to support decision on influenza control and prevention strategies.

Board 65. Influenza Trends and Risk Factors Associated with Influenza-Like Illness in Damanhour District, Egypt, 2011–2016

A. Mansour[1], H. Mansour[1], R. Helmy[1], S. El Alkamy[2], S. El Shourbagy[3], E. Reaves[4], M. Genedy[3], A. Kandeel[3]
[1]CDC Country Office Egypt, Cairo, Egypt, [2]Ministry of Health and Population, Damanour, Egypt, [3]Ministry of Health and Population, Cairo, Egypt, [4]US Centers for Disease Control and Prevention, Dar Es Salaam, United Republic of Tanzania

Background: Influenza is a leading cause of acute respiratory infections (ARI) with significant morbidity and mortality, globally. Surveillance of influenza is crucial to understand its impact, identify outbreaks, and develop guidelines for control. **Methods:** Between May 2011 and December 2016, we prospectively identified patients with influenza-like illness (ILI) treated at outpatient departments in three governmental and two private hospitals in Damanhour District, Egypt. Naso-oropharyngeal specimens were tested for influenza viruses and typed using real-time, reverse transcription polymerase chain reaction. Epidemiological and clinical characteristics of ILI cases were described. **Results:** Of 3983 ILI case-patients enrolled, influenza viruses were detected in 13.1% (521/3973); influenza A 9.7% (357/3684) and influenza B 4.2% (165/3941). The proportions among influenza A subtypes were H3N2 6.2% (227/3683), H1N1 pdm09 3.5 % (120/3456), and seasonal H1N1 0.2% (6/3342). No H5N1 was detected from 3712 samples tested. Enrollment was in winter months (November-February) only during 2012–2014. ILI cases with influenza A infection were characterized by cough (96.1%), sore throat (76.8%), and diarrhea (11.0%); 52.4% (187/357) were males and 69.7% (249/357) were rural residents. Influenza A was most common in age groups 20-49 year (32.2%, 115/357) and 50-64 years (25.8%, 92/357). influenza B infection was characterized by cough (97.6%), sore throat (83.4%), and diarrhea 12.7 % (21/165), and was common among males 50.3% (85/165) and age group 20-49 years (48.5%, 80/165). Risk factors associated with influenza A infection identified by univariate analysis were exposure to someone with ARI or a household contact with respiratory symptoms, and contact with birds. There were no significant factors associated with influenza B infection. **Conclusions:** influenza

viruses are a common cause of ARI among patients presenting to outpatient departments in Damanhour, Egypt. Risk factors differ between influenza types and may guide tailored control measures. Continued surveillance of influenza types is crucial to health security in Egypt and globally.

Board 66. Influenza Trends in Morocco: An Overview of Surveillance Data

M. Obtel[1,2], R. Rachid[1,3], L. Obtel[4], M. Elhakim[5], A. El Kholy[6], S. Rahman Malik[5], R. Abouqal[3], K. Idrissi Sbai[7,8]
[1]Laboratory of Community Health, Preventive Medicine and Hygiene, Rabat, Morocco, [2]WHO Consultant., Rabat, Morocco, [3]Laboratory of Epidemiology, Clinical Research and Biostatistics, Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [4]Lahcen Lyoussi College, Sefrou, Morocco, [5]Infectious Hazard Management, Health Emergencies Department, EMRO/WHO, Cairo, Egypt, [6]World Health Organization, Cairo, Egypt, [7]Laboratory of Community Health, Preventive Medicine and Hygiene, Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [8]Mohammed V Hospital of Military Instructions, Rabat, Morocco

Background: This review aims to identify reliable sources of influenza surveillance data, in Morocco, to be used for better description of morbidity and mortality trends of the disease. **Methods:** Influenza sentinel surveillance data were retrieved from the data reported to FluNet of World Health Organization (WHO). Also, a standardized questionnaire was introduced to a random sample of people living in Fez region, in Morocco, to identify the main reasons behind low rates of vaccine intake in the region. **Results:** During the last decade, the highest number of reported positive cases of influenza in Morocco was influenza A(H1N1)pdm09, specially during the pandemic period in 2009 and 2010. Influenza activity during the end of 2016 showed high activity with influenza A(H3N2) virus being the predominant circulating type with co-circulation of influenza B. Thousands of specimens were tested during this period showing 3366 positive cases for influenza viruses, 2924 (86.9%) typed as influenza A and 442 (13.1%) as influenza B. From the sub-typed influenza A, 2318 (68.9%) were influenza A(H1N1)pdm09, 538 (16%) were influenza A(H3N2) and 68 (2%) were seasonal influenza A(H1N1) and influenza A(not-subtyped). In addition, the influenza like-illness cases in Morocco showed seasonal pattern with the peak occurring every year during winter season, around Epi week 40 (October) to Epi week 12 (March). The main results of this study were: a lack of information in the general population regarding influenza vaccine; inaccuracy of its efficacy and efficiency; and non-availability of the vaccine in the Moroccan medical structures. **Conclusions:** Data provides a comprehensive description of the influenza trends in Morocco. Policy makers should take serious measures regarding the awareness of general population regarding the influenza vaccine.

Board 67. National Surveillance for Influenza-Like Illness in Lao PDR, 2013-2017

K. Vilivong, O. Keosavanh
National Center for Epidemiology and Laborarory, Vientiane Capital, Lao People's Democratic Republic

Background: Influenza-like-illness (ILI) is an important public health problem worldwide. In 2006, the Ministry of Health established national influenza surveillance to monitor the circulation of influenza viruses. The results from the hospital-based sentinel surveillance system for ILI in seven hospitals in Lao PDR from January 2013 to December 2017 are presented. **Methods:** We undertook retrospective analyses of monthly trends in influenza virus activity using Lao PDR national influenza surveillance data. Clinical and epidemiologic data were collected in outpatient pediatric and adult departments in 6 provincial hospitals and 1 military hospital, designated as influenza surveillance sites, from patients with influenza-like-illness (ILI). ILI was defined as fever or history of fever and cough with illness onset within 7 days. Nasal and throat specimens were collected and tested for influenza virus type and subtype by RT-PCR. Data were analyzed to describe frequency, seasonality, and distribution of circulating strains. **Results:** A total of 7404 patients with ILI were enrolled, 1265 (17.1%) were influenza positive. Of the 1,265 influenza positive patients 724 (57.2%) tested positive for influenza A, and 541 (42.8%) for influenza B. Among the influenza A patients, 515 (71.1%) tested positive for influenza A(H3N2), 208 (28.7%) for influenza A(H1N1)pdm09 and 1(0.1%) were influenza A/untyped. The percent of ILI specimens testing positive for influenza exceeded 17% during two peaks (August-November and January-February) in 2013, 2014, 2015, and 2017. Influenza activity only exceeded 17% during one peak (August-December) in 2016. Influenza B was detected in the 541cases during 5 years surveillance and the predominant influenza A hemagglutinin subtype detected was 111, 109, 193, 113, and 200 cases in 2013-2017, respectively. The number of ILI cases tested, and the percentage testing positive for influenza, were 172(8.8%), 386(19.5%), 259(27.1%), 351(18.2%), and 97 (16.6%) in the age group of less than 23 months, 2-7 years, 8-18 years,19-45 years, and more than 45 years, respectively. The percentage that tested positive was significantly higher in the school aged group (8-18 years) than other age groups. **Conclusions:** Influenza circulates year round, often with two peaks. School children were most likely to test positive and vaccination strategies should consider the seasonal peaks observed in Lao PDR.

Board 68. Seasonal Influenza among Unvaccinated Children in Khartoum State during February 2017–February 2018

E. Aljak[1], M. Eldegail[1], O. Elbadri[2], A. Osamn[1], L. Badi[1], M. Azhari[2], R. Mohammed[3]
[1]National public Health Laboratory, Khartoum, Sudan, [2]Ferdral Ministry Of Health, Khartoum, Sudan, [3]Mohammed Alamin Hamid Hospital, Khartoum, Sudan

Background: This study was carried out to detect the rate of seasonal Influenza among unvaccinated children as a part of surveillance program in Khartoum state during Feb 2017–Feb 2018 influenza season is an annually recurring time period characterized by the prevalence of outbreaks during the cold half of the year. Influenza is a contagious respiratory illness caused by influenza viruses that infect the nose, throat, and sometimes the lungs. It can cause mild to severe illness, and at times can lead to death Anyone can get the influenza (even healthy people), and serious problems related to the influenza can happen at any age, but some people at high risk of developing serious influenza-related complication (the immune compromised people, pregnant woman, the elderly, and children. **Methods:** Upper respiratory tract specimens (nasopharyngeal swabs) were collected in viral transport media VTM to detect influenza virus using molecular assay RT-PCR. **Results:** During the period from Feb 2017– Feb 2018, 200 patients from Mohamed Alameen Hamed Hospital were enrolled. Of speci-

mens tested, 10 (5%) were positive for influenza A. The majority 8 (4%) were seasonal influenza A(H3 N2), which was the dominant circulating influenza A virus subtype; while the rest 2 (1%) were unsubtypable. All the cases were children aged 5–17 month (males constituted 55%; while females constituted 45%). **Conclusions:** Influenza surveillance among children in Khartoum state confirmed that is circulating seasonal influenza virus although there is no active influenza vaccination program, so vaccination is very important factor that can control the spread of the virus.

Board 69. Epidemiological and Molecular Description of an Outbreak of Influenza A (H1N1)pdm09 in Tunisia during 2017-2018 Season

A. El Moussi[1], S. Abid[1], L. Charaa[1], N. Jarroudi[1], I. Landolssi[1], D. Arab[1], M. Nasr[1], L. Maazoui[2], N. Ben Alaya[2], A. Slim[1]
[1]National Influenza Centre-Tunis, Unit Virology, Microbiology Laboratory, Charles Nicolle Hospital, Tunis, Tunisia, [2]Primary Health Care Directorate, Tunis, Tunisia

Background: Influenza viruses are significant human respiratory pathogens that cause both seasonal, endemic infections and periodic, unpredictable pandemics. The incidence of recurring epidemics is primarily attributed to the high frequency of mutational changes in the HA and NA genes. **Methods:** The detection and subtyping of influenza viruses was conducted by real time RT-PCR. We performed sequencing and phylogenetic analysis of HA gene influenza A viruses collected from severe and fatal cases to verify previously known and novel mutation that can be the virulence factors. **Results:** A total of 1654 patient were enrolled during the 2017-2018 season. 641 patients positive for influenza A or B viruses, and 537 (83.7%) of them were confirmed with influenza A subtype A (H1N1)pdm09, 99 (15.44%) cases has the subtype A(H3N2) and only 5 cases were confirmed with influenza B. During this period, A (H1N1)pdm09 was the predominant epidemic strain and caused 90% of severe cases and 98.5% of fatal cases. A total of 68 deaths was directed correlated due to the infection of A (H1N1) pdm09. The highest rate of positivity (85%) was observed during the week 52. The phylogenetic analysis of HA gene of A (H1N1)pdm09 revealed the emergence of a specific Tunisian cluster differentiated by the amino acid substitutions S74R, S164T, R223Q, and I295V into the vaccine clade 6B.1. **Conclusions:** Epidemiological data show increase of pandemic influenza A activity in Tunisia in comparison with previous seasons which is the subtype A(H3N2) was the predominant virus. The ARI incidence was above 90 %. The virulence of A(H1N1) pdm09 virus can be explained by the high genetic variation observed in HA gene. We observed a severity of influenza A virus infection was related to underlying patient diseases, such as chronic lung disease and deaths. But further studies are needed to confirm associations between mortality and genetic substitutions in the viruses.

Board 70. Viral Acute Lower Respiratory Infections among Elderly in a Community Cohort in North India

G. Gopal[1], R. Kumar[1], R. Amarchand[1], S. Saha[2], D. Purakayastha[1], A. Wahi[1], R. Chhokar[1], A. Choudekar[1], R. Kumar[1], S. Kapoor[3], L. Dar[1], K. Lafond[4], S. Jain[4], A. Krishnan[1]
[1]All India Institute of Medical Sciences, New Delhi, India, [2]Centers for Disease Control and Prevention, New Delhi, India, [3]Centre for Chronic Disease Control, New Delhi, India, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Viruses are important etiologic agents for acute lower respiratory infections (ALRI) among elderly. However, there are no data from India on the viral etiology of community-acquired ALRI among this group to inform preventive and treatment strategies. This study presents the viral pathogens detected among ALRI cases in a community-based cohort of elderly in rural north India. **Methods:** Between January 2015 and January 2017, we enrolled consenting elderly as they aged ≥60 years and screened weekly for acute respiratory infection (ARI) by trained workers. ARI was defined as either new onset or worsening of any of the following symptoms in past 7 days: cough, sore throat, breathing difficulty and running nose. Trained nurses examined the ARI cases to classify as ALRI if the respiratory rate was >20/minute, and presence of one of the following: chest pain on respiration, wheezing, or sputum production. Nasal and throat swabs were collected and transported in viral transport medium to the laboratory within 24 hours in cold chain. We tested samples for influenza viruses, respiratory syncytial virus (RSV), human metapneumovirus (hMPV), and parainfluenza viruses (PIV) using real-time polymerase chain reaction (RT-PCR). **Results:** During the study period, we enrolled 1404 elderly, which included 357 with chronic respiratory disease (CRD). We detected 977 ALRI cases and collected samples, majority (70.4%; 688/977) of which were from persons with CRD. We detected at least one virus in 6.4% (62/977), which included influenza (23/62; 37.1% (95% CI: 25.2 – 50.3)), RSV (19/62; 30.6% (95% CI: 19.6 – 43.7)), PIV (12/62; 19.4% (95% CI: 10.4 – 31.4)) and hMPV (9/62; 14.5% (95% CI: 6.9 – 25.8)). Among 23 influenza positive samples, we detected 13 A (H3N2), 7 A(H1N1)pdm09 and 3 B viruses. There were few viral co-detections (2; 0.2%). Overall viral detection was significantly higher (11.1% vs. 4.4%, $p<0.001$) among non-CRD ALRI (32/289) compared with ALRI (30/688 CRD), as was influenza detection (4.8% vs. 1.3%, $p<0.001$). **Conclusions:** Influenza was the most common virus detected among elderly with ALRI in this rural Indian population. The low viral yield among elderly ALRI cases and lower viral detection among those with CRD needs further investigation. Further community-based research is required to understand the etiologic spectrum and incidence of ALRI among the elderly in India to help inform future vaccine policies in India.

Board 71. Severe Acute Respiratory Infection (SARI) in Qatar, January–December 2017

H. Al -Romaihi, N. Ganesan, S. Nadeem, S. Hamad J. Al Thani, A. Elberdiny
Ministry of Public Health, Doha, Qatar

Background: Influenza can cause severe acute respiratory infection in young children and elderly people worldwide. The aim of this study was to identify viral pathogens of SARI associated hospitalization among children and elderly patients in Qatar. **Methods:** A retrospective study was conducted at Hamad General Hospital (January 1 to December 31, 2017). Eligible patients who met the standardized SARI case definition were enrolled. Demographic, epidemiological information, as well as nasopharyngeal and/or oropharyngeal swabs was collected for respiratory virus isolations by RT-PCR. **Results:** Of 534 enrolled patients, 70.4 % were male and 29.6 % were female. Almost 99.6% presented with a cough, followed by fever (99.1%), shortness of breath (22.8%), and nasal congestion (57.5%). During hospitalization, 22 of 534 (4.1%) were admitted to intensive care unit (ICU), and 3 of 534 (0.6%) died. Of patients who were positive for SARI, most (117/534, 21.9%) were between 18 to 49 years old. Most of the patients who were positive SARI

had pneumonia (97.4%). Patients with one, two, and three respiratory virus was isolated in 310/534 (58.1%), 30/534(5.6%), and 4/534 (0.7%) respectively. 202/534 (37.8%) were positive for influenza viruses, of which (173/534, 32.4%) were influenza A and (29/534, 5.4%) were influenza B. Other respiratory virus testing results included 63 (11.8%) for respiratory syncytial virus, 30 (5.6%) for *Mycoplasma pneumoniae*, 26 (4.9%) for rhinovirus, 15 (2.8%) for human coronaviruses, 13 (1.9%) for parainfluenza viruses, 12 (2.2%) for human metapneumovirus, 10 (0.9%) for adenovirus 5 (0.9%) for Boca virus. Seasonal incidence rates of 4.1%, 7.9%, and 7.3% was observed in October, November, and December, respectively. **Conclusions:** Seasonal influenza plays a prominent role for all SARI in Qatar. Additional focus on the role of other respiratory viruses will help to minimize mortality and morbidity related to pneumonia .Surveillance activities should be strengthened to curtail pneumonia related respiratory illnesses in Qatar.

Board 72. Analysis of SES of SARI in the Republic of Kazakhstan 2014/2015 & 2015/2016

A. Myrzabekova
Epidemiological Surveillance Department of Consumers' Rights Protection, Shymkent, Kazakhstan

Background: SES of SARI was introduced in Kazakhstan in 2008.The purpose-to analyze SES of influenza among SARI patients in Kazakhstan during 2 influenza seasons 2014-15&2015-16 **Methods:** Comparative analysis was conducted of SARI morbidity during 2 seasons -2014/2015 (2014) and 2015/2016 (2015) in online base (http:\\ses.dec.kz). In database during season 2014 were 1,398 SARI patients and 1,985 during 2015. Clinical, epidemiological, and lab data on SARI cases were collected based on the questionnaire and were put into the electronic system. Swabs from nose and throat were taken for lab testing from SARI patients who met the standard case definition. The samples were examined in virology labs of sentinel regions using PCR and «*AmpliSens*» test systems made in Russia. **Results:** The first positive results for influenza during 2014 were obtained on 48 week, during 2015 – on 46 week. The highest SARI incidence rate during 2014 were observed during 01 - 03 weeks of 2015: from 389 to 466 per 1,000 hospitalized. The SARI incidence rate was fluctuating from 171 to 444 per 1,000 hospitalized in 2015. Patients admitted to the ICU during 2015 were 3.0% (60) SARI patients, compared to 2.7% (38) in 2014 (p=0.3); obtaining oxygen therapy 1.0% (21) compared to 0.3% (5), accordingly, (p=0.009); with shortness of breath 74.8% (1,486) compared to 72.6% (1,015), (p=0.07). During 2015 the prevailing subtype of influenza A was A/H1N1-09, it was observed in age group 30-64: 32.5% (169/520). During 2014 influenza A/H3N2 was observed in age group 15-29: 43.6% (106/243). Among children under 14 influenza A/H1N1-09 during 2015 - 37.3% (194/520), during 2014 influenza A/H3N2 – 34.9% (85/243). **Conclusions:** Earlier beginning of the influenza season was in 2015-2016 and a longer period of hospitalization of SARI patients, with high SARI morbidity rates, unlike 2014-2015. 2015-2016 was characterized by prevailing circulation of virus of flu A/H1N1-09, mainly in age gr. 30-64, and also among children under 14. During 2014-2015 the virus circulating in the country was A/H3N2, which was observed mainly in age gr. 15-29 and among children under 14.

Board 73. Withdrawn

Board 74. Respiratory Disease Surveillance on the United States–Mexico Border, 2016–2017

P. Kammerer[1], P. Kriner[2], M. Fierro[2], E. Fabian[3], Y. Medrano[3], A. Hawksworth[1], P. Graf[4], C. Myers[4]
[1]Henry M. Jackson Foundation for the Advancement of Military Medicine, Bethesda, CA, USA, [2]Imperial County Department of Public Health, El Centro, CA, USA, [3]California Department of Public Health, Sacramento, CA, USA, [4]Naval Health Research Center, San Diego, CA, USA

Background: The Naval Health Research Center collaborates with the Border Infectious Disease Surveillance program and state and local public health agencies to conduct respiratory disease surveillance along the US–Mexico border. Influenza-like illness (ILI) surveillance is conducted in 4 outpatient clinics. Severe acute respiratory infection (SARI) surveillance is conducted in 3 hospitals. We present the results of this surveillance for 2016-2017 and report on the performance of the Quidel Sofia rapid influenza diagnostic test (RIDT). **Methods:** Nasal swabs were collected from patients with ILI (fever ≥ 100˚F and sore throat or cough) or SARI (fever ≥ 100.5°F (or reported fever) and a cough/sore throat with a hospital admission, or a child < 5 years with hospital admission for suspected pneumonia). Specimens were tested for respiratory pathogens with polymerase chain reaction (PCR) techniques. For the outpatients with ILI, a nasal swab was also used to run the Quidel Sofia RIDT. RIDT results were compared with PCR results to determine sensitivity and specificity. **Results:** In 2016–2017, 503 specimens were collected from ILI patients and 304 specimens from SARI patients. The most common ILI pathogen was rhinovirus (18%), and the most common SARI pathogen was respiratory syncytial virus (RSV; 30%). Influenza A was detected in 17% of the ILI specimens and 7% of the SARI specimens. Overall sensitivity and specificity of the Quidel Sofia RIDT were 72% and 93%, respectively. Influenza A sensitivity and specificity were 75% and 98%, while influenza B were 50% and 94%, respectively. **Conclusions:** Border surveillance provides a means to identify emerging diseases, characterizing the changing patterns of respiratory pathogens. Of interest, we found RSV at higher levels in SARI patients than in past years, identified in as many as 33% of the specimens in one hospital. The Quidel Sofia performance was similar to prior years and better that the previously used Quidel QuickVue RIDT.

Board 75. Influenza-Associated Hospitalization among Children Less Than Five Years of Age in Suzhou, China, 2011- 2016

J. Yu[1], X. Zhang[1], W. Shan[1], J. Gao[1], J. Hua[2], J. Tian[2], Y. Ding[2], J. Zhang[3], L. Chen[3], Y. Song[4], S. Zhou[4], D. Iuliano[4], C. Greene[4], T. Zhang[1], G. Zhao[1]
[1]Fudan University, Shanghai, China, [2]Suzhou University Affiliated Children's Hospital, Suzhou, China, [3]Suzhou Center for Disease Prevention and Control, Suzhou, China, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Although seasonal influenza vaccination is recommended for young children in China, coverage is low. Studying the burden of severe illness from influenza infection in young children will inform vaccine policy and program investment. **Methods:** We conducted prospective, severe acute respiratory infection (SARI) surveillance at Suzhou University Affiliated Children's Hospital (SCH) to identify influenza-associated hospitalizations in SCH in children <5 years of age from Oct 2011 to Sept 2016. SARI was defined as fever (mea-

sured axillary temperature ≥38°C) and cough or sore throat/inflamed or red pharynx in the past 7 days that required hospitalization. Nasopharyngeal swabs were collected from all respiratory ward SARI patients whose guardians consented. Using SARI surveillance data and a healthcare utilization survey, we defined the catchment population to estimate the burden of influenza-associated SARI hospitalizations in the city of Suzhou in this age group during the 5 years. We adjusted the number of SARI patients in the catchment area to the 67% residents who sought care at SCH. **Results:** Of 36,313 SARI cases identified, 2,297 from respiratory wards were sampled; of these, 259 (11%) were influenza positive. Estimated annual influenza-associated SARI hospitalization rates per 1,000 children <5 years of age were: 23 (95% confidence interval[CI]: 20-27) in the 2011-2012 season with A/H3N2 as the predominant virus (59%); 5 (95% CI: 4-7) in the 2012-2013 season with B as the predominant virus (46%); 11 (95% CI: 9-13) in the 2013-2014 season with A/H3N2 as the predominant virus (71%); 6 (95% CI: 4-7) in the 2014-2015 season with A/H3N2 as the predominant virus (55%); and 7 (95% CI: 5-9) in the 2015-2016 season with both A/H1N1pdm09 (50%) and B (50%) predominating. Age-specific influenza-associated SARI hospitalization rates for the 5 years were 17 (95% CI: 11-22) per 1,000 children aged 0-5 months; 12 (95% CI: 10-14) per 1,000 children aged 6-23 months; and 7 (95% CI: 6-8) per 1,000 children aged 24-59 months. **Conclusions:** From 2011-2016, influenza-associated SARI hospitalization rates among children <5 years in Suzhou, China were high, particularly in children aged 0-5 months. Immunization for children >6 months, and maternal and caregiver immunization for those <6 months, could reduce influenza-associated hospitalizations among young children in Suzhou.

Board 76. Trends of Viruses Causing Respiratory Illness in Qatar, January–December 2017

S. Nadeem, A. Elberdiny, H. Romaihi, N. Ganesan
Ministry of Public Health, Doha, Qatar

Background: Respiratory illnesses are a significant cause of morbidity and mortality globally. In Qatar, a comprehensive surveillance system exists, comprising of influenza-like illness (ILI) and severe acute respiratory infection (SARI) and identification of the viruses causing the respiratory illnesses in the country. **Methods:** Nasopharyngeal and/or oropharyngeal swabs were collected from eligible patients (using WHO standard case definitions) from selected patients with ILI at the sentinel primary health care center sites and all patients with SARI admitted to sentinel hospitals for the year 2017. At the NIC, samples were analyzed by real-time polymerase chain reaction. **Results:** In the study period, 24,435 patients were enrolled and tested; 19,970 (81.7%) of which tested positive for respiratory virus infection. Out of these, 6,113 (25.0%) were positive for influenza; 4,556 (74.5%) of which were influenza A and 1,557 (25.5%) were influenza B. Sub-typing of influenza A showed 2,798 (61.4%) were influenza A(H1N1)pdm09. Other respiratory viruses isolated included rhinovirus 4,252 (17.4 %), RSV 3,215 (13.2%), Parainfluenza virus 1,320 (5.4%), Adenovirus 1,518 (6.2%), Coronaviruses 1,118 (4.6%), Boca virus 746 (3.1%), human metapneumovirus (hMPV) 643 (2.6%), *Mycoplasma pneumoniae* 285 (1.2%), and Parechovirus 127 (0.5%). Out of total reported respiratory illness cases in 2017 Qatari's account for 34.2% (8364) followed by Indians 13.1% (3204) and Filipinos 9.8 % (2402). The higher proportion was seen amongst males 56.1% (13698). For the entire respiratory panel as well as influenza A, the age group of less than 4 years was the most affected [50.3% (12 301) of all enrolled cases and 42.0% (2566) of influenza positive]. The distribution of cases shows seasonality; the peak of influenza virus was observed during October to December (weeks from 40 to 52). The highest cases were reported during week 50. **Conclusions:** Most of the respiratory illnesses in Qatar for 2017 were seen to be caused by Influenza A, Rhino Virus, RSV, Influenza B and Adeno Virus; this would thus influence the appropriate public health preventive measures, the clinical management and outcome of the patient. The influenza A & B cases can be effectively prevented by the seasonal flu vaccination every year. Moreover, it suggests the importance of public health education on non-pharmaceutical preventive measures.

Board 77. Epidemiology and Assessment of a SARI Sentinel Site in Egypt

M. Elhakim[1], S. Kandil[1], K. Mahmoud[1], M. Obtel[2], W. Anwar[1]
[1]Faculty of Medicine, Ain Shams University, Cairo, Egypt, [2]Faculty of Medicine and Pharmacy, Mohammed V University, Rabat, Morocco

Background: Sentinel surveillance for severe acute respiratory infections (SARI) in Egypt began in 2009 and occurs in eight hospitals. Avian influenza is endemic, and human cases of A(H5N1) are reported annually since 2006. This study aims to assess the SARI sentinel surveillance in a major sentinel site in the country. **Methods:** Data was collected from 2013-2015 from Abbasia Fever Hospital in Cairo. Epidemiology of SARI cases was studied, as well as, a questionnaire was developed and used to collect necessary data for assessment of the surveillance system at the sentinel site. **Results:** During the study period, 1254 SARI cases, conform with WHO case definition, were admitted to the hospital representing 5.6% of admitted patients for all causes and 36.6% from acute respiratory infection patients. 1250 cases (99.7%) were tested, and 263 cases (21.04%) tested positive. 128 cases (48.7%) were influenza A viruses, while 66 cases (25%) were influenza B. From influenza A, 64 cases (24%) were influenza A(H1N1)pdm09, 60 cases (23%) were influenza A(H3N2), and 4 cases (2%) were influenza A(H5N1). Under 5-year-old is the predominant age group with 443 cases (35.3%). The seasonality of the influenza data is conform with the northern hemisphere pattern . The influenza vaccination rate among patients was less than 1%. A questionnaire for assessment of sentinel site was developed using a checklist extracted from WHO and CDC guidelines. **Conclusions:** The study shows that SARI leads to substantial morbidity in Egypt. SARI sentinel surveillance is mandatory for a country like Egypt, with more than 90 million population. There is a great need for a high-quality surveillance system; especially with endemic respiratory threats in the country like the avian influenza A(H5N1), as well as in the neighboring countries like the Middle East respiratory syndrome (MERS) in Saudi Arabia.

Board 78. Seasonal Influenza and Severe Acute Respiratory Infection Surveillance, Lebanon, 2015-2018

N. Ghosn[1], N. Haddad[1], M. Saleh[1], R. Farah[1], M. Al Buaini[2], P. Zalloua[2], P. Mrad[3], A. Rady[3], L. Bazzi[4], R. Saidy[5], I. Ismail[2], M. Lteif[6], O. Kiwan[7], N. Nahouli[8], D. Merhej[9], R. Ahmad[10], E. Saad[11], F. Abou Rjeily[12], W. Ammar[1]
[1]Ministry of Public Health, Beirut, Lebanon, [2]Rafic Hariri University Hospital, Beirut, Lebanon, [3]World Health Organization, Beirut, Lebanon, [4]Saida Governmental Hospital, Saida, Lebanon, [5]Elias Hraoui Zahleh Governemental Hospital, Zahleh, Lebanon, [6]American University of Beirut - Medical Center, Beirut, Lebanon, [7]Ain Wa Zein Hospital, Ain Wa Zein, Lebanon, [8]Hammoud Hospital, Saida, Lebanon, [9]Centre Hospitalier Universitaire Notre Dame de Secours,

Jbeil, Lebanon, [10]Tripoli Governmental Hospital, Tripoli, Lebanon, [11]Mounla Hospital, Tripoli, Lebanon, [12]Khoury Hospital, Zahleh, Lebanon

Background: Seasonal and pandemic influenza constitutes a health burden for countries. Effectiveness of seasonal and pandemic influenza preparedness plan relies on availability of national and global surveillance data. Since 2014, the Ministry of Public Health (MOPH) has established severe acute respiratory infection (SARI) surveillance with the support of World Health Organization (WHO). The objectives of SARI surveillance are to understand national influenza epidemiology, detect novel viruses and contribute to global influenza surveillance network. **Methods:** Case definition is any person presenting fever with cough requiring hospital admission. Sentinel surveillance approach is adopted with selection of hospitals from public and private sectors covering different provinces. In each site, focal person is designated and trained on case detection, case investigation and data management. Nasooropharyngeal swab is collected, preserved in viral transport media and referred to the National Influenza Center (NIC). At NIC, specimen is tested by polymerase chain reaction for influenza A/B panels. Results are communicated to MOPH, hospitals, and WHO platforms. Data is archived in hospital database concatenated in national database at MOPH level. For feedback, monthly bulletin is disseminated via official website and mailing list. **Results:** Three seasons are described. From September 2015 to February 2018, 12 hospitals participated in SARI surveillance. 3185 cases were detected and 93% sampled for nasooropharyngeal swabs. 10% were influenza positive. Among positive, 56% were male, 34% aged under 5 years, 14% 5-14y, 34% 15-64y and 17% at least 65y. 46% were in pediatric ward, 39% in internal medicine, and 9% in intensive care units. 19% had chronic conditions. 2% received seasonal influenza vaccine. Influenza seasons showed 1 or 2 waves, starting earliest at week 40 or latest at week 52. Peaks varied from week 52 to week 9. Dominant types/subtypes were B (43%), H3 (31%), and H1pandemic2009 (20%). Seasons included 3 types (2015/2016 and 2017/2018) or 2 types (2016/2017). **Conclusions:** There is no standard pattern for seasonal influenza. There is need to monitor continuously influenza infection. Such knowledge will set baseline profile, alert/outbreak thresholds, estimate diseases burden, identify severity factors and guide influenza prevention program.

Board 79. Results of Sentinel Epidemiological Surveillance of Severe Acute Respiratory Infections (SARI) in the Republic of Kazakhstan during Epidemiological Seasons 2012/2013-2016/2017

M. Sultanova[1], G. Muratbayeva[2]
[1]Committee of Public Health Protection of Ministry of Health of the Republic of Kazakhstan, Astana, Kazakhstan, [2]CDC/Central Asia Regional office, Almaty, Kazakhstan

Background: Sentinel epidemiological surveillance of SARI was started in Kazakhstan in 2008 in three regions. There are 25 sentinel hospitals in 9 regions of the republic located in various geographic areas now. The purpose of this work was description of SARI morbidity during the last 5 epidemiological seasons (2012/2013–2016/2017) in Kazakhstan. **Methods:** The studied populations were the residents of the sentinel regions who have addressed sentinel hospitals for medical aid with sample collection for laboratory tests of patients above one year old, who met the standard case definition of SARI case (WHO Euro, 2011). **Results:** During the last 5 epidemiological seasons, SARI morbidity rate increased from 300 per 1,000 hospitalized in 2012-2013 to 700 in 2016-2017. The main SARI symptoms were temperature ≥38ºC and cough, which were observed in 100% of cases. Shortness of breath had children aged one to 4, up to 70% and 70% among persons above 65 year old, which were observed during last 5 seasons. The percent of influenza positive results among pregnant women ranged from 36% (48/132) in 2014-2015 season to 47% (169/361) in 2016-2017. During 2012-2013 season circulation of viruses A/H1N1/09pdm and A/H3N2 was noted, with prevalence of virus A/H3N2-52% (150/287). During the following 2013-2014 season influenza virus B was not detected. During epidemiological season 2015-2016 in 80% (451/565) of cases influenza virus A/H1N1/09pdm circulated and during season 2016-2017 influenza virus A/H3N2 – 58% (409/704) and B 42% circulated (295/704). **Conclusions:** In various epidemiological seasons circulation of various influenza viruses were observed. During season 2016-2017 the SARI morbidity has grown by 3.5 times due to improvement of epidemiological surveillance. Growth of the number of positive influenza results among pregnant women was observed due to the improvement of their selection according to the standard case definition.

Preparedness and Global Health Security

Board 80. Challenges and Opportunities for Building Zoonotic Disease Surveillance Systems through GHSA Efforts in Sierra Leone

D. Peprah
USAID, Freetown, Sierra Leone

Background: Sierra Leone's Ebola Virus Disease (EVD) outbreak exposed gaps not only in human but also animal disease surveillance systems. However, the country's measurable improvements in human disease surveillance have not been reflected on the animal side. Zoonotic disease surveillance and laboratory systems received the lowest scores in the country's Joint External Evaluation (JEE) in November 2016. USAID, through its Global Health Security Agenda (GHSA) efforts in Sierra Leone, is addressing this gap through a suite of projects to improve animal disease surveillance, behavior change communication for zoonotic diseases, animal health workforce development and One Health strengthening at district and national levels. With many of the projects approaching mid-point, it is important to understand progress, challenges and opportunities for the remainder of GHSA programming. **Methods:** Primary methodology utilized reviews of country-specific zoonotic disease assessments, program reports and evaluations. They included but were not limited to the Joint External Evaluation, quarterly GHSA inter-agency reports and FAO's surveillance evaluation tool (SET) for livestock surveillance. **Results:** USAID's GHSA projects in Sierra Leone have revived the country's only veterinary diagnostic laboratory, supported zoonotic disease prioritization and trained community animal health workers. While these efforts have provided the foundation for a zoonotic disease surveillance system, several systemic challenges persist. They include government hiring restrictions for new animal health workers, lack of policies to guide the animal health sector, a weak national One Health platform and limited coordination among donor organizations. These challenges threaten to undermine ongoing efforts and opportunities for improved zoonotic disease surveillance. **Conclusions:** Improvements to zoonotic disease surveillance systems remain essential to preventing future outbreaks and protecting the health of Sierra Leoneans and the global community. However, current investments in Sierra Leone's animal

disease surveillance can only be optimized if systemic issues related to sector governance and donor coordination are addressed.

Board 81. A Survey on Implementation of the One Health Approach for Preparedness and Control of MERS-CoV in the Gulf Cooperation Council (GCC) and Middle East Countries

E. Farag[1], M. Nour[1], E. Ahmed[2], J. Berrada[3], A. Moustafa[1], M. Mehmood[1], M. Mahmoud[4], A. El-Sayed[1], F. Alhajri[4], M. Al-Hajri[1], O. Hassan[5], H. Al-Romaihi[1], M. Al-Thani[1], S. Al-Marri[1], M. Koopmans[6], M. Haroun[4]
[1]Ministry of Public Health, Doha, Qatar, [2]FAO, Roma, Italy, [3]Institut Agronomique et Vétérinaire Hassan, Rabat, Morocco, [4]Ministry of Municipality and Environment, Doha, Qatar, [5]Institute of Health and Society, Center for Global Health ,Oslo University, Norway, Oslo, Norway, [6]Erasmus Medical Center, Rotterdam, Netherlands

Background: The response to the newly recognized Middle East respiratory syndrome coronavirus (MERS-CoV) was challenging due to many uncertainties regarding modes of transmission, the growing evidence of the potential camels' role in the virus transmission, along with the inherent value of camels in the Arabic culture, and the consequent need for collaboration between public health and veterinary authorities. Challenged for the first time with a serious zoonotic outbreak, Gulf Corporation Council (GCC) countries were introduced to One Health as a model to foster a coordinated action joining health and veterinary authorities in investigation, control of MERS-CoV. The purpose of this study is to gauge a preliminary understanding as to which extent the involved countries' policies and practices were in accordance with the one health approach. Also, the study explored policies and practices related to the One Health approach in support of surveillance and control of MERS-CoV at the human-animal interface. **Methods:** A survey was conducted in GCC countries Egypt and Jordan with the aim to monitor the early preparedness and response trends, policies, and practices determining the potential of these areas responding to the Middle East respiratory syndrome coronavirus (MERS-CoV) based on the One-Health approach. **Results:** The obtained results revealed that involved countries adopted One Health in varying degrees while responding to MERS-CoV. The majority of the countries established joint emergency committees and had joint teams for investigation and response. the study highlighted the lack of political will as one of the key gaps in the adoption of One Health, it called for taking the epidemic as a chance to promote the inter-sectorial collaboration to contain MERS-CoV and enhance preparedness for other possible emerging zoonotic diseases. **Conclusions:** Based on the experience gained in addressing MERS-CoV at the human-animal interface, One Health appears to gaining momentum in some GCC countries, but much remains to be done, particularly at the level of policy makers, also bolstering collaboration mechanisms during peacetime with priority given to capacity building, resource allocation, joint research, laboratory diagnostic services, the implementation of feasible biosecurity measures, and emergency risk communication.

Board 82. Standardized Quantitative and Qualitative Analysis of Software Solution Decisions for the Task Force for Global Health

M. Yost-Daljev[1], J. Padgett[2]
[1]J Michael Consulting, Buford, GA, USA, [2]Breckenridge and Associates, Woodstock, GA, USA

Background: The Task Force for Global Health (TFGH) requires a standardized, quantitative process for choosing software solutions that meet their program needs. Software selection is vital to all health agencies and this method provides a process to document the suitability of multiple solutions and reach consensus on the software to which best meets the requirements of the agency. **Methods:** The method for software solution evaluation includes seven process steps. Step 1 starts with an environmental scan to identify solutions that potentially meet the needs of the TFGH program. The team researches industry literature and corporate information as part of the environmental scan. In step 2, the team further analyzes and reduces the field of potential solutions. A questionnaire is sent to the select vendors, along with TFGH requirements and business process information. In step 3, the team schedules preliminary software demos and interviews with vendors who received the questionnaire and are interested in providing a demo. In step 4, the team further reduces the field based on the preliminary demos and interviews. The vendors with the most promising solutions are then invited to provide a more formal and extensive solution demonstration and presentation. Step 5 involves analyzing evaluation results from the formal demonstrations and reducing the number of solution vendors to around 2-4 competitors. Request for Proposals (RFPs) are then sent to these solution vendors. In step 6, each vendor proposal is reviewed and scored. The scoring methodology is based on the Analytic Hierarchy Process (AHP) and includes specified evaluation criteria and weighted scoring models. Step 7 brings the review team together to discuss and gain a consensus on the final ranking of the vendor solutions. **Results:** This process yields fully documented, quantifiable evidence regarding how well the software vendors meet the requirements of the stakeholders. **Conclusions:** By using a process that includes both extensive research and live demonstrations of potential solutions, better software solution decisions can be made. This method can be scoped to large or small software needs across any health or scientific industry.

Board 83. Using Rapid Diagnostic Tests in a Public Health Response: A Framework Approach for Thinking Beyond Test Accuracy

G. Rainisch, B. Greening, C. Atkins, V. Jeisy Scott, W. Lonergan, A. Balish, M. Meltzer
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Rapid Diagnostic Tests (RDTs) are increasingly available and offer simplicity, quick results, and generally affordable price. However, the public health benefits from using RDTs in a response setting are rarely evaluated. **Methods:** We developed a modeling framework to evaluate and compare RDT utilization strategies and testing algorithms. The framework produces estimates of clinical outcomes, resource requirements, and estimates how these measures vary with phase and scale of an outbreak and test accuracy uncertainty. During the 2014-2016 Ebola epidemic in West Africa, we used the framework to compare RDTs being considered for either of two utilization strategies: 1) Triage of patients presenting at medical facilities with clinical symptoms of Ebola, and 2) Testing cadavers in the community. We used the framework to calculate positive and negative predictive val-

ues (PPVs/NPVs) for the RDTs at different values of Ebola prevalence, analyzing them as standalone tests, or as part of 2-test algorithms. We then converted PPV and NPV values into the percent of patients expected to be treated appropriately and inappropriately to compare RDTs and the two utilization strategies. RDT performance data were obtained from public sources and Ebola prevalence was estimated. **Results:** Using the 3% estimated Ebola prevalence at the time of analysis, we show that the optimal algorithm (fewest false positives/negatives) for patient triage used two different RDTs sequentially, resulting in a 2-test 10% false positive rate and <1% false negatives. Based on the single RDT available to test cadavers, and an estimated 7% prevalence of Ebola-infected cadavers, we estimated 24% false positives and <1% false negatives. **Conclusions:** Our framework allows direct evaluation of health outcomes associated with RDTs, as well as resource requirements during an outbreak. It provides public health officials a more complete picture of RDT impacts, evaluating more than just test accuracy.

Board 84. Global Emergency Vaccine Stockpiles: Progress and Persistent Challenges

A. Hill[1], S. Richardson[2], T. Nguyen[1]
[1]World Health Organization, Geneva, Switzerland, [2]Research Department of Epidemiology and Public Health, International Centre for Life Course Studies in Society and Health, University College London, London, United Kingdom

Background: WHO-supported stockpiles of therapeutics exist to provide a timely, coordinated response to complex, large-scale outbreaks of vaccine-preventable diseases at the global level. Their governance aims to ensure availability of, fair and consistent criteria for access to, and equitable allocation of, scarce resources. Their mechanisms for funding, procurement, request coordination and vaccine release criteria vary. Three stockpiles are managed by the International Coordinating Group on Vaccine Provision (ICG), which reviews emergency vaccine requests from individual countries and other institutions and makes decisions on allocation. **Methods:** We reviewed the governance and allocation mechanisms of meningitis, yellow fever and cholera emergency vaccine stockpiles, and performed a descriptive analysis of vaccine requests to the ICG in 2016–2017. Time durations for each part of the ICG process were compared against time performance targets and challenges in implementing timely vaccine allocation were identified. **Results:** All 54 vaccine requests were circulated to the ICG for decision-making within one working day. Decisions were reached in ≤2 working days for 95%, 94% of 88% of meningitis, yellow fever and cholera requests respectively. Time between decision and reception of vaccines by affected countries was ≤7 days for 31%, 25% and 10% of requests. Over 50 million emergency vaccine doses were shipped to 16 countries for crisis response. Delays occurred in completion of ICG requests by requestors, vaccine shipment and in-country customs clearance. Gaps in laboratory, surveillance, logistics and outbreak response capacity remain challenges at the country level. **Conclusions:** Significant progress has been made in widening access to life-saving vaccines. The ICG mechanism has helped overcome the "first-come, first-served" approach which led to inefficient and inequitable vaccine allocation in the past. Delays may have undermined the effectiveness of vaccination campaigns. Vaccine shortages underscore the continuing importance of the ICG mechanism in ensuring equity in access and allocation. Vaccination is only truly effective alongside comprehensive disease control strategies that include strengthening surveillance, outbreak response and healthcare access at the country level.

Board 85. Prevention of Infectious Diseases Associated with Mass Gatherings Through Use of Vaccines: International Perspectives and Outstanding Questions

S. Malik[1], M. Obtel[2], P. Mala[1], Z. Memish[3], M. El Hakim[1]
[1]World Health Organization, Eastern Mediterranean Regional Office, Cairo, Egypt, [2]Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [3]College of Medicine, Alfaisal University, Riyadh, Saudi Arabia

Background: Mass gatherings (MGs) are usually pre-planned large events, and its association with the occurrence and spread of vaccine-preventable infectious diseases are well described. The aim of this presentation is to identify risks of vaccine-preventable diseases in MGs, evidence gathered so far on the effectiveness of vaccination policies for MG events, and the outstanding questions that need to be addressed for future considerations of new vaccines. **Methods:** A literature review has been conducted on this subject summarizing the documented risk of vaccine-preventable diseases in mass gatherings, available evidence on the effectiveness of vaccination policies for reducing disease transmission associated with these events and the outstanding questions that need to be addressed for future consideration of some new and promising vaccines. **Results:** The Hajj, the annual Muslim pilgrimage, stands out as the only MG event where limited data on vaccine–preventable health risks are available, including policies on vaccines use for the attendees and plausible effectiveness of such policies. Data on the vaccination requirements for attendance in other mass gathering events such as Kumbh Mela and other religious, sports and entertainment events are lacking. Apart from the Hajj information, no data is available on the possible impact of a vaccination policy on the control of infectious disease transmission in mass gatherings. **Conclusions:** The current lack of evidence on the exact burden and magnitude of vaccine preventable health threats associated with MG events limits recommendations regarding immunization in mass gatherings. The wider lessons from the Hajj is that the use of vaccines in mass gatherings can be effective not only in conferring protection to the vaccinated individuals but also to unvaccinated contacts, contributing to the development of herd immunity and also in preventing rapid international spread of preventable health risks. Appropriate research is warranted to address knowledge gaps required to improve the development and dissemination of vaccine strategies in MGs. In addition, some outstanding questions need to be addressed before considering the use of new vaccines, which offer promising public health benefits in MG events.

Board 86. Finding Outbreaks Faster: A Framework for Measuring the Public Health Response to Infectious Disease Outbreaks

A. Crawley, N. Divi, L. Gresham, M. Libel, M. Smolinski
Ending Pandemics, San Francisco, CA, USA

Background: Rapid detection, reporting, and response to infectious disease outbreaks are critical to the global health community's efforts to prevent outbreaks from becoming regional epidemics or pandemics. As countries strive to meet obligations under the International Health Regulations (IHR) there is a notable gap in the current global health architecture in measuring the timeliness of the public health response to infectious disease threats. Through a series of retrospective pilot studies in twenty-eight countries, Ending Pandemics worked with governments and partner organizations to assess a framework for tracking timeliness of response metrics at the national level. **Methods:** Ending

Pandemics, in collaboration with Ministries of Health, Field Epidemiology Training Programs, and NGOs, provided support and technical assistance to 28 countries to implement retrospective examination of 5-10 years of data on the timeliness of the public health response to priority diseases. These measures included quantifying the time interval between disease onset of the index case in an outbreak and (a) the date of outbreak detection, (b) the date of outbreak reporting to health authorities, (c) the date of laboratory confirmation from an epidemiologically linked case, and (d) the date of implementation of initial control measures. **Results:** Baseline measurements of outbreak response timeliness were established, against which future progress can be measured. Results varied due to differences in country's priority diseases and capacity for responding to disease outbreaks. Few countries collect the required timeliness data in a routine manner, requiring extensive data collection and extraction processes. Missing data and heterogeneous data collection practices were common. Nevertheless, many countries noted improvements in timeliness measures and found significant value in assessing gaps highlighted by these evaluations. **Conclusions:** This study lays the groundwork for refining a framework of timeliness metrics as indicators of outbreak preparedness. National and international partners are essential to help fill IHR surveillance gaps identified in this study.

Board 87. Successful Pilot of Event-Based Surveillance in Viet Nam

A. Mounts[1], T. Do[1], A. Dao[1], C. Bernadotte[2], H. Nguyen[3], Q. Nguyen[3], T. Phu[4], Q. Tran[4], A. Balajee[5]
[1]US Centers for Disease Control and Prevention (CDC), Hanoi, Viet Nam, [2]PATH, Seattle, WA, USA, [3]PATH, Hanoi, Viet Nam, [4]Vietnam Ministry of Health, General Department of Preventive Medicine, Hanoi, Viet Nam, [5]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA

Background: The World Health Organization defines two types of surveillance, indicator-based, which requires regular reporting based on case definitions and event-based surveillance (EBS) to detect signals that represent the emergence of outbreaks. In Viet Nam, the Ministry of Health (MOH) piloted a comprehensive program of EBS in 2017 that incorporated signal reporting from community level and health care facilities (HCFs) in six provinces. **Methods:** A program evaluation was conducted using a combination of online questionnaires, summary analysis of reported events, field visits with focused interviews at each administrative level. **Results:** A total of 331 outbreak events were reported during the 14 months of pilot from the six provinces involved. The majority (82%) of outbreaks were reported by from the commune level from the community level from a variety of sources with village health workers and teachers being the most common. Reported events included clusters of vaccine preventable diseases, dog-bites, and poultry die-offs. Several challenges were noted: (1) guidance for EBS reporting was interpreted to sometimes be in conflict with existing reporting requirements, (2) some signals were not well understood, and (3) CHWs and their supervisors felt that monetary incentives were important for sustainability. **Conclusions:** Currently, the MOH is working on a final revision of EBS guidelines with the intention implementing the program nationally in 2018. Successful adoption of the program by the MOH was credited to the following factors: the EBS program (1) fit within the existing legal framework. Without the legal mandate to report, EBS could not have been supported by the local government or implemented by the local departments of health. (2) It enhanced the existing surveillance platform by providing guidelines and SOPs for operationalizing EBS. (3) It addressed MoH stated need for early detection and rapid reporting of outbreaks.

Board 88. Assessing Applied Epidemiology Competencies in the South Carolina Department of Health and Environmental Control (SC DHEC) Workforce

D. Drociuk, M. Barker, L. Bell, M. Overman
South Carolina Department of Health and Environmental Control, Columbia, SC, USA

Background: In 2005, the Centers for Disease Control and Prevention (CDC) and Council of State and Territorial Epidemiologists (CSTE) developed applied epidemiology (epi) competencies that provided a foundation for expectations and training programs. Using these competencies, we assessed SC DHEC epidemiologists in the central office Division of Acute Disease Epidemiology (DADE) and our Regional Outbreak Response Teams (ORTs). **Methods:** Two online survey tools were developed reflecting the CDC/CSTE competencies. The first assessed epi capabilities among four multi-disciplinary Regional ORTs, via an assessment performed by each Regional Epidemiology Program Manager (REPM). The REPMs assessed the "Competency," "Training needs," and "Relevance to daily function" of their ORT across 23 epi skills. The second survey was directed to DADE epidemiologists, who were to self-assess their "Competencies," "Importance in their current position," and "Frequency of use" for 31 epi skills identified in the CDC/CSTE Tier 2 Epidemiologist competency assessment. The survey goal was to determine a base-line of skills and competencies for which targeted training will be developed. Responses were measured via Likert scales and comparisons were made by descriptive statistics and weighted rank order. **Results:** Four of 4 REPMs (100%) and 21 of 25 DADE epidemiologists (84%) responded to their respective surveys. Responses from REPMs indicated highest competence and lowest need for training for skills related to "carrying out an outbreak investigation using existing guidance and resources". Lowest competence and highest need for training were indicated for "use of statistical software" and "creating an analysis plan." Responses from DADE epidemiologists indicated highest competency in "articulating the need for further investigation from provided data." Lowest competence was reported in "providing epi input for community planning processes" and "developing program logic models/theories of action." **Conclusions:** Ongoing assessments and targeted training are effective methods to maintain an effective, highly functioning public health workforce. SC DHEC has a robust epi capacity with varying levels of experience at both the state and regional level. DADE will use these results to design targeted training to continue developing our epi workforce response capability.

Board 89. Reestablishment of Diagnostic and Surveillance Laboratory Activities at the Puerto Rico Department of Health after Hurricane Maria

M. Hardy
CDC, Atlanta, GA, USA

Background: The devastation caused by Hurricane Maria did not spare public health laboratories, which are considered critical facilities following a natural disaster. This manuscript documents the difficulties of reinitiating laboratory testing in Puerto Rico and what specific efforts were needed after an event that affected the United States' largest jurisdiction to lose its public health laboratories (PHL). This

report describes the reestablishment of laboratory testing at the Puerto Rico Department of Health (PRDH). **Methods:** Deployed staff conducted laboratory assessments. The CDC Laboratory Team (23 Spanish-speaking deployers from October 2017 through May 2018) aligned recovery activities with laboratory QMS principles, and developed and integrated QMS tools to response and recovery efforts. In addition to the procurement of critical lab supplies in collaboration with CDC Foundation, infectious disease testing needed to be reestablished. To reestablish interim clinical diagnostic testing and surveillance for priority pathogens identified by PRDH and CDC, sample shipping and tracking systems were implemented in coordination with local, federal, state, and non-governmental partners. **Results:** The implementation of enhanced QMS practices for specimen shipping and tracking led to a reduction in shipping time from 1.3 days in November 2017 to 1.0 days in December. The resources created during this response are being made available in the public domain, including a Sample Shipping and Tracking Log Template; an Inventory and Priority Supplies Template; an Emergency Laboratory Quality Kit; and, a Training Manual for Laboratory Team deployers. The freely available templates and tools enable laboratory staff and administration to review, edit as appropriate, and incorporate these elements into their own preparedness plans. **Conclusions:** The response conducted by the CDC Laboratory Team could be used by other jurisdictions to inform their Continuity of Operations Plans and improve their response to a future event. The same tools that assisted with the reestablishment of services can provide a framework for preparedness. The goal is to enhance preparedness of public health laboratory facilities by implementing workflows for preparedness and mitigation tools. Due to the seasonal nature of hurricanes, the information should be appropriately disseminated across the PHL network.

Board 90. Improving Medical Preparedness for Highly Infectious Diseases in Taiwan from 2015 to 2017

H. Ko, H. Kao, P. Guo, P. Liu, S. Chou, C. Chen
Taiwan Centers for Disease Control, Taipei, Taiwan

Background: The Communicable Disease Control Medical Network (CDCMN) has been established in Taiwan since the SARS outbreak in 2003, to receive patients with highly infectious disease and further ensure surge capacity during epidemics. In 2014, the framework of CDCMN had been readjusted from 22 responding hospitals (RH) and 17 supporting hospitals (SH) to 6 regional RH and 6 regional SH on the ground of centralization of medical resources without change of total amount of governmental budget. We evaluated the operation of the CDCMN from 2015 to 2017 after the adjustment. **Methods:** The evaluation of the adjustment strategy of the CDCMN is conducted by compiling data from the annual reports of each RH, SH and local health bureaus since 2015. The amount of budget, the number of training activities, the maintenance of medical workforce and the status of negative pressure isolation rooms was retrieved from 2015 to 2017. In addition, areas which needed improvements were identified through the meetings of regional consultation committee. **Results:** Within unchanged total budget, the mean amount of yearly budget per RH from 2015 to 2017 averagely increased by 148.4% (range from 60.5% to 227.4%) compared to the budget in 2013. The budget was used for the maintenance of negative pressure isolation rooms and training program for healthcare workers. The qualification rate in the annual performance testing of negative pressure isolation rooms in 2017 (85%) improved by 15% compared to the rate in 2015 (70%). In terms of personnel training, the passing rate of first-shift healthcare workers in RH increased from 70% in 2015, 85% in 2016, to 100% in 2017. The regional support workforce's training completion rate averagely increased from 68% in 2015, 89% in 2016, to 89.5% in 2017. Identified areas that needed improvement include the need for negative pressure isolation ward inspection and the development of core skills and scenarios in the training program. **Conclusions:** The strategy adjustment of the CDCMN in 2014 resulted in the raised budget per facility through centralization of resources and was associated with enhanced performance of RH and SH. The CDCMN will continue its core preparedness work and enhance the quality of isolation wards and training events to effectively combat highly infectious pathogens and to ensure patients and healthcare workers' safety.

Board 91. Beyond Ebola: Are We Ready?

S. Vanairsdale[1], J. Hillman[2], C. Kraft[2], A. Vasa[3]
[1]Emory University Hospital, Atlanta, GA, USA, [2]Emory University, Atlanta, GA, USA, [3]Nebraska Medicine, Omaha, NE, USA

Background: When providing care to patients with Ebola and other special pathogens, safety is essential for the patient, healthcare providers, and community. As the United States began to care for citizens with Ebola in August 2014, gaps within the healthcare system became evident after two nurses were infected with Ebola while providing patient care in a Texas hospital. In early 2015, the US Department of Health and Human Services (HHS) initiated programs to address Ebola clinical care preparedness and response. The National Ebola Training and Education Center (NETEC), a collaboration between three academic medical centers, was created by HHS to increase the capability of US healthcare systems to safely and effectively manage individuals with suspected and confirmed Ebola and other special pathogens. **Methods:** In response to the 2014 Ebola outbreak, HHS Office of the Assistant Secretary for Preparedness and Response and the Centers for Disease Control and Prevention contacted US facilities who successfully treated patients with Ebola to develop an infrastructure to disseminate best practices, standardize patient care, and improve the safety for patients and healthcare professionals. These three institutions have collaborated to create NETEC. NETEC promotes quality and excellence in patient care by developing risk assessment metrics, completing onsite hospital assessments, implementing educational offerings, designing an online resource repository for preparedness tools, and creating a research infrastructure for experimental measures. NETEC strives to optimize high-reliability performance related to efficient, effective, and safe patient-centered care. **Results:** Between July 2016 and June 2017, NETEC held 24 educational activities, including didactic courses, simulation courses, webinars, and conference presentations, reaching 3490 people, nearly a 9-fold increase compared to the previous year. Forty states, the District of Columbia, and 5 US territories were represented at in-person trainings. There were 31,687 NETEC.org page views, and 606 technical assistance requests regarding protocols and procedures were addressed. **Conclusions:** The 2014 Ebola outbreak provided an opportunity to take inventory of US preparedness. In today's world of global travel, infectious diseases pose a threat to all healthcare workers. NETEC is positioned to help the United States be prepared for the next outbreak.

Board 92. Political Corruption and State Failure: How Macro Level Pathologies Increase the Risks of Emerging Infectious Disease

T. Hirschfeld
University of Oklahoma, Norman, OK, USA

Background: Since the end of the Cold War a number of macro level changes have combined to increase global health risks from emerging infectious diseases. Most notably, institutions of democratic governance have weakened or failed in many countries, leaving large populations without the protections of citizenship, statehood or a functioning public health sector. The disruption of sanitation and vector control initiatives in these spaces increases the risks of preventable diseases like cholera and yellow fever. A second set of risks emerges from the predatory intrusion of violent non-state actors (VNSAs) such as warlords and organized crime groups in these "ungoverned spaces." **Methods:** This paper will begin with an overview of recent research in the field of international political economy detailing how macro level trends such as increasing rates of grand corruption have challenged the ability of fragile states to comply with IHR requirements, and increased population health risks in two recent epidemics of emerging infectious disease. **Results:** The case studies presented underscore the need for incorporating political fragility as a variable in epidemiological risk modeling. **Conclusions:** The IHR facilitates global health security by formalizing collaborative work between WHO Member States to identify, detect and respond to lethal outbreaks. Political pathologies such as instability, warlordism, armed conflict, and grand corruption, however, may lead to interruptions in public health prevention activities and reduced compliance with IHR guidance. Recognizing these potentialities will improve predictive risk modeling for future outbreaks.

Board 93. Towards Early Detection, Assessment, and Response to Acute Public Health Events: Tunisian Experience

H. Bouguerra[1], S. Bougatef[1], S. Chelly[1], H. Letaief[1], S. Rejaibi[1], M. Nachtnebel[2], L. Hollenweger[2], D. Kücükali[2], H. Bellali[1], N. Ben Alaya[1]
[1]National Observatory of New and Emerging Diseases, Tunis, Tunisia, [2]German Partnership Program for Excellence in Biological and Health Security, Robert Koch Institute, Germany

Background: Due to the worldwide changes occurring lately, including population movement, emergence of new diseases, chemical and nuclear incidents and other public health threats, adapting public health surveillance systems is essential. In this context and according to International Health Regulations (IHR), countries should implement an early warning and response system (EWARS) with its Event-Based surveillance (EBS) component in addition to the routine Indicator-Based surveillance (IBS). **Methods:** We described the development of the national Communicable Diseases Surveillance System and the implementation process of EWARS in Tunisia. We also assessed the progress achieved and the challenges faced. **Results:** The national Surveillance System of Communicable Diseases in Tunisia is based on two main institutions under the supervision of the Ministry of Health: the Primary Health Care Directorate; national IHR focal point and in charge of IBS, and the National Observatory for New and Emerging Diseases; created in 2008 with principal mission the establishment of EWARS. EWARS was progressively improved by involving partners not only from other disciplines such as ministries of Agriculture and Environment but also the private health sector (clinicians and laboratories). EWARS was strengthened in 2015 by the implementation of EBS through an epidemiological teleconference platform (EpiTec). This platform allows the most relevant stakeholders in surveillance both at the national and the regional level (regional directorates) to share new health events at weekly intervals. Many workshops for developing standardized procedures and curricula as well as trainings and simulation exercises were organized with stakeholders' participation. **Conclusions:** In Tunisia, significant progress has been made in the implementation of EWARS in order to comply with IHR requirement with the ultimate aim the contribution to global public health. However, many challenges remain, especially on organizational, financial and operational aspects. More efforts should also focus on better contribution of other sectors and better sharing of information.

Board 94. The Joint Mobile Emerging Disease Intervention Clinical Capability (JMEDICC): A Mobile Clinical Trials Capability for Rare and Highly Infectious Pathogens

K. Martins[1], J. Ake[2], D. Brett-Major[3], C. Cando[4], A. Cardile[5], G. Christopher[6], D. Clark[7], M. Doan[8], A. Fox[9], C. Hatcher[5], J. Hepburn[7], H. Kibuuka[10], M. Kozlowski[4], M. Lamorde[11], S. Mate[12], C. Ritchie[1], S. Zaman[7]
[1]USAMRIID, Laulima contractor, Fort Detrick, MD, USA, [2]US Military HIV Research Program, Bethesda, MD, USA, [3]Uniformed Services University, Bethesda, MD, USA, [4]Medical Countermeasure Systems BioDefense Therapeutics (MCS-BDTX), Fort Detrick, MD, USA, [5]USAMRIID, Fort Detrick, MD, USA, [6]Medical Countermeasure Systems, Fort Detrick, MD, USA, [7]Henry M Jackson Foundation, Bethesda, MD, USA, [8]NMRC, Fort Detrick, MD, USA, [9]Naval Medical Research Unit 3, Ghana Detachment, Accra, Ghana, [10]Makerere University Walter Reed Project, Kampala, Uganda, [11]Infectious Disease Institute, Kampala, Uganda, [12]WRAIR, Silver Spring, MD, USA

Background: Licensure of medical countermeasures (MCMs) effective against rare or highly lethal pathogens is complicated by the difficulty in obtaining human clinical efficacy data. The US FDA has developed the "Animal Rule" that enables licensure when given sufficient and appropriate animal efficacy data and human safety data. However, following the 2014-2016 Ebola virus outbreak in West Africa, the FDA released additional guidance indicating that human efficacy data may be required for MCMs targeting "rare" pathogens. The US Department of Defense (DoD) funds the development of a number of MCMs for rare pathogens, including filoviruses. **Methods:** DoD has established the Joint Mobile Emerging Diseases Intervention Clinical Capability (JMEDICC) to deliver mobile clinical trials capability in an outbreak setting. In 2016, the DOD launched a pilot capability in Uganda with a focus on filovirus therapeutics. This capability requires not only clinical trial readiness from a regulatory standpoint but also enhanced infection prevention and control processes, international engagement, and a mobile response. **Results:** In the last eighteen months, the US and Ugandan JMEDICC teams 1) established a research hub site as a platform for ongoing research activities, which allows for retention of staff and continual training; 2) hired and trained clinical, laboratory, data management, and logistics teams in the quality control and documentation practices critical for FDA regulated clinical trials; 3) engaged with US, Ugandan, and international stakeholders to ensure transparency and to identify regulatory and political obstacles; and 4) established a community engagement network to reduce

the fear and skepticism associated with both filovirus outbreaks and clinical research protocols. Priorities of FY18-FY19 include establishment and exercise of the mobile capability. **Conclusions:** Through this effort, the team has identified complications and risks that may help inform treatment-oriented response efforts in future outbreaks. Moreover, while the pilot focused on filovirus therapeutics, the JMEDICC platform has the potential to be utilized for vaccine, diagnostic, and therapeutics studies for products targeting numerous pathogens that are endemic to Uganda.

Board 95. Role of Private Sector Extractive Industries during the Ebola Virus Disease Crisis in West Africa

S. Scribner[1], L. Flynn[2], W. Strong[1], S. Sylla[3], S. Duale[2]
[1]DAI Global, Bethesda, MD, USA, [2]USAID P&R Project / DAI Global Health, Bethesda, MD, USA, [3]USAID P&R Project / DAI Global Health, Conakry, Guinea

Background: During the 2014-2016 Ebola outbreak in West Africa, private sector companies, especially from extractive industries, were active participants in response efforts. The USAID Preparedness and Response (P&R) Project, as part of its mandate to help countries strengthen long-term capacity to prevent, detect, and respond to pandemic threats, undertook a study in 2016 to learn how these companies viewed their experience. **Methods:** P&R surveyed 23 oil, gas, and mining companies operating in West Africa to understand the actions of the firms during the response and assess what they think industry's role should be in future outbreaks. Companies in Guinea and Ghana were selected because each country has large extractive industries and mounted a response to Ebola. P&R also wanted to see the differences between a country that had to respond to Ebola and one that did not have an outbreak but prepared for one. The survey was conducted in different ways: P&R interviewed participants at a workshop and also conducted in-person and phone interviews. **Results:** All companies reacted to varying degrees to the Ebola outbreak. All implemented compulsory handwashing at entry points to buildings and concessions. Thermal screening was used at entry points and at company offices. Most companies coordinated with non-government organizations (NGOs) to assist with distribution of supplies, such as rice and sanitation kits (buckets, soap, chlorine tablets). Many companies funded NGOs to sensitize communities on hand washing, feet washing, culturally appropriate risk mitigation measures, and screening. Most companies had to adjust their supply chains, and some had significant disruptions, but the biggest social and economic challenge was the closing of national borders and transportation routes. **Conclusions:** Private sector extractive industry contributed in substantial ways to the Ebola response in West Africa. Companies agreed that governments must lead and coordinate preparedness and response planning; however, industry should have a role. The public sector should engage key private sector actors in preparedness planning before the next large outbreak.

Board 96. Improving International Health Regulations Capacity through Point of Entry Public Health Preparedness and Response, Tanzania

S. Ward[1], R. Kakulu[2], J. Mohammed[3], P. Kinyunyi[2], F. Kilamile[2], T. Midaba[2], J. Ngoda[4], O. Grady-Erickson[1], K. Massa[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Ministry of Health, Community Development, Gender, Elderly, and Children, Dar es Salaam, United Republic of Tanzania, [3]Ministry of Health, Zanzibar, United Republic of Tanzania, [4]Tanzania Civil Aviation Authority, Dar es Salaam, United Republic of Tanzania

Background: Globalization of travel has greatly increased the need to strengthen border health systems, including public health detection and response capacities at points of entry (POE). Multisectoral engagement in the development of public health emergency response plans (PHERPs) and standard operating procedures (SOPs) enables countries to better prepare for, detect, and respond to public health events at POE. The International Health Regulations (IHR) require World Health Organization Member States to establish and maintain defined public health core capacities, including plans at POE to mitigate the international spread of disease. Also, the International Civil Aviation Organization requires its Contracting States to comply with pertinent provisions of the IHR and to have a national aviation public health preparedness plan. **Methods:** To develop a national aviation public health preparedness plan, and PHERPs and SOPs at multiple POE, Port Health Services of the Tanzania Ministry of Health, Community Development, Gender, Elderly, and Children convened a series of multiday, multisectoral workshops at national and POE levels. These were followed by training national and POE staff on the SOPs. Competency was evaluated by applying the SOPs in role-play scenarios. A train-the-trainer approach empowered participants to train other POE staff. **Results:** Tanzania developed and validated a multisectoral national aviation public health preparedness plan and PHERPs for three major international airports. Additionally, the airports as well as two international seaports established SOPs for identifying ill persons, notifying health authorities, managing ill persons, and referring them to a health facility. Port Health Services trained over 250 staff on the plans and procedures and conducted a tabletop exercise at one airport. **Conclusions:** Tanzania increased its IHR compliance at five major POE and is better positioned to continue to build capacity of additional POE and staff to respond to public health events. With these plans and procedures in place, Tanzania's POE can more efficiently implement interventions to detect and respond to ill persons and, thereby, help protect communities nationally and globally from the spread of infectious diseases.

Board 97. Strengthening Public Health Emergency Preparedness Systems and Capacities through the Development of Point of Entry Specific Public Health Emergency Contingency Plans (PHECP) in Nigeria

O. Bamsa, S. Alabi, O. Akinloluwa
Pro-Health International, Abuja, Nigeria

Background: The International Health Regulations 2005 (IHR 2005) recommends that all designated points of entry have public health emergency contingency plans (IHR annex 1b) to modulate response. The events that followed the arrival of the index case of Ebola virus disease at Murtala Mohammed International Airport (Lagos, Nigeria) from Monrovia (Liberia) in 2014 brought to light the need to strengthen disease surveillance and response structures at Nigerian points of entry. **Methods:** A core planning team (CPT) that included representatives of all stakeholder agencies functioning at the point of entry was constituted with the sole purpose of driving the drafting of the PHECP. The CPT was headed by Port Health Services and the meetings were facilitated by public health specialists from PHI. The CPT commenced its activities by agreeing on standard protocol for routine public health-related activities, these processes were then documented for review and adoption. A tabletop simulation exercise to assess the first completed draft of the PHECP is conveyed. Findings from the tabletop

simulation informs a CPT session to update the PHECP. Revised version of the plan is then adopted by all members of the CPT, the plan is then forwarded to the table of the Honourable Minister of Health for approval. This is then followed by the incorporation of PHECPs into the point of entry operational manual. Training sessions on the use of the PHECP and related SOPs is then convened to disseminate the plan to relevant personnel outside of the CPT. A live simulation exercise is conducted to test the direct applicability of the plan in real-time. **Results:** More than 12 months after the completion of the first draft of the PHECP, the international airports in both Lagos and Abuja have a PHECP signed and authorized for use by the Honourable Minister of Health. The same is true for the Idiroko Ground Crossing, whilst the PHECP for both Mallam Aminu Kano International Airport (Kano State) and Seme Ground Crossing (Lagos) are under revision following tabletop exercises. **Conclusions:** This model can be replicated in points of entry similar to those found in Nigeria, with numerous agencies (and the resulting turf issues) and an under resourced border health security agency. Such points of entry are typically found in low-income countries where ensuring border health security is critical to prosperity and stability.

Board 98. Integration of International Health Regulations into National Health System: A Case for Fostering Their Implementation in the Eastern Mediterranean Region

D. Samhouri[1], K. Ijaz[2], Z. Mirza[3], J. Mahjour[4]
[1]WHO-EMRO Health Emergency Programme (WHE), Cairo, Egypt, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [3]WHO-EMRO Director Health Systems Development, Cairo, Egypt, [4]WHO-EMRO Director Program Management, Cairo, Egypt

Background: Significant public health threats exist in many countries of the Eastern Mediterranean Region (EMR). The vast majority of threats to public health security are posed by emerging and re-emerging outbreak-prone infectious diseases. However, threats related to release of chemical, radiological and nuclear agents are of increasing concern. The International Health Regulations (IHR) 2005, as the overarching instrument for global health security, are designed to prevent, detect and manage public health threats. The recent international public health events such as the 2014 Ebola and 2016 Zika outbreaks, the ongoing poliovirus outbreak, and the recurrence of MERS-CoV and cholera outbreaks, underscored the inadequate implementation of IHR capacities, regionally and globally, and the need to integrate them into the national health system. The findings of global and regional assessments and reviews marked the need for new approaches to monitor and evaluate the implementation of IHR capacities. This prompted WHO to develop IHR Monitoring and Evaluation Framework (IHR MEF). **Methods:** Critical evaluation of data from the existing empirical work on IHR implementation in the EMR, global health security, health system preparedness and resilience was conducted from 2012-2017. This included assessments, field visits, and investigations, as well as sub-regional and regional meetings and training workshops. **Results:** During 2012-2017 time period, 54 assessments, 72 field visits and investigations, 15 meetings, and 25 training workshops were conducted in the EMR. Nine core capacities (legislation and finance, infection prevention and control, laboratory system, biosafety and biosecurity, health workforce, all hazard surveillance, preparedness and response, medical countermeasures) were identified within IHR that can be built on within national health systems. To date, of the health capacities, only health preparedness, medical countermeasures, and response have been integrated into the overall national health system in only 27% countries in EMR; yet in a fragmented manner. **Conclusions:** Although the development and implementation of the IHR MEF has been globally recognized and acknowledged, however it would require innovative approaches for actual implementation of IHR capacities by integration into existing national health system for enhanced preparedness and response to public health threats.

Vector-Borne Diseases I

Board 99. Epidemic Arboviral Diseases in the Eastern Mediterranean Region: Findings from a Systematic Review

M. Obtel[1,2], M. Elhakim[3], N. Minh[3], G. Al Garraya[4], H. Hassan Mohamed[4], A. Abubakar[3], S. Rahman Malik[3]
[1]Laboratory of Community Health, Preventive Medicine and Hygiene, Laboratory of Epidemiology, Clinical Research and Biostatistics, Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [2]WHO Consultant, Rabat, Morocco, [3]Infectious Hazard Management, Health Emergencies Department, EMRO/WHO, Cairo, Egypt, [4]Index Medicus for the Eastern Mediterranean Region (IMEMR), EMRO/WHO, Cairo, Egypt

Background: Despite the emergence of arboviral disease as a significant public health threat globally, little is known on the risk of epidemic arboviral diseases in the Eastern Mediterranean Region (EMR) of WHO. The aim of this systematic review was to better describe the risk of epidemic arboviral diseases in the EMR. **Methods:** We systematically conducted the search in accordance with Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA). Studies/reports containing information on the burden (Mortality and morbidity reported either during an epidemic or during an endemic transmission of the disease), risk factors including demographic, socio-economic and geographic distribution of cases and epidemic occurrence in the EMR's countries were considered eligible for inclusion in the review. **Results:** Sixty-six articles published between 2000 and 2016 from seven countries met the inclusion criteria. The diseases with information published on burden and risk factors were dengue, chikungunya, yellow fever and West Nile fever. The prevalence of dengue fever varied from 13.5% (95% CI; 13.43-13.57) to 73% (95% CI; 72.88-73.12) in Pakistan, while in Saudi Arabia, it varied from 37.5 (95% CI; 33.7-41.2) to 53.5% (95% CI; 53.16-53.94) in Yemen around 19.7% (95% CI; 19.65-20.5) and 9.4% (95% CI; 7.1-12.3) in Sudan. The seroprevalence of West Nile fever varied from 8% (95% CI; 7.97-8.03) in Jordan, 24% in Egypt (95% CI; 22.9-35.0) and 30.4% in Afghanistan (95% CI; 30.37-30.43) and other studies reported deaths of West Nile fever in Tunisia. Outbreaks of yellow fever and chikungunya were mainly investigated in Sudan and Yemen, respectively. **Conclusions:** This review presents information on the burden of epidemic arboviral diseases in the Eastern Mediterranean Region. There are substantial gaps in understanding on temporal and spatial distribution of *Aedes* mosquitoes in the Region as well as on epidemiology and characteristics of circulating arboviruses causing epidemics in the EMR.

Board 100. Risk of Epidemic Arboviral Diseases in the Eastern Mediterranean Region: Current Information Gaps

M. Obtel[1,2], M. Elhakim[3], N. Minh[3], G. Al Garraya[4], H. Hassan Mohamed[4], A. Abubakar[3], S. Rahman Malik[3]
[1]Laboratory of Community Health, Preventive Medicine and Hygiene and Laboratory of Epidemiology, Clinical Research and Biostatistics, Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [2]WHO Consultant., Rabat, Morocco, [3]Infectious Hazard Management, Health Emergencies department, EMRO/WHO, Cairo, Egypt, [4]Index Medicus for the Eastern Mediterranean Region (IMEMR), EMRO/WHO, Cairo, Egypt

Background: A number of countries in the Eastern Mediterranean Region (EMR) of WHO has reported outbreaks from epidemic arboviral diseases, some with widespreading impact. This study aimed to present the information and data gaps on the prevalence and epidemic risk of arboviral diseases in the EMR. **Methods:** We reviewed the data from a systematic review conducted on epidemic risk of arboviral diseases in the EMR. Any published outbreak investigation or outbreak report on arboviral diseases in the region between 2000 and 2016 were included in this review. **Results:** Our findings indicate that studies on risk of epidemic arboviral diseases in the EMR remain limited and insufficient. Among the 22 countries in the Region, published data on epidemic arboviral diseases are available only from 11 countries (50%). Pakistan, Sudan, and Saudi Arabia are the three countries in the Region, which have published most of the studies (82%) on this area. The main arboviral diseases for which studies are available and published include dengue fever (52/66; 78%), West Nile fever (8/66; 12%), yellow fever (2/66; 3%), and chikungunya (2/66; 3%). Data are still missing for most of the countries in the Region for these arboviral diseases. Data on distribution of *Aedes* mosquitoes, epidemiology, risk factors and information on characterization of either endemic or epidemic strain of these diseases are absent in the literature. Owing to inconsistencies in the study design and study populations of these published articles, no comparison could be done on the relative risks and rates across different countries. **Conclusions:** More research on the threat and burden of epidemic arboviral diseases in population-based studies are urgently needed and published to get a better understanding on the burden and risk factors of epidemic arboviral diseases particularly in countries where outbreaks from these diseases shave been reported in recent time.

Board 101. Human West Nile Virus Infection in Tunisia: Three Outbreaks in the Past 20 Years

H. Bouguerra[1], S. Bougatef[1], S. Chelly[1], H. Letaief[1], A. Hechaichi[1], R. Salsabil[1], F. Saffar[1], A. Cherif[1], R. Laamouri[1], A. Bahrini[1], W. Hachfi[2], O. Bahri[3], H. Triki[4], N. Ben Alaya[1]
[1]National Observatory of New and Emerging Diseases, Tunis, Tunisia, [2]Infectious Diseases Department Farhad Hached Hospital, Sousse, Tunisia, [3]Aziza Othmana Laboratory, Tunis, Tunisia, [4]Virology Laboratory Pasteur Institute, Tunis, Tunisia

Background: West Nile virus (WNV) is an important mosquito-borne and zoonotic arbovirus. Although in most cases, human WNV infection is asymptomatic or a minor illness, it may lead to fatal neuro-invasive disease. Nowadays, WNV is increasingly widespread. In Tunisia, three outbreaks occurred in the past 20 years. Our objectives are to describe these outbreaks and to identify areas on which further investigations should be developed to control this infection in Tunisia. **Methods:** It is a descriptive study of data collected from the WNV surveillance system. It is a passive surveillance system based on the notification of cases of meningitis and meningoencephalitis by public and private health sectors and enhanced if any viral activity is detected. For confirmation, suspected cases (fever associated to neurological symptoms) have serum and cerebrospinal fluid specimens for IgM and IgG antibodies testing and serum-neutralization if possible. **Results:** The first outbreak occurred in September 1997. A total of 173 suspected case-patients were notified from the center-east region (Governorates of Sfax, Mahdia, Monastir, Sousse, and Kairouan). The number of confirmed cases was 148; 8 patients had a fatal outcome. In October 2003, 50 cases of which 21 confirmed and 3 deaths were reported from the same regions (Sfax, Mahdia, and Monastir). The third outbreak occurred in July 2012, with 86 confirmed cases and 12 deaths. The same regions were affected in addition to southern areas around oases. Male-to-female sex ratio was 1.5. The median age was 54 years (extremes 3 months to 87 years). **Conclusions:** Tunisia has witnessed three major WNV outbreaks since 1997 with common features; affecting coastal central areas between late summer and early fall. These areas are often along the route of different migratory birds from Africa to Europe, especially in summer and autumn in addition to a higher activity of mosquitos. There is a need to strengthen surveillance during these seasons.

Board 102. Epidemiological Profile, Incidence, and Trends of West Nile Virus in Tunisia during Five Years

S. Chelly, H. Bouguerra, R. Salsabil, F. Saffar, L. Hajer, A. Lahchaichi, A. Cherif, S. Bougatef, N. Ben Alaya
National Observatory of New and Emerging Diseases, Tunis, Tunisia

Background: West Nile virus (WNV) is a virus most commonly spread to people by mosquito bites. WNV has become an important cause of human and animal disease worldwide including Tunisia where two outbreaks were reported in 1997 and in 2003. Since 2010, a human surveillance system was implemented in Tunisia. The aim of this study was to describe the epidemiological profile, incidence and the trends of WNV in Tunisia from 2012 to 2016. **Methods:** It was a prospective longitudinal descriptive study. A passive surveillance system based on the reporting of suspected cases of neuroinvasive infection by the public and private health care. If viral activity is detected, this passive surveillance is enhanced. Data collected from the notification of cases that reach to the National Observatory of New and Emerging Diseases. Data were entered and analyzed with SPSS 20.0. We include only the probable and confirmed cases to calculate attack rate, crude incidence and trends. We estimated chronological trends using spearman correlation coefficient (r‘). **Results:** A total of 1759 cases were notified and only 258 were probable and confirmed cases. Median age was 32 years and 68.2% were aged more than 20 years with male predominance (sex ratio=1.22). In 2012, it was an outbreak with an attack rate 1.65/100 000 inhabitants. From 2013 to 2016, there is an endemic of WNV with crude incidence rate 0.18/100 000 inhabitants per year. There was a slight significant decrease of the number of probable and confirmed cases from 2013 to 2016 ;(r’=0.399; p<10-3). **Conclusions:** This result showed that it was an epidemic of WNV with an endemicity during the other years. Also, it revealed a remarkable decrease of the number of cases over these five years. We should implement integrated surveillance system, which include human, animal and vector.

Board 103. Clinical Parameters and Lethality of West Nile Virus Infections in Humans, Tunisia, 2012-2016

S. Chelly, H. Bouguerra, S. Rejeibi, F. Saffar, H. Leteif, A. Lahchaichi, A. Cherif, S. Bougatef, N. Ben Alaya
National Observatory of New and Emerging Diseases, Tunis, Tunisia

Background: Symptoms associated with West Nile virus (WNV) infection range from fever to neuroinvasive disease. The objective of this study was to determine epidemiologic, clinical parameters and lethality among probable and confirmed cases during these five years. **Methods:** It was a prospective longitudinal descriptive study. A passive surveillance system based on the reporting of suspected cases of neuroinvasive infection by the public and private health care. If viral activity is detected, this passive surveillance is enhanced. Data collected from the notification of cases that reach to the National Observatory of New and Emerging Diseases. Data were entered and analyzed with SPSS 20.0. **Results:** A total of 258 probable and confirmed cases among 1759 notified cases. Median age was 32 years and most were aged older than 20 years (68.2%) with male predominate (Sex Ratio= 1.22). The most frequent clinical manifestation was meningitis, encephalitis and meningoencephalitis (59%). The lethality was 3.6%; however, age was the only risk factor for death identified which is significant higher in people older than 50 years. **Conclusions:** Our study highlights the neurological manifestation was the most common among reporting clinical WNV syndromes. Actually, there is potential for further synthesis of the risk factors of WNV illness, such as climatic factor which we should study them in the future research, and mortality.

Board 104. Severe Disease Presentations Are Correlated with Previous Exposure of Multiple Members of the *Flaviviridae* Family in the Caribbean Island of Sint Maarten

M. Raafat, R. Sgroi, P. Pagador, T. Kirtek, M. Samiullah, J. Barney, K. Shupe
American University of the Caribbean, Cupecoy, Sint Maarten (Dutch Part)

Background: The purpose of this study was to investigate the prevalence and varying presentations associated with the three tropical arboviruses common in the Caribbean area, specifically the Cupecoy area of Sint Maarten. These arboviruses are dengue fever, chikungunya, and Zika virus. Although the three diseases share similar symptoms, many cases can go unreported as they are not severely symptomatic, while other cases have a very intense disease presentation as noted in the literature. This study illustrates the association of presentation of symptoms associated with being infected with one or two or more diseases at one time. **Methods:** A free virus screening for the viruses of interest was conducted on the American University of the Caribbean School of Medicine campus in Cupecoy, Sint Maarten, over a six-month period. Approximately 281 participants volunteered, and were tested for positive IgM and IgG ELISA reactions to the three diseases. Surveys assessing symptoms were completed by all participants, were analyzed, and compared to serology results. **Results:** Of the 281 participants, our screening indicated a 9% prevalence of the Zika virus, 11% of the chikungunya virus, and 30% with the already endemic dengue fever. Survey analysis showed that patients who were previously infected with the Zika virus, were more likely to report a more severe disease presentation (p=.04) with dengue fever than those with Zika infections alone or dengue fever infections alone. Disease presentation was much less severe for patients who only tested positive for one of the infections. **Conclusions:** Patients with a suspected severe Zika virus infection, should also be tested for dengue fever serology as well as other members of the *Flaviviridae* family. Interaction between these two members of the same virus family indicates a possible mechanism of antibody dependent enhancement as historically seen with different strains of dengue fever.

Board 105. Enhanced Surveillance for Heartland Virus in Tennessee

K. Orejuela[1], T. Moore[1], A. Rodriguez[1], M. Fill[1], J. Schmitz[2], K. Bloch[2], A. Moncayo[1]
[1]Tennessee Department of Health, Nashville, TN, USA, [2]Vanderbilt University, Nashville, TN, USA

Background: Heartland virus (HRTV) is an emerging tickborne phlebovirus that was first isolated in Missouri in 2009. Clinical characteristics of infection include leukopenia, thrombocytopenia, and fever; at least 2 deaths have been reported in Tennessee. HRTV cases have been identified in the Midwestern and southern United States; however since commercial testing is unavailable, the frequency and spectrum of clinical disease is not well established. We sought to better understand the prevalence and clinical presentations of HRTV in Tennessee. **Methods:** Enhanced laboratory testing for tickborne diseases (TBD), including HRTV, was conducted on whole blood samples from Tennessee residents from 2011 and 2014–2017. Residual samples were obtained from Vanderbilt University Medical Center on patients suspected of having ehrlichiosis, and tested in the Tennessee Department of Health Vector-Borne Diseases Laboratory. Samples underwent RNA purification and molecular detection of HRTV through real-time reverse transcription polymerase chain reaction. Medical record review was conducted for HRTV–positive Tennessee residents. **Results:** Of 691 samples, 8 (1.2%) tested positive for HRTV; 8/8 (100%) had available medical records for review. Of the 8 patients, 6 (75%) were male and 2 (25%) were female; and all were aged ≥60 years (median = 69 years; range = 62–79 years). All patients had comorbidities, reported tick exposure, and survived their infection. Common reported symptoms included fever (8/8; 100%) and rash (4/8; 50%). Laboratory findings were consistent with TBD, including leukopenia (6/8; 75%) and thrombocytopenia (6/8; 75%). **Conclusions:** Enhanced laboratory surveillance demonstrated that ~1% of samples from patients with clinical suspicion for a TBD tested positive for HRTV, indicating some baseline prevalence in Tennessee. Medical record review reinforced that HRTV presents with clinical manifestations similar to many TBD. Although deaths from HRTV have been reported, milder infections may be more common. The finding of HRTV in whole blood samples suggests humans could potentially contribute to the anthroponotic transmission of HRTV by infecting ticks during their viremic period. More research is needed to better determine the prevalence and spectrum of clinical disease from HRTV.

Board 106. Increase in Reported Rocky Mountain Spotted Fever Cases — Indiana, 2017

T. Stevens, J. Brown
Indiana State Department of Health, Indianapolis, IN, USA

Background: Rocky Mountain spotted fever (RMSF) is caused by the bacterium *Rickettsia rickettsii,* which is transmitted in Indiana by the American dog tick. RMSF is fatal in 5–10% of cases. On June 8, 2017, a fatal RMSF case in a pediatric Indiana resident was widely reported in local, state, and national media. We analyzed surveillance

data to determine whether this event had an effect on case reporting. **Methods:** RMSF cases reported to the Indiana National Electronic Disease Surveillance System (I-NEDSS) during 2012–2017 that met the confirmed and probable national surveillance case definitions were analyzed. Because case reports for 2017 were not finalized at the time of this writing, analysis was restricted to cases with specimen collection date during January 1–September 30 for each year for consistency. Overall case counts and proportions of pediatric patients, hospitalized patients, and emergency department (ED) visits for 2017 were compared with the averages for 2012–2016 using chi-square statistics with one degree of freedom. An alpha level of 0.05 was used to determine statistical significance. **Results:** During 2012–2016, 155 RMSF cases were reported (average: 31/year; range: 28–38); none were fatal. Specimens were collected before June 8 in 44 (28%) cases (average: 9/year; range: 4–13) and after June 8 in 111 (72%) cases. Twelve (8%) cases occurred in pediatric patients, 38 (25%) were hospitalized, and 60 (39%) patients visited an ED. In 2017, 79 RMSF cases were reported (X^2=74.32; p <0.00001). Specimens were collected before June 8 in 21 (27%) cases and after June 8 in 58 (73%) cases (X^2=0.0001; p=0.992021). Six percent of cases occurred in pediatric patients (X^2=0.005; p=0.943628), 20% were hospitalized (X^2=0.01; p=0.920344), and 41% visited an ED (X^2=0.0003; p=0.987385). The case reported in the media was the only fatality. **Conclusions:** There was a statistically significant increase in reported RMSF cases in Indiana in 2017 that began prior to the media reporting of a fatality on June 8. The lack of a statistically significant increase in the proportion of cases reported after June 8 suggests that media coverage had minimal impact on case reporting. The stable proportions of hospitalized cases and ED visits suggests that overall illness severity did not increase in 2017. The cause of the increase in reported cases remains unknown.

Board 107. Bioclimatic Indicators of Rift Valley Fever Activity

A. Anyamba[1], R. Soebiyanto[1], J. Small[2], S. Britch[3], K. Linthicum[3]
[1]Universities Space Research Association / NASA Goddard Space Flight Center, Greenbelt, MD, USA, [2]NASA Goddard Space Flight Center, Greenbelt, MD, USA, [3]US Department of Agriculture (USDA) - Center for Medical, Agricultural & Veterinary Entomology (CMAVE), Gainesville, FL, USA

Background: Recent Rift Valley fever (RVF) epizootics indicate that the timing, persistence and coupling between rainfall and ecological dynamics – measured by satellite-derived vegetation index – as a leading indicators of RVF activity. Both rainfall and vegetation are known to be important factors influencing the emergence, abundance and longevity of RVF vectors (*Aedes* and *Culex* species). Here, we take an in-depth analysis of climate conditions leading to RVF activity in Africa, by analyzing satellite-derived rainfall, normalized difference vegetation index and land surface temperature at the outbreak locations. **Methods:** We processed rainfall time series from NOAA's Africa Rainfall Climatology (ARC) project (1983 to present), Normalized Difference Vegetation Index and Land Surface Temperature measurement from NASA Moderate-Resolution Imaging Spectroradiometer (MODIS) sensor. We utilize data anomaly methods to differentiate between potential RVF activity & non-activity periods. We evaluate conditions leading to initial index case (animal or human) using histogram comparisons. We discern number of days that lapsed between the start of above normal rainfall and RVF activity to determine how soon an early warning can be given for any region of concern. **Results:** Results indicate that > 90% of the locations where RVF activity occurred were preceded by 3-4 months of persistent and above normal rainfall & vegetation conditions, and below normal land surface temperatures. These conditions favor the emergence and propagation of large populations of RVF virus-infected vectors, leading to outbreaks. However, about 10% of locations of reported activity showed inconsistent results. We attribute this inconsistency to inaccuracies and delays in RVF reporting, livestock migration from the location of initial infection or secondary infections. **Conclusions:** We have illustrated the role and timing of bioclimatic indicators in determining the timing of RVF activity. It highlights the utility of remotely sensed data in building early warning systems at both continental and regional levels. However, there is still need for early vector surveillance and livestock in response to these warnings. More importantly, we need to gain a better understating of livestock/heard immunity and climate variability leading to episodic outbreaks of RVF.

Board 108. Epidemiology and Cost of Lyme Disease-Related Hospitalizations—United States, 2005-2014

A. Schwartz[1], M. Shankar[2], K. Kugeler[1], R. Max[1], A. Hinckley[1], M. Meltzer[2], C. Nelson[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: An estimated 300,000 cases of Lyme disease occur in the United States annually. Disseminated Lyme disease may result in carditis, arthritis, facial palsy, and meningitis, sometimes requiring hospitalization. We describe the epidemiology and cost of these Lyme disease-related hospitalizations. **Methods:** We analyzed 2005-2014 data from the Truven Health Analytics® MarketScan Commercial Claims and Encounters Databases to identify inpatient records possibly associated with Lyme disease based on International Classification of Diseases, 9th Revision (ICD-9) codes. We stratified costs by disease manifestation, demographic characteristics, month of admission, and region. **Results:** Of 19,983,165 admission records contained in the inpatient databases over the study period, we identified 2,823 (0.01%) that were categorized as Lyme disease-related hospitalizations. Over half of the identified records contained an ICD-9 code for carditis (n=429), meningitis (n=614), arthritis (n=375), or facial palsy (n=400). Nearly 60% of hospitalized patients were male. The costs were non-normally distributed (skewness=7.5; kurtosis=110.7) with a median cost of $11,688 (range: $140- $323,613) per hospitalization. The manifestation with the highest median cost per stay was carditis ($17,461), followed by meningitis ($15,177), arthritis ($13,012), and facial palsy ($10,491). Median length of stay was three days (range: 1-52) among all Lyme disease-related hospitalizations. Median cost was highest in the 15-19 year age group ($12,991). Admissions occurring in January had the highest median cost ($13,777) for all years, and residents of the non-endemic western region of the United States incurred highest median cost of admission ($16,830). **Conclusions:** Lyme disease-related hospitalization costs were highest among persons for whom Lyme disease may be low on the differential diagnosis list due to age, season, or geography; these findings underscore the need for continued provider education to encourage earlier disease recognition and communication regarding prevention. Information from this analysis can aid economic evaluations of interventions that prevent infection and advances in disease detection.

Board 109. Targeted Metagenomics as a High-Throughput Tool for Surveillance and Discovery of Tickborne Agents in Clinical Specimens

S. Sheldon[1], L. Kingry[1], S. Oatman[1], B. Pritt[2], M. Anacker[3], J. Bjork[3], D. Neitzel[3], D. Boxrud[3], G. Liu[3], L. Respicio-Kingry[1], A. Strain[3], J. Berry[2], L. Sloan[2], K. Kugeler[1], P. Mead[1], J. Petersen[1]
[1]Centers for Disease Control and Prevention, Division of Vector-Borne Diseases, Fort Collins, CO, USA, [2]Mayo Clinic, Rochester, MN, USA, [3]Minnesota Department of Health, Saint Paul, MN, USA

Background: An updated understanding of the scope and geographic distribution of bacterial tickborne pathogens infecting humans in the United States is essential for improving clinical recognition, laboratory diagnosis, and prevention. Nearly 50,000 cases of vector-borne disease are reported in the US each year, with the vast majority caused by bacterial pathogens transmitted by ticks. At least 14 different bacterial species are known causative agents, with ~25% of species discovered in the last decade. Lyme disease, relapsing fever, anaplasmosis, tularemia, ehrlichiosis, and spotted fever group rickettsioses can be severe or life-threatening diseases. To modernize surveillance for novel and known tickborne pathogens, a broad high-throughput metagenomics approach, capable of detecting all bacterial tickborne pathogens, was developed. **Methods:** Clinical specimens (blood, cerebral spinal fluid, or synovial fluid) from patients with suspected tickborne illness are submitted from throughout the US. Total DNA is extracted from clinical specimens, the V1-V2 region of the 16S rRNA gene is amplified, multiplexing indices are added by PCR, and the final libraries are pooled and subjected to paired-end next generation sequencing using the Illumina MiSeq. The resulting sequence reads undergo quality trimming, paired reads are merged, and taxonomic designations are assigned using MiniKraken. **Results:** Targeted metagenomic testing of >8,000 clinical samples from patients suspected of tickborne illness identified two new bacterial tickborne species (*Borrelia johnsonii* and an *Anaplasma* species) not previously associated with human illness as well as nine known tickborne bacterial pathogens in the *Anaplasma*, *Ehrlichia*, and *Rickettsia genera*. Two samples co-infected with *A. phagocytophilum* and either *B. mayonii* or *B. burgdorferi* were also identified. **Conclusions:** Broad detection of known and novel tickborne pathogens in clinical samples illustrates that targeted 16S rRNA metagenomics is a powerful surveillance approach for bacterial tickborne pathogens in patients with suspected tickborne illness. Ultimately, these findings will upgrade our understanding of bacterial tickborne species associated with human disease in the United States and the geographic regions these species cause human disease.

Board 110. Validating Targeted Metagenomic Identification of Bacterial Species in Specimens from Patients Suspected of Tickborne Illness

S. Oatman[1], S. Sheldon[1], L. Kingry[1], L. Respicio-Kingry[1], B. Pritt[2], M. Anacker[3], J. Bjork[3], D. Neitzel[3], D. Boxrud[3], G. Liu[3], A. Strain[3], J. Berry[2], L. Sloan[2], K. Kugeler[1], P. Mead[1], J. Petersen[1]
[1]Centers For Disease Control and Prevention, Fort Collins, CO, USA, [2]Mayo Clinic, Rochester, MN, USA, [3]Minnesota Department of Health, St. Paul, MN, USA

Background: Bacterial agents are responsible for the majority of tick-transmitted infections reported in the United States, with at least 14 different bacterial tickborne pathogens known to cause human illness. To enhance surveillance for known, emerging, and novel bacterial tickborne pathogens in US patients, we have developed a multi-center collaborative effort to screen specimens from patients with a suspected tickborne illness, using a 16S metagenomics/bioinformatics approach. This method allows for comprehensive taxonomic identification of bacteria in clinical samples. Independently corroborating these taxonomic designations is important for establishing accuracy and utility of this method for laboratory based surveillance. **Methods:** Clinical samples (blood, cerebral spinal fluid, and synovial fluid) from patients throughout the US with a suspected tickborne illness were tested using a high-throughput bacterial V1-V2 16S ribosomal RNA (rRNA) metagenomic/bioinformatics workflow. To verify taxonomic designations assigned by this approach, samples positive for tickborne and other bacterial genera were independently analyzed by multi-locus sequence typing (MLST), genus or species-specific real time PCR, and/or sequencing of the V1-V4 region of the 16S rRNA gene. **Results:** Secondary testing of over 350 samples positive for either known tickborne pathogens or other bacteria, demonstrated that the taxonomy assigned by the workflow was 100% accurate for genus level designations and over 90% accurate for species level designations. Additionally, two tickborne bacteria not previously associated with humans were identified, revealing the utility of this approach for detection of novel pathogens. **Conclusions:** Independent verification of taxonomic designations validates the accuracy of a targeted 16S metagenomic/bioinformatics approach for surveillance of known and discovery of new tickborne pathogens. Moreover, other pathogens that may produce clinical symptoms similar to tickborne illnesses can be detected with this method. The ability to identify bacterial tickborne pathogens accurately and comprehensively will enhance our understanding of tickborne diseases in the US and aid in the clinical recognition, laboratory diagnosis, and prevention of these conditions.

Board 111. Geographic Information for Vector Surveillance (GIVeS): Collaboration for GIS Capacity Building for Vector Surveillance

D. Evans[1], M. Stanton[2], S. Dunkley[2], A. South[2], O. Manders[1], N. Desousa Williams[1], L. Martin[1], A. Gates[1], R. Levine[3], M. Coleman[2], A. Lenhart[3]
[1]Emory University, Atlanta, GA, USA, [2]Liverpool School of Tropical Medicine, Liverpool, United Kingdom, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The GIVeS program was developed as part of the 2016 Zika Virus response to improve Geographic Information System (GIS) capacity for vector surveillance in Latin America and the Caribbean (LAC) using QGIS, a freely available GIS program. **Methods:** We conducted a baseline needs assessment to assess existing GIS capacity for vector surveillance across 34 LAC countries. Baseline data were used to develop a curriculum on QGIS, a freely available and open source mapping program. Five introductory (Tier 1) trainings were conducted between April and November 2017, with 116 participants from 31 LAC countries attending. Participants ranged from field entomologists to key vector surveillance decision makers. Individual learning was assessed using pre- and post-testing and a course evaluation to gauge course effectiveness. Quantitative data were entered and analyzed in Epi Info 7. **Results:** Only 20 percent of responding participants (n=95) reported being comfortable with GIS software before the workshop compared to 45% post-training. A third (30%) of participants reported at pre-test that they could create maps from entomological surveys; nearly all (92%) reported they could do so at post-test. At pre-test 22% of participants were incapable of accessing/creating spatial data, which dropped to 4% after the workshop. **Conclusions:** The GIVeS

program successfully met its objectives, receiving positive feedback across evaluation metrics for its introductory level trainings. A second level (Tier 2) training is currently under development; this training will focus on expanding basic skills, data analysis, and the interpretation and presentation of spatial data. Next steps include expansion of the programs' geographic focus beyond the LAC region. Others focused on vector and disease surveillance may benefit from the adoption of GIS software - particularly widely used, freely available programs such as QGIS.

Board 112. Molecular Prevalence of Selected Canine Vector-Borne Pathogens in the United States (2008-2015)

E. Persico[1], B. Qurollo[2], B. Thomas[2], B. Hegarty[2], E. Breitschwerdt[2], P. Diniz[3]
[1]University of Minnesota, Minneapolis, MN, USA, [2]North Carolina State University, Raleigh, NC, USA, [3]Western University of Health Sciences, Pomona, CA, USA

Background: Sentinel animal populations allow for monitoring of changes in abundance, geographic location, and potential novel organisms which can be transmitted between individuals and species. Large compilations of data related to vector-borne pathogen surveillance by molecular diagnostic techniques are limited to universities and private laboratories. For over a decade, clinicians have submitted canine samples to the Vector Borne Disease Diagnostic Laboratory (VBDDL) at North Carolina State University (NCSU-CVM) for PCR panel testing of the following genera: *Anaplasma, Babesia, Bartonella, Ehrlichia, Leishmania, Mycoplasma,* and SFG *Rickettsia*. This is the first report of the molecular prevalence of selected vector-borne pathogens in dogs in the US from 2008 to 2015. **Methods:** Results from 9,477 US-based canine EDTA-blood samples submitted to the VBDDL NCSU-CVM between 2008 and 2015 were tested via PCR for the presence of pathogen DNA. PCR products (amplicons) were also available for species identification. Duplicate samples were identified as any sample tested for the same pathogen within 180 days of the first positive result; these samples were flagged and analyzed separately. **Results:** Overall, *Babesia* (328/6318, 5.2%) was the most prevalent canine vector-borne pathogen (CVBP) at the genus level, followed by *Ehrlichia* (211/5255, 4.0%), *Mycoplasma* (106/3415, 3.1%), *Anaplasma* (83/3519, 2.4%), *Bartonella* (58/5491, 1.1%), and *Rickettsia* (26/3678, 0.7%). Despite a higher prevalence of *Leishmania* (23/319, 7.2%), a limited number of samples were tested compared to the other CVBPs. By region, *Anaplasma* was most prevalent in the Northeast; *Ehrlichia, Leishmania,* and *Rickettsia* (Mid-Atlantic); *Babesia* (Midwest); *Mycoplasma* (South); and *Bartonella* (West). Excluding *Leishmania* spp., by year, the most prevalent genera detected in 2008-2010 and 2013 was *Babesia*; 2011 and 2012 (*Rickettsia*); 2014 (*Mycoplasma*) and 2015 (*Ehrlichia*). These are preliminary results, which are subject to change. **Conclusions:** Complete statistical analyses are pending. Our study provides the most current, extensive, and pathogen-specific data regarding canine vector-borne pathogens in the United States, and will serve as a reference for temporal and spatial pathogen distribution.

Board 113. Prioritization of Vector-Borne Diseases in Canada under Current Climate and Projected Climate Change

V. Ng[1], A. Chemeris[2], P. Breadner[3], A. Otten[1]
[1]Public Health Agency of Canada, Guelph, ON, Canada, [2]University of Guelph, Guelph, ON, Canada, [3]University of Waterloo, Waterloo, ON, Canada

Background: The habitat ranges of arthropod vectors in Canada are expected to expand with milder temperatures and increasing precipitation due to climate change. As such, vector-borne diseases (VBDs) are becoming an increasing public health concern. As resources are limited, it is necessary to prioritize diseases to direct resources into those posing the greatest risk to public health. **Methods:** We used multi-criteria decision analysis (MCDA) to rank VBDs thought to have the potential to emerge and/or expand in Canada under current and projected climate change. A total of 43 VBDs were ranked in order of priority according to 11 disease criteria; these included six epidemiological criteria (incidence, severity, trend, case-fatality, treatment and prevention), one economic criterion (cost to the healthcare system) and four climate change criteria (potential for introduction/expansion/establishment under current/projected climate change). An expert working group derived weights for disease criteria that formed the baseline disease priority list. The MCDA tool was designed to allow users to compare their priority list against the baseline by adjusting the weighting of disease criteria. Endemic diseases were ranked separately to non-endemic diseases. **Results:** The baseline weights (100 points in total) applied by the expert working group for the disease criteria were as follows: expansion/establishment under projected climate (22), expansion/establishment under current climate (17), introduction under current climate (13), introduction under projected climate (9), prevention (8), severity (8), treatment (6), economic impact (5), case-fatality (5), disease trend (4) and disease incidence. Preliminary results show priority endemic diseases for Canada include Powassan virus, Cache Valley virus and Lyme disease while priority non-endemic diseases include La Crosse encephalitis and St. Louis encephalitis. These diseases are most likely to emerge or expand in Canada due to climate change given the preferential weighting of the four climate change criteria. **Conclusions:** This is the first study focusing on the prioritization of VBDs in Canada under current climate and projected climate change. The MCDA tool built for this project will be used by Canadian researchers to formulate a strategy for directing research and surveillance efforts into VBDs that are most likely to be impacted by climate change.

Surveillance I

Board 114. Can Wearable Sensors Detect Influenza Epidemics? Correlation of Anomalous Fitbit Data with Influenza Surveillance Data

J. Radin, G. Queer, S. Steinhubl
Scripps Translational Science Institute, La Jolla, CA, USA

Background: Acute infections can cause elevated heart rates as a result of fever and other inflammatory responses. Illness is also likely to cause an individual's sleep and activity to deviate from their norm. Consequently, it may be possible to identify population trends of seasonal respiratory infections, such as influenza, through wearable

sensors that collect heart rate, sleep and activity data. **Methods:** We gathered Fitbit data from 60,473 individuals in the US who wore a Fitbit consistently from March 1, 2016 to February 28, 2017. We identified weeks when an individuals' Fitbit measurements deviated from the norm compared to their yearly averages. We then calculated the proportion of Fitbit users with anomalous measurements each week and correlated this with CDC influenza-like illness rates in both the US and California. **Results:** We collected 14 million daily resting heart rate measurements, 16 million days of activity tracking, and 11 million days of sleep measurements. The highest correlations were found when we classified anomalous measurements as a weekly heart rate mean that was more than half a standard deviation above average and a weekly mean step count that was more than one standard deviation below an individual's yearly average. We found a very strong Pearson correlation to ILI rates in California ($r=0.92$, $p<0.0001$) and a moderately strong correlation to ILI rates in the US as a whole ($r=0.78$, $p<0.0001$). **Conclusions:** There are a growing number of people in the US and globally who wear activity and physiological trackers to monitor their individual health: currently, there are more than 25 million active Fitbit users worldwide. By accessing this data in a timely manner it may be possible to provide more geographically specific and timely surveillance for infections than are currently available via traditional methods. In the coming months, we plan to further assess this method using data from the 2017-18 flu season.

Board 115. Estimating Weekly Call Volume to a National Nurse Telephone Triage Line in an Influenza Pandemic

B. Adhikari[1], L. Koonin[1], M. Mugambi[2], K. Sliger[3], M. Washington[1], E. Kahn[1], M. Meltzer[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]University of Washington, Seattle, WA, USA, [3]ORAU, Oak Ridge, TN, USA

Background: Telephone nurse triage lines (NTLs) may help reduce the surge in demand on health care facilities during an influenza pandemic by providing telephonic advice about clinical care and access to prescription antiviral medication. An example of an NTL is CDC's Flu on Call® project. **Methods:** We developed a Call Volume Projection Tool to estimate potential call volume for Flu on Call®, which may be activated nationally during an influenza pandemic. The Tool incorporates two influenza clinical attack rates (20% and 30%), four different levels of pandemic severity, different "seed numbers" of cases (10 or 100), and allows variation in which week Flu on Call® is activated. The Tool calculates call volume by using call-to-hospitalization ratios (CHR) based on pandemic severity informed from data from the Minnesota FluLine that operated during the 2009 H1N1 pandemic. **Results:** Assuming a 20% clinical attack rate and a case hospitalization rate of 0.8% - 1.5% (1968-like pandemic severity), we estimated the number of calls during the peak week of the pandemic to range from 1,551,882 to 3,523,902. Assuming a more severe 1957-like pandemic (case hospitalization rate = 1.5%-3.0%), the number of estimated calls during the peak week of the pandemic ranged from 2,909,778 to 7,047,804. **Conclusions:** These results will aid in planning and developing NTL's such as Flu on Call® for use during the next influenza pandemic.

Board 116. Enhancing Surveillance for Emerging Respiratory Infectious Diseases through Clinician Participation: An Assessment of Pneumonia of Unknown Etiology Surveillance in China, 2016

N. Xiang[1], Y. Song[2], Y. Wang[3,4], J. Wu[5], A. Millman[2], C. Greene[2], Z. Ding[6], J. Sun[7], W. Yang[7], G. Guo[6], R. Wang[8], P. Guo[9], Z. Ren[10], L. Gong[5], S. Zhou[2], Q. Li[1]
[1]Chinese Center for Disease Control and Prevention, Beijing, China, [2]US Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Beijing Municipal Center for Disease Control and Prevention, Beijing, China, [4]Beijing Research Center for Preventive Medicine, Beijing, China, [5]Anhui Provincial Center for Disease Control and Prevention, Hefei, China, [6]Fuyang Prefecture Center for Disease Control and Prevention, Fuyang, China, [7]Lu'an Prefecture Center for Disease Control and Prevention, Lu'an, China, [8]The Second People's Hospital of Fuyang City, Fuyang, China, [9]Lu'an People's Hospital, Lu'an, China, [10]Changchun Prefecture Center for Disease Control and Prevention, Changchun, China

Background: The Pneumonia of Unknown Etiology (PUE) System, a passive surveillance system, has detected human infections with novel avian influenza viruses in China since 2004. Underutilization and inconsistent reporting persist. We assessed factors affecting PUE case reporting. **Methods:** From February 29–May 29 2016, surveillance officers conducted active case finding at two hospitals performing daily screening of all acute respiratory infection (ARI) admissions using a pre-defined list of ARI-related diagnoses, and enrolled patients with illnesses of unknown etiology that met all four PUE case criteria: 1) axillary temperature >38◦C, 2) radiographic pneumonia, 3) low/normal leukocyte or lymphocyte count early in disease, and 4) no improvement/worsening symptoms after 3–5 days antimicrobial treatment per guidelines. Surveillance officers used standardized questionnaires to collect demographic and exposure data from medical records, and collected throat samples that were tested for influenza viruses. Surveillance officers interviewed all consenting clinicians using a standardized questionnaire to assess familiarity with the PUE system and factors affecting case reporting. **Results:** Surveillance officers screened 2619 ARI admissions; 335 (13%) met the PUE case definition and none were reported to the national system. Of 311 specimens tested, 18 (6%) were positive for seasonal influenza; none were positive for avian influenza. The proportion of medical records of enrolled PUE cases that documented whether or not there was animal exposure was 6%, contact with other persons with respiratory illness was 5%, and travel history was 17%. Awareness of the PUE system was higher among clinicians with >10 years work experience (100%) vs. 5-9 years (84%) and <5 years (23%). The most common reasons for not reporting included not being aware of the PUE system (76%) and not understanding the case definition (53%). **Conclusions:** Most clinicians are not using the PUE system. Adding relevant exposure history to the current case definition, increasing clinicians' awareness of the system, and including exposure items related to emerging respiratory infections in standard medical record histories may enhance clinicians' identification and reporting of patients at greater risk for emerging respiratory infections.

Board 117. Establishing Influenza Surveillance Thresholds for India

A. Prabhakaran[1], V. Potdar[2], S. Bardhwaj[2], S. Saha[1], D. Iulliano[3], K. Lafond[3], M. Chadha[2]
[1]Influenza Program, US Centers for Disease Control and Prevention, New Delhi, India, [2]National Institute of Virology, Pune, India, [3]US Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: India has influenza surveillance, but no defined thresholds to detect the start or end of a season (seasonal threshold) or an unusually high season (alert threshold). We analyzed influenza-like illness (ILI) surveillance data to describe typical influenza activity (average epidemic curve) and develop thresholds, adapting the World Health Organization method. **Methods:** We used data from 23,140 ILI cases sampled between January 1 2011 and December 31 2013 from 7 surveillance laboratories in India to define typical influenza activity. Each laboratory collected samples weekly from ILI cases selected randomly from 2-3 sentinel health facilities and tested through RT-PCR. We calculated the weekly percent of samples positive for influenza. Seasonal threshold (ST) was defined as median weekly influenza percent positive during the 3 years. We identified the median of peak weeks for years 2011-13 and aligned the peak week of epidemic curves with this median week-number. We calculated mean of weekly percent positives of aligned epidemic curves to plot the mean epidemic curve (AEC) and the 90% upper confidence limit to plot alert threshold (AT). We categorized intensity of influenza activity as unusually high when positivity was equal or more than the AT. We considered the influenza season to start when positivity exceeded the ST and end when positivity receded below the ST, both for 2 consecutive weeks. We expressed the season in-terms of week numbers starting from first week of January. For sensitivity analysis, we assessed intensity of influenza activity in pandemic years (2009 and 2010) against these thresholds. **Results:** We observed year-round influenza detection with annual percent positive ranging from 10-14%. We calculated the ST as 8%. The AEC showed influenza season typically occurred from week 19 to week 35 and peaked at week 28. AT for weeks 19, 28 and 35 were 14%, 43% and 22% respectively. For each reference years, we observed one major season and 1 or 2 additional peaks. We observed 75% (39/52) weeks above ST, out of which 39% (15/39) weeks had unusually high intensity in 2009. **Conclusions:** Thresholds can provide timely alerts about the start of influenza season, which would be useful for adopting appropriate control measures. More years of surveillance data are needed to accurately identify these thresholds.

Board 118. Performance of a Large-Scale Implementation of a Participatory Influenza-Like-Illness Surveillance System in Guatemala

J. Prieto[1], J. Jara[1], A. Espinosa-Bode[2], S. Kaydos-Daniels[2]
[1]Centro de Estudios en Salud, Univerisdad del Valle de Guatemala, Guatemala, Guatemala, [2]US Centers for Disease Control and Prevention, Guatemala, Guatemala

Background: Background: Public participation in surveillance of influenza-like-illness (ILI) symptoms could strengthen limited and delayed information from hospital- and laboratory-based surveillance in Latin America. In 2017, we validated and published results on the use of text messages and an app to collect ILI surveillance information. In this study, we evaluate effectiveness of the approach during an influenza season in a large-scale implementation in Guatemala. **Methods:** In February 2018, we sent 30,000 text messages to invite people to submit weekly reports via a mobile-accessible, web-based survey or the Android app "Nuestra-Gripe" through April 2018, on respondent's location, age, symptoms of ILI, health-seeking behavior, and history of influenza vaccination. Half of participants (group 1) were offered influenza prevention tips, the other half (group 2) the chance to participate in ten lotteries of 15 dollars of phone credit. **Results:** Following the transmission of invitation text messages, 109 unique numbers in group 1 (0.7%, 109/15,000) and 254 unique numbers in group 2 (1.7%, 254/15,000) accepted to participate. In total, 350 respondents submitted at least 1 report through the web-based survey; 33.7% (118/350) reported symptoms of ILI. One tenth of respondents with symptoms of ILI (14/118) reported history of influenza vaccination within the current year. Respondents reported from 18 out of 22 Guatemalan departments. The median age was 27 years (range: 13-54). In addition to the survey reports, we recorded 37 reports through the app, 17 of them indicating symptoms of ILI. **Conclusions:** We received reports originating in four-fifths of the country departments, suggesting promising representativeness of the system. Acceptability was low, but participating in a monthly lottery of phone credit may be more attractive than receiving health-promoting information for participants. We will send 30,000 additional text-messages to recruit new participants and learn more about the value of crowdsourced data for influenza surveillance in Guatemala.

Board 119. Establishing an Online Platform for Influenza Data Sharing and Analysis – Experience from the Eastern Mediterranean Region of WHO

M. Elhakim[1], A. Elkholy[1], A. Barakat[1], B. Shrestha[1], W. Khan[2], A. Abubakar[1], M. Obtel[3], S. Malik[1]
[1]World Health Organization, Eastern Mediterranean Regional Office, Cairo, Egypt, [2]University of Bath, Bath, United Kingdom, [3]Faculty of Medicine and Pharmacy, Mohammed V University, Rabat, Morocco

Background: WHO Regional Office for the Eastern Mediterranean established a platform for influenza data sharing and analysis, Eastern Mediterranean Flu (EMFLU) Network. The aim of this review is to present preliminary outcome of the platform's development on influenza data sharing in EMR. **Methods:** EMFLU is a web-based platform, used to enter real time influenza data at country level, providing information on trends and estimates of influenza and helping to detect any abnormal patterns of circulating viruses in the region. Quantity and quality of data shared, specifically SARI data, was assessed and the number of reporting countries was compared before and after the launching of the platform in May 2016. **Results:** EMFLU focuses on collecting SARI data from sentinel surveillance sites according to a specific case definition. This helped to improve the quality of data shared and to define the circulating viruses causing severe cases of influenza in the region. The number of influenza cases shared on FluNet in 2014/2015 season, last influenza season before launching EMFLU, was 34,671 cases shared by 11 countries; these cases included SARI, ILI and clinical influenza cases. During 2016/2017 season, 9 countries shared 29,817 cases on the EMFLU (almost 86% of the number previously shared on FluNet during previous seasons) and these cases represent SARI cases only. The number of countries using EMFLU increased to 14 countries, in February 2018, sharing regularly their influenza data on the platform. Three of these countries have never shared influenza data previously with any other platform. **Conclusions:** EMFLU encouraged the countries in EMR to focus on sentinel surveillance of influenza, with data collected from a limited number of health facilities representing the country's population. This supported

collection of high-quality and reliable influenza data needed by decision makers at different levels.

Board 120. Comparing the 2016-17 and 2017-18 Influenza Seasons with Participant-Reported Symptoms from Flu Near You

K. Sewalk[1], K. Baltrusaitis[1], A. Crawley[2], J. Brownstein[1]
[1]Boston Children's Hospital, Boston, MA, USA, [2]Ending Pandemics, San Francisco, CA, USA

Background: Flu Near You (FNY) is a participatory syndromic surveillance system in the United States that allows for users to report influenza-like symptoms for themselves and their household members. Flu Near You provides an opportunity for individuals to engage directly in public health surveillance via weekly reminders to report any influenza-like illnesses they experience. Flu Near You captures disease activity at the community level and in non-medically attended populations. Flu Near You can compliment existing surveillance systems for assessing community-level disease trends. Given the significant levels of influenza activity during the 2017-18 season, FNY reporting can add important insight into symptom trends and care-seeking behavior. **Methods:** We compare self-reported symptoms during the 2017-18 influenza season to the 2016-17 influenza season, to determine any differences in symptom reporting and healthcare-seeking behavior observed between the two years. Symptoms include: fever, headache, diarrhea, fatigue, nausea, rash, cough, sore throat, body ache, chills/night sweats, shortness of breath, and runny nose. **Results:** During the current 2017-18 influenza season, week of 10/2/2017 through week of 5/14/2018, 37.9% (11,822/31,181) participants reported at least one symptom through FNY that was either self-reported (users) or submitted on their behalf (household members). Compared with the 2016-17 influenza season, week of 10/3/2016 through week of 5/15/2017, where 44.5% (13,628/30,638) participants reported at least symptom through FNY. We also observed that 18.6% (n=2,193 11,822) participants with at least one symptom sought medical attention during the 2017-18 influenza season, compared to 26.5% (n=3,618/13,628) participants during the 2016-17 influenza season. **Conclusions:** We observe a decrease in symptom reporting during the 2017-18 influenza season to date, compared to the 2016-17 flu season. We also observed a decrease in participants experiencing symptoms who seek medical attention.

Board 121. A Real-Time Automated SMS Tool for Monitoring Persons Potentially Exposed to Avian Influenza Twice Daily

C. Kara-Zaïtri[1], M. Schweiger[2], H. ter Waarbeek[3], K. Ohrimenko[4]
[1]University of Bradford, Bradford, United Kingdom, [2]Retired Consultant in Communicable Disease from Public Health England, Leeds, United Kingdom, [3]GGD Zuid Limburg, Heerlen, Netherlands, [4]inFact UK Ltd, Bradford, United Kingdom

Background: The circulation of influenza A(H5N1) virus around the world in 2006 has raised fears of the possible emergence of new highly pathogenic pandemic influenza strains. This has prompted many countries to establish rapid surveillance systems for their early detection. Surveillance officers commonly contact exposed persons through a daily telephone follow-up, which can readily be costly, ineffective and impractical in an epidemic situation. **Methods:** The success of an SMS tool implemented in 2014 to monitor persons returning from West Africa and who have been exposed to Ebola, has motivated the development of a secure web-based SMS tool for the (twice) daily collection of syndromic avian influenza data, embedded in a surveillance and management system for infectious disease control (HPZone). Potentially exposed persons, who may have one or more exposure episodes, are registered in HPZone with their mobile phone numbers, risk category and the date of the last know exposure date. The tool starts by sending an initial SMS to establish contact with the exposed person. It then sends the morning SMS to check if the exposed person has any ILI symptoms soliciting a Yes or No answer. A second SMS is sent in the afternoon and then twice daily (with reminders within the hour) for 10 days after the last exposure to infected birds or environments. **Results:** The SMS tool has been used to monitor a large number of exposed persons. HPZone has been augmented to receive all responses automatically and now includes an alert for each No and Yes response to prompt a monitoring officer to carry out an immediate follow-up, an action to reassess the associated risk category, a dashboard facility for viewing at a glance those in higher risk categories, those who are OK and those who have not responded, and additional workflows for AI exposed persons, cases and outbreaks. **Conclusions:** The real-time SMS tool can readily enhance AI syndromic surveillance and might be the only way to conduct surveillance in a very large outbreak in a cost-effective way. HPZone users have the opportunity to monitor the automated process running in real-time, view the responses as they are received in easy-to-interpret tables and graphs to rapidly identify aberrant patterns. Plus, the potential value of using such a tool is not limited to industrialized countries.

Board 122. Identification of Unplanned Closure of K-12 Schools via Twitter and Online Systematic Search: A Pilot Study of Public Schools in Michigan, September 2015 – June 2016

A. Jackson[1], L. Mullican[2], Z. Tse[3], J. Yin[2], D. Kumar[3], I. Fung[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Georgia Southern University, Statesboro, GA, USA, [3]University of Georgia, Athens, GA, USA

Background: Unplanned school closures (USCs) can be used to mitigate the transmission of infectious diseases such as influenza or rotavirus. Currently, CDC researchers use online systematic searches to evaluate interpandemic patterns of publically announced USCs lasting ≥1 day in the United States. We determined whether Twitter provides complementary data. **Methods:** Twitter handles of Michigan public schools and school districts were identified. All tweets associated with these handles were downloaded. USC-related tweets were identified using five keywords. Descriptive statistics and multivariable logistic regression were performed in R for each data collection method, with individual schools as the unit of analysis. Sensitivity of each data collection method was calculated using all the schools with USCs identified by either method as the denominator (assumed as true positive). **Results:** Among 3,469 Michigan public schools, 2,003 maintained their own active Twitter accounts or belonged to school districts with active Twitter accounts. Of these 2,003 schools, in the 2015–2016 school year, at least one USC announcement was identified for 349 schools via the current method only, 678 schools via Twitter only, and 562 schools via both methods. No USC announcements were identified for 414 schools. Assuming true positives for either method, the sensitivity of the current method is 57% (911/1,589) and that of the Twitter method is 78% (1,240/1,589). Rural schools were less likely than city schools to have active Twitter coverage (adjOR = 0.2171, 95% CI, 0.1734–0.2708) and to announce USCs on Twitter (adjOR =

0.3341, 95% CI, 0.2477–0.4491), but more likely to have USCs identified by the current method (adjOR = 2.3420, 95% CI, 1.9230–2.8564). **Conclusions:** Each method identified USCs that were missed by the other. Our results suggest that identifying USCs on Twitter complements the current method.

Board 123. Using Legal Epidemiology to Assess Electronic Disease Reporting Laws to Overcome Issues with Manual Disease Reporting and to Improve Surveillance of Emerging Diseases

J. Black[1], R. Hulkower[1], T. Ramanathan[2], M. Penn[2]
[1]Cherokee Nation Assurance, CDC, Public Health Law Program, Office for State, Tribal, Local and Territorial Support, Atlanta, GA, USA, [2]CDC, Public Health Law Program, Office for State, Tribal, Local and Territorial Support, Atlanta, GA, USA

Background: Laws requiring disease reporting are vital to limiting the spread of disease through surveillance. While all 50 states have statutes and regulations requiring healthcare entities to report cases of diseases to their health departments, many states also have electronic disease reporting systems. Electronic disease reporting is used for diseases on reportable disease lists and for emerging, novel, new, or unusual diseases or clusters of diseases, as prescribed in each state's law. Electronic disease reporting for clinical and laboratory reports improves disease surveillance capacity. Studies show that electronic disease reporting systems improve the timeliness and completeness of data. However, no analysis exists for the entire landscape of laws that affect electronic disease reporting's implementation and use by states. **Methods:** CDC's Public Health Law Program conducted a cross-sectional study using legal epidemiology methods to assess electronic disease reporting laws across the 50 states, DC, and Puerto Rico. Researchers developed 35 coding questions, including types of healthcare providers, facilities, and other features, to assess the content of laws. **Results:** The presenter will describe methods used and results of data collection, including statistical analysis of data on state electronic disease reporting laws. While this research is under way, preliminary results show 41 states have statutes, regulations, or both that either require or allow disease reporting to be done electronically. The majority of these laws are written to require the same standards for electronic disease reporting as are required for manual disease reporting, rather than incorporating new requirements specific to electronic reporting. **Conclusions:** Health departments can use this information to understand the implications of state laws on the use of disease reports. The implications are also relevant for international health departments since using electronic disease reporting may help identify emerging diseases and outbreaks more quickly and improve detection capacity.

Board 124. A Rapid Communication Protocol for Sharing Infectious Disease Risk Alerts with Cross-Border Partners in the Euregion of Germany, Belgium and the Netherlands

H. ter Waarbeek[1], C. Kara-Zaitri[2]
[1]Public Health Service South Limburg, Heerlen, Netherlands, [2]inFact, Shipley, United Kingdom

Background: Disparate un-integrated national surveillance systems and the lack of a common notification protocol has led to gaps in timeliness and accuracy in international infectious disease data exchange, causing delays in detection and response. This can have significant impact in cross-border regions. There is therefore an urgent need for a simple but effective notification protocol for alerting cross-border public health professionals and exchanging key information required for improved cross-border infectious disease control. **Methods:** Extensive Delphi workshops involving communicable disease consultants from the three countries were held to develop a practical, effective and standardized communication protocol for transmitting and receiving essential notifications of cross-border concern, which – if necessary – could result in a timely and cooperative cross-border response. **Results:** Five clearly defined Cross-border Risk Alert Levels (CRAL), immediately conveying the risk level of a given notification (based on disease, spread, management, cross-border impact and response actions). Minimal data sets (MDS) for case, outbreak and exposure. A simple euregional flow chart for cross-border notification including quick check boxes indicating actual cross-border links (contact, context, residency or media /public interest), crossborder response (cross-border cooperation or special awareness required) and the likely spread across the border. The above has been put together into an agreed Cross-border Notification Template (CNT), which conveys at a glance the current risk level (CRAL) and a basic description of the notification (including multidrug resistant organisms), with the associated MDS and the flow chart data. **Conclusions:** The outcomes were tested successfully in a cross-border hepatitis A simulation exercise and evaluated as part of daily work. The professionals found the communication protocol developed clear, easy to use, effective and practical. The email-friendly CNT is now routinely used in infectious disease control in the Euregion of Germany, Belgium and the Netherlands. It has also been rolled-out in a cross-border software tool (Dashboard).

Board 125. Baseline Measurement of Invasive Mold Infections before Hurricane Harvey—Hospitals A and B, Houston, Texas, 2016–2017

K. Skrobarcek[1], M. Toda[1], R. Chemaly[2], N. Chow[1], J. da Silva[1], B. Garcia[3], B. Murthy[1], L. Ostrosky-Zeichner[4], A. Pennington[1], K. Short[6], J. Shuford[5], S. Solomon[7], J. Strysko[1], B. Jackson[1], T. Chiller[1], K. Beer[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]University of Texas MD Anderson Cancer Center, Houston, TX, USA, [3]Texas Department of State Health Services, Houston, TX, USA, [4]McGovern Medical School, Houston, TX, USA, [5]Texas Department of State Health Services, Austin, TX, USA, [6]Houston Health Department, Houston, TX, USA, [7]Harris County Public Health, Houston, TX, USA

Background: In August 2017, Hurricane Harvey caused extensive flooding in Southeast Texas exposing residents to high levels of mold from water-damaged buildings. Immunocompromised patients are at risk for invasive mold infections (IMI), which are often fatal. However, public health surveillance for IMI has been limited, and the few post-hurricane IMI studies have been too small to evaluate risk. In September 2017, the Texas Department of State Health Services requested emergency assistance establishing a surveillance system for IMI to identify risk factors and guide prevention measures. **Methods:** We conducted case finding at Hospitals A and B from August 2016–August 2017 by identifying microbiology cultures or indirect blood tests positive for mold species. Cases were evaluated during medical chart review. Proven and probable cases were defined using currently published case definitions. Clinical cases did not meet these definitions but were those diagnosed and treated for IMI. **Results:** We reviewed 297 charts at Hospital A, a tertiary hospital system, and 72 charts at

Hospital B, a cancer center, identifying 37 proven, 15 probable, and 26 clinical cases. Median age was 64 years (range: 5–89) and 60% were male. Underlying comorbidities included recent immunosuppressive medications (65.4%), cancer (64.3% [45/70]), and transplant (21.0% [13/62]). The most common clinical presentations were lower respiratory tract infections (60.3%), sinusitis (12.8%), or disseminated infection (10.3%). Most (92.3%) received anti-fungal treatment. Median case count was 6 (range: 3–9) in the 13 months prior to Hurricane Harvey. **Conclusions:** This hospital-based, rapid response IMI surveillance system is the largest of its kind to date. Baseline data collected, including predominant etiologies and underlying comorbidities, were consistent with other studies of IMI in specific patient populations. This surveillance system will continue to be used to identify new IMI cases and allow ongoing assessment of IMI incidence following the hurricane.

Board 126. Evaluation of a Case Definition for Surveillance of Invasive Mold Infections: Hurricane Harvey—Houston, October 2017

M. Toda[1], J. DaSilva[1], K. Skrobarcek[1], J. Strysko[1], A. Pennington[1], N. Chow[1], B. Murthy[1], S. Solomon[2], K. Short[3], L. Gaul[4], T. Chiller[1], B. Jackson[1], K. Beer[1], L. Ostrosky-Zeichner[5], D. Kontoyiannis[6]
[1]CDC, Atlanta, GA, USA, [2]Harris County Public Health, Houston, TX, USA, [3]Houston Health Department, Houston, TX, USA, [4]Texas Department of State Health Services, Austin, TX, USA, [5]University of Texas Health Science Center at Houston, Houston, TX, USA, [6]The University of Texas MD Anderson Cancer Center, Houston, TX, USA

Background: After severe flooding during Hurricane Harvey, concerns regarding mold growth and possible increased risk of invasive mold infections (IMI), presented the need for rapid hospital-based IMI surveillance. An IMI case definition by the Mycoses Study Group (EORTC/MSG) has been validated for use in clinical trials, however no IMI surveillance case definition currently exists for use in public health. We conducted surveillance using the EORTC/MSG definition in addition to a set of more comprehensive clinical criteria (CC) that included the EORTC/MSG criteria, but were designed to emulate clinical diagnosis by an infectious diseases physician. We evaluated the attributes of these case definitions as part of a surveillance effort to determine risk of IMI following flooding and target prevention efforts. **Methods:** We queried databases from two large Houston-based hospital systems for microbiology cultures yielding mold species from September 1, 2016 to October 1, 2017. Clinicians reviewed associated charts and classified each according to EORTC/MSG criteria (proven/probable/not a case) and CC (yes/no). We then calculated sensitivity and specificity of EORTC/MSG criteria against the CC definition, using the more comprehensive CC as gold standard. **Results:** Of 395 mold cultures, we identified 86 (21.7%) IMI cases by either criteria, 51 (12.9%) by both, 57 (14.4%) by EORTC/MSG criteria and 80 (20.3%) by CC. Among EORTC/MSG cases, 40 (70.1%) were classified as proven and 17 (29.9%) as probable. Sensitivity of EORTC/MSG criteria was 63.7% (95% confidence interval: 52.2%–74.2%) and specificity was 98.1% (95% confidence interval: 95.9%–99.3%). The CC definition identified 36.2% more cases than EORTC/MSG alone. **Conclusions:** The first evaluation of the EORTC/MSG definition for public health surveillance shows it has poor sensitivity, but high specificity; a third of cases were missed using the EORTC/MSG definition alone. A surveillance-driven IMI case definition with higher sensitivity should be used for future surveillance efforts.

Board 127. Hurricane-Associated Mold Exposures Among Patients at Risk of Invasive Mold Infections—Houston, TX, 2017

C. Nancy[1], M. Toda[1], K. Beer[1], E. Anassi[2], R. Atmar[3], J. Da Silva[1], B. Garcia[4], M. Al-Mohajer[5], B. Murthy[1], A. Pennington[1], J. Schulte[6], J. Shuford[4], K. Skrobarcek[1], S. Solomon[7], J. Strysko[1], B. Jackson[1], T. Chiller[1], L. Ostrosky-Zeichner[8], D. Kontoyiannis[9]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Harris Health, Houston, TX, USA, [3]Baylor College of Medicine, Houston, TX, USA, [4]Texas Department of State Health Services, Austin, TX, USA, [5]St. Luke's Medical Center, Houston, TX, USA, [6]Houston Health Department, Houston, TX, USA, [7]Harris County Public Health, Houston, TX, USA, [8]Memorial Hermann, Houston, TX, USA, [9]MD Anderson, Houston, TX, USA

Background: Hurricane Harvey caused record flooding in late August 2017. Flood damage causes mold growth and health agencies advise people to assume mold growth if flood-affected surfaces are not dried promptly. In addition, immunocompromised persons are at risk of fatal invasive mold infections (IMI) and CDC advises patients to avoid contact with mold-damaged areas. However, little is known about patient activities that may place them at risk of IMI. We aimed to characterize behaviors of high-risk patients following Hurricane Harvey. **Methods:** We conducted phone interviews with 110 immunocompromised patients at high risk of IMI using a standardized questionnaire. Inclusion criteria included: use of immunosuppressive medications from July 15–October 15, 2017 or receipt of solid organ transplant from October 15, 2016–October 15, 2017. Questionnaires were administered in English and Spanish. **Results:** Of 110 patients interviewed, 42 (38%) cleaned or remediated their own or other people's homes that were affected by the hurricane. Of 42 who performed any cleaning activities following the storm, only 11 (26%) wore a recommended respirator, 30 (71%) wore gloves, 9 (21%) wore boots, 3 (7%) wore goggles and only one person (2%) wore all recommended personal protective equipment. Remarkably, of 42 who did any cleaning, 24 (57%) participated in heavy cleaning and only 10 (42%) of those wore a recommended respirator. Over a third of at-risk patients were exposed to flood-affected or mold-damaged structures and not all patients wore personal protective equipment while performing remediation. **Conclusions:** Immunocompromised patients reported extensive exposure to mold after Hurricane Harvey, including participating in cleaning activities that dislodge mold spores and many did not wear recommended personal protective equipment despite health agencies' guidance. Additional messaging and outreach about strategies to prevent mold exposure are needed for patients at higher risk of developing IMI.

Board 128. Developing and Pilot Testing an Early Warning System for Epidemic-Prone Events Based on Syndromic Surveillance System (SSS) in Iran: Initial Results

M. Gouya[1], P. Hemmati[1], S. Yousefzadeh-Chabok[2], M. Rezvani[2], K. Seif Farahi[3], M. Amini Moridani[2], J. Ahmadi Gasem Kheili[4], P. Parchami[5], A. Haghdoost[6]
[1]Iranian Center for Communicable Diseases Control (CDC), Ministry of Health & Medical Education, Tehran, Islamic Republic of Iran, [2]Gilan University of Medical Sciences & Health Services, Rasht, Islamic Republic of Iran, [3]Independent Researcher, Toronto, ON, Canada, [4]Independent Software Analyzer, Tehran, Islamic Republic of Iran, [5]Iran University of Medical Sciences & Health Services,

Tehran, Islamic Republic of Iran, [6]Kerman University of Medical Sciences & Health Services, Kerman, Islamic Republic of Iran

Background: The public health events of international concern (PHEIC) such as Ebola, pandemic influenza and so on, are growing concerns for global health security. IHR2005 requires all countries to detect any PHEIC at the earliest. Although, some global authorities believe that such a capacity is currently lacking in many countries. From 2011 through 2016, Iranian CDC started a regional initiative with the support of WHO/EMRO on a syndromic-based early warning surveillance (EWS) even sensitive to emerging diseases. We intended to compare SSS with conventional surveillance methods to describe the quality of SSS and flag areas that need improvement. **Methods:** A list of 14 syndromes was developed by a joint team of national and WHO authorities. We implemented 6 prerequisite sub-projects before coming to the 7th i.e. development and implementing the SSS electronic platform in a pilot province. SSS quality was evaluated according to some WHO recommended criteria such as completeness, timeliness, sensitivity, etc. **Results:** Before WHO mission on SSS to Iran, its completeness was 20% in health houses, 69% in health centers and 97% in hospitals. Using capture-recapture, we estimated median sensitivities of SSS and traditional methods for bloody diarrhea, fever and maculopapular rash syndromes as 82% vs 60% and 65% vs 54% respectively. 90% of cases of fever and maculopapular rash had been reported 1.41 days earlier than instant telephonic reporting. The decrease of 3+ and 2+ smear-positive TB cases in favor of an increase of less severe cases, was another indication of timeliness as a fruit of "chronic cough" syndrome. **Conclusions:** This study indicated that SSS is an effective EWS tool complementing some drawbacks of conventional methods such as timeliness, sensitivity, etc. Despite the shortage of SSS in Iran and Eastern Mediterranean region, the initial results inspire its effectiveness and has flagged area that need improvement.

Board 129. Improving Cross-Border Public Health Surveillance and Response through a Participatory Approach to Population Movement Mapping, Togo and Benin

R. Merrill[1], A. Chabi[2], J. Kouassi[2], M. Alleby[2], E. Tchedeli[2], C. Dagbémè[2], A. Abdias[2], S. Ward[1], E. Mcintyre[3], T. Agbeko[4], C. Kakaï[5]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Abidjan Lagos Corridor Organization, Cotonou, Benin, [3]Booze Allen, Atlanta, GA, USA, [4]Ministry of Health, Lomé, Togo, [5]Ministry of Health, Cotonou, Benin

Background: Local and regional human population movement is common and complex and contributes to the risk of geographic spread of communicable diseases, as evidenced by the 2014-to-2016 Ebola epidemic in West Africa and repeated multinational cholera outbreaks across Africa. Integrating a better understanding of domestic and cross-border population movement patterns in surveillance and response systems may help tailor cross-border public health collaboration and mitigate the international spread of disease. **Methods:** The novel method to integrate information on population connectivity across borders ("PopCAB") involves national- and community-level key informant interviews and focus group discussions, each with participatory mapping, to identify geographic areas of public health priority; characterize and visualize the population movement patterns into, through, and from those areas; and apply the results to better coordinate and tailor public health surveillance and response. Since 2016, the Togo and Benin Ministries of Health (MOH) have integrated PopCAB into their national cholera outbreak responses, a cross-border outbreak response, and regional collaboration. **Results:** The Benin MOH used newly identified cross-border community connectivity between Benin and Nigeria among a population experiencing a cholera outbreak to update national preparedness strategies and to initiate a four-country collaboration to review national-level cholera surveillance data to improve regional coordination. During Lassa fever outbreaks in 2017 and 2018, Togo and Benin MOH used binational PopCAB results to target cross-border communities at risk of disease importation and support collaborative response more rapidly than in previous cross-border outbreaks. **Conclusions:** Togo and Benin MOH used PopCAB results to improve cross-border public health surveillance and response to communicable disease events and to initiate regional public health collaboration. Integrating a participatory approach to understanding population movement patterns into public health programs can help countries mitigate international spread of disease in support of improved global health security and International Health Regulations requirements.

Board 130. Tools for Monitoring and Evaluation of Event-Based Surveillance in Vietnam

A. Clara[1], T. Do[2], P. Dao[2], K. Alroy[1], C. Bernadotte[3], H. Nguyen[4], Q. Nguyen[4], T. Phu[5], Q. Tran[5], A. Mounts[2], A. Balajee[1]
[1]U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]US Centers for Disease Control and Prevention, Hanoi, Viet Nam, [3]PATH, Seattle, WA, USA, [4]PATH, Hanoi, Viet Nam, [5]Vietnam Ministry of Health, General Department of Preventive Medicine, Hanoi, Viet Nam

Background: In 2016 Vietnam's Ministry of Health (MOH) established a pilot program for event based surveillance (EBS). As a new surveillance type, there were no tools and few practical reports on EBS monitoring and evaluation. The MOH, CDC and PATH, a non-governmental organization, developed a series of EBS specific M&E tools. This evaluation describes these tools and lessons learned from their implementation. **Methods:** Vietnam's MOH launched EBS in September 2016 in 4 provinces. An M&E framework was designed based on World Health Organization (WHO) guidance and WHO Interim Guidelines for EBS. Monitoring tools were developed and made available to all levels, including logbooks, monthly report forms, and supervision checklists. An EBS evaluation was conducted in two-parts: a 6 mo mid-term review in March 2017; and an evaluation in June 2017, 9 months after implementation. A series of data collection tools were created: a desk review, key informant interviews (KII), focus group discussions (FGD), deep-dive interviews, a timeliness extraction tool, and an online survey of acceptability and perceived usefulness. **Results:** The desk review tool was effective to compile training information, use of logbooks, and the number of signals and events. While there was some overlap, the KII and FGD tools provided a practical guide to obtain qualitative information from all levels on the challenges, successes and recommendations from EBS implementation. Deep dive interviews clarified the EBS process and timeline for selected events. The extraction tool helped to gather timeliness data yet was difficult to complete. The online survey was low cost and easily implemented. The survey was open for 3 weeks and response rates varied between 23-100% for different levels. **Conclusions:** The M&E strategy and tools enabled a comprehensive collection of high quality quantitative and qualitative data on EBS implementation. Early data review allowed evaluators to reduce potential bias. While some challenges remained, such as a lack of direct impact indicators, time-consuming site visits, and the presence of selection and information bias, this

evaluation represents the first report of EBS M&E strategic plans and tools. Even when impact cannot be directly measured, a well-planned evaluation can provide useful insights into the effectiveness of EBS.

Board 131. Daily Surveillance of Laboratory Records: Enhanced Outbreak Response for Military Readiness

B. Poitras[1], R. Scagos[2], N. Seliga[2], G. Nowak[3]
[1]Defense Health Agency, J3, Armed Forces Health Surveillance Branch, Portsmouth, VA, USA, [2]Oak Ridge Institute for Science and Education, Portsmouth, VA, USA, [3]Navy and Marine Corps Public Health Center, Portsmouth, VA, USA

Background: Reportable medical events (RMEs) form the cornerstone of public health surveillance. These events represent potential public health threats that may be prevented through specific control measures. Healthcare personnel in the Department of Defense (DOD) have the responsibility of disclosing RME cases for all military beneficiaries in their area of responsibility. The processes used to search for cases are time consuming and may result in missed cases, and largely rely on ad hoc system queries. The Epi-Data Center (EDC) at the Navy and Marine Corps Public Health Center provides daily surveillance of laboratory data which not only facilitates the identification of RMEs, but also plays a supporting role in outbreak identification and response. The goal of this project is to describe the benefits of the daily case finding process on outbreak response. **Methods:** The Armed Forces Reportable Medical Event Guidelines & Case Definitions laboratory criteria are used by the EDC to develop algorithms for the identification and classification of 54 RMEs in military health system (MHS) laboratory data. Each day, infectious disease cases are identified from laboratory data using disease specific algorithms. Identified cases are loaded into the Disease Reporting System, internet (DRSi) for centralized access. **Results:** The EDC case finding process has been an integral piece in the DOD outbreak response for diseases such as Salmonella, influenza, pertussis, Zika and *E. coli. Unusual patterns in specific diseases may alert healthcare personnel of a potential outbreak in a specific geographic location. This process assists medical event recorders with the identification of RMEs and has improved efficiency and completeness of routine and outbreak surveillance.* **Conclusions:** Daily analysis of laboratory records provides a platform for near real-time surveillance and identification of possible infectious disease outbreaks among DOD beneficiaries.

Laboratory: Detection and Diagnosis

Board 132. Rabies Surveillance: Training and Implementation of Next Gen Sequencing

G. Gallagher[1], T. Fink[1], S. Winnicki[2], D. Park[2], S. Hennigan[1], N. Yozwiak[2], D. Hennigan[1], V. Pani[1], M. Farris[1], C. Tomkins-Tinch[2], P. Sabeti[2], S. Smole[1]
[1]Division of Molecular Diagnostics and Virology, Department of Public Health, Massachusetts State Public Health Laboratory, Jamaica Plain, MA, USA, [2]Broad Institute of MIT and Harvard, Cambridge, MA, USA

Background: In 2017, the Massachusetts State Public Health Laboratory (MA SPHL) partnered with the Broad Institute of MIT and Harvard (Broad) to provide ongoing hands-on trainings for advanced techniques in viral sequencing and bioinformatics of rabies virus samples. Capitalizing on the Broad's expertise in training laboratorians to perform genomic disease surveillance, the MA SPHL collaborated to develop and implement a training program. **Methods:** Participants were identified within the Northeast Public Health and Environmental Laboratory Directors (NEEPHLD) group. Rabies was selected as a prototype virus due to its ease of availability within the public health setting. Participants were invited to ship samples to the MA SPHL in preparation for the course. In 2017, 84 Rabies DFA-positive brain tissue samples from domestic and wild animals were provided by six states (MA, ME, RI, CT, and DE); in 2018, four additional public health laboratories (VT, NH, NJ, and NYS) are providing additional geographic samples. Vaccinated MA SPHL staff performed a validated sample processing, nucleic acid extraction, and inactivation method on frozen, original rabies DFA-positive animal brain tissue. Inactivated, extracted samples were sent to Broad for trainees to perform QC assessment of the 18S RNA and/or a viral target, RNA processing of the sample to deplete rRNA and cRNA followed by cDNA synthesis, Nextera XT Library preparation, MiSeq sequencing, and data analysis using DNAnexus. **Results:** Preliminary genomic analyses confirms the detection of raccoon and bat variants; raccoon subclades structured by region; and new bat variants. **Conclusions:** In total, these data are expected to better inform national rabies surveillance within the public health system using a standardized protocol.

Board 133. The Recovery of Nontyphoidal *Salmonella* from CIDT-Positive Stool Specimens

K. Dillon[1], J. Hensley[1], A. Blackstock[2], M. Patel[1], E. Trees[2], J. Besser[2], H. Carleton[2], A. Huang[2], A. Williams-Newkirk[3]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]IHRC, Inc., Atlanta, GA, USA

Background: Nontyphoidal *Salmonella* is estimated to cause 1,000,000 infections, over 19,000 hospitalizations, and 380 deaths each year in the US. Clinical laboratories are adopting culture-independent diagnostic tests (CIDTs) to detect *Salmonella* and other enteric pathogens because they provide clinical information faster than traditional microbiological techniques. However, CIDTs do not yield isolates, which are currently required for outbreak surveillance. A standard protocol for isolate recovery from CIDT-positive stools would reduce barriers to isolate availability. This study examined the impact of transport temperature, plating media, transport media, and transport time on the recovery of two *Salmonella enterica* serovars from human stool. **Methods:** 5 stool samples from clinically healthy, anonymous donors were homogenized and pooled to make one standard stool which was divided and seeded with either *Salmonella enterica ser.* Newport or Oranienburg at 10^4 or 10^2 CFU/mL. Seeded stool and unseeded negative controls were used to inoculate vials of each transport media (Cary-Blair Transport Medium or Gram-Negative broth). Three replicates of each seed level were held at each transport temperature (4°C or 22°C). Sampling occurred at three transport times (4, 8, and 14 days), and two plating medias (Hektoen Enteric Agar or Xylose Lysine Deoxycholate Agar) were inoculated for each. Plates were incubated at 37°C for 24 hours. Up to 3 colonies morphologically consistent with *Salmonella* and a sweep were collected from each plate. Colony and sweep identity was confirmed by qPCR. **Results:** At 22°C *Salmonella* was recovered from 100% of the seeded stool samples. At 4°C *Salmonella* was recovered from 83% of 10^4 CFU/mL samples, and 1% of samples at 10^2 CFU/mL (42% overall). Recovery rates did not differ significantly by serotype, transport time, plating media, or transport media. **Conclusions:** Results from this study strongly support trans-

porting *Salmonella* CIDT-positive stool specimens at 22˚C to optimize isolate recovery even at low pathogen loads. Future work will examine screening approaches and enrichment media used in conjunction with the optimal conditions identified here to allow recovery from samples with lower *Salmonella* levels and/or after longer transport times.

Board 134. Comparison of the Cepheid GeneXpert Carba-R and Streck ARM-D Kit, β-Lactamase for the Detection of Carbapenem Resistant Enterobacteriaceae

B. Craft[1], D. Edwards[2], E. Santos[2], J. Jordan[1], A. Tran[2]
[1]The George Washington University Milken Institute School of Public Health Department of Epidemiology and Biostatistics, Washington, DC, USA, [2]The District of Columbia Department of Forensic Sciences, Public Health Laboratory Division, Washington, DC, USA

Background: Carbapenem-resistant Enterobacteriaceae (CRE) are a growing group of antibiotic resistant bacteria. These organisms spread rapidly in healthcare settings and can cause infections that are severe and often untreatable. The rapid identification of true CRE will lead to more focused public health control efforts in healthcare settings. There is currently a lack of data on the performance of these carbapenem-resistance gene detection methods. We evaluated two assays for the detection of resistance genes for CRE. **Methods:** A well characterized panel of 50 bacterial isolates with a variety of known carbapenem-resistance genes was provided by the CDC. Of these, 45 had at least one carbapenem-resistance gene. The resistance genes reported for each isolate were identified by either WGS (n=47) or PCR (n=3). The Cepheid GeneXpert Carba-R test kit (Carba-R) and the Streck ARM-D, β-Lactamase kit using an Applied Biosystems Real-Time PCR system (ARM-D) were evaluated for this study. All 50 isolates were tested with both methods. The Carba-R detects the KPC, NDM, VIM, OXA-48, and IMP β-lactamase genes. Additionally, the ARM-D detects the CMY-2, CTX-M-15, CTX-M-14, and DHA β-lactamase genes in addition to those detected in Carba-R. **Results:** The Carba-R accurately identified all carbapenem resistant isolates that are able to be detected by the test. The ARM-D also identified all resistant isolates, but falsely reported two isolates as carbapenem resistant. Of the 45 isolates, the Carba-R identified 60% and ARM-D 72% of all resistance genes. The Carba-R identified all 27 specific genes it tests for while ARM-D identified all 36 genes it tests for, however, it incorrectly identified 13 carbapenem resistance genes that were not present. **Conclusions:** The high accuracy and streamlined workflow of the Carba-R makes it an ideal test for carbapenem resistance. While Carba-R and ARM-D both reported all resistant isolates with genes that were tested for, ARM-D had multiple false positives for specific genes, with all false positives being in isolates with other resistance genes. Of the 45 resistant isolates, ARM-D was able to detect a higher percentage of resistant isolates than the Carba-R. This added value of the ARM-D makes it a useful test to characterize a wider variety of resistance, despite the over reporting of genes.

Board 135. Development of a Targeted Sequencing Panel to Detect Antimicrobial Resistance Determinants in Human Stool

J. Hensley[1], J. Chen[2], K. Dillon[1], B. Aspinwall[1], A. Huang[3], J. Besser[3], H. Carleton[3], E. Trees[3], A. Williams-Newkirk[2]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]IHRC, Inc., Atlanta, GA, USA, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Fast characterization of the resistome of complex metagenomic samples has broad potential applications for medicine, public health, environmental monitoring, and food safety. Highly multiplexed amplicon sequencing (HMAS) panels are a new tool that enables the rapid detection of hundreds of antimicrobial resistance genes (ARGs) directly from clinical samples without the need for isolation. However, baseline data on healthy stool resistomes is needed to interpret ARG signals, and assay specifications need to be established. Here we assessed an ARG HMAS panel's limit of detection and reproducibility to determine assay specification. We then examined ARG content in healthy stools. **Methods:** We used the Juno Targeted DNA Sequencing Library Preparation System (Fluidigm) to amplify 749 amplicons targeting 111 ARGs. Targets were selected from a published microarray for relevance to enteric pathogens. Amplicons (180-240 bp) were sequenced on the Illumina MiSeq. Stool DNA was spiked with 2 *Salmonella* isolate DNAs with known ARGs at 10^1 to 10^8 CFU/mL and analyzed in triplicate. In addition, 22 unique, healthy stools samples were screened from younger and older adults. Sequence reads were assembled, quality filtered, trimmed, and mapped to ARG reference sequences obtained from ResFinder using standard tools. Reference coverage and depth were used to determine gene presence. **Results:** Six of 12 ARGs from *Salmonella* isolates were detectable in stools with 10^7 CFU/mL spike-ins. At 10^8 CFU/mL spike-in, 9/12 ARGs were strongly detected, and 3 were weakly detected. This detection limit is equivalent to 0.2-2% of the total input DNA. Detection was consistent across triplicates. Eleven ARGs were detected in the 22 healthy stools (1-6 ARGs/sample, mean 3.8). The most common was *mefA* (22 samples), followed by *ermB* (19) and *ermG* (16). **Conclusions:** This study suggests that the Juno can detect ARGs against a stool background, but the sensitivity likely varies with primer specificity and gene copy number. Limited sampling of healthy stools suggests that some ARGs may be too common in stool to be useful in disease surveillance. The Juno may be a viable platform for deployment of HMAS sequencing panels to public health laboratories. Future studies include expanded testing of healthy and diarrheal stools, and additional assessments of assay interpretation and limitations.

Board 136. Replication of Human Norovirus in Human Intestinal Enteroids as a Model to Measure Virus Inactivation

V. Costantini[1], E. Morantz[2], H. Browne[3], K. Ettayebi[4], X. Zeng[4], R. Atmar[4], M. Estes[4], J. Vinje[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Synergy America, Inc., Atlanta, GA, USA, [3]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [4]Baylor College of Medicine, Houston, TX, USA

Background: Human noroviruses are the most common cause of epidemic gastroenteritis worldwide and a leading cause of foodborne illness in the US. Since the discovery of norovirus in 1972, many attempts to grow human norovirus in cell culture have failed or have

been difficult to reproduce in other laboratories. Due to the lack of a robust cell culture system, evaluation of inactivation methods and products have relied on the use of cultivable surrogate viruses, with variable results depending on treatment and surrogate virus. Recently, non-transformed human intestinal enteroids (HIEs) derived from proliferating crypts isolated from human small intestinal tissue have shown to support replication of human norovirus. The aim of this study was to test the effect of chlorine and alcohols on infectious human norovirus. **Methods:** In this study, we inoculated duplicate 96-wells of HIE monolayers with 82 human norovirus positive stool samples [12 genogroup (G) I, 67 GII and 3 GIV] from outbreaks and sporadic cases of acute gastroenteritis collected between 2000 and 2017. Among the strains that successfully replicated, three GII.4 strains (GII.4 Den Haag, GII.4 New Orleans, GII.4 Sydney) were chosen to assess virus inactivation with increasing concentrations of chlorine (0 to 5000 ppm) and with 70% ethanol or isopropanol. **Results:** Successful replication was shown for six different norovirus GII genotypes (GII.1, GII.2, GII.3, GII.4, GII.14 and GII.17) including 3 different GII.4 variants. Identical levels of replication were obtained consistently for several human norovirus strains tested at several time points over 1 year period. The 50% infectious dose was 2.1 x 10^3 genome copies/well for GII.4 Den Haag strain, 5.6 x 10^2 genome copies/well for GII.4 Sydney strain and 3.9 x 10^3 genome copies/well for GII.3 strain. Regardless of exposure time (1 or 5 min), alcohols slightly reduced, but did not completely inactivate, human norovirus replication. In contrast, complete inactivation of the three GII.4 viruses occurred at concentrations as low as 50 ppm of chlorine. **Conclusions:** Taken together, our data confirm the successful replication of human noroviruses in HIEs and their utility as tools to study norovirus inactivation strategies.

Board 137. Eukaryotyping: A Novel Typing Method Developed for Sexual Eukaryotes and Its First Application to *Cyclospora cayetanensis*

J. Barratt, S. Park, F. Nascimento, J. Hofstetter, S. Casillas, M. Plucinski, R. Bradbury, M. Arrowood, Q. Yvonne, E. Talundzic
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: *Cyclospora cayetanensis* is an intestinal protozoan responsible for seasonal outbreaks of foodborne illness in the United States (US) due to importation of contaminated fresh produce from endemic countries. No independently validated molecular tools are available to aid cyclosporiasis outbreak investigations. *Cyclospora* reproduces sexually and possesses three discrete genomes, one nuclear and two organellar, resulting in a complex genetic structure, which complicates typing using traditional phylogenetic approaches. Additionally, the availability of only two published *C. cayetanensis* genomes hinders selection of informative typing markers. **Methods:** We sequenced 11 *C. cayetanensis* genomes and identified three Polymerase Chain Reaction (PCR) enrichment friendly markers, including two nuclear loci and one mitochondrial locus. We applied PCR enrichment and Sanger sequencing of these loci to 74 fecal specimens containing *C. cayetanensis*, including 27 that had been epidemiologically linked to US cyclosporiasis outbreaks. Next, we developed eukaryotyping, which incorporates machine learning approaches to identify genetic clusters that represent parasite familial relationships, and used it to analyze the sequence data. Eukaryotyping differs from other methods as it considers intra-isolate heterozygosity, a feature of sexual eukaryotes partly attributable to their mechanisms of nuclear inheritance. This is an important advancement, as this heterozygosity confounds traditional typing approaches. **Results:** Eukaryotyping resolved the *C. cayetanensis* parasites within the 74 fecal specimens into 10 genetic clusters, represented as a 2D scatter-plot for ease of interpretation. These clusters were corroborated by the epidemiological data for a large number of specimens. Therefore, the tool shows promise for assisting epidemiological trace-back. **Conclusions:** We present eukaryotyping; a method for typing sexual eukaryotes that shows promise for aiding investigations of cyclosporiasis outbreaks. Unlike other typing approaches, this method considers intra-isolate heterozygosity often observed at nuclear loci in sexual pathogens. While the markers examined here are specific to *C. cayetanensis*, the bioinformatic principals behind eukaryotyping will likely extend to other sexual eukaryotic pathogens.

Board 138. Improved Differentiation of *Streptococcus pneumoniae* from Other Streptococcal Species Using Pyrosequencing and *comC* PCR in Respiratory Autopsy Tissues

A. Denison, S. Zaki, J. Bhatnagar
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Streptococci cause a wide range of human clinical syndromes, and the genus contains a variety of pathogenic and commensal species. Phenotypic methods (e.g. optochin resistance, bile insolubility) have been most widely used to differentiate species of Streptococci, but require an isolate for testing. Molecular mechanisms of identification are complicated by the naturally transformable quality of Streptococci, such that genetic elements are exchanged between species. PCR and subsequent Sanger sequencing to the 16S rRNA, pneumolysin, autolysin, and other genes has often been used to differentiate species, but whole genome analyses have shown that differentiation between *Streptococcus pneumoniae*, *Streptococcus mitis*, and *Streptococcus pseudopneumoniae* cannot always be accomplished with PCR to these genes due to genetic exchange. While whole genome sequencing can be helpful in determining the causative species, it is expensive and tedious to perform. **Methods:** To simplify and more accurately identify Streptococci found in respiratory tissue samples obtained at autopsy, we have developed a pyrosequencing assay that utilizes two sequencing primers specific to the V1 and V2 regions of the Streptococcal 16S rRNA gene. Combined with PCR and Sanger sequencing to a 300 bp amplicon of the *comC* gene, we sought to differentiate species of Streptococci. These results were compared with PCR and Sanger sequencing to the 16s rRNA, pneumolysin and autolysin genes traditionally used in our laboratory to differentiate Streptococci. **Results:** Eleven different Streptococcal species controls were tested using pyrosequencing/*comC* PCR. All results were in agreement, and in one case, contamination with *S. pneumoniae* was confirmed. In respiratory tissues from 14 autopsy cases, pyrosequencing and Sanger sequencing of the *comC* PCR amplicon could effectively differentiate between species, particularly when the percentage of sequence identity was high. Results were comparable to those obtained with traditional assays, including cases where a determination could only be made to the genus level. **Conclusions:** Combining these two assays, the total number of diagnostic tests performed can be reduced and more effectively surveil the number of pathogenic Streptococci that cause fatal respiratory disease.

Board 139. Real-Time PCR for Diagnosis and Differentiation of Relapsing Fever *Borrelia*

E. Dietrich, A. Replogle, S. Sheldon, M. Schriefer, J. Petersen
Centers for Disease Control and Prevention, Fort Collins, CO, USA

Background: *Borrelia* species in the relapsing fever (RF) group include multiple recognized and emerging pathogens. The known pathogenic RF *Borrelia* can be divided into three phylogenetic clades. The first clade includes *B. hermsii*, the most common cause of tick-borne relapsing fever (TBRF) in the United States, and related species found in North America. The second clade includes species such as *B. duttonii*, which causes TBRF in Africa, and *B. recurrentis*, which causes louse-borne relapsing fever (LBRF). The third clade comprises only *B. miyamotoi*, which causes a distinct clinical syndrome known as hard-tick relapsing fever or *B. miyamotoi* disease. Distinguishing among the clades is important for epidemiological surveillance and may impact clinical management. Because these organisms are associated with spirochetemia levels $\geq 10^4$/ml, they are good candidates for sensitive molecular detection in blood samples. **Methods:** We developed a multiplex real-time PCR assay using hydrolysis (TaqMan) chemistry to detect RF *Borrelia* and to distinguish between the three clades in clinical samples. This assay uses a single primer pair designed to amplify all known pathogenic RF *Borrelia*, but not *B. burgdorferi* sensu lato genospecies, which cause Lyme disease. Three different fluorescently labeled probes detect and differentiate among the clades. **Results:** The assay is capable of detection of all pathogenic RF *Borrelia* tested with a limit of detection of 10 pg bacterial DNA, or approximately 7 genome equivalents. No amplification was detected in normal human blood or in any of 45 non-RF bacterial species tested, including 10 *B. burgdorferi* sensu lato genospecies. **Conclusions:** This assay will be useful for improving the ability to diagnose RF in early disease, and will aid in surveillance and clinical management of RF patients.

Board 140. Utilization of High-Throughput Multi-Locus Sequence Typing for Strain Characterization of *Borrelia* Directly from Patient Samples

L. Respicio-Kingry[1], M. Anacker[2], B. Pritt[3], J. Bjork[2], G. Liu[2], S. Sheldon[1], D. Boxrud[2], A. Strain[2], S. Oatman[1], J. Berry[3], L. Sloan[3], P. Mead[1], D. Neitzel[2], K. Kugeler[1], J. Petersen[1], L. Kingry[1]
[1]Division of Vector-borne Diseases, US Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Minnesota Department of Health, St. Paul, MN, USA, [3]Mayo Clinic, Rochester, MN, USA

Background: In the United States, Lyme borreliosis (LB) and relapsing fever (RF) are caused by bacterial tickborne species within the *Borrelia* genus. Genospecies of the *Borrelia burgdorferi* sensu lato group are the causative agents of LB, the most common vector-borne disease in the Northern Hemisphere. Over the last decade, novel *Borrelia* species causing human infection have emerged and the geographic distribution of LB cases has expanded. As culture of *Borrelia* species from clinical specimens is difficult and uncommonly performed, development of new, culture independent methods is beneficial for enhancing our understanding of the epidemiology of *Borrelia* infections, including improving our knowledge of species associated with human disease. **Methods:** To characterize *Borrelia* species directly from clinical specimens (blood, cerebral spinal fluid, and synovial fluid), DNA extraction and PCR amplification of 8 housekeeping genes, comprising a previously developed multi-locus sequence typing (MLST) scheme, was coupled with next generation sequencing (NGS) of the resulting amplicons. The resulting reads were mapped to *Borrelia* reference gene sequences. Consensus housekeeping gene sequences were concatenated for phylogenetic analyses and speciation. **Results:** All 8 genes were amplified and analyzed from patient specimens (blood, cerebral spinal fluid, or synvovial fluid) positive for known LB causing pathogens *B. burdgorferi* and *B. mayonii*, and relapsing fevers borreliae, *B. miyamotoi*, *B. hermsii*, and Candidatus *B. johnsonii*, a species not previously associated with human illness. Due to the depth of sequence coverage offered by this approach, high quality sequence data was readily obtained, significantly enhancing the sensitivity of this approach as compared to conventional Sanger based sequencing. **Conclusions:** These results demonstrate a culture independent, high throughput, high quality MLST approach utilizing NGS sequencing, is a powerful tool for identifying and characterizing *Borrelia* species directly in patient samples. Implementation of this method will help to advance our understanding of the epidemiology of *Borrelia* infections in US patients, including uncovering the spectrum of *Borrelia* species causing human disease and improving understanding of their geographic distribution.

Board 141. Unexpected Viruses Detected in Patients Presenting with Lyme-like Symptoms

K. Forberg, M. Berg
Abbott Laboratories, Abbott Park, IL, USA

Background: Lyme disease is a tick-transmitted illness caused by infection with the *Borrelia* spirochete for which disease incidence and distribution are on the rise. Signs of Lyme often occur in 3 stages, beginning with the hallmark erythema migrans rash, followed by common flu-like symptoms including fever, headaches, fatigue, and joint pain, which can progress to arthritis. Metagenomic NGS (mNGS) was deployed to study patients testing negative for a physician-ordered Lyme antibody test. **Methods:** Plasma was commercially sourced from patients presenting with Lyme-like symptoms that were IgM negative. A panel of 38 samples spiked with an internal control (IC) were extracted along with positive and negative controls, converted into mNGS libraries by random priming and Nextera, and sequenced on 5 MiSeq runs multiplexing 8 samples. Data analysis was performed with SURPI and a custom informatics pipeline. **Results:** An average of 4.1 million reads per sample were obtained, with IC detected in all 38 patient libraries and 9 different viruses each detected at log 4.0 copies/ml in the positive control. No evidence of tick-borne bacteria or parasites was observed, nor any divergent viruses, although several unexpected, known viruses were identified. Four patients were positive for HCV, 2 of which were acute cases. Three patients were individually positive for HBV, parvovirus B19, and the recently described HPgV-2. A new variant of human rhinovirus C (HRV-C) was detected in 9/38 specimens. However, given the low abundance of these reads, the identical sequence found in each, and the failure to detect it in nucleic acid derived from an alternate extraction method, we concluded HRV-C was a contaminant. Thus, 31/38 specimens were negative for any pathogen. **Conclusions:** Screening numerous samples together under standardized conditions allowed data to be interpreted holistically, avoiding the erroneous link of HRV-C to Lyme-like symptoms which may have resulted from sequencing one sample at a time. The detection of multiple unexpected viruses also known to cause non-specific symptoms similar to Lyme highlights the potential of mNGS as an early diagnostic. While expensive compared to PCR tests targeting one or more viruses or bacteria and currently not reimbursed, mNGS can detect all pathogens simultaneously, or none at all, and may arguably be more cost effective long term as it links patients to care and avoids lengthy hospital stays.

Board 142. Development and Use of *In-Vitro* RNA Transcript as a Positive Control for Detection of Dengue serotypes by Real-time RT-PCR

A. Ahmad[1], K. Bedi[1], J. He[1], B. Werner[1], G. Santiago[2], D. Bagarozzi[1], D. Petway[1]
[1]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [2]Centers for Disease Control and Prevention (CDC), San Juan, Puerto Rico

Background: Dengue is the most common and clinically important arbovirus disease caused by one of four dengue viruses (serotype DENV-1-4) and the potential co-circulation of other arboviruses can lead to complications during diagnosis. Therefore, timely and precise detection is critical for clinical management and surveillance. Currently, real-time RT-PCR (qPCR) is the most preferred method for the detection of virus RNA and serotype identification. The reliability of qPCR results depends on having proper positive controls that resemble a real positive sample or amplification to facilitate interpretation especially for low positive signals. Using native RNA as an internal positive control for qRT-PCR requires culture of viruses in a BSL-2 facility and inactivation of viruses. Our aim was to develop and validate *in-vitro* RNA transcript as a positive control for the detection of dengue by qRT-PCR. This would eliminate the need for production of virus cultures for positive controls. **Methods:** We started with the DENV-1 and used DENV-1/US/BID-V1739/1998 (Accession # FJ205872.1) genome. We synthesized a 669bpgene fragment that contains the target for the CDC DENV-1-4 Real Time RT-PCR assay capped with T7 promoter at 5' end and cloned in a vector. The *in-vitro* transcription template and the RNA product was verified by Sanger sequencing and fragment analyzer respectively. The validation of transcript was performed according to the CDC DENV1-4 Real-Time RT-PCR assay using ABI 7500 Fast Dx qPCR instrument. **Results:** We successfully synthesized ~35µg of RNA transcript from 500ng of template, where 100ng transcript contains approximately 2.7×10^{11} copies of transcript. We targeted a Ct range of 20-30 to standardize a low to high Ct curve. After dilution (1:10^3 to 1:10^{12}), we obtained Ct values in the range of 22-30 with 10^4–10^5 copies of transcript. To evaluate potential cross-reactivity, we tested the RNA transcript with the primer sets specific for DENV-2 and -4 and found no evidence of cross-reactivity. **Conclusions:** We successfully developed and validated DENV-1 *in-vitro* RNA transcript as an internal positive control for the detection of DENV-1. We will apply the same approach for development and validation of *in-vitro* RNA transcript for identification of the other serotypes of DENV.

Board 143. LeDantec Rhabdovirus Human Infection in Uganda: Identification of the Transmitted/Founder Virus

J. Salazar-Gonzalez[1], M. Salazar[1], H. Jerome[2], P. Namuwuya[3], H. Bukenya[3], B. Kigozi[3], E. Mbidde[3], J. Bwogi[3], R. Downing[3], P. Kaleebu[1], E. Thomson[2]
[1]MRC/UVRI and LSHTM Uganda Research Unit, Entebbe, Uganda, [2]MRC Centre for Virus Research University of Glasgow, Glasgow, United Kingdom, [3]Uganda Virus Research Institute, Entebbe, Uganda

Background: LeDantec virus (LDV) has been reported to be pathogenic in suckling mice causing hind-limb paralysis, ataxia, tremor and death. Two human cases have been reported, one in Senegal in 1965 and a second case in Wales in 1969. The later was a dockyard worker unloading a ship from West Africa - sometime later he developed Parkinson's disease but no causal relationship was established. Little is known about the determinants of zoonotic spillovers of emergent and re-emergent viruses despite their implications for human public health. **Methods:** We used metagenomic next-generation sequencing, single genome amplification and sequencing, phylogenetic analysis, and real-time PCR to identify and characterize an LDV genome found in a plasma sample taken from a 9-year Ugandan boy presenting with an acute febrile illness of unknown origin on May 2012. **Results:** Metagenomic analysis of the acute plasma RNA revealed a contiguous sequence of 11,423 nucleotides that had a 94% identity with a 1965 LDV strain isolated from a Senegalese girl (DakHD763 strain, KM205006) by phylogenetic analysis. The metagenomics sequence was confirmed by PCR and Sanger sequencing of a 5'-half genome fragment. The consensus sequence has an intact proteome for the five canonical rhabdoviral protein genes. End-point dilution and single genome amplification analysis of a 2.3 Kb fragment (partial glycoprotein and polymerase genes region) revealed identical and near-identical sequences coalescing to a single consensus sequence, that we inferred to represent the transmitted/founder virus that initiated infection. An RNA aliquot equivalent to three microliters of acute plasma yielded a Ct value of 30 using an in-house developed real-time TaqMan assay that is consistent with a high-level viremia typically seen in acute viral infections. **Conclusions:** This is the first human case of infection with LDV in East Africa, and the third case reported worldwide. A molecular diagnostic assay is readily available for surveillance of human cases and wildlife reservoirs. We present evidence of a strong genetic bottleneck in LDV transmission to humans, likely representing a zoonotic spillover. This is the first inferred transmitted/founder LDV, which will enable us to determine its biological and pathogenic properties.

Board 144. Molecular Diagnosis of Hemorrhagic Fever with Renal Syndrome

M. Korva[1], K. Resman Rus[1], N. Knap[1], P. Bogovič[2], E. Pal[3], F. Strle[2], T. Avšič Županc[1]
[1]University of Ljubljana, Faculty of Medicine, Institute of Microbiology and Immunology, Ljubljana, Slovenia, [2]Department of Infectious Diseases, University Medical Centre Ljubljana, Ljubljana, Slovenia, [3]Department of Infectious Diseases, Regional Hospital Murska Sobota, Murska Sobota, Slovenia

Background: Hemorrhagic fever with renal syndrome (HFRS) is endemic in Slovenia with yearly recorded sporadic cases and seasonal epidemic outbreaks. The incidence of HFRS in Slovenia is modest, but the complex ecology of the Balkan Peninsula supports the existence of diverse rodent species, which harbour several genetic lineages of Dobrava (DOBV) and Puumala (PUUV) viruses. The diagnosis of HFRS is based on clinical and epidemiological information as well as laboratory tests. Routine laboratory diagnosis of acute hantavirus infections is based on serology, since in most cases, antibodies are already present at the onset of symptoms. There are two major disadvantages in using the serological approach: high cross-reactions among different hantaviruses and identification of early cases in the epidemic years. Therefore, the detection of viral RNA is a valuable addition to the existing approach. **Methods:** A prospective study was performed in 2 epidemic years (2012 and 2017), when we tested 1187 HFRS suspected cases. RNA isolation was performed in different clinical samples (serum, plasma, EDTA blood or urine) using automated methods. One-step multiplex qRT-PCR assay for simultaneous detection of both DOBV and PUUV was developed based on the whole S segment of Slovenian strains. A limit of detection was established to

be 10-40 RNA copies/mL. **Results:** Using standard serological methodology, 263 patients were found HFRS positive (244 PUUV and 19 DOBV) and 249 (94.7%) were also positive with multiplex RT-PCR. Additionally, we detected PUUV RNA in 4 patients which were initially serologically negative and seroconverted 3 days later. Average Ct value in PUUV-infected patients was 33.2 and 31.2 in DOBV-infected patients. In acute samples, viral RNA was detected in all sample types, but urine was positive only in 12% of tested samples. The viremia was highest and detected the longest in blood samples, lasting on average 12 days post infection. **Conclusions:** A molecular diagnosis of HFRS is a very useful tool for routine diagnostics in epidemics, when early appearance of cases is expected and, especially in areas, where different hantaviruses are circulating. However, the high genomic diversity among hantaviruses hampers the development of universal molecular diagnostics and requires a vigilance in monitoring PCR sensitivity.

Board 145. An Evaluation of Four Molecular Assays Used for the Diagnosis of Zika

N. Deot[1], A. Tran[2], A. Cunanan[2], P. Raj[2]
[1]George Washington University, Washington, DC, USA, [2]The District of Colombia Department of Forensic Science, Public Health Laboratory Division, Washington, DC, USA

Background: The recent Zika virus outbreak has resulted in the availability of a multitude of molecular diagnostic assays. Molecular diagnosis of Zika virus infection provides a definitive answer for the disease. Although molecular methods such as real-time reverse transcription-PCR (rRT-PCR) and transcription-mediated amplification (TMA) have proven to be a reliable method of detecting Zika virus, there has not been proper characterization and comparison between the various assays. The goal of this study was to compare and determine the limit of detection (LOD), sensitivity, and specificity of four Zika virus assays to better understand the most accurate test for molecular diagnosis. **Methods:** The four tests evaluated in the study were the Centers of Disease Control and Prevention (CDC) Trioplex, CDC Singleplex, Altona Diagnostics RealStar Zika Virus RT-PCR, and Aptima Zika Virus Assay. A panel of 98 Zika positive and 100 negative serum and urine specimens were conducted on all four different assays and compared to determine sensitivity and specificity. In order to evaluate the LOD, ten negative urine and serum specimens were spiked with Zika culture fluid to create a range of 10^5 PFU/mL to 1 PFU/mL. **Results:** The sensitivity of the Aptima Zika Virus Assay was the highest followed by Altona Diagnostics RealStar Zika Virus RT-PCR, CDC Trioplex, and CDC Singleplex. All four molecular assays had a specificity of 100% with the panel provided. The Aptima Zika Virus Assay also had the lowest LOD of the assays evaluated, detecting the virus in as little as 1 PFU/mL. **Conclusions:** The Aptima Zika Virus Assay is the most sensitive assay and has the ability to detect the lowest concentration of Zika virus in human serum and urine, as compared to the other molecular assays evaluated. This coupled with the fully automated and random access nature of the Aptima assay provides a good platform for both public health and clinical microbiology laboratories to utilize.

Board 146. Multiplex Arbovirus IgM and IgG Serology Assay Evaluation for Rapid Presumptive Diagnosis of Zika Virus Infection

N. Venkateswaran[1], J. Sarwar[2], N. Parameswaran[2], K. Krishnan[3], W. Nelson[1], K. Venkateswaran[2]
[1]Tetracore, Inc., Rockville, MD, USA, [2]Omni Array Biotechnology, Rockville, MD, USA, [3]University of California, Davis, Davis, CA, USA

Background: Vector-borne diseases account for more than 17% of all infectious diseases. Arthropod-borne viruses (arboviruses) are a source for many debilitating diseases common in tropical countries and are emerging as a significant threat in recent years in the western hemisphere. Timely and correct diagnosis of the causative viruses is essential for effective public health measures to combat the spread and devastating effects of these diseases. Potential cross-reactivity of immunoglobulin M (IgM) and immunoglobulin G (IgG) antibodies against different viruses of the arbovirus family limits the generalized use of serodiagnosis. Differential diagnosis of Zika virus (ZIKV) infection against dengue virus (DENV), West Nile virus (WNV), yellow fever virus (YFV) and some other related flaviviruses infection is vital for clinical management in Zika infection. We developed an arbovirus fluorescent microsphere array multiplex assay (AV-FAMA) for simultaneous detection of ZIKV and many different flaviviruses and chikungunya virus (CHIKV) as an effort to overcome current challenges of serodiagnosis. **Methods:** An 18-Plex AV-FAMA was developed with covalent attachment of 13 different recombinant arboviral antigens to Luminex fluorescent microspheres. There are five different internal controls included in this assay. The individual fluorescence results are normalized using the internal controls. AV-FAMA is configured to measure virus-specific IgM or IgG antibodies in the human blood sample in a sandwich immunoassay format. We have also developed a multiplex data analysis algorithm for clearly delineating ZIKV antibody response from other arboviruses. Entire AV-FAMA can be completed in about 2 hours for detection and differentiation of recent, past, or co-infections that may occur in endemic regions. AV-FAMA performance was assessed using over 200 samples procured from commercial sources including ZIKV, DENV, CHIKV, WNV, EBV, CMV, INFV positive and normal samples. **Results:** Good agreement was seen with the vendor supplied sample results. ZIKV NS1 antigen showed better specificity than ZIKV envelope antigen for accurately detecting ZIKV infection. ZIKV envelope antigen showed cross-reactivity with many samples positive for other flaviviruses. **Conclusions:** AV-FAMA has great potential for rapid and presumptive detection ZIKV and arboviral antibodies in human blood.

Board 147. Comparison of Zika Virus Inactivation Methods for Reagent Production

A. Chida, J. Goldstein, X. Tang, J. Lee, O. Herzegh, J. Moon, K. Bedi, L. Hughes-Baker, D. Bagarozzi Jr
CDC, Atlanta, GA, USA

Background: Background: Zika virus (ZIKV) infection leading to birth defects is still a public health concern and there is a great demand for the virus production in coming years. Every lot of virus production requires confirmation of inactivation and stability testing. The aim of our study is to establish standard method for production of inactivated ZIKV while maintaining antigenicity and RNA integrity. Inactivated virus constitutes an important component of our current Trioplex kit and MAC-ELISA, required to confirm active and recent infections,

respectively, in infected individuals. **Methods:** Method: Viral supernatants were tested by 4 different inactivation methods for comparison, including heat inactivation at 56^{0}C and 60^{0}C; gamma-irradiation; chemical inactivation (decontamination) and chemical inactivation by Beta-propionolactone (BPL). Inactivation was judged by cytopathic effect (CPE) and plaque assays. RNA integrity and antigenicity of the viral supernatants were confirmed by Real time PCR and MAC-ELISA, respectively. All assays included mock and live virus control samples. **Results:** Results: Our results indicate that virus concentration, volume and tube material are critical factors dictating the effectiveness of heat inactivation methods. For gamma irradiated samples, virus titer and dose of gamma irradiation are important. BPL inactivation is dependent on the percentage of BPL. Microchem (5%) kills the virus in couple of minutes. Real time PCR results indicate that RNA integrity is maintained in all the inactivation samples. However, heat inactivated and gamma irradiated samples lost the antigenicity according to MAC-ELISA data, but BPL samples showed binding depending on the percentage of BPL. **Conclusions:** Conclusion: Heat treatment and gamma irradiation inactivate ZIKV by destroying the antigen but not the RNA. However, both antigenicity and RNA are preserved with 0.035% BPL treated for 3hrs or 6hrs at 4^{0}C. Microchem (5%) is the most efficient chemical for killing the virus in a short time.

Board 148. Development and Characterization of Mouse Monoclonal Antibodies Against Zika Virus Non-Structural Glycoprotein 1 (NS1)

J. Goldstein, A. Chida, L. Hughes-Baker, J. Lee, X. Tang, D. Bagarozzi
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The pandemic of Zika virus (ZIKV) and its linkage to birth defects and neurological symptoms prompted the development of novel reagents for diagnostics. ZIKV nonstructural-1 glycoprotein (NS1) is a glycosylated 48-kD protein involved in viral replication and immune evasion. It is candidate biomarker during active infection based on studies with Dengue virus. **Methods:** Seven monoclonal antibodies (mAbs) were isolated from BALB/c mice immunized with mammalian r-NS1 recognized by ZIKV positive human serum. Characterization using multiple biochemical and cellular methods (ELISA, bio-layer interferometry, immunofluorescence and immunoblotting) with active virus and r-NS1 revealed certain mAbs were ZIKV-specific with limited cross-reactivity among other flavivirus members, notably dengue. **Results:** Among 350 IgG positive clones, seven were selected for study based on their unique assay performance. Four of these mAbs were specific to ZIKV NS1 with detection in viral-infected cells as well as higher MW forms of r-NS1. **Conclusions:** We have developed murine mAbs for development of immunoassays to detect ZIKV infection. 3C2 is most reactive to native antigen with the capability of sensitive virus immunofluorescence studies. 4B3 and 6B1 are primary candidates for sandwich assays. 4C1 clone is clearly preferential for DENV1 r-NS1. These mAbs are in development of assays to differentiate Flavivirus species.

Board 149. A Systematic Review of Environmental Survival across 27 Viral Families

A. Willoughby[1], E. Hagan[1], J. Kerwin[2], K. Olival[1]
[1]EcoHealth Alliance, New York, NY, USA, [2]Brooklyn College, New York, NY, USA

Background: Outside of their hosts, viruses typically decay and loose infectiousness rapidly. Our understanding of factors that influence virus survival in the environment, however, is currently limited as most experimental studies are species- or family-specific. Understanding broad taxonomic patterns and the importance of specific environmental factors is crucial to understanding viral transmission via fomites and exposure to infected substrates. Additionally, the effect of abiotic factors like temperature, pH, and desiccation on viruses can be translated into intervention methods. **Methods:** We conducted a systematic review of virus survival from the literature using PRISMA methods, identifying papers that experimentally tested viral decay. From each study, we extracted taxonomic viral information, laboratory methods, abiotic variables, publication theme, and virus survival metrics. For studies on human viruses quantified by TCID50, we conducted a meta-analysis on viral half-life. **Results:** We identified 297 studies on 85 viral species from 27 viral families that fit our systematic review criteria. Viral survival studies are dominated by enteric viruses in the Picornaviridae family (36% of our database). Most studies test temperature (60%) or pH (46%) effects rather than decay changes due to humidity (4%). For the most part, metrics for both viral quantification and viral persistence are widely variable and make comparative analyses difficult. We conducted meta-analyses on 88 studies of human viruses. Half-life ranged from less than an hour to three weeks, with an average of 65 hours across viral families. Relevant variables included viral composition and transmission pathway, along with environmental conditions. **Conclusions:** Virus survival studies are often pathogen-specific and siloed across various disciplines. Most research centered on water quality, hospital hygiene, veterinary health, and food safety. Our review highlights key gaps in the knowledge of virus survival in the environment, such as zoonotic hantaviruses. We also identify areas to improve standardized experimental procedures and reporting of data from laboratory studies.

Late Breakers

Board LB-01. Changes to the Federal Policy for the Protection of Human Research Subjects and Why They Matter for Public Health Surveillance

L. Youngblood
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: On June 18, 2018 the United States Department of Health and Human Services, and 16 other federal agencies issued a Final Rule delaying the general compliance date for the revised Federal Policy for the Protection of Human Subjects, also known as the Common Rule, until January 2019 while permitting institutions to adopt certain burden-reducing provisions early beginning July 19, 2018. Among the provisions that may be adopted early is the revised definition of research, which removes certain public health surveillance activities from the scope of IRB review requirements. **Methods:** Although the core definition of "research" remains a systematic investigation designed to develop or contribute to generalizable knowledge, the revised Rule deems certain public health surveillance activ-

ities not to be research, including many activities that are routinely conducted in the context of outbreak investigations and public health emergency response: identifying, monitoring, assessing, or investigating public health signals, disease outbreaks, and conditions of public health importance; and activities undertaken to provide timely situational awareness and inform priority setting during an event or crisis that threatens public health. **Results:** The removal of these activities from the definition of research obviates the need to consider whether such activities are designed to develop or contribute to generalizable knowledge. Historically, the concepts of "design" and "generalizability" have been challenging to interpret in the context of public health surveillance, and have often led to such activities being classified as research. **Conclusions:** Clarification of the definition has the potential to reduce administrative burden and facilitate timely response by providing a clear basis for classifying such activities as non-research, and thus outside the scope of IRB review requirements. Change does not impact other applicable laws, regulations, policies, or standards. Consideration of ethical standards, such as the Belmont principles, should be a key component of any process by which regulatory status is determined.

Board LB-02. Training in Applied Epidemiology: A Strategic Impact to Respond to Emergent Infectious Diseases

D. Herrera Guibert, A. Hilmer
TEPHINET, Decatur, GA, USA

Background: Field Epidemiology (and Laboratory) Training Programs, FE(L)TPs, share a common value of "learning through service." It is a training model that relies on mentorship from experienced public health practitioners. Currently, 69 FETP programs working in 100 countries around the world are, integrated into the Training Program in Epidemiology and Public Health Interventions Network (TEPHINET). This study presents results of a survey conducted by the TEPHINET secretariat to update the current situation of the FETP programs and completed in May, 2018 targeting TEPHINET member programs. **Methods:** A 30-question online survey was designed to gather information on 1) FETP program type and composition; 2) participation of alumnae in outbreak investigations and other public health activities, 3) alumnae profile; and 4) other areas of interest. Data were collected from (date) through (date), and information was analyzed by program, region and globally. Analyses were completed during the first semester of 2018. **Results:** Survey response rate was 87% (60/69 surveyed programs). 38 of the programs started after 2000; 50 FETPs were advanced training programs, 7 intermediate and 3 are conducting only basic programs. By region, 25% of the programs are located in Africa and the Americas while 28% are in Asia. 81% of the programs are incorporated within the MOH and 20% in universities or other institutions. Between 2016 – 2017, program graduates conducted more than 1,174 outbreak investigations and 1,338 general surveillance and other public health activities. We have 668 cohorts of graduates (10,933 from the advanced, 703 from the intermediate, and more than 300 from the basic programs). 80% of the graduates work for the MOH. **Conclusions:** Results of the survey highlight the interdisciplinary makeup of the cohorts, the participation of graduates in field activities, and the interaction with MOH, all clear evidence of the impact of the training in the public health service.

Board LB-03. Tanzania GHSA Program: Meeting IHR Core Capacities One Milestone at a Time

W. Gatei[1], J. Mghamba[2], P. Mmbuji[3], M. Mponela[4], M. Freeman[1], C. Massambu[2], A. Nyanga[2], M. Mohamed[2], G. Kauki[2], M. Kelly[5], S. Nyanga[5], A. Mohamed[2], J. Harris[1], M. Bakari[2], R. Eidex[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Ministry of Health, Child Development, Gender, Elderly and Community, Dar es Salaam, United Republic of Tanzania, [3]Avram Corporation, Dar es Salaam, United Republic of Tanzania, [4]Centers for Disease Control and Prevention - Tanzania, Dar es Salaam, United Republic of Tanzania, [5]National Health Laboratory Quality Assurance and Training Center, Dar es Salaam, United Republic of Tanzania

Background: Tanzania was the first country to complete the Joint External Evaluation in 2016 and a costed National Action Plan for Health Security in 2017. Substantial progress to date on Global Health Security Agenda implementation has been achieved through strong CDC program management and guidance, multi-agency coordination, innovative partners, and the highly engaged government of Tanzania. We describe progress in four core areas of Laboratory, Surveillance, Workforce Development, and Emergency Preparedness. **Methods:** Three tiers of the Field Epidemiology and Training Program (FETP) were implemented between 2008 and 2016. In 2015, the Public Health Emergency Operation Center (PHEOC) opened at the Ministry of Health, Community Development, Gender, Elderly and Children. Starting in January 2016, 11 regional laboratories and the National Health Laboratory Quality Assurance and Training Center (NHLQATC) received support for microbiology reagents, training, mentorship, and quality management. At the same time, community-based surveillance was piloted in five districts to develop national guidelines, and influenza surveillance was expanded to include other respiratory illnesses at nine sentinel sites. **Results:** As of July 2018, 100 field epidemiologists have been trained in advanced, 25 in intermediate, and 154 in frontline FETPs, covering 43 of 184 districts. Three managers trained at CDC Atlanta in public health emergency management and trained 19 others to use the incident management system. By January 2018, 69 scientists received microbiology training, and regional laboratories were reporting cholera and other priority bacterial pathogens weekly to PHEOC. More than 900 influenza-negative specimens were tested at NHLQATC and results reported to epidemiologists. At least 50 events, including cholera recurrences, have been investigated by FETP graduates, with PHEOC providing coordination and risk communications using data to improve detection and response. **Conclusions:** Tanzania is progressing towards meeting IHR core capacities in a short time. Funding uncertainties threaten these gains. Concerted efforts to expand the resource base, including domestic funding and engagement with other multilateral or unilateral donors, will ensure Tanzania maintains the pace needed to meet IHR core capacities and sustain gains.

Board LB-04. Strengthening Public Health in Colombia through National Public Health Institutes Partnerships

A. Espinosa-Bode[1], E. Barzilay[2], C. Marin[3], D. Jarvis[2], M. Gonzalez[3], L. Hernandez[2], L. Peruski[2], S. Binder[4], S. Bratton[2], M. Ospina[3]
[1]Centers for Disease Control and Prevention, Guatemala City, Guatemala, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Instituto Nacional de Salud de Colombia, Bogotá,

Colombia, [4]International Association of National Public Health Institutes, Atlanta, GA, USA

Background: Fragmentation of public health efforts among multiple organizational units and limited technical capacity and infrastructure hinder an optimal delivery of core public health functions. The development or strengthening of national public health institutes (NPHI) can enhance public health systems serving as a single focal point that leads or coordinates public health activities. **Methods:** To support Colombia's NPHI (INS) to strengthen core public health functions and operations, INS, the International Association of National Public Health Institutes (IANPHI), and CDC's Division of Global Health Protection have engaged in a multi-year partnership to address INS priorities. Topics included surveillance of communicable diseases, laboratory safety and security, public health data quality and access, and national public health research agenda. In addition, the Staged Development Tool (SDT), an assessment tool-kit, was implemented in 2017 to help INS clearly define their current capacities and barriers to help them move to a higher level of functioning. **Results:** Preliminary outcomes aligned with priorities include the development of a fully functional Public Health Emergency Operations Center (EOC), improved emerging viral laboratory capacity, enhanced surveillance, and a strengthened risk communications strategy. Impact is reflected on INS robust response to recent major public health events in Colombia, and 225 nationwide epidemiologic alerts have been tracked by EOC's early warning system since 2017. Using SDT, a series of gaps within nine public health functions where identified. A list of about 100 activities was proposed to help mitigate these challenges in the short and middle term. **Conclusions:** This partnership provides a very successful case on advancing global health through supporting an existing NPHI in Latin America. CDC and IANPHI are using a similar approach to NPHI strengthening in other developing countries, supporting them to better collect and use public health data, implement and monitor evidence-based public health programs, and, ultimately, save lives and resources.

Board LB-05. Building Public Health Workforce Capacity in 12 Countries over 15 Months: The Establishment of FETP Frontline across the Americas as a Rapid Response Strategy to the Zika Epidemic

A. Hilmers[1], M. Mansur[1], L. Alonso[2], J. Arrasco[3], L. Boodram[4], A. Cabello[5], P. Dely[6], M. Garcia[7], J. Ojeda[8], R. Pimentel[9], F. Prieto[10], D. Herrera[1]
[1]TEPHINET, Atlanta, GA, USA, [2]Ministry of Health - Uruguay, Montevideo, Uruguay, [3]CDC-Peru, Lima, Peru, [4]CARPHA, Port of Spain, Trinidad and Tobago, [5]Ministry of Health - Paraguay, Asuncion, Paraguay, [6]Ministry of Health - Haiti, Port au Prince, Haiti, [7]Ministry of Health - Brazil, Brasilia, Brazil, [8]Ministry of Health - Ecuador, Quito, Ecuador, [9]Ministry of Health - Dominican Republic, Santo Domingo, Dominican Republic, [10]National Institute of Health, Bogota, Colombia

Background: In 2016, Zika virus (ZIKAV) spread rapidly throughout the Americas with more than 700,000 cases. The magnitude of the outbreak triggered urgent action and coordinated response. Field Epidemiology Training Program (FETP) Frontline, a 3-month, supervised, in-service training, was considered the best strategy for strengthening epidemiological capacity in the region. We describe the implementation and early outcomes of this training targeting public health workers at the local level of the health system. **Methods:** A descriptive study was conducted using data collected from March 2017 – May 2018. Site selection was based on the following criteria: risk for ZIKAV transmission; availability of qualified mentors; Ministries of Health (MoH) commitment to assist with roll-out and build program sustainability according to country work plan. Instructors and mentors were experienced health surveillance professionals. Pre- and post-tests assessed participants' performance. Successful completion requirements were 100% attendance and presentation of four field projects. 3-6-month post-training monitoring visits were conducted in four countries. TEPHINET provided regional technical oversight. **Results:** Participating countries were Brazil, Colombia, Dominican Republic, Ecuador, Grenada, Haiti, Jamaica, Paraguay, Peru, St. Vincent and Grenadines (SVG), Trinidad, and Uruguay. 783 public health workers completed training during the study period. Median age of participants was 37 years (range = 22-67); 78% were female. Higher retention rates were observed in Ecuador, Jamaica, and SVG (100%) compared with Grenada (73%). Trinidad and Uruguay achieved 100% coverage with at least one graduate per subnational structure. 169/267 of all field investigations were on arboviral diseases. Post-tests showed 40% improvement across all competencies. At least 70% of graduates applied learned skills 3-6-month post-training. **Conclusions:** Successful FETP Frontline implementation relied on regional coordination and collaborative planning with MoH. Program acceptability has remained high in all countries. National initiatives have been undertaken to further expand and retain qualified workforce. Country program evaluations are needed to determine impact on the surveillance system.

Board LB-06. Successes and Lessons Learned from CDC's Employee Monitoring Program during the Ebola and Zika Emergency Responses

P. Delinois Roberts, M. Glover
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The 2014-2016 West Africa Ebola outbreak was the first time the Centers for Disease Control and Prevention (CDC) began conducting post-deployment assessments and health surveillance of its employee responders during a public health emergency response. CDC also implemented post-deployment assessments during the 2016 Zika response. We demonstrate the value of conducting individual health surveillance assessments of responders returning from areas of concern as an effective health and wellness surveillance program. **Methods:** CDC's Employee Monitoring Team implemented Emergency Responder Health Monitoring and Surveillance (ERHMS) strategies to identify, enroll, and monitor all potentially exposed employees. Post-deployment assessments were conducted via email and phone with emergency responders within 48 hours of departure from areas of concern. **Results:** Throughout the 61 weeks of the Ebola response, 1,491 post-deployment assessments were completed and 2,610 post deployment assessments were completed during the 85 weeks of the Zika response. During each of the responses, 11% of those who deployed reported health and wellness concerns. To our knowledge, there were no reports of serious health conditions. **Conclusions:** Post-deployment health and surveillance monitoring of public health emergency responders is essential to the mission of any emergency response. A responder health and wellness surveillance program allows for timely information gathering that will identify as early as possible, the extent, if any, which individuals have been adversely affected by their work. CDC's approach in establishing and refining the Employee Monitoring Program is relevant across the spectrum of disaster preparedness and

response and highlights strategies that helped ensure these responders remained healthy, safe, and able to continue their work.

Board LB-07. Assessing the Role of Built Environment Improvements on Doffing High-Level Personal Protective Equipment in Biocontainment Units

M. Wong Sala[1], Z. Matić[1], G. Campiglia[1], J. DuBose[1], C. Zimring[1], P. Shah[2], J. Jacob[2]
[1]SimTigrate Design Lab, College of Design, Georgia Institute of Technology, Atlanta, GA, USA, [2]Division of Infectious Diseases, Department of Medicine, Emory University School of Medicine, Atlanta, GA, USA

Background: The 2014-2015 Ebola outbreak highlighted doffing personal protective equipment (PPE) as possibly the highest risk activity for healthcare workers (HCWs) in biocontainment units (BCUs). In this recently completed study, we explored how environmental design impacts the behavior of those doffing PPE and can reduce individual cognitive load, potentially leading to increased HCW safety. **Methods:** Based on the performance results, ergonomic principles, and anthropometry, we selected the two highest scoring aids (one fixed and one mobile) and defined optimal layouts to test in round two. Nine students doffed PPE in both layouts following a step-by-step protocol. Using the same performance metrics and questionnaire responses, we determined the best layout for the doffing area and are currently testing it with HCWs as part of the PEACH project. **Results:** In the first phase, participants performed best when using the horizontal grab bar or stability bar. In phase 2, when provided with an optimized layout for a specific stabilization aid, participants' performance improved over 20% across all performance metrics in both layouts tested. The questionnaire responses confirmed these findings: two-thirds of the participants reported a preference for the more restricted layout with a fixed stabilization aid and reported that using color as a visual cue effectively communicates the proper location of tools and where one should stand while doffing. **Conclusions:** Using ergonomic principles and empirical guidelines, the built environment can reduce the frequency of risky behaviors and cognitive and physical burden for HCWs. Low-cost design strategies can guide HCWs to safer behavior and lead to enhanced HCW safety.

Board LB-08. Developing Influenza Vaccine Supply Hubs in Low- and Middle-Income Countries

S. Goldin, C. Nannei, C. Chadwick, A. Moen
World Health Organization, Geneva, Switzerland

Background: Effective influenza pandemic response requires pandemic vaccines to be produced and distributed within 6 months of the pandemic vaccine master seed's transfer to industry. To achieve this goal, seasonal influenza vaccine production facilities must be operational to be quickly converted to pandemic vaccine production sites. Global response to a potential pandemic should include regional suppliers in low- and middle-income countries (LMICs). **Methods:** The Global Action Plan for Influenza Vaccines (GAP) from 2006-2016 was a catalyst for global expansion of influenza vaccine manufacturing capacity, providing a framework for increasing the number of LMICs with influenza vaccine production capacity in place. Through a technology transfer, the World Health Organization (WHO) and partners provided technical and financial support to 14 manufacturers to produce influenza vaccines. Currently, 10 manufacturers have approved products (some are prequalified) or are in late stage of development. In 2018, WHO commissioned four analyses on the 1) legal and trade agreements, 2) sustainable business models, 3) geopolitical and diplomatic relationships, and 4) procuring perspectives to better understand the future of sustainable local production of influenza vaccines in developing countries. **Results:** Through the supply hub analyses, WHO and partners considered factors that enable the creation of global and/or regional supply hubs for influenza vaccines. The results of these studies provide the foundation for influenza vaccine use and sustainable vaccine production in low- and middle-income countries. **Conclusions:** Maintaining influenza vaccine production capacity and enhancing equitable access to influenza vaccines are crucial components of future pandemic influenza preparedness. By presenting the recommendations of these analyses, WHO can provide insight into considerations for low- and middle-income countries as they prepare for future influenza outbreaks.

Board LB-09. Pandemic Influenza Severity Assessment — Modelling Canadian Influenza Epidemic Activity and Severity Thresholds Using the Moving Epidemic Method

C. Sevenhuysen[1], Y. Shi[2], A. Sinilaite[2], L. Lee[2], C. Bancej[2]
[1]Public Health Agency of Canada, Winnipeg, MB, Canada, [2]Public Health Agency of Canada, Ottawa, ON, Canada

Background: Comparable seasonal influenza surveillance is essential for pandemic preparedness. Countries participating in the WHO Pandemic Influenza Severity Assessment (PISA) project use thresholds based on historical data to compare influenza activity across three parameters: virus *transmission*, *seriousness* of disease, and societal or healthcare *impact.* In Canada, three national surveillance indicators were selected for the PISA assessment based on their comparability over recent seasons. In this analysis, we explore the value of additional indicators in broadening the assessment of seasonal influenza severity. **Methods:** For the parameter of *transmission*, two FluWatch indicators are used: the percentage of laboratory specimens positive for influenza, and the percentage of sentinel primary care visits for influenza-like illness. For the *seriousness* parameter, the number of sentinel pediatric hospitalizations with influenza is used. Two additional FluWatch indicators are considered: number of influenza outbreaks in long-term care facilities and hospitals (for *transmission*), and influenza-associated hospitalization rate per 100,000 population (for *seriousness*). The Moving Epidemic Method was applied to these five national surveillance indicators. **Results:** During the 2017-18 influenza season, the three indicators compared for the *transmission* assessment crossed the seasonal threshold within a week of each other. The outbreaks indicator crossed the high threshold at the peak of the season, while the other two indicators stayed within the moderate level. Both indicators for *seriousness* crossed the seasonal threshold at a similar time, but the assessment levels using hospitalization rate were more variable over the course of the season. **Conclusions:** PISA assessments permit in-season assessments of transmission and severity of an influenza season relative to historical norms in near real time. The 2017-18 PISA assessment for Canada revealed a moderate influenza season compared with previous years. The assessments using influenza outbreaks and hospitalization rate may reflect the different impact on adult and pediatric populations. The PISA assessment for Canada may be improved by age-stratification or changing data into proportions.

Board LB-10. Applying Machine Learning Models with an Ensemble Approach to Make Accurate Real-Time Influenza Forecasts in Taiwan

H. Cheng[1], Y. Wu[2], M. Lin[1], Y. Liu[3], Y. Tsai[2], J. Wu[2], K. Pan[2], C. Chen[1], D. Liu[1], I. Lin[4], J. Chuang[1]
[1]Taiwan Centers for Disease Control, Taipei, Taiwan, [2]Acer Inc., New Taipei City, Taiwan, [3]Taiwan, Taipei, Taiwan, [4]Yang-Ming University, Taipei, Taiwan

Background: Taiwan Centers for Disease Control has built nearly real-time national surveillance systems on influenza-like illness (ILI) since 2007. By using those data, we aimed to develop an ensemble approach together with machine learning models to provide real-time ILI forecast estimates and facilitate influenza preparedness. **Methods:** The data source included the ILI visit records in emergency rooms (from Real-time Outbreak and Disease Surveillance System) and outpatient clinics (from National Health Insurance database) and the national notification records of influenza patients with severe complication. Four machine learning models (autoregressive integrated moving average, random forest, supportive vector machine, and extreme gradient boosting) were established to produce weekly ILI predictions for up to 4 weeks ahead at the end of every week. An ensemble approach, which takes each model's recent performance into consideration, was used to integrate those predictions from other models. We established a framework of those machine learning models by using the historical data during January 2008 to December 2014 to automatically calculate and adopt the best parameters for each model to make predictions. Predictive ability was then evaluated during January 2015 to December 2017 for each of the four weekly time horizons. A dashboard was also built to visualize the predictions. **Results:** The prediction of our ensemble approach outperforms every prediction of each machine learning model. The 1-week-ahead prediction has good accuracy with mean absolute percentage error (MAPE) as low as 6.0% and hit rate about 70%, while the 2-week and t3-week predictions still maintain comparable accuracy (MAPE 9.6% and 12.0%). The automatic featuring framework of models could catch different features from the past epidemic for individual model; therefore, our models could provide accurate predictions with some preserved variety for policy makers to consider every possible change. **Conclusions:** Our results show that applying the ensemble model on nearly real-time ILI surveillance data could make considerably accurate 4-week-ahead predictions and help the epidemic preparedness.

Board LB-11. Active Surveillance for Avian Influenza Virus in Poultry in Vietnam, 2016 – 2018

L. Nguyen[1], M. Phan[1], D. Nguyen[1], A. Nguyen[1], P. Tran[1], T. Nguyen[1], T. Nguyen[2], H. Do[2], D. Mai[2], J. McFarland[3], T. Nguyen[4], N. Ha[4], T. Davis[3], D. Pham[1]
[1]Department of Animal Health of Viet Nam, Ha Noi, Viet Nam, [2]National Centre for Veterinary Diagnosis, Ha Noi, Viet Nam, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Office of the U.S. Centers for Disease Control and Prevention in Viet Nam, Ha Noi, Viet Nam

Background: Vietnam borders China, Laos, and Cambodia, and avian influenza (AI) viruses have been endemic in these countries, with H5N1, H5N6, and H7N9 particularly important to both veterinary and public health. Humans and poultry cross the borders daily and illegally, with risk of introduction of AI viruses into Vietnam. From June 2016, we conducted regular active surveillance for AI viruses in poultry. **Methods:** Six live bird markets (LBMs) per selected province were sampled monthly for up to 6 months per year. Up to 8 pooled samples were collected at each LBM; 5 pooled oropharyngeal swabs from domestic poultry (chickens, ducks and Muscovy ducks) and 3 pooled environmental samples from feces and water. Culling areas for smuggled poultry were also sampled. Pooled samples contained 5 swabs per pool and were first tested for the influenza A matrix (M) gene, and positives were tested for H5N1, H5N6, and H7N9 HA and NA subtypes using real-time RT-PCR. **Results:** Between June 2016 and April 2018, 7,395 pooled samples were collected at 141 LBMs and 30 culling areas in 15 provinces; 5,758 pooled poultry swabs from 28,790 individual poultry; and 1,637 pooled environmental samples. 2,187 (30%) samples were positive for influenza A virus RNA, among which 202 (9.2%) were positive for H5 or H7, with 120 positive for H5N1 (5.5%), 55 for H5N6 (2.5%), and 7 for H7 (0.3%). None of the H7 positive samples were N9 positive. Next-generation sequencing and real-time RT-PCR is ongoing to determine the subtypes of positive samples and the genetic clades/lineages of the H5 and H7 positive samples. **Conclusions:** 30% of samples collected in this study were positive for influenza A virus, but H7N9 virus was not detected in these samples. More than 9% were positive for H5 (H5N1, H5N6) or H7 virus RNA. Subtyping by either real-time RT-PCR or sequencing is ongoing to characterize these viruses; preliminary data indicate the majority are H9N2 positive. Continued surveillance for AI virus in Vietnam is critical for timely detection and response.

Board LB-12. Features of the Influenza Epidemic Season in Azerbaijan (2016 – 2017).

N. Abdullayeva, S. Ibrahimova, N. Ustun, R. Ismailova, R. Abdullayev
Republic Anti-Plague Station, Baku, Azerbaijan

Background: Acute respiratory infections (ARIs) are the most prevalent among registered diseases in Azerbaijan. After eight incidents of avian flu A(H5N1) in 2006 (five of them fatal), specific monitoring of A(H5N1) was implemented in the country. In this study we analyzed the incidence of viral ARI infections and influenza in Azerbaijan during the epidemic season 2016-2017. **Methods:** We took nose and throat smears from the persons with symptoms of ARIs in the first 3 days from the onset of clinical manifestations. Laboratory diagnostics included detection of the influenza viruses PCR combined with RT-PCR using universal primers and probes. **Results:** In 437 analyzed during the epidemic season samples, we detected 43 (9.84%) of the influenza A(H3N2) virus, and one (0.23%) related to the B/ Victoria line B virus. Parainfluenza virus of type 3 was found in 5 samples (1.14%), and adenovirus in 8 samples (1.83%). A(H3N2) virus is known to have higher prevalence during epidemic seasons, and the highest percentage of its release occurred in the 50th to 51st weeks (58.13%). 242 samples out of 437 were collected from children under the age of 17. Children were more often registered with adenovirus infection. **Conclusions:** Sequencing of 10 samples of A(H3N2) demonstrated that all samples had sufficient sialidase activity for resistance to the inhibitors oseltamivir and zanamivir in sialidase inhibition assays. They were all sensitive to both inhibitors. Further monitoring of influenza viruses in Azerbaijan is needed for detecting their changes, quickly responding to influenza outbreaks, and analyzing the efficiency of available antiviral drugs.

Board LB-13. Epidemiological Characterization of Acute Respiratory Viral Infections and Influenza Dynamics in the Republic of Kazakhstan in 2015-2017

I. Alymova[1], B. Kartpayeva[2], I. York[1], A. Rakhimbayeva[2], A. Tabayeva[3]
[1]Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Almaty City Branch of the National Center of Sanitary-Epidemiological Expertise, Almaty, Kazakhstan, [3]Department of Hygiene & Epidemiology, Al-Farabi Kazakh National University, Almaty, Kazakhstan

Background: The National Reference Laboratory (Astana) and 16 regional sentinel centers of the National Center of the Sanitary-Epidemiological Expertise (CSEE) survey influenza and other respiratory viruses in Kazakhstan. **Methods:** Here, weekly CSEE reports were analyzed to determine and compare the number of ARVI and influenza cases and hospitalizations and their distribution among population groups. **Results:** The total number of ARVI and ARVI-associated hospitalizations, and ARVI incidence per 100,000, were comparable in 2015/2016 and 2016/2017 (600,893; 56,112; and 3,496.44 vs. 603,945; 56,848; and 3,277.64, respectively). More cases of ARVI were observed in pregnant women in 2016/2017 than in 2015/2016, and the peaks of total ARVI and associated hospitalizations were recorded 3 weeks earlier (week 2/2017) than in 2015/2016. Influenza played a larger role in ARVI in 2016/2017 than in 2015/2016, with 2,542 laboratory-confirmed cases from sentinel centers and 1,706 associated hospitalizations reported in 2016/2017 compared to 926 and 565, respectively in 2015/2016. The peak of total positive influenza specimens was observed earlier in 2016/2017 (week 2/2017) than 2015/2016 (week 8/2016), as was the peak of influenza-associated hospitalizations (weeks 52/2016 and 2/2017 in 2016/2017 compared to week 5/2016 in 2015/2016). Both influenza A and B viruses (IAV and IBV) contributed to 2015-2017 morbidity, with IAV more common than the IBV cases. In 2015/2016, there were 41.7% H1N1, 56.2% H3N2, and 2.1% IBV. In 2016/2017, there were no H1N1, 61.5% H3N2, and 38.5% IBV. **Conclusions:** The 2015/2016 and 2016/2017 seasons had distinct influenza seasonality and circulating viruses, highlighting the importance of country-specific surveillance in defining ARVI and influenza dynamics for better preparedness.

Board LB-14. School Closures and Mitigation of Influenza B, Hong Kong, 2018

S. Ali, B. Cowling, E. Lau, V. Fang, G. Leung
The University of Hong Kong, Pokfulam, Hong Kong

Background: In Hong Kong, school closures have been used to mitigate SARS in 2003, seasonal influenza in 2008, and pandemic influenza in 2009. On 8 February 2018, the authorities in Hong Kong elected to close schools to mitigate an epidemic of influenza B/Yamagata, 1 week earlier than the scheduled Chinese New Year school holiday. **Methods:** We analyzed surveillance data on influenza activity in Hong Kong in order to infer the impact of school closures on community transmission. We estimated transmissibility through the effective reproduction number, Rt, assuming that the serial interval distribution was a Weibull distribution with mean 3.2 days and standard deviation 1.3 days. We examined changes in transmissibility during the school closure period, and simulated epidemics with and without school closures from 8-15 February to estimate the impact of the closures on incidence. **Results:** The estimate of Rt was 1.03 (95% CI: 0.73, 1.34) before the start of the school closure, and it was reduced to 0.87 (95% CI: 0.54, 1.21) during the closure week, corresponding to a 16% (95% CI: 10%, 26%) reduction in transmissibility. We then simulated incidence under the counterfactual scenario of no school closures between 8 and 15 February, estimating that closures led to a reduction by 4.2% (95% CI 1.5%, 6.7%) in the cumulative incidence of infections. **Conclusions:** School closure after the epidemic peak had a small effect on transmission, and we estimated a 4.2% reduction in overall incidence of infections. There were approximately 400 laboratory-confirmed influenza deaths by the end of the 2017/18 winter season, fewer than those in recent A(H3N2) epidemics, but still indicating a moderate to high impact of influenza in the 2017/18 winter. A reduction in incidence of infections by 4.2% might have reduced hospitalizations and deaths by a similar fraction, with the caveat that most infections occur in children while most deaths occur in older adults.

Board LB-15. The Curious Case of Influenza Twice: Case Presentation of Two Sequential, In-Season Infections with Influenza A(H3N2) in a Usually Healthy, Vaccinated Child

J. Temte[1], A. Uzicanin[2], M. Goss[1], S. Barlow[1], L. Comp[1], E. Temte[1], T. Haupt[3], E. Reisdorf[4], M. Wedig[4], P. Shult[4], N. Florek[4]
[1]University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Wisconsin Division of Public Health, Madison, WI, USA, [4]Wisconsin State Laboratory of Hygiene, Madison, WI, USA

Background: Cocirculation of influenza types, strains, and lineages allows coinfection and intraseason sequential infection. We report a case of sequential, influenza A(H3N2) infections within one season. **Methods:** ORCHARDS (ORegon CHild Absenteeism due to Respiratory Disease Study) is a longitudinal school-based influenza study in Oregon, WI. Parents of children with influenza-like illness (ILI) symptoms voluntarily call a study hotline. Students are screened for ILI, and, if eligible, visited at home. Research staff collect nasal and pharyngeal specimens for rapid influenza diagnostic testing (RIDT; Quidel Sofia FIA), influenza RT-PCR (IVD CDC Human Influenza Virus RT-PCR Diagnostic Panel), multipathogen testing (Luminex NxTAG RPP), as well as symptom and epidemiologic data. Families may participate in a home transmission study, in which nasal swabs are obtained from family members the day of the visit (day 0) and 7 days later, along with a day-7 nasal swab from the student. **Results:** Case Presentation: On 1/31/2018, a usually healthy, vaccinated, 9-year-old female 4th-grader with moderate illness was screened. Although the RIDT was negative 25 hours after symptom onset, RPP and RT-PCR were (+) for coronavirus HKU1 and influenza A(H3N2) (Ct=31.5). The day-7 swab was PCR-negative for influenza, as were specimens from family members on days 0 and 7. On 3/09/2018, the subject was again screened due to a new ILI, and had specimens collected 49 hours after symptom onset. Her RIDT was (+) for influenza A; PCR results confirmed only influenza A(H3N2) (Ct=26.5). The subject's day-7 swab was also (+) for influenza A(H3N2) (Ct=33.3). No other family members had laboratory-confirmed influenza on day 0 or day 7. Whole genome sequencing, performed at the Wisconsin State Laboratory of Hygiene, revealed clade 3C.2a for both episodes. **Conclusions:** The absence of influenza in the subject's first day-7 swab with recovery from ILI confirms the distinct nature of two influenza episodes. This is the first known case of two distinct episodes of influenza A(H3N2) in the same season. The

presence of a recurrent, clinically significant ILI caused by the same influenza A(H3N2) clade in the same season warrants further epidemiologic and virologic analyses to help elucidate this case.

Board LB-16. Influenza Prevalence and Self-Medication Practices among Patients with Self-Reported ILI Presenting to Community Pharmacies — Guatemala, 2018

B. Ramay[1], M. Moreno[1], J. Jara[1], P. Lupo[1], C. Serrano[1], J. Alvis[1], C. Arriola[2], S. Kaydos-Daniels[3]
[1]Influenza and Other Respiratory Viruses program, Center for Health Studies, Research Institute, Universidad del Valle de Guatemala (UVG), Guatemala City, Guatemala, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Centers for Disease Control and Prevention, Guatemala City, Guatemala

Background: Self-medication with antibiotics for influenza like illness (ILI) is commonly practiced in community pharmacies in Guatemala, but little is known about the spectrum of illness of these ILI community cases. This study aimed to estimate the proportion of clients presenting to study pharmacies with ILI, current influenza vaccination status, self-medication practices, and the proportion attributable to influenza A or B. **Methods:** We conducted a cross-sectional study in six pharmacies selected among a range of neighborhoods geographically spread across Guatemala City. Enrollment occurred from 3-8 pm to screen the highest number of clients possible. We defined ILI as reported fever plus cough and/or sore throat. Spanish-speaking customers with ILI were invited to participate in the study; those who had been prescribed medication from a physician were excluded. Oseltamivir, antibiotics, and multi-ingredient cold medications are non-prescription medications in Guatemala. Study personnel collected nasopharyngeal and oropharyngeal swabs from participants and tested for influenza A and B using real-time RT-PCR. Participants' ILI-associated medication purchases were documented with receipts. Influenza vaccination status in the current year was self-reported. **Results:** From March 13 – May 15, 2018, 7,555 people presented to study pharmacies during study hours; 477(6%) self-reported ILI. Among those who self-reported ILI, 16% (75/477) agreed to participate in the study and to be tested for influenza; 31% (23/75) had a positive test for influenza A. Thirty percent of the total items purchased by all participants were multi-ingredient cold medication (23/77 total items purchased), 16% were nonsteroidal anti-inflammatory drugs, 10% were antibiotics, and 44% were other items. Nearly all participants (74/75) denied receiving the influenza vaccination for the current flu season, but 77% (58/75) indicated interest in receiving influenza vaccination in the pharmacy. **Conclusions:** A high proportion of participating ILI patients presented with influenza A during the final weeks of the 2018 influenza season in Guatemala City. We report a low rate of current influenza vaccination among participants but high level of interest in receiving the influenza vaccine.

Board LB-17. The Host-Targeted Iminosugar UV-4B Inhibits Influenza Virus without Selecting for Resistance

K. Spurgers[1], L. DeWald[1], E. Plummer[2], R. Halpin[3], B. Peters[4], U. Ramstedt[5], M. Callahan[5], S. Das[6], K. Warfield[1]
[1]Emergent Biosolutions, Inc, Gaithersburg, MD, USA, [2]La Jolla Institute for Allergy and Immunology, San Diego, CA, USA, [3]J. Craig Venter Institute, Rockville, MD, USA, [4]La Jolla Institute for Allergy and Immunology, La Jolla, CA, USA, [5]Unither Virology, Silver Spring, MD, USA, [6]Vanderbilt University Medical Center, Nashville, TN, USA

Background: The development of antiviral drug resistance is a continuous concern for many viruses, particularly for viruses with high mutation rates such as influenza. Drugs directly targeting viral proteins can place the virus under selective pressure and increase the development of antiviral drug resistance. The use of antivirals targeting host proteins required for viral replication are less likely to select for resistant viruses and may increase the broad-spectrum antiviral potential as some host enzymes are required for the replication of diverse viruses. The iminosugar UV-4B is a host-targeted glucomimetic that inhibits α-glucosidase I and II enzymes in the endoplasmic reticulum resulting in improper glycosylation and misfolding of multiple viral envelope glycoproteins. UV-4B has broad-spectrum antiviral activity *in vitro* against distinct RNA and DNA viruses including dengue, Ebola, vaccinia, and influenza. Oral treatment with UV-4B protects mice against lethal infection with mouse-adapted oseltamivir-sensitive influenza A (H1N1 and H3N2), oseltamivir-resistant influenza A/Perth/261/2009 (H1N1), and influenza B. **Methods:** To examine the ability of influenza virus to generate resistance against UV-4B, mouse-adapted influenza virus was passaged in mice in the presence or absence of UV-4B and virus isolated from lungs at the peak of virus replication was used to infect (~ 1 LD_{90}) the next cohort of mice, for five passages. Deep sequencing was used to identify changes in the viral genome during the passaging in the presence or absence of UV-4B. **Results:** Only seven nonsynonymous mutations were identified with an absence of apparent viral escape mutants following sustained exposure to UV-4B. Recombinant viruses containing individual and combination nonsynonymous mutations unique to UV-4B pressure were still sensitive to UV-4B treatment in mice. **Conclusions:** These results provide additional evidence that there is a high genetic barrier to the generation and selection of escape mutants exposed to host-targeted iminosugar antivirals.

Board LB-18. A Universal Influenza Vaccine against Multi-Strain Flu Viruses

W. Wei, J. Chang, W. Liu
Development Center for Biotechnology, Taipei, Taiwan

Background: Seasonal influenza epidemic is always a serious threat to lives all over the world. Owing to the diversity of influenza viruses, human and other species like swine and avian are infected by different flu subtypes, which could cause a disastrous influenza pandemic when cross-infection between species occurred. **Methods:** A universal influenza vaccine was designed for long-lasting protection against multiple strains of viruses. A vaccinated peptide (JJ) from a well-conserved sequence of hemagglutinin (HA) in 16 different subtypes of flu viruses was discovered in the stem portion of HA with a low mutation rate. The JJ1 and JJ3 peptides were modified for digestion resistance and kept the antigenicity that cross-react back to the original region. Animals were immunized with JJ1 and JJ3 peptides, and anti-sera was subject to IgG production analysis, hemagglutination inhibition assay, and virus micro-neutralization assay, **Results:** Results showed that anti-sera could induce immunity with JJ1 and JJ3 peptides, which high titer of specific antibody was generated that could cross back to the original viral sequence. These anti-sera were also able to inhibit the hemagglutination in a variety of HA subtype, such as H1, H3, H5, and H7 hemagglutinin. Furthermore, MDCK cells were protected by JJ1- and JJ3-immunized anti-sera from natural viruses including H1N1, H3N2, H5N1 and H7N9 viruses in a micro-neutralization assay. **Conclusions:** This peptide vaccine showed that prevents the multi-strain

of flu viruses in our research, which can be regarded as a universal flu vaccine. Adjuvant system for delivering this peptide vaccine is under development.

Board LB-19. Unraveling the Evolutionary Origin of Low Vaccine Efficacy in the H3N2 Influenza Virus

J. Alvarez, W. Zhai, H. Chen
Genome Institute of Singapore, Singapore, Singapore

Background: As a dominant seasonal virus, H3N2 influenza evolves rapidly in human and poses constant threats to public health. Despite many years of efforts, there has been an alarming decrease in the efficacy of H3N2 vaccine. Even though antigenic drift (mutation and selection in the human host) and passage adaptation (substitutions accumulated during vaccine production in embryonated eggs) have been implicated in low vaccine efficacy, their contributions remain controversial. **Methods:** Using a powerful Bayesian method of sequence evolution known as mutational mapping, we were able to analyze an unprecedented amount of H3N2 hemagglutinin sequences (n=32,278). **Results:** We found that passage adaptation in embryonated eggs is driven by repeated convergent evolution over 14 codons. Based on substitution patterns at these sites, we develop a metric of Adaptive Distance (AD) quantifying the strength of passage adaptation and identify a strong negative correlation between AD and vaccine efficacy. **Conclusions:** This study resolves the long-standing puzzle on vaccine efficacy and provides direct evidences that passage adaptation in embryonated eggs is a major determinant of recent drops in H3N2 vaccine efficacy. A computational package (MADE) was developed to measure the strength of passage adaptation and predict the efficacy of a candidate vaccine strain. Our findings shed light on strategies reducing Darwinian evolution for effective vaccines in the coming future.

Board LB-20. Efficacy of Live Attenuated and Inactivated Influenza Vaccines against Laboratory-Confirmed Influenza Infection among Children in Rural Ballabgarh, India: A Randomized, Triple-Blinded, Placebo-Controlled Trial

A. Krishnan[1], R. Kumar[1], R. Amarchand[1], S. Saha[2], V. Narayan[1], L. Dar[1], K. Lafond[3], M. Widdowson[3], S. Jain[3]
[1]All India Institute of Medical Sciences, New Delhi, India, [2]Influenza Program, Centers for Disease Control and Prevention, New Delhi, India, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Few data exist on the efficacy of live attenuated influenza vaccine (LAIV) and trivalent inactivated influenza vaccine (IIV) in lower resourced countries. We conducted a randomized placebo-controlled trial among children to assess the absolute efficacy of intra-nasal LAIV and its relative efficacy compared with IIV. **Methods:** In June 2015, we enrolled children aged 2-10 years in six villages of Ballabgarh in northern India and randomly allocated to four arms: LAIV, IIV, intra-nasal placebo, or injectable inactivated polio vaccine (IPV) in ratio of 2:2:1:1. In year 1, children received either a single dose of LAIV/intra-nasal placebo or two doses of IIV/IPV four weeks apart (except children aged 9-10 years who received only one dose of IIV/IPV). In June 2016, children received a single dose of vaccine or placebo as per the first-year allocation. Post-vaccination, we conducted weekly surveillance for febrile acute respiratory infection (FARI) for 1 year. Nurses collected nasal and throat swabs from children with FARI weekly and sent the specimens within 24 hours of collection to laboratory under cold chain for influenza testing using reverse-transcription polymerase chain reaction (rt-PCR). We used modified intention to treat analysis censoring children lost to follow-up before influenza infection or the end of the study period. We estimated vaccine efficacy for each year separately using a Cox-proportional hazard model and combined IPV and placebo groups as the control group. **Results:** In year 1, we enrolled 3,041 children with 1,015 allocated to LAIV, 1,010 to IIV, 509 to IPV, and 507 to nasal placebo arms. In year 2, 2,902 participants remained enrolled: 967 allocated to LAIV, 973 to IIV, 485 to IPV, and 477 to nasal placebo. In year 1, absolute efficacy against all A and B viruses was 40% (95%CI: 25 - 52) for LAIV and 59% (48 - 68) for IIV, and the relative efficacy of LAIV compared with IIV was -46% (-89 - -13). In year 2, absolute efficacy against all viruses was 52% (42 - 60) for LAIV and 50% (39 - 59) for IIV, and relative efficacy of LAIV was 4% (-20 - 24). No serious adverse events attributable to vaccines were reported. **Conclusions:** In this rural Indian cohort of children aged 2-10 years LAIV and IIV vaccines were safe and efficacious against influenza infection. The efficacy of single dose of LAIV was less than that of two doses of IIV in the first year in this influenza vaccine naive population.

Board LB-21. Utilization of Antisera Generated in Immunized Chickens for Antigenic Characterization of A(H5N1) Viruses in Vietnam

D. Nguyen[1], S. Shepard[2], D. Burke[3], J. Jones[2], S. Thor[2], L. Nguyen[4], T. Nguyen[5], A. Balish[2], T. To[5], M. Iqbal[6], D. Wentworth[2], J. MacFarland[7], E. Spackman[8], H. Doorn[9], C. Davis[2], J. Bryant[9]
[1]Department of Animal Health, Ministry of Agriculture and Rural Development of Vietnam, Ha Noi, Viet Nam, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Department of Zoology, Cambridge University, Cambridge, United Kingdom, [4]Department of Animal Health, Ha Noi, Viet Nam, [5]National Center for Veterinary Diagnostics, Ha Noi, Viet Nam, [6]The Pirbright Institute, Pirbright, United Kingdom, [7]Office of the U.S. Centers for Disease Control and Prevention in Viet Nam, Ha Noi, Viet Nam, [8]Southeast Poultry Research Laboratory, United States Department of Agriculture, Athens, GA, USA, [9]Oxford University Clinical Research Unit, Ha Noi, Viet Nam

Background: Highly pathogenic avian influenza (HPAI) A(H5N1) viruses pose significant economic burdens to the poultry sector of Vietnam and have pandemic potential. Poultry vaccination against A(H5N1) viruses has been an important component of HPAI control measures in Vietnam. However, ensuring optimal "antigenic match" for poultry vaccines to protect flocks against A(H5N1) virus in Vietnam poses an enormous challenge due to the rapid evolution of the virus as well as temporal and geographic distribution of antigenically distinct clades. When novel genetic variants of A(H5N1) virus are detected, there is a need for rapid antigenic characterization and vaccine efficacy studies to guide vaccination policies. **Methods:** A panel of chicken and ferret antisera was raised against Vietnamese HPAI A(H5N1) viruses representing clade variants detected between 2001 and 2014. The antisera were used for haemagglutination inhibition (HI) assays to generate datasets for analysis by antigenic cartography, allowing direct comparison of results obtained from HI assays using chicken and ferret antisera. The data were also used to evaluate the antigenic relationships between circulating viruses and existing A(H5N1) poultry vaccines and how these relationships correlated to in vivo protection in vaccinated chickens. **Results:** Irrespective of the animal model used

to raise antisera, antigenic cartography revealed similar patterns of antigenic relationships and clustering of viruses that were dependent on the clade of viruses analyzed. Antigenic relationships between existing poultry vaccines and circulating field viruses also correlated with in vivo protection profiles determined by challenge studies. **Conclusions:** Our results establish the feasibility and utility of chicken antisera for the antigenic characterization of A(H5N1) viruses and support further experimental and modeling studies to investigate quantitative relationships between genetic variation, antigenic drift, and correlates of poultry vaccine protection in vivo. The developed methods provide a systematic approach to evaluating antigenic variation and help inform vaccine strain selection for future A(H5) poultry vaccine intervention strategies in Vietnam.

Board LB-22. Relative Effectiveness of Cell-Based Influenza Vaccines Compared with Egg-Based Influenza Vaccines, Active Component U.S. Service Members, 2017–18 Season

A. Eick-Cost, Z. Hu
Defense Health Agency – AFHSB, Silver Spring, MD, USA

Background: In 2016, the first cell-based influenza vaccine (CBIV) was licensed in the United States. Since that time, the use of CBIV has increased, especially among the U.S. military. During the 2017–18 influenza season, 50% of service members immunized received a CBIV. This study was conducted to determine the relative effectiveness of CBIV versus egg-based influenza vaccines (EBIV) against multiple influenza outcomes among U.S service members during the 2017–18 influenza season. **Methods:** Data from the Defense Medical Surveillance System (DMSS) were used for the study. The study was conducted among active component (AC) U.S. service members who received either a CBIV or an EBIV from 1 Aug 2017 – 28 Apr 2018. Two different study designs were used: (1) case test-negative control methodology for laboratory-confirmed influenza cases and (2) cohort studies for influenza-like illness or influenza-specific diagnoses in any medical encounter or during a hospitalization only. Crude and adjusted (age, sex, month of vaccination, and prior season influenza vaccination) odds ratios or incidence rate ratios and VE estimates were calculated for each outcome. **Results:** For the case test-negative design, 2,467 individuals received a CBIV (506 cases) and 3,239 individuals received an EBIV (757 cases). The adjusted relative VE of CBIV compared to EBIV was 5 (95% CI: -10, 17). The cohort analyses consisted of 796,691 to 822,001 individuals, depending on the outcome of interest and censoring. For all cohorts, 50% received a CBIV. The adjusted relative VE of CBIV to EBIV was 2 (95% CI: 1, 4), 16 (95% CI: -9, 35), 16 (95% CI: 11, 20), 46 (95% CI: -18, 76) for any ILI, hospitalized ILI, any influenza, and hospitalized influenza, respectively. **Conclusions:** The relative VE of CBIV was similar to or greater than that of EBIV depending on the outcome of interest among AC U.S. service members. The adjusted relative VE point estimates were in favor of CBIV for all outcomes, but only reached statistical significance for ILI and influenza-specific medical encounters. Additionally, the relative effectiveness of CBIV compared to EBIV increased with increasing specificity and severity of the outcome. These results indicate that CBIV may provide greater effectiveness against influenza among AC U.S. service members.

Board LB-23. High Mortality by Severe Acute Respiratory Syndrome among Patients in Long-Term Hospital Care, Goias, Brazil, 2018

A. Alves[1], C. Silva[1], M. Carvalho[2], A. Oliveira[3], W. Júnior[3], É. Dias de Jesus[3], L. Michelone[4], M. Costa[3], G. Aires[5], S. Furtado[5], T. Sardeiro[5], L. Pereira[6], E. dos Santos[1]
[1]Ministry of Health of Brazil (MoH), Health Surveillance Secretariat (SVS), Field Epidemiology Training Program (EpiSUS), Brasilia/DF, Brazil, [2]State Health Secretariat of the State of Goiás (SES-GO)/Health Surveillance Secretariat (SUVISA) /Epidemiological Surveillance Management (GVS), Goiânia/Goias, Brazil, [3]State Health Secretariat of the State of Goiás (SES-GO)/Health Surveillance Secretariat (SUVISA)/Epidemiological Surveillance Management (GVS)/Health Surveillance Strategic Information Center (CIEVS), Goiânia/Goias, Brazil, [4]SES-GO/SUVISA/Mortality Surveillance Coordination (CVO), Goiânia/Goias, Brazil, [5]SES-GO/SUVISA/GVS/Vaccine Preventable, Respiratory and Viral Hepatitis Diseases Coordination (CDIRHV), Goiânia/Goias, Brazil, [6]SES-GO/Public Health Laboratory Dr. Giovanni Cysneiros (LACEN), Goiânia/Goias, Brazil

Background: In early 2018, a sudden increase in the number of deaths due an acute febrile illness with respiratory symptoms occurred in a long-term hospital among disabled and socially vulnerable patients in a Goiás State county in Brazil. An investigation was carried out to describe the occurrence and identify factors associated with those deaths. **Methods:** Suspected case was a patient who presented fever and malaise with onset of symptoms between January/March 2018. In a case-control study, the cases were patient who met the Severe Acute Respiratory Syndrome (SARS) definition: suspected case with cough or sore throat and dyspnea or oxygen saturation <95% with fatal outcome, between February/May 2018, and controls who had SARS and did not die. Laboratory diagnosis was performed through RT-qPCR, from nasopharyngeal secretion. Association measure was odds ratio (OR), 95% confidence interval (95%CI), and chi-square test ≤0.05. For logistical regression were considered the variables with p≤ 0.20. **Results:** Among 327 patients, 93(28.4%) met suspect case definition; for those, the median age was 43.6 (±13.9) years and 53.7% were females. Of 93 suspected cases, 47(50.5%) met SARS definition and 34.0% (16/47) had fatal outcome. Seven cases had RT-qPCR detectable for Flu A(H1N1)pdm09 and 3 for Respiratory Syncytial Virus (RSV). The seasonal influenza vaccine coverage for patients in April/2017 was 98.5%. In the bivariate analysis, factors associated were age ≥40 (OR=5.7; 95%CI:1.1-29.70;p<0.02); dysphagia (OR=18.6; 95%CI:3.27-106.2;p<0.01); orotracheal intubation (OR=78.0;95%CI:8.31-732.0;p<0.01), did not receive oseltamivir (OR=144.0; 95% CI:11.68-775,0;p<0.01). After logistic regression analysis, dysphagia remained as independent associated factor (AOR-=12.0;95%CI:2.55-56.37;p<0.01). **Conclusions:** This Flu A(H1N1) pdm09 outbreak occurred with other respiratory viruses, affecting a highly vaccinated population. The strongly association with dysphagia indicates possible nutritional deficiencies and a greater susceptibility to worsening pulmonary condition, which may have contributed to the high lethality among those patients. The implementation of treatment protocols and prevention measures were recommended to reduce flu transmission.

Board LB-24. Probable Diphtheria's Death Case in Nan Bosquets, Fond-Parisien, Croix-des-Bouquets, Haiti, April 2018

L. Jean Louis
Field Epidemiology Training Program Intermediate Level Trainee, Port-au-Prince, Haiti

Background: Diphtheria is an acute bacterial infection disease caused by *Corynebacterium diphtheria* or *Klebs Loeffer's bacillus*. This bacterium synthesizes a toxin that leads to multiple complications. At the 15th Epidemiological Week (SE) 2018, the Western Health Directorate (DSO) was alerted of probable diphtheria's death in Nan Bosquets, locality of Croix-des-Bouquets commune. This led to an investigation. **Methods:** A descriptive analysis was made. Data about the death case were collected using standardized diphtheria survey form of the Directorate of Epidemiology, Laboratory and Research (DELR); interviews were conducted with case relatives. An active research of other probable diphtheria cases was conducted; cases were identified using DELR diphtheria's case definition. Socio-demographic, clinical and risk factor data were collected. Samples were collected and transferred to the national laboratory for PCR testing. Microsoft Excel was used for analysis and results presentation. **Results:** Data analysis reveals that the case was a boy aged 8 years; he presented swelling of the neck and dyspnea, He died on April 16th a few hours after showing symptoms; he was vaccinated a week ago before death. Active research led to four more probable cases, all female. The median age was 7 years old. All live in the same household as the investigated death case and all were vaccinated. The PCR test was positive for three (75%) of them. Sanitary cordons and chemotherapy were conducted in the household and around. An educational session on diphtheria transmission's mode, symptoms, and awareness rising on vaccination was conducted in Nan Bosquets. **Conclusions:** The investigation leads to confirmation of more diphtheria cases linked to death case reported in Croix-des-Bouquets. It is recommended to evaluate the efficiency of the vaccines.

Board LB-25. Measles Outbreak in a Daycare Related to Overseas Travel--Johnson County, KS

T. Wallin[1], E. Holzschuh[1], C. Walls[1], T. Coleman[2]
[1]Johnson County Department of Health and Environment, Olathe, KS, USA, [2]Linn County Health Department, Pleasanton, KS, USA

Background: Measles was declared eliminated from the United States in 2000 thanks to a highly effective vaccination program. On March 7, the Johnson County Department of Health and Environment received a call about an 11-month-old daycare child who had previously been admitted, with symptoms of rash, facial swelling, cough, and fever. The patient was IgM positive for measles, which had not previously been reported. **Methods:** Interviews were conducted with the family of the initial case-patient as well as staff at the daycare that the child attended. Records from visits the patient made to different medical providers were collected. An immediate review was conducted of the children who were in the patient's class at the daycare. Isolation and control measures were put into place initially in this room, then in the rest of the daycare when cases in children outside the room were discovered. **Results:** A family with an infant in the daycare recently traveled to Pakistan and had come back to the United States with symptoms consistent with measles, which was misdiagnosed by her healthcare provider. It was also discovered that the older sister, who is 2 years of age and has received 1 MMR vaccination, also had symptoms that were misdiagnosed by the same pediatrician. Later serology confirmed this on both, as well as a genotype of B3, which was circulating in Pakistan. Out of the 8 children in the infant room, 7 came down with symptoms. The last infant in the room to come down with symptoms began on day 21 of her quarantine period. Outside of the infant class, an additional older child came down with symptoms; the diagnosis of measles was lab-confirmed, prompting further quarantine. Of the 2 older children, one had been vaccinated once and one had not. One case was in an older daycare teacher who had been vaccinated in the 1960's. Illness in the teacher and one of the infants prompted investigations in 2 counties south of Johnson County. **Conclusions:** This investigation is ongoing. There are no new cases in Johnson County or Miami County. Current investigation is pending on 5 cases in Linn County. Avidity testing and PRN assay testing are pending.

Board LB-26. Locking Down a Bad Bug--*N. meningitidis* Serogroup Y Outbreak in a Transitional Correctional Facility, Georgia, 2017-2018

M. Tobin DAngelo[1], A. Moore[1], L. Lorentzson[1], N. Oosmanally[1], T. Parrott[2], R. Thornton[3]
[1]Georgia Department of Public Health, Atlanta, GA, USA, [2]Georgia Public Health Laboratory, Decatur, GA, USA, [3]Coastal Health District, Savannah, GA, USA

Background: *Neisseria meningitidis* (Nm) infections, although uncommon, result in morbidity and mortality. Nm serogroup Y (NmY) is rare in the United States, with 53 cases (14% of Nm) reported in 2016. CDC defines an institutional outbreak as 2 or more cases of the same serogroup within 3 months. From December 2017-February 2018, the Georgia Department of Public Health (GDPH) and the Coastal Health District (CHD) investigated 2 NmY cases from a transitional correctional facility (TF A). **Methods:** Invasive Nm infections are reportable. GDPH collected clinical and epidemiologic data from case interviews and medical charts. Isolates were submitted to the Georgia Public Health Laboratory for serogrouping and forwarded to CDC for multilocus sequence typing (MLST) analysis using whole genome sequencing. We identified close contacts of case-patients, consulted with CDC on outbreak control measures, and examined GA NmY trends from 2016-2017. **Results:** Case-patients were aged 35 and 48 years, were black non-Hispanic males; illness onset was 12/10/17 and 2/7/18, respectively. Both presented with encephalopathy and were hospitalized for a range of 10-14 days; both survived. Serogrouping and MLST analysis of a blood isolate from Case-Patient 1 and CSF specimen from Case-Patient 2 identified NmY, Sequence Type 11 (ST11)/Clonal Complex 11 (CC11). Case-Patient 2 denied knowing Case-Patient 1 who was released from TF A in January 2018. Prophylaxis and vaccination with quadrivalent meningococcal conjugate (MenACWY) were offered, with most staff (n=41) and residents (n=269) of TF A receiving ciprofloxacin (99% acceptance) and vaccine (82% acceptance). Transfers of new inmates to TF A were limited for 3 months. From 2016-2017, 7 GA NmY cases were reported in patients with the following characteristics: 4 female, 7 white, 4 Hispanic, 7 residents of North Georgia, 4 ST11/CC11. **Conclusions:** The NmY outbreak case-patients were demographically distinct but were infected with similar strains (ST11/CC11) to recent GA NmY case-patients. ST11/CC11 is rare among NmY infections and is associated with serogroups W and C. Outbreaks in transitional correctional facilities are challenging due to people's short stays and outside contacts so that identifying the population at risk is difficult. Similar to Nm outbreaks on college campuses, we will monitor TF A and the surrounding community for cases for 1 year.

Board LB-27. Phylogenetic Diversity of Environmental Isolates *Legionella pneumophila* Serogroup 5 and 6 by *rpoB* Gene in Korea

H. Lee, D. Han, D. Han, S. Park
Korea National Institute of Health, Korea Centers for Disease Control & Prevention, Cheongju, Republic of Korea

Background: Legionnaires' disease (LD) spreads by aerosols from environmental water sources contaminated with *Legionella*. *Legionella pneumophila* serogroup 1 (*L. pneumophila* sg 1) is the major causative agent of LD in the world and it has genetic diversity. Although other *L. pneumophila* serogroups have also been isolated from clinical and environmental samples, only a few studies about molecular diversity for other serogroups have been reported until now. In Korea, *L. pneumophila* sg 5 and sg 6 in the environmental aquatic systems are predominant strains after sg 1. The *rpoB* gene, encoding the β-subunit of RNA polymerase has been widely used for identifying of *Legionella* isolates and for phylogenetic studies as a molecular marker since 2002. **Methods:** In the present study, the genetic diversity of *L. pneumophila* sg 5 and sg 6 isolates from aquatic environment water in Korea was analyzed using the *rpoB* gene. Phylogenic analysis was carried out by MEGA7 package program. **Results:** To analyze *rpoB* gene, we selected 57 isolates of sg 5 and sg 6 at random. Of these, sg 5 and sg 6 were 32 and 25, respectively. The 27 and 30 strains were isolated from cooling tower water and hot water, respectively. In reticulate network phylogenetic tree, sg 5 isolates from cooling tower water belonged to one clonal group that was different from the reference strain (*L. pneumophila* sg 6) and the strains from hot water showed a similar pattern. However, sg 6 showed various clonal patterns in both isolates from cooling tower water and hot water. **Conclusions:** These results showed that the population of *rpoB* gene from environmental isolates in Korea was different from reference strains. In particular, the isolates from hot water had various molecular diversity. In addition, our results would be helpful for epidemiology, ecology, and evolution studies of *L. pneumophila* isolates in Korea.

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Oral Presentation Abstracts

E1. Novel Surveillance Strategies

3:30-5:00 pm GrandBallroom A/B

Strengthening Global Event Based Surveillance Capacity – Epidemic Intelligence from Open Sources (EIOS) Project

C. Hercik[1], G. Division of Global Health Protection[2]
[1]CDC Foundation assigned to CDC/CGH/DGHP, Atlanta, GA, USA, [2]CDC/CGH/DGHP, Atlanta, GA, USA

Background: In 2008, the Global Health Security Initiative (GHSI) endorsed the development of the Early Alerting and Reporting (EAR) platform – a web-based, open-source collection, analysis and alerting tool, designed to strengthen epidemic intelligence. The EAR project served as a successful proof of concept that largescale intercountry partnerships for event-based surveillance (EBS) are feasible; outcomes of this pilot project demonstrated the value of collaborative event characterization and analysis. **Methods:** To build upon existing EBS systems, including EAR, in 2017 the WHO, GHSI, and collaborating partners launched the Epidemic Intelligence from Open Source (EIOS) project to streamline EBS efforts globally, and enhance communication across surveillance communities. Developed by the Joint Research Centre with input from EBS analysts, EIOS effectively aggregates unclassified epidemic intelligence from leading sources such as GPHIN, MEDISYS, ProMed, and other open sources, using scripted searches of the Internet for key words, such as "unknown disease" or "hemorrhagic syndrome." A built-in translation tool allows records to be translated into English. EIOS stores articles in respective categories, or "filters," for ease-of-review by users. The portal is further curated, full-time, by human analysts who generate email notifications about select noteworthy articles. EIOS continues to refresh the collection that is displayed in real-time, effectively automating EBS workflow. **Results:** EIOS is currently in its beta test development phase, however the system already maintains the ability to collect nearly 100,000 articles per day from >10,000 selected media sources, in more than 40 languages. Information can be shared directly among different user groups of the platform (including the WHO, GHSI, Africa CDC, FAO/OIE, GOARN, among others) enhancing near real-time communication across a wide range of networks. EIOS will be accessible to all WHO member states and will help strengthen member state capacity for early detection of health threats aligning with the International Health Regulations (2005). **Conclusions:** EIOS has demonstrated promising potential to expand the breadth and depth of open-source epidemic intelligence coverage, which can diminish the time needed to detect a public health threat thus strengthening global health security.

EpiHackTM - an Innovative Process for Developing Local Solutions to Infectious Disease Surveillance Challenges

A. Crawley, N. Divi, M. Smolinski
Ending Pandemics, San Francisco, CA, USA

Background: Every nation faces unique circumstances that underscore disease surveillance challenges, including, but not limited to: burden of endemic diseases; risk of emerging diseases; available public health resources; local infrastructure; and other social and environmental factors. Many of these disease surveillance challenges may be addressed through new tools and technologies that are developed by and for local stakeholders. One approach to developing these solutions is through the use of hack-a-thon style events. During these events, prototypes are created for users to test, refine and further implement. An EpiHack™ is a hack-a-thon that convenes software developers and health professionals to identify and develop solutions that address specific challenges to disease surveillance. **Methods:** EpiHack participants engage for approximately five days to create prototypes of new technology tools that may be further developed into applied solutions in the host country. During an EpiHack, human and animal health experts collaborate with software developers and other technologists to identify key challenge areas and work throughout the week to iterate on potential solutions. All EpiHack products are free and open source to enable post-event sharing, adoption, and development by stakeholders. Online, www.epihack.org features a curriculum for prospective EpiHack organizers and facilitators. **Results:** From 2013 to 2018 EpiHacks have hosted nearly 500 participants in the USA, Albania, Brazil, Tanzania, Uganda, Cambodia, Laos, Thailand, Myanmar, Sri Lanka and Vietnam. These Epihacks have resulted in successful outcomes that include two community-based reporting hotlines, two mobile One Health surveillance tools, three population health crowdsourcing platforms, and several alerting and analytic tools. Many of these tools have been adopted by and integrated into local or national government surveillance frameworks. **Conclusions:** EpiHacks provide an innovative, replicable mechanism to identify surveillance challenges, convene relevant stakeholders in a collaborative environment, and arrive at sustainable, locally relevant technology solutions to infectious disease challenges.

Lessons Learned from Community Event-Based Surveillance Implementation in Ghana

S. Merali[1], F. Asiedu-Bekoe[2], M. Adjabeng[2], P. Mensah[3], P. Avevor[3], D. Pwayidi[3], S. Ohene[4], R. Merrill[5], S. Ward[5], C. Walker[6], N. Hempfield-Henderson[6], A. Balajee[7]
[1]Synergy America, Inc., contracting agency to the Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Disease Surveillance Department, Ghana Health Service, Accra, Ghana, [3]International Organization for Migration, Accra, Ghana, [4]World Health Organization Ghana Country Office, Accra, Ghana, [5]Division of Global Migration and Quarantine, National Center for Emerging and Zoonotic Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]Division of Global Health Protection/Ghana, Center for Global Health, Centers for Disease Control and Prevention, Accra, Ghana, [7]Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Ghana uses the Integrated Disease Surveillance and Response (IDSR) strategy for its national surveillance system. The IDSR relies heavily on a largely passive health facility-based reporting, and thus a delay can occur between the appearance of health events or outbreaks and their detection in the community. To address this gap, the US Centers for Disease Control and Prevention (CDC) partnered with Ghana Health Service (GHS), the International Organization for Migration (IOM), and the World Health Organization (WHO) to launch a community event-based surveillance (cEBS) pilot in two districts, Ketu

South and Kassena-Nankana West, bordering Togo and Burkina Faso, respectively. The objectives of this pilot were to: (1) expand cEBS to include precise definitions of unusual health events, (2) strengthen cEBS at points of entry to encourage cross-border communication and coordination, and (3) improve the national surveillance and reporting system. **Methods:** Technical guidelines, training materials, and communications materials for cEBS were developed and implemented, with emphasis placed on the integration of cEBS into IDSR and national surveillance and reporting systems. **Results:** From April to May 2017, 492 public health personnel and community-based surveillance volunteers were trained to carry out the functions of cEBS in 375 participating communities, covering a population of over 264,500 people. Since the pilot launch of cEBS in June 2017, trained volunteers detected and reported 581 signals, of which 350 (60.2%) were verified by trained personnel as events. Notable events included cases of suspected measles, suspected cholera, suspected meningitis, suspected polio, animal die-offs, and foodborne illnesses. **Conclusions:** The implementation of the cEBS pilot in Ghana demonstrates how this form of surveillance can improve early detection and notification. Experiences and lessons learned from this pilot are contributing to the scale-up of cEBS to more districts and regions in Ghana.

Leveraging Community Health Worker Engagement for Early Detection and Reporting of Emerging Infectious Diseases.

S. Kanga[1], J. Nesbit[2], I. Holeman[2], A. Crawley[3], J. Edwards[4]
[1]Medic Mobile, Nairobi, Kenya, [2]Medic Mobile, San Francisco, CA, USA, [3]Ending Pandemics, San Francisco, CA, USA, [4]Medic Mobile, Atlanta, GA, USA

Background: Over the past decade community health worker (CHWs) networks have increasingly become a cornerstone for primary healthcare delivery in many countries around the world, particularly in sub-Saharan African. Medic Mobile (MM) designs, builds, delivers, and supports open-source software for health workers and health systems. Working in 23 countries MM has trained and equipped over 20,000 CHWs. **Methods:** In Uganda and Kenya, MM is working alongside Ministries of Health and Living Goods (LG) to integrate infectious disease outbreak reporting into their existing open-source, offline-enabled mobile app for CHWs. The system facilitates door-to-door outbreak surveillance, provides decision support for CHWs and families, enables rapid reporting of potential outbreaks, and automates sharing of surveillance data with health authorities. The CHW app supports symptom-driven identification of suspected cases for priority diseases, with automated alerts based on government-set thresholds. Alerts are escalated by SMS to key surveillance contacts, supporting follow-up action. Dashboards provide visibility into community health data and trends for suspected cases. **Results:** 155 CHWs have been trained on the CBDS workflow to date in both Kenya and Uganda. 77 suspected cases have been reported in Uganda. During the month of August, the MoH in Uganda issued an alert for a measles outbreak. In the 3 months preceding August, 23 suspected cases of measles were reported through the application. 116 CHWs in Kenya reported 200 suspected illnesses in the first month. **Conclusions:** This initiative has demonstrated that CHWs can provide an excellent entry point and opportunity to involve communities in health security. The lessons learned include: (1) mHealth can be effectively deployed to strengthen CHW capacity to detect outbreaks; (2) mHealth provides the additional advantage of mapping and locating foci of disease outbreaks; and (3) there is a need to integrate health facilities to complete the disease surveillance loop in investigating suspected cases at the community level.

Association between Community-Level Ethnic and Linguistic Distributions and the Spatiotemporal Spread of Ebola Virus Disease — Liberia, 2014

L. Zambrano[1], P. Thomas[2], L. Bawo[2], T. Nagbe[2], R. Merrill[1]
[1]National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Ministry of Health and Social Welfare, Republic of Liberia, Monrovia, Liberia

Background: Viral hemorrhagic fever risk can be modeled with multivariable indices that include measures of population connectivity. In rapid response environments, however, population connectivity may be difficult to quantify or characterize. Community-level ethnolinguistic distributions may inform population connectivity patterns; therefore, we evaluated regional ethnolinguistic diversity to determine its association with risk of disease spread. **Methods:** Liberia's national Ebola virus disease (EVD) case dataset contains 667 village-level geocoded cases with disease onset from March 9 – August 16, 2014. We calculated a space-time permutation scan statistic, which involved Monte Carlo hypothesis testing to explore spatial and temporal characteristics for each detected case. Ethnolinguistic composition of administrative clans was categorized as having one ethnic or linguistic type (homogeneous) or more than one (heterogeneous) using WorldMap data modified by Liberian Ministry of Health co-investigators. We explored the association between ethnolinguistic heterogeneity and the presence of an EVD case in a significant 74km or 24km spatiotemporal case cluster through Poisson regression, controlling for clan distance to major roads and population size. **Results:** Of Liberia's 305 clans, 232 were ethnically and linguistically homogenous, 51 were ethnically and linguistically heterogeneous, and 22 were ethnically homogenous but linguistically heterogeneous. When compared to ethnically homogenous clans (n=240/305), ethnically heterogeneous clans (n=65/305) were more likely to have an EVD case in a 72km cluster (aRR: 2.86; 95% CI: 1.45 – 5.65; P=0.002) and a 24km cluster (RR: 3.21; 95% CI: 1.45 – 7.14; P=0.004). Similar effect sizes were found with language diversity **Conclusions:** There was major overlap between ethnic and linguistic heterogeneity across clans in Liberia. Clans with more than one ethnic or language group were at significantly increased risk of EVD circulation. Future multivariable indices designed to predict regions at risk for disease importation during an outbreak should account for ethnolinguistic heterogeneity, which may serve as a proxy for population connectivity.

Use of SaTScan to Identify Clusters of HIV Diagnoses to Guide Public Health Investigation

A. Board[1], C. Zhang[2], A. Oster[3], L. Linley[3], A. France[3]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]ICF, Atlanta, GA, USA, [3]Division of HIV/AIDS Prevention, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, CDC, Atlanta, GA, USA

Background: Identifying clusters of HIV diagnoses is critical for guiding public health investigations; however, traditional surveillance analytic approaches, which rely on analysis of data within a pre-specified geographic area, may not capture clusters that cross jurisdictional boundaries. Spatial scan statistics software such as SaTScan® is increasingly being used in public health to identify such clusters,

but may not always yield clusters that are sufficiently geographically focused to allow for a feasible investigation. We aimed to determine whether SaTScan could be used to identify geographically focused HIV clusters, particularly those that crossed jurisdictional boundaries, using national HIV surveillance data. **Methods:** HIV diagnoses for 2014–2016 were analyzed at the county level for the United States (50 states and the District of Columbia) and Puerto Rico. Space-time analyses were conducted in SaTScan using the discrete Poisson model. The spatial scanning window was adjusted based on percentage of the population at risk (up to 50%) and maximum radius size (93, 62, and 31 mi) to assess the number, geographic range, and jurisdictional composition of resulting clusters. A cluster was defined as an area in which the observed number of cases exceeded the expected based on population size. **Results:** Using parameter settings based on population at risk, SaTScan identified between 11 and 72 statistically significant ($p<0.05$) clusters in the US and Puerto Rico during 2014-2016. Maximum cluster radius sizes ranged from 104 to 1,639 mi, and between 3 and 7 clusters crossed jurisdictional boundaries. Using parameter settings based on a maximum radius of 93, 62, or 31 mi for the scanning window, 41, 55, and 72 statistically significant clusters were identified, respectively. Maximum radius sizes were 91, 54, and 31 mi, and 11, 9, and 7 clusters crossed jurisdictional boundaries, respectively. The majority of clusters were located in the Southeast. **Conclusions:** When maximum radius sizes were specified, SaTScan identified more geographically focused clusters of HIV diagnoses that could allow for feasible investigations, including several that crossed jurisdictional boundaries. SaTScan should be considered as a complement to cluster detection methods based on traditional surveillance approaches.

E2. Emerging Threats in Healthcare

3:30-5:00 pm InternationalBallroom D

Council for Outbreak Response: Healthcare-Associated Infections and Antibiotic Resistance (CORHA)

G. Clabaugh[1], M. Kainer[2], D. Terashita[3], K. Heyer[4], M. Ngoh[4], M. Anderson[5], N. Bryan[6]
[1]Iowa Department of Public Health, Des Moines, IA, USA, [2]Tennessee Department of Health, Nashville, TN, USA, [3]Los Angeles County Department of Public Health, Los Angeles, CA, USA, [4]Association of State and Territorial Health Officials (ASTHO), Arlington, VA, USA, [5]Council of State and Territorial Epidemiologists, Atlanta, GA, USA, [6]Gwinnett County Medical Center, Lawrenceville, GA, USA

Background: Healthcare-associated Infections (HAIs) including antimicrobial resistant (AR) pathogens cause hundreds of thousands of illnesses and deaths among US patients each year. Despite significant progress, patients continue to experience illnesses associated with outbreaks and other adverse events due to delayed detection of emerging infectious diseases in healthcare settings. Consistent and coordinated approaches are needed to accelerate detection of new threats and develop tools to support outbreak investigation. To address these needs, a variety of public health and healthcare organizations have partnered to create the Council for Outbreak Response: HAI/AR (CORHA). **Methods:** The Council functions as a multidisciplinary collective of organizations representing the interests of healthcare consumers; the medical community; state, local and territorial public health authorities; professional associations; clinical & public health laboratories; and federal agencies. Multiple workgroups have been formed to create products and identify resources aimed at improving HAI/AR outbreak response. **Results:** CORHA has developed a variety of outbreak detection and response products through workgroups composed of representatives from each member organization. The Outbreak Detection and Reporting workgroup has developed investigation/reporting thresholds and proposed outbreak definitions for selected conditions including *Candida auris, Clostridium difficile,* carbapenem-resistant Enterobacteriaceae (CRE), scabies, and nontuberculous mycobacteria. The Outbreak Investigation and Control workgroup developed investigation guidance for *C. auris* and *C. difficile* and created a data dictionary/activity tracking system to assist health departments and large healthcare systems in managing information for investigations of HAI-AR outbreaks. **Conclusions:** Because of its multidisciplinary nature, CORHA is well equipped to identify and address the needs for HAI/AR outbreak detection and response activities across the healthcare spectrum. The Council continues to grow in terms of member organizations, expanding workgroup activities, and new product/resource development.

Epidemiologic Approach for an Outbreak Investigation by *Ralstonia mannitolilytica* in Dialysis Units, Colombia, 2017-2018

S. Rivera Vargas[1], M. Pardo Bayona[2], Y. Mosquera[3], M. Ovalle[1], J. Diaz[1], A. Padilla[1], J. Moreno[1], C. Duarte[1], F. Prieto[1]
[1]The National Institute of Health, Bogotá, Colombia, [2]The Andes University, Bogotá, Colombia, [3]Deparment of Health the Valle del Cauca, Santiago de Cali, Colombia

Background: On December 2017 four dialysis clinics in Colombia reported a *Ralstonia mannitolilytica* outbreak. The National Institute of Health team on Hospital Acquired Infections addressed this outbreak, finding its source and stopping further propagation. We aim to present the methodology used for investigating and ending the outbreak. **Methods:** A cross-sectional study was conducted in patients from four dialysis units in three cities of Colombia between December 2017 and February 2018. The case definition was established as patients treated in dialysis clinics with signs and symptoms of infection and a positive blood culture for *Ralstonia spp.* We collected information about the location of the hemodialysis seats and shifts of the infected patients, characterized patients, their clinical procedures and administered medications seven days before the positive culture. Members of a surveillance team supervised hospital control measures for infections. Samples of intravenous solutions possibly implied with the outbreak were cultured. Microbiologic analysis was ran using mass spectrometry (MALDI-TOF MS), and clonality studies are currently being processed using Pulsed-field Gel Electrophoresis. **Results:** A total of 136 cases of infection by *R. mannitolilytica* were detected. The epidemic curve showed a common, intermittent source. Ninety-six percent of infected patients had central catheter for dialysis, with an attack rate of 22%. No relation was found between infected patients, dialysis machines and patients shifts. Supervision of control measures showed deficiencies in hand hygiene, medication mixing and production of dialysis water processes. Medication tracing showed Heparin prefilled syringes from a specific pharmaceutical were used in all infected patients, and isolates of *R. mannitolilytica* were recovered from these samples. Once a definite recall of the Heparin took place, the outbreak stopped. **Conclusions:** The applied methodology helped establish Heparin as a possible source of the outbreak, and led towards effective control measure implementation and laboratory sample processing. Distracting elements that hindered the identification of the source and delayed the timely withdrawal of the Heparin were detected in the analysis. These lessons should serve for future dialysis clinic outbreak investigations.

Estimating the Attributable Disease Burden and Effects of Inter-Hospital Patient Sharing on *Clostridium difficile* Infections

D. Sewell, J. Simmering, S. Justice, P. Polgreen
University of Iowa, Iowa City, IA, USA

Background: *Clostridium difficile* infection (CDI) is an important cause of morbidity, mortality and excess healthcare costs and is one of the most common healthcare associated infections (HAIs). Hospital-level CDI rates are associated by the strength and number of connections that hospitals have with other hospitals via patient sharing. However, the extent to which CDI cases are attributable to hospital transfers is unknown, and the cascading effects of transferring patients from highly contaminated hospitals is not well understood. **Methods:** We used data from the Healthcare Cost and Utilization Project California State Inpatient Database (2005-2011) to identify 27,200,873 admissions and 532,329 patient transfers. We first constructed transfer networks based on monthly average patients discharged from one hospital and admitted to another on the same day. We then considered the monthly average number of CDI cases per hospital as well as salient hospital level characteristics. Using network autocorrelation models, we studied the contamination effects between hospitals on CDI. From this inferential framework, at a hospital level we estimated the increase in expected number of CDI cases due to transfers as a function of the CDI rate of the source hospital. Using a transformation of the model parameters we were also able to estimate the proportion of CDI cases attributable to the patient sharing network. **Results:** The proportion of CDI cases due to the diffusion of *Clostridium difficile* through the patient sharing network was found to be 7.6% (95% CI: 3.0%-12.2%). Further, we derived an equation describing the expected number of cases of CDI in a hospital as a function of the number of transfers coming in as well as the contamination level of the source hospitals. **Conclusions:** Patient sharing among hospitals contributes substantially to the overall CDI burden. Because of patient sharing, a hospital's patients may be at increased risk of CDI due to an increase in the contamination level of neighboring hospitals. Our results suggest that a minority but substantial burden of CDI infections are attributable to hospital transfers. A hospital's infection control may thus be nontrivially influenced by its neighboring hospitals. This work adds to the growing body of evidence that intervention strategies designed to minimize HAIs should be done at the regional, rather than local, level.

Healthcare-Associated Infections Related to Medical Devices — United States, 2017

I. Benowitz, K. Perkins, J. Perz, M. Arduino
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Investigations of healthcare-associated infection (HAI) and antimicrobial-resistant (AR) pathogen transmission and infection control breaches can identify emerging or recurrent infection control issues such as improper medical device reprocessing and handling and local or intrinsic medical device contamination. Upon invitation, the Centers for Disease Control and Prevention's Division of Healthcare Quality Promotion (DHQP) investigates and responds to infections and related adverse events in healthcare settings. **Methods:** We reviewed DHQP's internal records for consultations with state and local health departments involving medical devices performed in 2017. We collected data on healthcare setting, pathogen, investigation findings including possible exposure or transmission, and public health actions. **Results:** Of 285 consultations, 48 involved a specific medical device or general medical device reprocessing. Most occurred in an acute care hospital (n=30, 63%) or clinic (n=9, 19%). The most frequent pathogens were environmental pathogens including nontuberculous mycobacteria (n=10, 21%), *Candida* spp. (n=5, 10%), and *Burkholderia* spp. (n=4, 8%). Investigations identified medical devices contaminated in manufacturing, incorrect reprocessing of endoscopes or ventilators, and inappropriate medical device use or reuse; transmission was not confirmed in most events. Actions included medical device recalls, improved infection control and reprocessing procedures, patient notification and testing, and disciplinary action against healthcare providers. **Conclusions:** DHQP most frequently provided assistance for medical device-related events in acute care hospitals and specialty clinics. Environmental pathogens were often the triggers for these investigations. There is a need for on-going vigilance for the possible role of medical devices in HAI and AR transmission. Healthcare providers, infection preventionists, and public health authorities should ensure adherence to medical device reprocessing guidelines and instructions, maintain

an appropriate index of suspicion for the possible role of contaminated medical devices in HAI and AR pathogen transmission, and seek to strengthen infection control practices even in the absence of demonstrated transmission.

High Prevalence of Metallo-β-Lactamase Carbapenemase-Producing *Acinetobacter baumannii* in Tripoli, Libya: Dominance of OXA-23 and NDM-1

A. Zorgani[1], N. Abukhatwa[2], N. Elgrew[2], B. Bezan[2], N. Sufya[2], A. Bashien[2], O. Elahmer[2]
[1]Faculty of Medicine, Tripoli, Libya, [2]University of Tripoli, Tripoli, Libya

Background: *Acinetobacter baumannii* is an opportunistic pathogen causing various nosocomial infections. The aim of this study was to characterize the molecular support of carbapenem-resistant *A. baumannii* clinical isolates recovered from two Libyan hospitals. **Methods:** Bacterial isolates were identified and antibiotic susceptibility testing was performed using automated system. Carbapenem resistance determinants were studied phenotypically using three different techniques: metallo-β-lactamase (MBL) E-test; chromogenic culture media and modified Hodge test (MHT). Polymerase chain reaction (PCR) amplification was used to determine the presence of metallo-β-lactamase bla_{NDM-1}, bla_{OXA23}, bla_{OXA48} and bla_{OXA51} genes among isolates. **Results:** A total of 108 *A. baumannii* isolates were characterized, overall the resistance prevalence was extremely high for aminoglycosides, fluoroquinolones, cepahosporens and carbapenemes (93.2-100%), all isolates were susceptible to colistin. In addition, 97.5% of isolates were identified as multidrug resistance (MDR). Varying degree of phenotypic detection of carbapenemes was determined; highest levels of carbapenemes were detected using chromogenic media (75.5%) compared with MBL E-test (45.5%) and MHT (71.4%). The carbapeneme resistance-encoding genes detected were bla_{NDM1} (70.6%), bla_{OXA23} (84%), bla_{OXA48} (46.2%) and bla_{OXA51} (73.1%); the highest carbapeneme genes were demonstrated in Burn and Plastic Surgery Hospital (73.7%). The co-occurrence of bla_{NDM1}, bla_{OXA23} and bla_{OXA48} genes were demonstrated in (30/119; 25.2%) showing dissemination of carbapenemes resistance MDR *A. baumannii* in hospitals. MLST analysis for A. baumannii isolates revealed also the presence of multiple clones in our study. The clones belonging to ST1 and ST2 were the most frequent **Conclusions:** This study shows that the high prevalence of NDM-1 and OXA-23 contribute to antibiotic resistance in Libyan hospitals and represents the high incidence of carbapenemases in an autochthonous MDR *A. baumannii* isolated from patients in Libya, indicating that there is a longstanding infection control problem in these hospitals.

Successful Control of a Multi-Patient Use Equipment Driven *Candida auris* Outbreak in a UK Intensive Care Unit

D. Eyre[1], A. Sheppard[1], H. Madder[2], A. Walker[1], T. Peto[1], D. Crook[1], K. Jeffery[3]
[1]University of Oxford, Oxford, United Kingdom, [2]Oxford University Hospitals, Oxford, United Kingdom, [3]Oxford University Hospitals, Oxford, United Kingdom

Background: *Candida auris* is an emerging and multi-drug resistant pathogen. Here we provide an update on the epidemiology of one of the largest identified *C. auris* outbreaks to date, centred around the neurosciences intensive care unit of Oxford University Hospitals, United Kingdom. **Methods:** Following identification of a cluster of *C. auris* infections, an intensive patient and environmental screening program was established. Patient and environmental isolates were Illumina and Oxford Nanopore whole-genome sequenced. We have shown previously using multivariate logistic regression that, controlling for length of stay, patient physiology, and biomarkers, multi-patient use skin surface axillary temperature monitoring was an important independent predictor of *C. auris* colonisation/infection (odds ratio 6.80 [95%CI 2.96-15.63]). Here we describe the progress of the outbreak after removal of these axillary temperature probes. **Results:** 66 patients were colonised or infected with *C. auris* between 02-February-2015 and 24-April-2017, after which all axillary temperature probes were comprehensively withdrawn. Up to 1-March-2018 a further 10 cases occurred, the last on 9-Nov-2017. All outbreak sequences formed a single genetic cluster within the *C. auris* South African clade. Within this, for most of the outbreak there was limited temporal or spatial phylogenetic clustering, and multi-use patient equipment sequences were identified throughout the phylogenetic tree of patient isolates, suggesting widespread transfer of *C. auris* between patients and equipment used throughout the unit. However, this pattern changed following removal of the temperature probes, with 7 of the 10 most recent patient isolates genetically-clustered, suggesting persistence from a point source. This was eventually eliminated but lasted several months despite a bundle of intensive infection control interventions and periods without similarly colonised patients on the unit. No new patient has been colonised or infected with *C. auris* in the last 112 days. **Conclusions:** Environmental survival appears key to *C. auris* persistence and transmission in healthcare settings. This reinforces the need to carefully investigate the environment, and in particular multi-use patient equipment, in otherwise unexplained healthcare-associated outbreaks.

E3. Vector-Borne Diseases

3:30-5:00 pm International Ballroom A/B/C

Yellow Fever Outbreak Response in Kebbi State, Northwestern Nigeria - January 2018

A. Hassan[1], O. Cosmas[2], E. Ebuka[2], R. Abdu-Aguye[3], A. Nauzo[3], I. Abubakar[3], H. Bala[4], S. Mohammed[5], M. Dalhat[3], M. Balogun[3], P. Nguku[3], O. Ojo[6], C. Ihekweazu[7]
[1]Nigeria Field Epidemiology and Laboratory Training Program, Nigeria Centre for Disease Control, Abuja, Nigeria, [2]National Arbovirus Research Institute, Enugu, Nigeria, [3]Nigeria Field Epidemiology and Laboratory Training Program, Abuja, Nigeria, [4]Kebbi State Ministry of Health, Birnin Kebbi, Nigeria, [5]World Health Organisation, Birnin Kebbi, Nigeria, [6]Nigeria Centre for Disease Control, Abuja, Nigeria, [7]Nigeria Centre for Disease Control, Abuja, Nigeria

Background: There is an apparent re-emergence of yellow fever in Nigeria. On 16 November 2017, an outbreak was reported in Kebbi State which shares international borders with Republics of Niger and Benin. We were deployed by the Nigeria Centre for Disease Control to describe the epidemiology, determine yellow fever vaccine coverage; and the presence of its vectors. **Methods:** We defined a presumptive case as any suspected case who tested positive for yellow fever in a Nigerian laboratory and a confirmed case as any presumptive case who tested positive for yellow fever in the reference laboratory in Dakar. We conducted active case search through record reviews at health facilities and in communities. We conducted larval surveys and used modified human landing catch (human bait), CDC UV light, biogent-sentinel traps and ovitraps to catch mosquitoes. We calculated a sample size of 384 for surveys of yellow fever vaccination coverage and yellow fever knowledge, attitude and practice among community members. We gave equal allocation of 12 questionnaires to each of 36 settlements in the ward and randomly selected 12 households per settlement for the interviews. We calculated frequencies and proportions of vaccinated and unvaccinated children; and computed percentage score of knowledge, attitude and practice of respondents. **Results:** Between 30th August, 2017 and 27th January, 2018, there were 151 reported cases, of which five (3.3%) were presumptive cases, one (0.7%) was a confirmed case, 113 (74.8%) were negative and 31 (20.5%) results were pending. The presumptive and confirmed cases were clustered. Ninety-seven (64.2%) were male. Median age was 12 years (inter quartile range = 6-25 years). Out of 39 mosquitoes trapped, 38 (97.4%) were *Culex spp.* Out of 432 eligible children, 130 (30.1%) had their yellow fever immunization cards sighted and 260 (60.2%) heads of households did not have knowledge on the protective effect of vaccination against yellow fever. **Conclusions:** There is a potential for future yellow fever cases and other arbovirus infections in these areas. We conducted mass risk communication and requested for reactive vaccination in affected areas from the International Coordinating Group on Vaccine Provision. We recommended rapid laboratory turnaround time and intensified community and laboratory surveillance for other arbovirus infections.

CDC's International Vector Response to the Zika Virus Outbreak: Strengthening Regional Public Health Entomology Networks

R. Levine, A. Lenhart
CDC, Atlanta, GA, USA

Background: The 2016 Zika virus outbreak highlighted capacity gaps in vector surveillance and control programs. Many countries were not able to respond to the outbreak as effectively or efficiently as they would have liked, at least partly due to resource and staffing constraints. In addition, there were limited opportunities for countries to share expertise in public health entomology and few formal mechanisms for countries to work together to bring vector borne disease outbreaks under control. **Methods:** CDC supported a network-based strategy to facilitate the ability of countries to leverage resources among themselves for vector surveillance and control. Regional networks were either developed or strengthened (where already in existence) to create frameworks for vector personnel from neighboring countries to share surveillance data, collaborate on vector control strategies, and improve information exchange. In addition, CDC and partners used the networks to organize multiple workshops on various aspects of vector surveillance and control. **Results:** Three entomological networks focusing on *Aedes* surveillance were either created or strengthened in Central America, the Caribbean, and West Africa, improving capacity for response to and control of *Aedes*-borne disease. As an example, by the end of 2017 a unified strategy was formalized for the island of Hispañola, whereby both Haiti and the Dominican Republic conducted joint border surveillance activities, agreed to share entomological data, and adopted the same entomological surveillance platform. The networks were also used to provide trainings to personnel from over 40 countries on topics including trapping methods, integrated vector management, insecticide resistance, mapping and use of GIS, surveillance platforms, and data management and analysis. **Conclusions:** A network-based approach may empower countries to support one another in vector surveillance and control using regional experts, which contributes to sustainable improvements in entomological capacity and outbreak response.

Environmental Suitability and Predicted Distribution of *Aedes albopictus* and *Aedes aegypti* Mosquitoes in Canada and the United States: Assessing Arboviral Risks in North America

S. Khan[1], N. Ogden[2], A. Fazil[3], A. Greer[1], V. Ng[3]
[1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]National Microbiology Laboratory, Public Health Agency of Canada, Saint-Hyacinthe, QC, Canada, [3]National Microbiology Laboratory, Public Health Agency of Canada, Guelph, ON, Canada

Background: *Aedes* species of mosquitoes, particularly *Aedes aegypti* and *Ae. albopictus*, are known vectors of over 20 arboviruses of global public health importance. With climate change, both species are predicted to expand their habitat range. This study aimed to apply a machine learning approach to assess the current environmental suitability and probable distribution of the vectors in Canada and the United States (US). **Methods:** We utilized *Ae. albopictus* (n=2,939) and *Ae. aegypti* (n=335) occurrence data from 2001 to 2016 in Canada and US and generated random pseudo-absence data-points; four for each occurrence and constrained to below 60°N. We modeled the vec-

tor occurrences using ecological and anthropogenic predictors including temperature, precipitation, enhanced vegetation index (EVI) and urbanicity. Boosted regression trees were used to assess the relative contribution of each predictor, determine the predictive performance of the model, and to map the probability of the ecological niche of *Ae. albopictus* and *Ae. aegypti*. **Results:** The probable distribution of *Ae. albopictus* in Canada and the US was primarily associated with increasing number of days with an average temperature of 10°C or higher (Relative contribution (RC): 45.2%), in urban locations (RC: 17.6%), with increasing amount of total monthly precipitation (RC: 9.7%), enhanced vegetation index (7.2%) and increasing minimum temperature (7.1%). *Ae. aegypti* demonstrated a preference for urban locations (RC: 47.2%), increasing number of days with an average temperature of 20°C or higher (13.9%), and increasing minimum (RC: 12.5%) and maximum (RC: 9.6%) temperatures. The predicted niche of *Ae. albopictus* ranged from southeast regions of the US to the southwestern borders of Ontario, and from the east coast of the US to the central US. Some small regions of the west coast also appeared suitable for *Ae. albopictus*. *Ae. aegypti* were predicted to have a similar distribution but scattered sparsely. **Conclusions:** A large proportion of North America appears to be suitable for *Ae. albopictus* and *Ae. aegypti* vector populations increasing the chance of local transmission of arboviruses of public health significance. Continued surveillance for the vectors in the high-risk regions will enable us to effectively use resources to identify circulating pathogens and their geographical range expansion.

Tracking the Spread of Insecticide Resistance in *Aedes aegypti* and *Ae. albopictus* for Informed Vector Control of Arboviral Diseases

D. Athinya[1], M. Hadi[1], S. Omondi[2], E. Ochomo[2], H. Pates Jamet[3]
[1]Vestergaard, Nairobi, Kenya, [2]Kenya Medical Research Institute, Kisumu, Kenya, [3]Vestergaard, Washington, DC, USA

Background: Vector borne diseases account for more than 17% of all infectious diseases and cause more than 700,000 deaths annually. *Aedes aegypti* and *Ae. albopictus* have been implicated as vectors of dengue, chikungunya, yellow fever and Zika virus. The prevention of mosquito-borne diseases relies heavily on insecticide based vector control tools and knowledge of the spatial distribution of insecticide resistance is essential. Enhanced vector surveillance is one of four pillars of the WHO Global Vector Control Response 2017-2030. IR Mapper (www.irmapper.com) was launched in 2012 to display reports of insecticide resistance in malaria vectors. In 2016, the mapping platform was expanded to geospatially display reports of insecticide resistance in *Ae. aegypti* and *Ae. albopictus*. **Methods:** IR Mapper comprises of a cloud database that is visualized on an interactive mapping platform. The database is updated monthly with newly published data from peer reviewed published literature on phenotypic (WHO susceptibility test and CDC bottle assay) and resistance mechanisms (target site and overexpressed metabolic enzymes) data. The mapping platform was built using ArcGIS for JavaScript API with advanced query functions incorporated to enable an interactive interface. **Results:** As of January 2018, *Aedes* IR Mapper consisted of 8,523 field records from 1,324 localities in 68 countries and territories. 72% of localities reported confirmed resistance to at least one class of public health insecticide for adult stage control. Insecticide resistance was more frequently investigated in *Ae. aegypti* (85% of localities) than in *Ae. albopictus* (25% of localities). The highest proportion of confirmed resistance was to organochlorines (89%) followed by pyrethroids (64%). The majority of data were available from Asia with very few data from Africa. **Conclusions:** IR Mapper is a useful tool for visualizing the spatial spread of insecticide resistance and identifying resistance data gaps.

Changing Trends in Age and Sex Distributions of Human Lyme Disease—United States, 1992-2016

K. Kugeler, P. Mead, A. Schwartz, A. Hinckley
Centers for Disease Control and Prevention, Fort Collins, CO, USA

Background: In the United States, the age distribution among Lyme disease cases is consistently bimodal. However, temporal changes in the relative frequency of cases across age groups are apparent. **Methods:** Lyme disease case records submitted to US Centers for Disease Control and Prevention (CDC) during 1992-2016 were divided into five time periods. Patient age was grouped into five-year age categories and converted into birth year. Average annual incidence was calculated by age, sex, and time period. We used incidence rate ratios (IRR) to compare incidence during 2012-2016 to 1992-1996. **Results:** During the 25-year period, 510,555 confirmed case records were transmitted to CDC; 481,827 (94%) contained patient age. Among children, cases consistently peaked among those 6-8 years. Among adults, cases initially peaked among those 35-49 years whereas by 2012-2016, cases peaked among 50-64 years. Persons born during 1950-1964 accounted for the peak among adults during the 25-year period. Incidence rates corrected for a changing population structure yielding peak incidence around age 60 irrespective of time period. Overall, incidence nearly doubled (IRR: 1.74; 95% CI:1.70-1.78). However, temporal increase in incidence differed by age and sex; greatest rate increases occurred among those 10-14 years (IRR: 2.23, 95% CI:2.05-2.42) and ≥70 years (IRR: 2.01, 95% CI:1.87-2.16). Incidence increased disproportionately among males, with IRRs among those aged 2-69 years 39%-89% higher than for females. **Conclusions:** Commonality of Lyme disease among children appears driven by age-related behavior and interaction with tick habitat rather than by size of the population at risk. In contrast, the increasing age of adult Lyme disease cases appears driven by an aging "baby-boom" generation and associated size of the population at risk. Although disease incidence nearly doubled during the past 25 years across most age groups and disproportionately among males, young children and older adults are consistently at highest risk for acquiring Lyme disease.

Evaluating the Risk of Tick-borne Relapsing Fever Among Occupational Cavers — Austin, TX, 2017

S. Campbell[1], A. Klioueva[2], S. Tomasi[3], C. Nelson[1], A. Replogle[1], M. Schriefer[1], J. Taylor[2], N. Kwit[3], A. Hinckley[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Austin Public Health, Austin, TX, USA, [3]Centers for Disease Control and Prevention, Morgantown, WV, USA

Background: Tick-borne Relapsing Fever (TBRF) is a potentially serious spirochetal infection caused by certain species of *Borrelia* and acquired through the bite of *Ornithodoros* ticks. In Texas, *Ornithodoros turicata* is found in caves and burrows and transmits the bacteria *Borrelia turicatae.* In 2017, Austin Public Health identified several TBRF cases among employees who worked in caves. We investigated the occurrence of TBRF and associated risk factors among occupational cavers, with the aim of developing targeted prevention recommendations. **Methods:** We conducted a cross-sectional serosurvey of employees from 8 organizations with cave-related work in three Austin-area counties. Participants were interviewed regarding

frequency and location of cave exposures, use of protective measures, and illness history. Serum was tested for antibody reactivity to *Borrelia* antigens using a 2-tiered testing algorithm. **Results:** Among 44 participants, 33 (75%) had entered 89 different Austin-area caves in the previous 12 months. Antibodies against TBRF-causing *Borrelia* were detected in serum of 5 participants, all of whom had entered caves in the past 12 months. Among these, 4 reported recent illness and had sought medical care; 3 were diagnosed with TBRF. Seropositive employees entered significantly more caves (23.6 vs 11.9, P=0.04) and were more likely to guide cave tours (80% vs 31%, P=0.05) than seronegative employees. Five caves were identified as the most frequently entered among the seropositive. There were no differences between seronegative and seropositive employees with respect to any protective measures used. **Conclusions:** Employees who frequently enter caves near Austin are at increased risk for TBRF. Five specific caves were identified as potentially high risk, several of which are in public use areas and open for tours. CDC and Austin Public Health developed materials to share with Austin area healthcare providers about TBRF and prevention recommendations for high-risk groups.

E4. Frontline Public Health

3:30-5:00 pm International Ballroom E

Missed Opportunities to Diagnose Infections Related to Injection Drug Use are Common: A Population-Based Investigation

A. Miller, P. Polgreen
University of Iowa, Iowa City, IA, USA

Background: The recent dramatic increase in opioid use has coincided with an increase in injection drug use (IDU). In addition to overdoses, infections are one of the most serious adverse events associated with IDU. Surveillance for IDU-related infections has relied on the co-occurrence of diagnostic codes for both the infection and drug use. However, infections caused by IDU may be missed if drug use is not diagnosed or concurrently recorded. Our objective was to estimate the incidence of IDU-related infections by identifying potentially missed IDU-related infections where there was evidence of drug use prior to, or following, the infection but where drug use was not recorded at the time of infection. We also analyze the factors associated with missed opportunities to diagnosis IDU. **Methods:** We conducted a retrospective cohort study using state inpatient and emergency department visits from the Healthcare Cost and Utilization Project for California (2005-2011), Florida (2005-2013), and New York (2006-2013). We identified all patients with a principal or secondary diagnosis of bacteremia or sepsis, endocarditis, osteomyelitis or septic arthritis, and skin or soft tissue infection. We first identified drug use recorded at the time of infection diagnosis. We next identified "missed" cases where drug use was diagnosed within 6 months before or after an infection. Finally, we compared patient and hospital characteristics between IDU-related infections that were concurrently identified and those where drug use was missed. **Results:** IDU-related infections have been steadily increasing since 2008 along with the number of cases where IDU was missed. Including missed IDU-related infections increases the number of IDU-related infections identified by 2 to 3 times each year. Factors associated with IDU being missed included emergency department setting, limited hospital experience treating drug use, patient age<18, and Medicare as the primary payer. **Conclusions:** The incidence of IDU-related infections may be dramatically underreported, and current surveillance methods may capture less than half of all IDU-related infections There are a number of hospital and patient characteristics that could be targeted to improve the diagnosis and identification of IDU and prevent IDU-related harms.

Hepatitis C Testing Among Health Department Clients in Tennessee

L. Sizemore[1], J. Black[1], K. Gill[1], C. Goff[2], T. Sondgerath[1], H. Wingate[1], C. Wester[1]
[1]Tennessee Department of Health, Nashville, TN, USA, [2]Tennessee Department of Health, Knoxville, TN, USA

Background: Approximately 75% of the estimated 3.5 million individuals infected with Hepatitis C (HCV) in the United States are unaware of their infection, limiting access to prevention and medical services. The US Preventive Services Task Force recommends HCV testing among Baby Boomers as well as individuals with risk factors, including high risk sexual behaviors. We sought to better understand the statewide burden of chronic HCV by providing testing among at-risk groups within health departments (HD). **Methods:** Routine

opt-out HCV testing was offered to patients attending HD sexually transmitted disease (STD) and family planning (FP) clinics in Tennessee, although participation in testing varied by region. Routine demographic and risk factor information were collected at the time of specimen collection. HCV antibody (Ab) testing with reflex to confirmatory RNA was conducted at the Tennessee Department of Health State Laboratory. **Results:** From April 3, 2017 through December 31, 2017, 14,933 HD clients underwent HCV Ab testing. The median age of clients tested was 28 years (range 2-87), 52% were female, 66% non-Hispanic White and 32% non-Hispanic Black. Eleven percent were born from 1945-1965, and self-reported risk factors included a history of incarceration (28%), non-professional tattoo (26%), snorting drugs (22%), and injection drug use (13%). Risk factors were not mutually exclusive. Thirteen percent of clients tested positive for HCV Ab (n=1,892), and 73% (n=1,377) of these clients were RNA positive, indicating active HCV infection. Men were more likely than women to be Ab-positive (14% versus 12%; P <0.001), and non-Hispanic Whites were more likely to be Ab-positive than all other races/ethnicities (19% versus 8%; P <0.0001). **Conclusions:** These findings indicate the feasibility and importance of incorporating routine HCV testing to clients attending HD STD and FP clinics. Through ongoing efforts, we can reduce the undiagnosed fraction and increase access to prevention services, and HCV care and treatment.

Repeat Chlamydial Infections among Women Aged 15 to 34 Years — Louisiana, 2000–2015

S. Cha[1,3], D. Newman[1], M. Rahman[1,2], T. Peterman[1]
[1]Centers for Disease Control and Prevention, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, Division of Sexually Transmitted Diseases Prevention, Atlanta, GA, USA, [2] Louisiana Department of Health-Office of Public Health-STD/HIV Program, New Orleans, LA, USA, [3]Center for Surveillance, Epidemiology, and Laboratory Services, Division of Scientific Education and Professional Development, Atlanta, GA, USA

Background: Chlamydial infections are usually asymptomatic among women. Infections and especially repeat infections can lead to pelvic inflammatory disease, ectopic pregnancy, and tubal factor infertility. Louisiana has the third highest chlamydia rate among women in the United States (961.2 per 100,000). We assessed the likelihood of reported repeat chlamydial infections and time interval between infections among all young women reported in Louisiana. **Methods:** Surveillance data on all chlamydial infections reported among women in Louisiana were analyzed for years 2000 to 2015. Women aged 15-34 years at the time of their first chlamydia diagnosis were included, with a potential follow up period of 16 years. Test results with duplicate specimen collection dates and chlamydial infections reported ≤30 days of a previous infection were excluded. **Results:** There were 268,215 infections reported among 177,591 women. Thirty-four percent (90,624) of chlamydial infections were repeat infections (maximum=15). Most repeat infections were among young women aged 15-19 years (54%; 48,621) and black women (81%; 73,276). The risk of subsequent reinfection increased with the number of previous reinfections. Among 15-19 year olds with one infection, the cumulative incidence of a second infection was 9% at 6 months, 16% at 1 year, and 26% at 2 years, compared to women aged 25-29 years (4%, 7%, and 10%, respectively). Thirty percent of 15-19 year old black women with one infection had a second infection within 2 years. **Conclusions:** In Louisiana, more than a third of reported chlamydia among women were repeat infections. Our findings likely underestimate the true number of infections because surveillance data represent only infections that were detected and reported. Interventions are needed to address the high rates of reinfections among women.

Sexual Activity, Abstinence, and Condom Use among Pregnant Women during the Zika Virus Outbreak — Puerto Rico

K. Turay[1], G. Earle-Richardson[1], P. Chavez[2], C. Prue[1]
[1]Centers for Disease Control and Prevention, National Center for Emerging and Zoonotic Infectious Diseases, Office of the Director, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention, Atlanta, GA, USA

Background: Background: In February 2016, public health authorities in Puerto Rico (PR) recommended condom use or sexual abstinence to prevent pregnant women from becoming infected with Zika virus. We aim to describe the prevalence of these Zika protective sexual behaviors among pregnant women in PR, and factors associated with engaging in the behaviors during the 2016-2017 outbreak period. **Methods:** Methods: From July to December 2016, and alternate months between February and June 2017, pregnant women from the PR Women, Infants, and Children (WIC) program database were randomly selected to participate in telephone interviews. Each month, callers interviewed approximately 150 women about their sexual behaviors and Zika risk perceptions. Frequencies of behaviors were calculated and chi-square tests assessed associations with trimester and risk perceptions. **Results:** Results: Data were available for 1,315 women. The prevalence of sexual abstinence during pregnancy increased during peak transmission periods – from 20% in July 2016 to 27% in September 2016. Among the 268 women who provided reasons for abstinence, 9% cited Zika prevention. Of all women interviewed, 35% reported having sex and using a condom every time, rising from 23% in July 2016 to 43% in October 2016. This increase was sustained in November (42%) and December (41%). Another 21% reported never using a condom. By June 2017, the proportion of pregnant women reporting either abstinence (16%) or condom use every time they had sex (24%) declined. Engaging in Zika protective sexual behaviors was not significantly associated with trimester (at interview) (p=0.40) or confidence in ability to protect self and baby from a Zika infection (p=0.53). **Conclusions:** Conclusions: Pregnant women's condom use behaviors changed over the course of the outbreak, starting at low levels, increasing during peak periods of Zika transmission, and declining as the outbreak ended in June 2017. Future analyses should examine facilitators of Zika protective sexual behaviors among pregnant women during the outbreak.

Level and Factors Influencing Uptake of Human Papilloma Virus Vaccine among Female Adolescents in Lira District, Uganda, 2016

E. Kisaakye, J. Babirye, J. Namakula
School of Public Health, College of Health Sciences, Makerere University, Kampala, Uganda

Background: Globally, cervical cancer is the fourth most common malignancy in women affecting 500,000 women each year with an estimated 266,000 deaths in 2012. Uganda has one of the highest cervical cancer incidence rates globally with an age-standardized incidence rate per 100, 000 of 47.5. This study aimed at assessing the level and the factors influencing the uptake of Human Papilloma Virus (HPV) vaccine by Female adolescents in lira district, Uganda. **Methods:** This

was a cross-sectional study of 460 female adolescents conducted in May 2016. Data was collected using a questionnaire. Uptake was defined as completing all the doses of the vaccine. Prevalence risk ratios were used as measures of association and were computed using modified poison regression. Statistical significance was at $p \leq 0.05$ and 95% confidence interval. **Results:** The mean age of the respondents was 13.97 (SD=1.24). Uptake was at 17.61% (81/460). Factors associated with uptake of HPV vaccine were: a positive attitude towards the vaccine (aPR 3.46, 95%CI 1.70 – 7.02), receiving vaccine doses from different vaccination sites (aPR 1.59, 95% CI 1.10 – 2.28), encouragement from a health worker (aPR 1.55, 95%CI 1.15 – 2.11) or Village Health Team (aPR 3.47, 95%CI 1.50 – 8.02) to go for the vaccine, existence of community outreaches (aPR 1.47, 95%CI 1.02 – 2.12), availability of vaccines at vaccination sites (aPR 4.84, 95%CI 2.90 – 8.08) and receiving full information about the vaccine at the vaccination site (aPR 1.90, 95%CI 1.26 – 2.85). **Conclusions:** HPV vaccine uptake was low in Lira District. Efforts to improve uptake of HPV vaccine should focus on ensuring consistent supply of vaccines at the vaccination sites, sensitization of the adolescents and caretakers about the vaccine and conducting community outreaches.

Measles Outbreak in an Underimmunized Community — Minnesota, 2017

J. Griffith, E. Laine, E. Muenchow, H. Omar, P. Gahr, K. Como-Sabetti, C. Kenyon, E. Banerjee
Minnesota Department of Health, St. Paul, MN, USA

Background: Endemic measles was eliminated in the United States in 2000 through high vaccination rates but is occasionally imported by travelers. In April 2017, a measles outbreak began among children in an underimmunized Somali-Minnesotan community, the second outbreak in this community in 6 years. While the MMR vaccine rate among all 2 year olds in MN is 94%, MMR rates among 2-year-old Somali-Minnesotans have declined, largely due to fears of autism, from 92% in 2004 to 42% in 2017. **Methods:** Cases were defined as those meeting the CSTE confirmed case definition for measles or those genotyped as B3, regardless of symptoms. Epidemiologic investigations were conducted for all suspect and confirmed cases. Exposures to measles cases were assessed in high-risk settings (childcare, schools, households and healthcare) to identify susceptible children and recommend post-exposure prophylaxis (PEP); susceptible children not receiving PEP were excluded from childcare or school for 21 days. Susceptibility of adults was not routinely assessed. An accelerated MMR vaccine schedule for children >=12 months was recommended. Intensive infection control measures were implemented in healthcare settings and targeted communication and outreach activities about measles and MMR vaccine occurred. **Results:** 75 cases were confirmed from April 11-July 11, 2017. 831 suspect cases were investigated and ruled out. The median case age was 2 years (94% were <=10 years), 61 (81%) were Somali-Minnesotan, 68 (91%) were unvaccinated, 21 (28%) were hospitalized; there were no deaths. The index case was not identified. Over 8,500 known exposures occurred in childcare, schools and healthcare, and additional, but unquantifiable exposures occurred in the community. 575 children were excluded and 51,706 doses of MMR vaccine above the expected baseline were administered. At the time the first case was confirmed, 8 children had undiagnosed measles and 20 were infected. **Conclusions:** The focus of our outbreak control strategy was to stop transmission among children as identifying susceptible adults in a population that is largely immune would have had limited impact. Aggressive public health, healthcare and community response resulted in quick control of this outbreak.

Tuesday, August 28

Poster Abstracts

Poster / Exhibit Hall

One Health II

Board 150. Wildlife Disease Surveillance as an Early Warning System for High Consequence Zoonotic and Animal Diseases

K. Richgels, D. Blehert, C. White, J. Sleeman
USGS National Wildlife Health Center, Madison, WI, USA

Background: Most emerging infectious diseases originate in wildlife species. Additionally, many of the zoonotic diseases that are predicted to increase or spread due to climate change have wildlife reservoirs. Thus, establishing wildlife surveillance systems may provide early warning of emerging or re-emerging infectious diseases that are concern for wildlife conservation, and for human or domestic animal health. **Methods:** The National Wildlife Health Center of the US Geological Survey provides national scope passive and active surveillance for pathogens in wildlife species. Our passive surveillance includes cause-of-death determinations for mortality events (>5 mortalities in a population) submitted by state, federal, and tribal land managers throughout the United States. In addition, we also conduct or participate in national scale designed surveillance for highly pathogenic avian influenza in wild birds, salamander chytridiomycosis (Bsal) in amphibians, and white-nose syndrome in bats. **Results:** For passive surveillance, the NWHC investigates approximately 225 mortality events per year, representing about 1,300 cause-of-death determinations. These submissions cover all taxa of wildlife, but are predominantly birds (67%), mammals (17%), or amphibians (12%). Passive surveillance has led to the discovery of diseases significant to human health or the agricultural economy. For example, we reported 136 identifications of high consequence diseases such as sylvatic plague, virulent Newcastle disease, highly pathogenic avian influenza, and botulism from wildlife mortality events in the past three years. **Conclusions:** The National Wildlife Health Center has unique capabilities to conduct national scope disease surveillance and is looking to expand its capacity to additional diseases of concern. We are also very partner- and One Health-focused, developing capabilities such as standardized and curated publicly available datasets, that will allow for better integration with other health agencies.

Board 151. Improving Response Time through Private Sector Contributions and One Health Approach in Guinea

T. Bah[1], S. Agbo[2], D. Ngaradoum[3], W. Kaschak[1], B. Ohoukou[4]
[1]USAID, Conakry, Guinea, [2]DAI, Abijan, Côte d'Ivoire, [3]CNFA, Conakry, Guinea, [4]FAO, Conakry, Guinea

Background: Unreliable and incomplete data flow for zoonotic diseases and lack of resources dedicated to field investigations lead to slow response time to outbreaks. The Global Health Security Agenda (GHSA), Guinea designed targeted programs in surveillance, workforce development, laboratory diagnostic capacities, and mechanisms to prevent detect and respond to zoonotic disease outbreaks. **Methods:** To reduce response time, the surveillance system relies on a strong national commitment that includes in-country coordination and detection capabilities. **Results:** In-country coordination based on the One Health approach for zoonotic diseases surveillance/control/prevention enables communication between key ministries for quick decision making prior or during outbreaks. Guinea National One Health platforms (OH) bring together public and animal health and environment representatives to address ongoing issues and plan for an action. The platform is institutionalized with a formal structure and inter-ministerial executive order. Animal and environment sectors combine their data to the National Health Security Agency (ANSS) weekly bulletin. The effective operation of the platform however requires strong commitment from host country governments expressed through budget allocation. A country's ability to detect zoonotic diseases depends on its resources (human, material, and financial) for investigation and laboratory capacity to analyze samples. Modest levels of donor support to address emergency plans and private sector partnership enable countries to quickly respond to outbreaks. Anthrax emergency plan enables Guinea to quickly deploy teams in the field to investigate and collect sample for laboratory testing without delay. The GHSA – public – private partnership model focuses on the private network of 79 veterinarians and unemployed young Guineans enrolled in an entrepreneurship program that promotes animal health and youth business opportunities. **Conclusions:** Country improved regulatory environment in a conducive environment for increased private investment in livestock sector to contribute to improving animal health surveillance thus reducing zoonotic disease outbreaks.

Board 152. One Health Approach Involving Rabies Control and Prevention in Thailand

S. Sungpradit[1], S. Lertsithichai[2], P. Panichabhongse[3], S. Martsri[4], W. Tabkaew[5], P. Ratanakorn[6]
[1]Department of Pre-clinic and Applied Animal Science, Faculty of Veterinary Science, Mahidol University, Nakhon Pathom, Thailand, [2]Faculty of Liberal Arts, Mahidol University, Nakhon Pathom, Thailand, [3]Bureau of Disease Control and Veterinary Services, Department of Livestock Development, Phayathai, Bangkok, Thailand, [4]Audio Visual Education Technology Officer, National Laboratory Animal Center, Mahidol University, Nakhon Pathom, Thailand, [5]Student Support Service Section, Ratchsuda College, Mahidol University, Nakhon Pathom, Thailand, [6]Department of Clinical Sciences and Public Health Medicine, Faculty of Veterinary Science, Mahidol University, Nakhon Pathom, Thailand

Background: Rabies, a mammal-borne disease caused by rhabdovirus (family Rhabdoviridae), is still a complicated life-threatening zoonotic disease worldwide including in Thailand. The World Health Organization (WHO) has announced that rabies will be eliminated in all countries by 2030. Even though there were a lot of campaigns in Thailand regarding rabies control and prevention, an average of seven Thai people died annually (year 2013-2017) from the disease. No single discipline could deal with the disease because of the disease's relevance to medicine, veterinary, economic, culture, and beliefs, etc. In order to introduce the "One Health" concept as a solution to the complicated rabies problem, Mahidol University (MU) set up the One Health model when it hosted the annual World Rabies Day 2011 and 2015 events. **Methods:** Several disciplines of the faculties, centers, institutes, and colleges at MU were invited to become involved in the One Health model. Each organization used its expertise to produce breakthrough products. **Results:** Three rabies cartoon animations (rabies knowledge,

control, and prevention) and a poem performed by MU International College; a rabies cartoon pocketbook, *Jood the Curious Puppy and a Rabies Story*, which was translated into many languages (English, Chinese, Vietnamese, and Indonesian) by the MU Research Institute for Language and Culture of Asia; a rabies Braille code pocketbook for the blind who could be rabies victims, completed by MU Ratchasuda College; and a stop-motion animation rabies cartoon produced by MU National Laboratory Animal Center. **Conclusions:** Not only is the health science discipline responsible for rabies, but non-health science disciplines should get involved as well to combat the complicated zoonotic disease of rabies.

Board 153. Determining the Minimum Level of Vaccination Needed to Prevent Re-introduction of Dog Rabies Once It Has Been Eliminated

S. Jeon, J. Cleaton, E. Kahn, M. Meltzer, E. Pieracci, R. Wallace
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Rabies virus causes approximately 59,000 human deaths annually worldwide, most of which are attributed to the canine virus variant. The World Health Organization recommends that countries vaccinate 70% of their dogs each year to eliminate canine rabies. However, it is unknown what level of vaccination must be maintained to prevent reintroduction of canine rabies. In this paper, we consider a scenario whereby canine rabies is reintroduced into a rabies-free population and demonstrate the cost-effectiveness of vaccination strategies to maintain canine variant rabies free status. **Methods:** We used a published model of canine rabies transmission, RabiesEcon, to estimate the percentage of dogs that must be annually vaccinated to prevent re-establishment of canine rabies. We allowed for differences in human-to-dog ratios (dog densities), dog turnover rates (life expectancy), transmission rates (basic reproduction number), and number of rabid dogs reintroduced. Finally, we calculated the economic costs and benefits of maintaining sufficient coverage over a 20-year time period. **Results:** Assuming 10 rabid dogs are introduced into a canine variant rabies free area of 1 million human and 67,000 dog population, 45% of dogs must be vaccinated annually to prevent re-establishment of canine rabies. Compared to discontinuation, continuing vaccination with 45% coverage can prevent approximately 73,000 rabid dogs and 17,000 human rabies deaths over a 20-year period. Average cost per rabies-related human deaths averted over a 20-year period was $72. We found that the results were most sensitive to transmission rates and dog turnover rates. **Conclusions:** Although canine rabies can be eliminated by vaccinating at least 70% of dogs, public health officials have to plan for the post-elimination risk of re-introduction. The estimates presented here will aid public health officials in implementing such plans.

Board 154. A Comparative Study of Enumeration Techniques for Free-Roaming Dogs in Rural Baramati, District Pune, India

H. Tiwari[1], A. Vanak[2], M. O'Dea[1], J. Gogoi-Tiwari[3], I. Robertson[1]
[1]Murdoch University, Perth, Australia, [2]Ashoka Trust for Research on Ecology and the Environment, Bengaluru, India, [3]Curtin University, Perth, Australia

Background: The presence of unvaccinated free-roaming dogs amidst human settlements is a major contributor to the high incidence of rabies in countries where the disease is endemic, such as India. Estimating free-roaming dog population is crucial to the planning and evaluation of interventions, such as mass immunisation, against rabies. Enumeration techniques are resource intensive and can vary from simple direct counts to statistically complex capture-recapture techniques primarily developed for ecological studies. In this study, we compared eight enumeration techniques to estimate the free roaming dog population and recommend a technique that yields a reasonably accurate count to use for effective vaccination coverage against rabies with minimal resource inputs. **Methods:** We used direct count, Lincoln–Petersen's index, Chapman's correction estimate, Beck's method, Schumacher-Eschmeyer method, Regression method, Huggin's closed capture models, and Application SuperDuplicates online tool using the data collected by seven sessions of photographic capture-recapture of free roaming dogs in Shirsuphal village of Baramati town in western India. **Results:** A total of 263 unique dogs were sighted at least once over 6 observation occasions with no new dogs sighted on the 7th occasion. The methods that do not account for individual heterogeneity yielded population estimates in the range of 248-270, which potentially underestimate the real FRD population size. The highest estimates were obtained with the Huggin's M_h-Jackknife (437±33), Huggin's M_{th}-Chao (391±26), Huggin's M_h-Chao (385±30), models and Application "SuperDuplicates" tool (392±20). When the sampling effort was reduced to only two surveys, the Application SuperDuplicates online tool gave the closest estimate of 349±36, which is 74% of the estimated highest population of free-roaming dogs in Shirsuphal village. **Conclusions:** Application SuperDuplicates online tool provides a reliable estimate of free-roaming dog population with the minimal use of resources and is recommended as a reliable technique.

Board 155. Deaths from Clinically Identifiable Human Rabies in Bangladesh: A Survey through Verbal Autopsy

S. Ghosh[1], U. Siddiqi[1], M. Rana[1], S. Chowdhury[2], S. Ullah[1], M. Islam[1], R. Shah[1], S. Tahmina[1], B. Ahmed[1]
[1]Communicable Disease Control, Directorate General of Health Services, Ministry of Health and Family Welfare, Bangladesh, Dhaka, Bangladesh, [2]Chittagong Veterinary and Animal Sciences University, Bangladesh, Chittagong, Bangladesh

Background: Despite a significant reduction of rabies deaths (>50%) in Bangladesh through integrated rabies control program over the last few years, a substantial number of deaths are still encountered. Mortality data are crucial to identify ways to reduce unnecessary deaths due to rabies. **Methods:** We used an enhanced type of verbal autopsy to identify the causes of 195 deaths reported in National Rabies Prevention and Control Centre of Bangladesh from January 2013 to December 2014. We also identify the factors affecting compliance to rabies post-exposure prophylaxis (PEP) among rabies patients. The diagnosis of the death was almost always a clinical one and not confirmed by laboratory tests. **Results:** A total of 191 people were diagnosed as rabies having a history of animal exposure with clinical signs of hydrophobia (100%), aerophobia (84.8%), photophobia (15.3%). Most rabies deaths occur in men (74%), in rural areas (78%), and in children below the age of 15 years (45%). Dogs were responsible for 83% (n=159) of all animal exposure; however, cats (11%, n=22), jackals (4%, n=8), and mongoose (1%, n=2) were also found to be responsible with unknown vaccination status. Lower limbs were the most commonly affected areas (74.3%) where the animal bites took place; the majority of the bites (95%) were WHO class III. The majority of the victims had no history of receiving any PEP (88%). Although the 22 case-patients received PEP, only 2 had completed the courses from local pharmacy but received no immunoglobulin (RIG). However,

85% first sought treatment from traditional healers or village doctors. Existing mis-belief, prejudice (68%), high cost of PEP (14%), and lack of proper knowledge (14%) were identified as major barriers for not receiving standard management in case of animal bite for preventing rabies. **Conclusions:** The findings from this study suggest that it is crucial to promote the standard and effective treatment-seeking behavior of the bite victims through awareness, proper education, and discouraging visiting traditional healers for bite treatment. Ensuring better accessibility and availability for the provision of rabies PEP in rural areas of Bangladesh can help to prevent this deadly disease.

Board 156. Dynamics of and Factors Affecting the Occurrence of Rabies in Humans and Animals in South America

M. Meske, L. Awada, L. Mur, K. Murai, S. Epperson, P. Tizzani
OIE - World Organisation for Animal Health, Paris, France

Background: The dynamic of rabies in South America is complex and includes two main cycles: a terrestrial cycle involving domestic animals, and an aerial cycle with the vampire bat (*Desmodus rotundus*) playing the main epidemiological role. The impact of the two cycles on public health is significantly different, with most of the human cases related to the aerial cycle. The objective of this work was to describe the dynamic of the disease in South America and to analyse the factors affecting its occurrence within the framework of the OIE strategy for the elimination of dog-mediated rabies. **Methods:** Rabies cases in humans and animals reported to the World Organisation for Animal Health (OIE) and the Pan American Health Organization (PAHO) by the national authorities from 2009 to 2015 were analyzed. **Results:** The global number of rabies cases declined significantly over time (rho = -0.5; $p<0.05$), with a marked reduction for wildlife (rho = -0.6; $p<0.05$) and humans (rho = -0.7; $p<0.05$). Rabies cases were reported in 67% of the 239 administrative divisions in the region, with two main clusters of animal cases in Colombia and Brazil, and one main cluster of human cases in Peru. The majority of human cases (90/129) were due to contact with wildlife, vampire bats being the main source of infection (87/90). Of the factors impacting the occurrence of rabies cases, a significant association ($p<0.05$) with deforestation was observed. **Conclusions:** Although rabies continues to cause significant losses in South America, its occurrence has significantly declined during the last years. Different clusters of infection were identified depending on the population affected, the vampire bats being the main source of infection for humans. This information will help to elaborate targeted control and preventive programs for reducing the exposure to rabies in the region.

Board 157. A Case of Mistaken Identity: HSV Encephalitis Confirmed in a Patient Highly Suspect for Rabies Infection

A. Feldpausch[1], J. Gabel[2], C. Drenzek[2]
[1]University of Georgia, College of Veterinary Medicine, Athens, GA, USA, [2]Georgia Department of Public Health, Atlanta, GA, USA

Background: On Friday morning, March 10, 2017, the Georgia Department of Public Health (DPH) was notified of a suspect rabies case in a human. The patient, an 85-year-old woman, presented to an emergency department on March 6 after she was found in her home unwell and exhibiting "strange" behavior. She was admitted and continued to exhibit behavior such as chewing on blankets and medical equipment, and even bit a personal visitor. On Tuesday, March 7, she began spitting out water and refusing oral fluids. The patient was assessed for seizure disorders, meningitis, and other common neurologic diseases. She continued to deteriorate with a rapidly progressing, unexplained encephalopathy. Rabies infection was suspected due to the patient's clinical picture, potential for exposure as a resident of a rabies endemic area, and lack of a more likely diagnosis. The patient expired in the evening of March 10, 2017. **Methods:** A rabies risk assessment and consultation with the Centers for Disease Control and Prevention (CDC) Rabies staff was conducted on March 10, 2017. DPH had no documentation of an animal bite report on the patient. Antemortem rabies specimens were collected the same day. Although lower on the list of differential diagnoses, prion disease and herpes simplex encephalitis (HSE) were considered. After the patient died, DPH collaborated with CDC to deploy a team to procure specimens for rabies and herpes simplex virus (HSV) testing. **Results:** On March 11 antemortem serum and cerebral spinal fluid were negative for rabies IgG and IgM antibodies by indirect fluorescent antibody testing (IFA) at CDC, and saliva and tissue biopsy were negative by RT-PCR. On March 17, rabies rapid fluorescent focus inhibition tests (RFFIT) were negative on all antemortem samples. Postmortem brain samples were negative for rabies by direct fluorescent antibody (DFA) test and RT-PCR. Postmortem tissue biopsy was positive by RT-PCR for HSV-1 and negative for HSV-2. **Conclusions:** Given the patient's clinical presentation, the medical team's thorough rule out of other causes, and her potential for exposure, rabies was at the top of the list of differential diagnoses. Results of ante- and postmortem testing confirmed HSV-1 infection and ruled out rabies infection. Despite a classic clinical picture for human rabies infection, it is important to always consider other agents in patients with a progressive infectious encephalitis.

Board 158. Genome Sequence of Akhmeta Virus, an Early Divergent Old World Orthopoxvirus

J. Gao[1], C. Gigante[1], P. Liu[2], K. Wilkins[1], K. Zhao[1], W. Davidson[1], E. Khmaladze[3], D. Carroll[1], G. Emerson[1], Y. Li[1]
[1]Poxvirus and Rabies Branch, Division of High-Consequence Pathogens and Pathology, Centers of Diseases Control and Prevention, Atlanta, GA, USA, [2]Emory University, Atlanta, GA, USA, [3]National Center for Disease Control and Public Health, Tbilisi, Georgia

Background: An outbreak of human cowpox-like case was investigated in Akhmeta in Georgia (the country) and viruses (AKMV_Akhm13-85 and -88) were recovered from two human patients. An additional virus (AKMV_Vani10) was identified near Vani in a retrospective screening of negative cutaneous anthrax samples. Phylogenetic analysis has revealed the three viruses form a new species in the genus of *Orthopoxvirus.* **Methods:** The genome sequences of the three viruses was determined using Illumina next generation DNA sequencing, and whole genome sequence comparison were conducted between AKMV and other OPXVs. **Results:** The AKMV genome is similar in genomic content and structure to that of cowpox virus (CPXV), but we observed lower sequence identity between AKMV and Old World OPXVs than between other known species of Old World OPXV. AKMV isolates formed a clade in the OPXV phylogeny, yet the sequence variability between AKMV isolates was higher than that between MPXV Congo basin and West African strains. An AKMV isolate from Vani contained a 7 kb sequence in the left terminal region that shared higher similarity with CPXV than with other AKMV isolates, while the rest of the genome was most similar to AKMV, suggesting recombination between AKMV and CPXV in a region containing several host range/virulence

genes. Mapping of the known CPXV host range factors to AKMV genome suggested that AKMV is likely to infect a wide range of animals. **Conclusions:** This work provides a foundation for further study of AKMV virulence and of poxvirus evolution.

Board 159. Behaviors of High-Risk Individuals in the Bushmeat Value Chain in the Democratic Republic of the Congo: Suggestions for Behavioral Interventions

K. Saylors[1], C. Clary[1], E. Obel[2], K. Reggiana[2], A. Lucas[1], P. Mbala[2]
[1]Metabiota, San Francisco, CA, USA, [2]Metabiota, Kinshasa, Democratic Republic of the Congo

Background: Eighty percent of newly identified human pathogen species are associated with animal reservoirs. Bushmeat hunting has played a role in emerging infectious diseases, including Ebola, HIV, and Marburg, yet behavioral risk and disease exposure practices of individuals who work in human-animal interfaces are not well characterized. We analyzed behaviors of individuals with close contact with animals to identify attitudes, beliefs and practices that could lead to zoonotic spillover. **Methods:** In the context of USAID PREDICT-2 human behavioral surveillance, we conducted 166 open-ended interviews and 10 focus groups across two sites in the Democratic Republic of the Congo: Kinshasa and Buta. All individuals interviewed reported consistent high-risk contact with animals, performing roles of hunting, trapping, slaughtering or butchering animals. All interviews were thematically coded using the program Dedoose. **Results:** Most interviewed individuals did not understand disease transmission dynamics or how individuals contract zoonotic diseases; many believed in divine etiology, that God determines who falls ill, rather than any exposure or transmission causality. The majority did not believe that manipulating bushmeat was risky. Several participants indicated that Ebola was caused by witchcraft. Most individuals expressed a lack of concern over contact with wild animal meat or blood; hunting is not considered a dangerous activity, but rather a traditional way of life. Despite frequent contact with animals, most individuals do not use personal protective equipment. **Conclusions:** PREDICT is examining the behavioral dimension of the animal value chain in the Democratic Republic of the Congo, particularly in bushmeat markets, with a focus on exploring potential interventions that could directly reduce risk of emerging pandemic threats. Interventions that reduce human contact with animal meat and blood could help decrease the likelihood of diseases transmission. Potential interventions include educational campaigns about zoonotic disease transmission, personal protective equipment, proper wound management, and diversifying protein sources. Iterative discussions with communities to explore feasible strategies are ongoing.

Board 160. Outbreak of Monkeypox in the Likouala Department, Republic of Congo, 2017

B. Petersen[1], R. Doshi[1], S. Guagliardo[1], A. Dzabatou-Babeaux[2], E. Pukuta[3], J. Burgado[1], M. Townsend[1], S. Panayampalli[1], V. Olson[1], A. McCollum[1], M. Reynolds[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Ministry of Health, Brazzaville, Congo, [3]Institut Nationale de Recherche Biomedicale, Kinshasa, Democratic Republic of the Congo

Background: Monkeypox (MPX) is caused by a zoonotic *Orthopoxvirus* with a clinical presentation similar to smallpox. Humans can acquire the virus through direct contact with infected animals or patients. MPX has been reported in the Republic of Congo in 2003 and 2009. In January 2017, laboratory-confirmed cases of MPX were reported in the Likouala Department, Republic of Congo, prompting an outbreak investigation. **Methods:** Between March 22 and 29, 2017, 38 suspect cases were investigated (defined as a case in any person with a history of fever and a vesicular–pustular rash and at least one of the following three characteristics: 1) rash on the palms and soles, 2) lymphadenopathy, and/or 3) fever preceding rash). Individuals were asked to provide demographic and animal exposure information for the month preceding illness onset. Vesicular and crust specimens were collected from lesions and tested for MPX virus and varicella zoster virus (VZV) DNA signatures by polymerase chain reaction (PCR) at the Institut Nationale de Recherche Biomedicale (INRB) in Kinshasa, Democratic Republic of Congo. Dried blood spots were collected by finger-stick on Nobuto blood filter strips; serological testing for *Orthopoxvirus* IgG and IgM antibodies was conducted at the CDC Poxvirus Laboratory, Atlanta, GA. **Results:** The median age among the 38 suspect cases was 12 years (interquartile range: 5-23) and 22 (59.5%) were female. Among the Likoula districts, Dongou reported 13 (34.2%) of suspect cases; 16 (42.1%) in Betou; 4 (10.4%) in Enyelle; and 5 (13.1%) in Impfondo. Among the 36 (94.7%) suspect cases that were IgG positive, 22 (57.9%) were IgM positive; of those IgM positive, 14 (63.6%) were Bahama pygmies. One of the two specimens tested at the INRB were PCR MPX-positive and 1 was VZV PCR-positive. No epidemiologic linkages were found across Likouala districts. **Conclusions:** Current data suggest the occurrence of distinct zoonotic events in each district. Inconsistent and incomplete reporting make it difficult to determine to the background rate of disease in Likouala. Implementation of a surveillance program modeled off other MPX endemic countries could be useful to determine the scale of this outbreak and endemic disease.

Board 161. Epidemiology and Molecular Characterization of Group A Rotavirus from Rhesus Macaques (*Macaca mulatta)* at Wildlife-Human Interfaces in Bangladesh

A. Islam[1], M. Hossain[2], M. Rostal[1], S. Mukharjee[2], N. Haider[2], M. Rahman[2], P. Daszak[1], M. Rahman[2], J. Epstein[1]
[1]EcoHealth Alliance, New York, NY, USA, [2]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh

Background: Rotavirus A (RVA) is an important cause of diarrhea in humans and numerous animal species globally. Animal-to-human interspecies transmission is one of the evolutionary mechanisms driving rotavirus strain diversity in humans. This study aims to detect and characterize RVA in rhesus macaques (*Macaca mulatta*) at wildlife-human interface in Bangladesh. **Methods:** Fecal samples (N=454) were collected from apparently healthy wild rhesus macaques from eight different areas of Bangladesh between February to March 2013. The samples were tested by one-step RT-PCR followed by nucleotide sequencing. **Results:** Four percent of samples (95% CI 2-7%) were positive for RVA. Age, sex, and habitat type had no significant effect on the presence of RVA in macaques. RVA positive samples were further genotyped by four structural proteins, VP1, VP4 (P genotype). Only 7 (35%) samples were able to be genotyped and G3, G10, P[3] and P[15] were identified. G3 was most prevalent (6/7; 86%; 95%CI: 42-99%) followed by G10 (1/7; 14%; 95%CI: 0.3-58); these were associated with VP4 as follows: G3P[3], G3P[15], and G10P[15].The phylogenetic analysis revealed a close relationship between the identified

strains with known human and animal strains from various countries, including Bangladesh. **Conclusions:** To our knowledge this is the first report of the detection and characterization of rotaviruses in rhesus macaques in Bangladesh. Data generated from this study will add crucial information on the prevalence of rotavirus in urban rhesus macaques and the phylogenetic distribution of RVA in the country. This study indicates there is likely viral sharing of RVA between humans and macaques in Bangladesh.

Board 162. Establishing New Protocol for Field Collection of Rodents for Disease Surveillance in the Country of Georgia

I. Sikharulidze, D. Putkaradze, M. Shavishvili, P. Imnadze, G. Babuadze, G. Chakhunashvili
National Center for Disease Control and Public Health, Tbilisi, Georgia

Background: Rodent-borne diseases pose a major public health threat to many military and civilian populations around the world. Personnel working in agriculture and those living in close proximity with livestock and other large animals are especially vulnerable to rodent-borne diseases since the rodents often seek food and shelter in and around animal feeding and bedding areas. In addition, these same rodents and other small mammals serve as hosts for a number of mite, flea, and tick species linked to other zoonotic diseases. The primary goal of this protocol is the collection of rodents for disease surveillance, not the test of a statistic hypothesis. The descriptive analysis will be performed to report data statistics and distribution. **Methods:** The field collection protocol determined the presence of diseases associated with wild rodents in the country of Georgia. Wild rodents were trapped, anesthetized, and humanely euthanized, and tissues were harvested for the purpose of establishing a baseline of diseases carried in rodent populations from different locations across Georgia. **Results:** All research and sample collections were conducted in accordance with United States federal laws in accordance with Georgia's laws, regulations, and policies. Using new approach for field work is based on international regulations, using high biosafety and biosecurity procedures, less harmless for the small mammals and coverage of the habitat more complete than using previous approach. **Conclusions:** Identifying and understanding the epidemiology of rodent-borne and associated ectoparasitic diseases is important for developing disease mitigation strategies. The first requirement is knowledge of the many ecological factors that affect small mammal population densities and how that knowledge relates to rodent infection rates. A second requirement is an understanding of how those rodent-borne pathogens are potentially transmitted to humans, particularly how human behaviors, activities, and land-use modifications increase the risk for exposure to the rodents and the diseases they may carry. The end result of this new animal protocol is to conduct rodent and rodent-borne disease surveillance in Georgia under the One Health concept.

Board 163. Study of Tularemia Prevalence in Commensal Rats from the Country of Georgia

V. Chitiashvili, T. Giorgadze, M. Shavishvili, L. Malania, P. Imnadze
National Center for Disease Control and Public Health, Tbilisi, Georgia

Background: *Francisella* spp. cause zoonotic infections and present in glandular, ulceroglandular, oculoglandular, oropharyngeal, and pneumonic forms with significant morbidity. *F. tularensis* is considered to be a biological threat agent that poses a substantial risk to public health. Mammals transmit the bacterium to humans directly through bites and scratches as well as through arthropod vectors and contamination of water and food sources. The disease is considered to be endemic for Georgia within a few focal areas. Small and large outbreaks are periodically reported (Velidjanashvili I, 1992; Sakvarelidze LA, et al, 1983; Chitadze N, et al, 2009). The goal of this study was to identify *Francisella tularensis* among commensal rats in different urban areas of the country. **Methods:** During 2016-2017 from 25 different cities in the country, 280 rats were trapped (*Rattus norvegicus; Rattus rattus*) from 115 different sites. Tissue samples were collected from all rats and investigated for the presence of *Francisella tularensis.* For the laboratory study was applied bacteriological investigation – culturing the tissue samples to obtain bacterial growth with further biochemical characterization. **Results:** Out of 280 collected rat samples, 165 cases were studied by bacteriological methods and none of them gave typical bacterial growth. 115 tissue samples still are under investigation. **Conclusions:** Zoonotic bacterial pathogens associated with the genus *Rattus* cause significant human morbidity and mortality. The urban environment provides an optimal opportunity for rodent-borne zoonosis with close contact between rodents, people, and other animals, facilitating disease transmission. After finishing the study we will have important data on the risk factors of zoonotic pathogens associated with synanthropic rodents indoors.

Board 164. Assessing Viral Diversity in Rodents and Shrews in Bangladesh

A. Islam[1], M. Rahman[2], M. Hossain[2], M. Rostal[1], E. Hagan[1], A. Islam[2], N. Haider[2], S. Anthony[3], P. Daszak[1], J. Epstein[1]
[1]EcoHealth Alliance, New York, NY, USA, [2]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [3]Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, NY, USA

Background: Rodents and shrews live in close proximity to humans and have been identified as important hosts of zoonotic pathogens. The Emerging Pandemic Threats: PREDICT project aims to identify novel zoonotic viruses in rodents, shrews and other key wildlife groups that have a high degree of contact with people and domestic animals. **Methods:** Rectal and throat swab samples collected from 427 rodents and shrews from 10 districts in Bangladesh between June 2011 and October 2013. Samples were screened for 10 viral families (adenoviruses, arenaviruses, astroviruses, bunyaviruses, coronaviruses, flaviviruses, hantaviruses, influenzas, paramyxoviruses, and rhabdoviruses) using consensus PCR and sequencing to confirm positive. **Results:** A BLASTN search and clade analysis revealed 52 viruses including five influenza A, 45 novel adenoviruses, one novel mamastrovirus and one novel West Nile virus strain. Influenza-A was present in 1.3% (n=150, 95%CI: 0.4-5.7) of *Suncus murinus*; 4.6% (n=22; 95%CI: 0.1-22.8) of *Mus musculus* and 2.2% (n=90; 95% CI 0.3-7.8) of *Rattus rattus*. Novel adenoviruses were present in 6% (n=150, 95% CI: 2.8-11.1) of *S. murinus*; 15.8% (n=76; 95%CI: 8.4-25.9%) of *Bandicota bengalensis*, 11.4% (n=9; 95%CI: 34-20.5%) of *B. indica* and 16.7% (n=15; 95%CI: 9.6-26.0) of *R. rattus*. The novel mamastrovirus and the novel West Nile were identified in *B. bengalensis* and *R. rattus*, respectively. **Conclusions:** These findings represent the first description of viral diversity in rodent and shrews in Bangladesh and form a basis for understanding the types of viruses circulating among small mammals. Additional genomic and experimental studies are required to ascertain the zoonotic potential of novel viruses.

Board 165. Two Case Examples Illustrating the One Health Approach to Identify Emerging Tick-Borne Diseases

J. Sidge[1], E. Foster[1], J. Tsao[2], M. Stobierski[1]
[1]Michigan Department of Health and Human Services, Lansing, MI, USA, [2]Michigan State University, East Lansing, MI, USA

Background: With six out of every ten infectious diseases in humans being spread from animals, and emerging diseases continually on the rise across the nation, a One Health approach to combat these diseases is critical. Lyme disease, which is caused by *Borrelia burgdorferi*-infected *Ixodes scapularis* ticks, is the most common vector-borne disease in the United States affecting both humans and companion animals. We present two tick-borne case examples illustrating the importance of One Health. **Methods:** In 2016, Michigan Department of Health and Human Services (MDHHS) received a report of a human Lyme carditis case and in 2017, MDHHS received a report of a canine anaplasmosis case. Both of these cases involved no travel history and the counties of residence were not known to have established populations of *Ixodes scapularis* ticks. Following these reports, MDHHS and university partners performed ecological follow-up both years, consisting of rodent trapping and dragging for questing ticks in and around the patients' homes. **Results:** In 2016, established populations of *Borrelia burgdorferi*-infected *Ixodes scapularis* ticks and infected small mammals were found at the case-patient's home and at a nearby state recreation area. Following ecological follow-up in 2017, white-footed mice (*Peromyscus leucopus*) were found to be infected with *Anaplasma phagocytophilum* near the canine patient's home. **Conclusions:** Both cases provide support that tick-borne diseases may be circulating among ticks and small rodent hosts, posing a risk for both people and canines in counties that were previously not known to have established *Ixodes scapularis* tick populations. Without the collaboration amongst human physicians, veterinarians, and the subsequent environmental sampling, these results would not be possible, illustrating the importance of the One Health approach when combating emerging infectious diseases.

Board 166. Characterization of Multiple Rift Valley Fever Virus Re-emergence Events in Uganda, 2017-8

T. Shoemaker[1], S. Balinandi[2], L. Nyakarahuka[2], A. Tumusiime[2], S. Mulei[2], J. Kyondo[2], B. Lubwama[3], R. Metras[4,5], S. Zufan[1], S. Whitmer[1], J. Klena[1], P. Rollin[1], S. Nichol[1], J. Lutwama[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uganda Virus Research Institute, Entebbe, Uganda, [3]Uganda Ministry of Health, Kampala, Uganda, [4]CIRAD, UMR ASTRE, Montpellier, France, [5]ASTRE, Univ Montpellier, CIRAD, INRA, Montpellier, France

Background: In March 2016, an outbreak of Rift Valley fever virus (RVFV) was confirmed in Kabale district, southwestern Uganda. This represented the first reported laboratory-confirmed human cases in Uganda since 1968. Since then, an additional 6 acute RVFV cases have been identified throughout the country in November 2017, with 5 cases being fatal. As part of UVRI and CDC's ongoing Viral Hemorrhagic fever program, expanded RVFV activities were initiated to identify incident human cases and identify risk factors associated with RVFV re-emergence in Uganda. **Methods:** Enhanced VHF surveillance and raising public awareness for RVFV in human and animal health sectors was initiated. Educational and informational materials were developed to heighten awareness and efforts directed to all districts through the Uganda MOH National Task Force. In addition, a cross sectional serosurvey combined with a multi-year longitudinal surveillance study of RVFV in animal herds was developed. An analysis of historical seroprevalence, spatial, environmental, and meteorological metadata is currently underway to identify areas at higher risk of RVFV occurrence and inform risk-based surveillance activities. **Results:** In the affected districts, 12% of livestock were found seropositive for RVF IgG, suggesting RVFV circulation. Full genome phylogenetic analysis from 3 of the human RVFV isolates shows the strains group closely with the Kabale 2016 RVFV isolates and all are related to the 2006-7 RVFV epizootic Kenya-2 lineage. Analysis of national livestock cross-sectional serology, environmental, and meteorological data from these affected districts is underway to identify risk factors for recent RVFV emergence in Uganda. **Conclusions:** Our findings from 2016 combined with these recent RVFV cases suggest active circulation of RVFV throughout Uganda. Our analysis of serological and genetic data also suggests RVFV may have been circulating undetected for many years and possibly introduced during the 2006-07 East Africa epizootic. Recent emergence may be due to environmental conditions or other unknown risk factors. Results from our ongoing risk factor analysis may help identify causes for RVFV emergence and identify areas at greatest risk in order to target surveillance and risk reduction interventions and education.

Board 167. Molecular Characterization of Ulceroglandular Tularemia Cases in Slovenia

M. Korva[1], U. Glinšek Biškup[1], R. Kogoj[1], T. Rojko[2], F. Strle[2], T. Avšič Županc[1]
[1]University of Ljubljana, Faculty of Medicine, Institute of Microbiology and Immunology, Ljubljana, Slovenia, [2]Department of Infectious Diseases, University Medical Centre Ljubljana, Ljubljana, Slovenia

Background: Tularemia is a zoonotic infection caused by the gram-negative facultative intracellular bacterium *Francisella tularensis*. It has a broad geographical distribution with sporadic cases and/or out-breaks occurring in many European countries. Slovenia is situated in Central Europe and has only rare and sporadic cases of tularemia. In the last 20 years up to 2 cases per year were reported. However, between 2012 and 2013 six patients with the ulceroglandular form of tularemia were recognised in the same town. Epidemiological data indicated transmission by a tick bite in 50 % of patients. In Slovenia, *I. ricinus* is the most prevalent species of ixodid ticks in the central part of the country. *D. reticulatus* is present only in the north-eastern part of Slovenia, where before 2012 most of tularemia cases were reported. Thus, the aim of the study was an investigation of genetic diversity of tularemia in Slovenian patients. **Methods:** In a ten year period (2007-2017) 38 patients were treated in Slovenia. In all patients the clinical diagnosis was confirmed with either serology and/or real time PCR. For molecular characterization of PCR positive samples a multilocus variable-number tandem-repeat analysis (MLVA) on 6 markers was performed. Additionally, from 1 patient *F. tularensis* was cultured in the BSL-3 laboratory and whole genome (WGS) was sequenced. **Results:** *F. tularensis* was cultured from lymph node aspirate on chocolate agar and colonies were observed after 3 days (very small, light grey, reflective, soft and easily emulsified colonies). Phylogenetic analysis based on WGS confirmed that isolated strain belonged to subspecies *holarctica*. By using the whole genome comparisons for single nucleotide polymorphism (canSNP) analysis our isolate clustered into type B27A MLVA revealed 4 unique subtypes, with all mutations present

only in 2 locuses (Ft-M03, Ft-M06), which are representing the most rapidly mutating markers. **Conclusions:** With molecular characterization we have confirmed that all clinical cases resulted from the infection with *F. tularensis* subs. *holartica*. In comparison to neighbouring countries, Slovenian tularemia strains showed low genetic diversity which most probably corresponds to localized disease clusters. But not all 6 case-patients from the same town shared the same MLVA subtype, which might suggest different possible reservoirs.

Board 168. Bat Hunting: Risk of Disease Emergence at Thriving Ecosystem Interface in Bangladesh

A. Islam[1], S. Shano[1], E. Hagan[1], B. Watson[1], M. Rostal[1], M. Hussain[3], M. Rahman[3], M. Flora[3], L. Francisco[1], J. Epstein[1], P. Daszak[1]
[1]EcoHealth Alliance, New York, NY, USA, [3]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh

Background: Hunting and butchering of wild animals may cause the transmission of zoonotic diseases to humans. Our understanding of the underlying causes of hunting, trading, and consumption of wildlife at the community level in Bangladesh is limited. **Methods:** This qualitative study proposes to understand hunting behavior, wildlife consumption patterns, and the wildlife value chain assessing the risk of zoonotic disease transmission in Faridpur communities. Participant observation and 15 targeted ethnographic interviews were conducted between October-December 2015. Participants included wildlife hunters, collectors, transporters, vendors, and consumers. **Results:** The studied "Sharder" community people hunt wild animals as their traditional practice and key protein source. This community is dependent on various sources of income, including: day labor, potter, barber, and cobbler. Hunting provides an additional source of income in the community. Hunters are mostly illiterate and unaware of zoonotic disease risks, such as Nipah from large fruit bats (*Pteropus medius*). None of the hunters use protective equipment during hunting and butchering. Men were involved in hunting whereas women were primarily involved in butchering. Sometimes children handled and played with hunted bats. The wild animal value chain is centered in Sharder communities, though some neighboring Muslim communities reported hunting wild animals as a free protein source. Participants were observed using bat bones to remedy joint pain and asthma. Hunters reported declining local bat populations due to over-hunting and ecological changes. A shared human and animal dependence on limited natural resources amplified biodiversity declines, however to be successful communities need sustainable alternative livelihoods solutions and protein sources **Conclusions:** Unprotected hunting practices and limited or no hygienic measures can yield greater risk of zoonotic disease spillover. Hunting and interaction with flying foxes in Bangladesh may represent a previously unrecognized pathway for Nipah emergence. The dearth of disease transmission knowledge posed by wildlife may facilitate zoonotic spillover.

Board 169. Serological Detection of *Pteropine orthoreovirus* in Singapore

A. Uehara, C. Tan, S. Mani, D. Anderson, L. Wang
Duke-NUS Medical School, Singapore, Singapore

Background: *Pteropine orthoreovirus* (PRV) is a member of the *Reoviridae* family and is known to cause respiratory and gastrointestinal complications in humans. First isolated from Australian bats in 1968, seroprevalence in humans of 4.4-13% have been reported in a number of Southeast Asian countries. Numerous reports of PRV exposure across the region suggest continuous spillover events are occurring between bats and humans. To our knowledge, no cases of PRV-related spillover events have been reported in Singapore. In lieu of using enzyme-linked immunosorbent assay (ELISA), we adopted the Luciferase Immunoprecipitation System (LIPS) – a previously reported antibody detection method that utilizes crude lysate and requires minimal sera input. **Methods:** Following previously published methodology, we generated LIPS constructs against two strains of PRV and screened a cohort of patients with febrile illness in Singapore. Convalescent samples were initially screened with pooled PRV constructs, and later constructs were deconvoluted for subsequent LIPS screen across different time points. Secondary confirmation was conducted through sera neutralization tests on samples with high LIPS values. **Results:** 856 samples were initially screened with pooled LIPS constructs. Further LIPS testing with deconvoluted constructs across different time points yielded 16 samples positive for PRV. Of the 16 individuals screened, seven displayed neutralizing antibody titers against PRV3M (also commonly known as Melaka virus). **Conclusions:** The current febrile cohort provided an opportunity to determine the seroprevalence of PRV in Singapore, albeit in a select population. Patients enrolled in the cohort presented with febrile illness, while PRV is known to cause respiratory and gastrointestinal symptoms, hence our findings are likely an underrepresentation of the PRV seropositivity in Singapore. We demonstrate that LIPS is an appropriate tool for rapid detection of antibodies with high level of sensitivity. Although ELISAs remain to be the gold standard in serology, LIPS provides a rapid alternative that negates the need for protein purification. This is especially crucial for pathogens that do not have well-established serological assays. Additionally, as the LIPS assay does not require a secondary antibody for detection, the same assay can be used for surveillance of zoonotic infections in both human and animal samples.

Board 170. Aquatic Animal-Inflicted Envenoming Injuries: Common Culprits and Emerging Pathogens

J. Diaz
Louisiana State University Health Sciences Center, New Orleans, LA, USA

Background: Marine envenoming stings, most commonly by jellyfish, occur frequently. Second only to jellyfish stings are lacerating stings caused by stingrays. Following stingray injuries, penetrating injuries caused by venomous fish of the Family Scorpaenidae are the next most common causes of aquatic animal-inflicted injuries. Although many species of bacteria have been isolated from aquatic animal-inflicted injuries sustained in salt and freshwater ecosystems, a small number of emerging, aquatic bacterial species cause skin, soft tissue, and invasive infections. **Methods:** An Internet-based analysis of published articles meeting the case definitions of stingray and Scorpaenidae injuries was conducted to describe the epidemiology, mechanisms of envenoming, and manifestations of stingray and Scorpaenidae injuries and to recommend management and prevention strategies. A stingray injury was defined as a penetrating injury inflicted by a stingray barb. Similar methods described the epidemiology, presenting clinical manifestations, diagnostic and treatment strategies, and outcomes of the superficial and deeper skin and soft tissue infections stratified by causative bacterial pathogens characterized as commonly encountered or newly emerging. **Results:** The presenting clinical manifestations of impetigo, erysipelas, cellulitis, pyodermas, or necrotizing soft tissue infections

will determine initial empiric antibiotic therapy. With the exception of minor wounds demonstrating localized cellulitis or erysipeloid-type reactions, most other aquatic infections, all gram-negative infections, and mycobacterial infections will demonstrate antibiotic resistances, especially to penicillins, and require therapy with susceptible antibiotic combinations. **Conclusions:** Clinicians should maintain high indices of suspicion for potentially catastrophic bacterial infections following marine injuries and exposures, especially *Vibrio vulnificus* in the Gulf of Mexico, *Chromobacterium violaceum* in the Western Pacific, and *Shewanella* infections in the Mediterranean and Western Pacific.

Waterborne Infections

Board 171. Characterizing Multiple Spatial Waves of the 1991-1997 Cholera Epidemic in Peru

N. Sterrett[1], O. Mujica[2], C. Munayco[3], C. Viboud[4], G. Chowell[1]
[1]School of Public Health, Georgia State University, Atlanta, GA, USA, [2]Pan American Health Organization, Washington DC, USA, [3]Centro Nacional de Epidemiología, Prevención y Control de Enfermedades, Lima, Peru, [4]Division of International Epidemiology and Population Studies, Fogarty International Center, National Institutes of Health, Bethesda, MD, USA

Background: Due to a lack of sanitary infrastructure and a highly susceptible population, Peru experienced a historic outbreak of *Vibrio cholerae* O1 that began in 1991 and generated multiple waves of disease for several years. Though case-fatality was low, the epidemic put massive strain on healthcare and governmental resources. Here we explore the transmission dynamics and spatiotemporal variation of cholera in Peru using mathematical models and statistical analyses that account for environmental conditions favoring the persistence of bacteria in the environment. **Methods:** The authors use dynamic transmission models that incorporate seasonal variation in temperature, concentration of vibrios in the environment, as well as separate human and environmental transmission pathways. The model is fit to weekly department level data obtained from the cholera surveillance system in Peru. The authors also assess the spatial patterns of cholera transmission and correlations between case incidence, time of epidemic onset, and department level variables. Basic reproduction numbers are compared across departments. **Results:** Our findings indicate that the epidemic first hit the coastal departments of Peru and later spread through the highlands and jungle regions. There is high seasonal variation in case incidence, with three clear waves of transmission corresponding to the warm seasons in Peru. Department level variables such as population size and elevation also played a role in transmission patterns. Finally, basic reproduction numbers most often ranged from one to eleven depending on department and time of year. Lima had the largest reproduction number, likely due to its population density and proximity to the coast. **Conclusions:** Incorporating environmental variables into an epidemic model predicts the multiple waves of transmission characteristic of *V. cholerae*, and effectively differentiates transmission patterns by geographic region even in the absence of unique parameter estimates. Mathematical models can provide valuable information about transmission patterns and should continue to be used to inform public health decision making.

Board 172. Assessing the Knowledge, Attitudes, and Practices Regarding Cholera Preparedness and Prevention in Owerri, South East Nigeria

P. Chinedu-Eleonu, C. Onyeneke
Imo State University, Owerri, Nigeria

Background: Background of the Study: The study assessed the knowledge, attitudes and practices of cholera prevention and preparedness in Naze community, Owerri, South East Nigeria. **Methods:** The survey research design was adopted for the study. The researcher collected data using a two-pronged method, namely structured questionnaire (open and closed-ended questions) to assess knowledge and attitudes about cholera, and observations to assess practices in the prevention and management of the disease. Additionally, the researcher took pictures with the respondents' permission. Eighty-four respondents were randomly selected and administered the questionnaire with a return rate of 96%. **Results:** Most of the respondents (92%) indicated they knew how cholera was contracted (86%), indicating water contamination as a source. Eighty-eight percent (88%) of the respondents indicated they knew how to prevent contracting cholera. All the respondents generally knew that cholera could be treated with medicine received at the community health center or health workers. Fewer respondents (42%) had specific knowledge such as the use of oral rehydration solutions. The researcher observed that the respondents' high level of prevention practices could be biased. The researchers discovered that many practices were not adhered to, such as not washing hands, not using toilet paper, and dropping waste in respondents' premises. **Conclusions:** The researcher concluded that Naze community had not reached a stage of adequate cholera prevention and preparedness in spite of their awareness of cholera risks and risk-reduction strategies.

Board 173. Case Management and Clinical Outcomes during an Outbreak of Typhoid Fever—Harare, Zimbabwe, October-December, 2017

J. Strysko[1], M. Vere[2], K. Masunda[2], C. Duri[2], R. Aubert[1], W. Davis[1], H. N'Cho[1], J. McAteer[1], P. Manangazira[3], E. Mintz[1], G. Mhlanga[3], E. Gorove[4], L. Chawira[4], B. Tippett Barr[5], G. Appiah[1]
[1]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]City of Harare Health Services, Harare, Zimbabwe, [3]Epidemiology and Control, Ministry of Health and Child Care, Harare, Zimbabwe, [4]Beatrice Road Infectious Disease Hospital Laboratory, City of Harare Health Services, Harare, Zimbabwe, [5]Division of Global HIV & TB, Centers for Disease Control and Prevention, Harare, Zimbabwe

Background: Typhoid fever is a potentially fatal illness caused by *Salmonella enterica* serovar Typhi (Typhi). In October 2017, a typhoid outbreak was detected in the Mbare suburb of Harare, Zimbabwe and high rates of ciprofloxacin-resistant Typhi were reported in the Kuwadzana suburb, prompting public health officials to recommend 3rd-generation cephalosporins as first-line treatment for residents of Kuwadzana. **Methods:** We reviewed Harare City Health Department surveillance data, hospital laboratory microbiology results, and medical records of patients with suspected typhoid fever admitted to Harare's typhoid treatment unit (TTU) and referral center between 1 October – 31 December 2017. Suspected cases had fever and ≥ 1 symptom: malaise, headache, vomiting, diarrhea, constipation, or cough. Confirmed cases had Typhi cultured from blood, stool, or rectal swabs. Antibiotic susceptibility testing performed by disc diffusion was inter-

preted using CLSI standards. We compared complication rates and illness durations using Fisher's exact χ^2 and Wilcoxon signed-rank tests. **Results:** During the study period, 2,026 suspected and 146 confirmed typhoid fever cases were reported in Harare. The TTU admitted 583 patients (29% hospitalization rate) and referred 36 for advanced care. Median age of inpatients was 20 years (5 months - 87 years); 55% were male; most resided in Mbare (45%) or Kuwadzana (12%). Inpatients received ciprofloxacin (70%), a cephalosporin (3%) or both (19%). Median length of stay was 2 days (0-36). Complications were reported in 79 (14%) inpatients, the most common being acute kidney injury (26), anemia (10), peritonitis (9) and deranged electrolytes (9). One patient had intestinal perforation and 5 patients died (none culture-confirmed). Cultures were processed for 286 inpatients; 74 (26%) yielded Typhi; 15 (33%) of 46 isolates tested were ciprofloxacin-resistant. Complication rates (19% vs 9%, p=0.26) and median illness duration (9 vs 7 days, p=0.15) were greater in patients with ciprofloxacin-resistant isolates. **Conclusions:** In a large typhoid outbreak in Zimbabwe, 33% of isolates from hospitalized patients were ciprofloxacin-resistant. Patients with resistant strains tended to have longer illness duration and higher rates of complications, but these differences did not reach statistical significance on univariate analysis.

Board 174. Etiologic Agents of Diarrhea in Vientiane Capital, Lao People's Democratic Republic

S. Houatthongkham
Ministry of Health, Lao PDR, Vientiane Capital, Lao People's Democratic Republic

Background: In Lao People's Democratic Republic (Lao PDR), 11% of deaths in children younger than five years of age are caused by diarrhea. There have been a limited number of studies on the etiologic agents of diarrhea in Lao PDR. **Methods:** In 2012, the National Center for Laboratory and Epidemiology started a project to collect clinical data and specimens (stools and rectal swabs) to perform microbiological examinations on patients with diarrhea who were hospitalized at eight diarrhea sentinel surveillance sites in Vientiane Capital. We retrospectively reviewed data from 2012 to 2015 (n=2,482). All patients were tested for bacteria, and children aged five years or younger were additionally tested for rotavirus during the winter season (November to April). **Results:** Those aged 1–5 years were 947 (38.0%). Of the 2,482 cases, at least one entero-pathogen was detected in 17.8% (441 cases). *Salmonella* spp. was the most commonly detected bacterial pathogen. Enteropathogenic *E.*coli (EPEC) and *Salmonella* spp. were the most commonly detected pathogens in the dry winter season and the wet rainy season, respectively. In terms of multiple entero-pathogens, rotavirus with bacterial pathogens was found most often. In 913 children, rotavirus was found in 39.1% (291 children). Bacterial pathogens were consistently found throughout the year and most frequently found during the dry winter season, with a peak in detection rate in February. **Conclusions:** *Salmonella* spp. was the predominant bacterial pathogen for single bacterial infection in individuals of all age groups, and rotavirus was most commonly involved in mixed infections among children who were five years old or younger. A further study examining other types of pathogens for diarrhea should be conducted in other provinces in Lao PDR in the future.

Board 175. Acute Gastroenteritis Outbreak in Union Council Neemargh, District Kalat, Pakistan, 2017

S. Riaz, A. Saeed
Field Epidemiology and Laboratory Training Program, Quetta, Pakistan

Background: On 6th July 2017, District Health Officer (DHO) Kalat reported 116 suspected cases of acute gastroenteritis from Union Council Neemargh to Provincial disease surveillance and response unit Quetta and requested for investigation. A team was deployed to the affected area to confirm outbreak, evaluate risk factors, and recommend control measures on 7th July 2017. **Methods:** A case was defined as sudden onset of 3 or more episodes of loose stools per day with or without vomiting in a resident of UC Neemargh district Kalat 5th July to 11th July 2017. A descriptive study was carried out in order to identify cases, through active case finding. Medical records were also reviewed to find cases, environmental assessments were conducted, and water samples were collected for lab. **Results:** A total of 116 cases were identified (overall attack rate=1.05%). No deaths were reported. Men were more affected 57% (n=67). Mean age of case-patients was 14.7 years (range =1-40 years). All cases were clinically diagnosed as acute gastroenteritis. Diarrhea n=116 (100%), vomiting n= 101 (87%), dehydration n=96 (82%), fever n= 23 (19%), and nausea n=15 (12%) were the most frequent symptoms. Environmental assessment revealed evidence of open defecation along the stream which was the main source of water they used. Fecal coliform was isolated from water samples. **Conclusions:** Drinking water contaminated by feces was associated with this community-wide acute gastroenteritis outbreak. Health education sessions were conducted and community was informed about the preventive measures to be taken for water borne diseases in general and acute gastroenteritis in particular. We recommended rigorous disposal of patients' feces, chlorination of piped water, and drinking of boiled or treated water. The community was informed about the benefits of boiling water and how to protect water from contamination. Hand hygiene and washing particularly after using the toilet and before eating was particularly stressed during the health education sessions.

Board 176. Antibiotic Resistance Detected in *Escherichia coli* and *Klebsiella* spp. Isolates from Household Water, Food Preparation Surfaces, and Soil in Compounds in Maputo, Mozambique: Implications for Environmental Transmission Outside the Clinic

D. Berendes[1], L. Dengo-Baloi[2], D. Holcomb[3], J. Knee[4], J. Brown[4]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]MISAU: Mozambican Ministry of Health, Maputo, Mozambique, [3]University of North Carolina, Chapel Hill, NC, USA, [4]Georgia Institute of Technology, Atlanta, GA, USA

Background: Environmental conditions may be important drivers of antibiotic resistant (AR) infections, especially in low-income, pathogen-rich environments. This study examined potential AR bacteria in households in a controlled before-and-after study of a sanitation intervention in Maputo, Mozambique. **Methods:** Samples of household source and stored water, food preparation surfaces, and soil (both at the household's and its latrine's doorstep) were collected in 30 intervention and 30 control compounds one year after the intervention. Samples were cultured in mTEC broth and confirmed as *E. coli* or *Klebsiella* spp., followed by disk diffusion to assess antibiotic susceptibility. From each sample, 1-2 isolates were tested for the 12 National Anti-

biotic Resistance Monitoring System for Enteric Bacteria antibiotics of interest for *E. coli*. Following completion of AR testing in May, we will compare AR household isolates by environmental conditions (e.g. WASH infrastructure) assessed at concurrent household surveys. **Results:** To-date, 101/505 (20%) of isolates have been tested for AR, with 21 (21%) confirmed as *E. coli* and 25 (25%) as *Klebsiella* spp. Of *E. coli* isolates, 12/21 were resistant to ampicillin; including 4/5 sample types (household stored water, food preparation surfaces, and household/latrine soil). Resistance to cefoxitin, nalidixic acid, streptomycin, tetracycline, and sulfamethoxazole-trimethoprim (SXT) was also observed. Most *Klebsiella* spp. isolates (9/10) were also resistant to ampicillin, with resistance to azithromycin, gentamicin, streptomycin, tetracycline, and SXT detected as well. **Conclusions:** Although <20% of household environmental isolates have been tested, we have already observed high levels of resistance to ampicillin—a first-line drug for pediatric enteric infections—among other AR profiles. These data provide early evidence of potential environmental exposures and sources of AR bacteria in dense, low-income household settings.

Board 177. Incidence Trend and Epidemiology of Legionnaires' Disease, Delaware, 2006-2017

N. Luong, S. Nagarajan, M. Luta
Delaware Division of Public Health, Delaware Health and Social Services, Dover, DE, USA

Background: Legionnaires' disease (LD) is a severe pneumonia. The number of *Legionella*-infected cases have reportedly increased in the United States in recent years. Understanding Legionnaires' epidemiology is important for prevention and control strategies. This study was to determine the incidence trend and characterize the epidemiologic features of LD in Delaware. **Methods:** We performed a retrospective study on persons having *Legionella* infection reported to Delaware Division of Public Health's Surveillance System during January 1, 2006-December 31, 2017. The charts of 237 persons were reviewed and included in the analysis. **Results:** A total of 237 confirmed cases of LD were reported to the state health department during 2006-2017. The overall yearly incidence rate had increased by 257%, from 1.4 cases in 2006 to 3.6 cases per 100,000 population in 2017. The incidence rate increased 195% in males and 400% in females. A majority (183 cases, 77.2%) were among those ≥ 50 years. LD occurred at any time during a year, however, it increased from May through November. During the study period, Legionnaires' attack rate was higher for men compared with women (28.1 vs. 23.2 cases per 100,000 population). Cases were dominant in whites (152 cases, 64.2%) compared with blacks (64 cases, 27%), and other races (19 cases, 8%); however, the highest attack rate was seen in blacks (31.2 cases/100,000 population). The overall case fatality rate was 7.2%, 91.9% of case-patients required hospitalization, 9.7% were travel-related, and all cases were community acquired. Only 1 outbreak was detected during the study period. **Conclusions:** LD is significant and can occur at any time in Delaware. The number of diagnosed cases and geographic expansion increased significantly in recent years with a high mortality. Public education, increasing awareness among medical practitioners about LD, and adequate water management programs are essential for prevention and control of LD.

Board 178. WGS Analysis of *Legionella pneumophila* Reveal Diversity Within and Across Water Samples Over Time in a Hospital Premise Plumbing System

V. Reeb[1], B. Raphael[2], W. Hottel[3], N. Hall[1], L. DesJardin[1]
[1]State Hygienic Laboratory at the University of Iowa, Coralville, IA, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]University of Iowa College of Public Health, Iowa City, IA, USA

Background: Legionnaires' disease is a life-threatening pneumonia most often caused by *Legionella pneumophila* (Lp) serogroup 1, although other Lp serogroups and *Legionella* species can cause disease. Strain typing with WGS is an emerging tool to link a human case to the environmental source. Since *Legionella* are ubiquitous in the freshwater environment and man-made water systems, a better understanding of the genomic diversity could help inform WGS analysis schemes. In this study, we investigate diversity over time in addition to diversity within a single water sample from a hospital premise plumbing system. **Methods:** *Legionella pneumophila* isolates were collected between 2013-2017 at various locations within a hospital water system during routine surveillance. One colony per sample was sequenced. Diversity in a single water sample was determined by selection of multiple colonies per sample for four samples collected on the same day in July 2017. Isolates were confirmed as Lp by MALDI-TOF and sequenced using the Illumina MiSeq. BioNumerics v.7.5 was used for whole genome multilocus sequence typing (wgMLST). **Results:** wgMLST determined that nearly all Lp isolated at the hospital formed a cluster sharing >98.6% identical alleles. A subset of these isolates were characterized as Lp serogroup 4. Sequence Based Typing (SBT) revealed that these isolates belonged to ST378, which has previously been reported from Canada and Europe but not yet in the United States. All isolates sequenced were distributed into three distinct subclades. Time of collection and location did not seem to drive this clustering. For example, some of the locations sampled over time were represented in all three subclades. Isolates selected from a single sample were restricted to one subclade but did not form a monophyletic group. Within this group, allele similarity differed by up to 0.4%, which is equivalent to the diversity that can be found among isolates collected at different locations and times at the facility. **Conclusions:** Lp isolates appear to be closely related throughout the hospital and persistent over time, although there are subclades which will be further analyzed using SNP analysis. *Legionella* species have a relatively high genetic diversity due to their mobile elements, so we will also investigate the role of recombination on the sequence diversity observed among these isolates.

Board 179. Epidemiology of Nontuberculous Mycobacteria Notifications and Association with Drinking Water Disinfectant in Queensland, Australia

C. Coffey[1], M. Kirk[1], S. Huxley[2], G. Jackson[2]
[1]Australian National University, Canberra, Australia, [2]Queensland Health, Brisbane, Australia

Background: Nontuberculous mycobacteria (NTM) are opportunistic pathogens associated with environmental sources. NTM is a notifiable condition in Queensland, Australia and cases have increased in recent years. As NTM occur in treated drinking water supplies we mapped cases of NTM and water quality results for chloramines to identify potential sources of infection. **Methods:** We mapped the notifiable condition register to the water monitoring database. Rate ratios (RR) and 95% confidence intervals were calculated using negative

binominal regression models for comparing rates across three time periods (2002–2006, 2007–2011, 2012–2017). Water disinfectant levels per sampling points were aggregated across selected supply zones in southeast Queensland and association between NTM notifications and disinfectant levels within the supply zones assessed using Poisson regression models. **Results:** Compared to 2002–2006 (2,895 (20%)), NTM rates were significantly higher in 2007–2011 (4,946 (34%), RR 1.49, 95% CI 1.07–2.07) and 2012–2017 (6,871 (47%), RR 1.51, 95% CI 1.11–2.07). *Mycobacteria intracellulare* predominated over the time period and notifications were approximately equal between men and women. Overall, the proportion of water samples with insufficient disinfectant levels (<0.2 mg/dL) increased across supply zones in southeast Queensland, 2012–2016 (p<0.01). There was no significant association between NTM rates and water disinfectant levels across selected supply systems. Aggregating all NTM species and annual NTM and water quality data to a supply zone level may have missed trends, reduced accuracy at a lower geographical scale, and failed to account for fluctuations in water quality. **Conclusions:** Spatial patterns and significant associations may depend on the aggregation and area used for mapping. Further examination of risk factor data, specific NTM species and the spatiotemporal clustering of NTM notifications and disinfectant levels per sampling points may be useful in increasing understanding of NTM epidemiology and promoting interventions.

Board 180. Evolving Epidemiology of Reported Giardiasis Cases in the United States, 1995–2016

C. Coffey[1], K. Benedict[2], M. Kirk[1], K. Fullerton[2]
[1]Australian National University, Canberra, Australia, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Giardiasis is the most common intestinal parasitic disease of humans identified in the United States and an important infection potentially transmitted by water. Giardiasis was under standardized surveillance from 1995 to 2002, when it became nationally notifiable. The national case definition changed in 2010 to reflect changing diagnostic practices. States voluntarily report giardiasis cases to CDC and can change this requirement each year. Our objectives were to describe the evolving epidemiology of US giardiasis cases for 1995–2016 using National Notifiable Disease Surveillance System (NNDSS) data. **Methods:** We used negative binominal regression models to compare incidence rates by age (0 to 4, 5 to 24, 25 to 44, 45 to 64, and 65 and older) across three time periods (1995–2001, 2002–2009, 2010–2016) over the study period. We present incidence rate ratios (IRR) and 95% confidence intervals. **Results:** During 1995–2016, the average number of reported cases were 18,887 per year (range: 14,624–27,446 cases). Compared to 1995–2001, incidence rates were lower in 2002–2009 and 2010–2016 across all age groups. The smallest decrease from the referent period was seen amongst cases aged 45 to 64 in 2002 to 2009 (IRR 0.89 [0.85-0.94]) and the largest decrease from the referent period was seen amongst cases aged 0 to 4 (IRR 0.36 [0.33-0.39]) in 2010 to 2016. **Conclusions:** The incidence of reported giardiasis in the United States is decreasing. This decrease differs by age group and may reflect either changes in surveillance methods (e.g., changes in case definitions or changes in reporting practices of states to CDC) or differences in exposures by age group. Incidence rates in older age group have not decreased as much as incidence rates in children, suggesting that differences in exposures and immunity by age group are important to the epidemiology of giardiasis. Investigation of risk factors for sub-populations with higher rates may facilitate prevention and control efforts.

Board 181. Molecular Surveillance of *Cryptosporidium* Infection in Children in Kuwait

J. Iqbal
Faculty of Medicine, Jabriay, Kuwait

Background: Cryptosporidiosis is an infection of young children and immunocompromised individuals especially in children less than 2 years of age. There has been an increase in the incidence of cryptosporidiosis especially in tropical and sub-tropical countries. More than 2 million migrant workers reside in Kuwait, the majority of whom come from these countries. Due to relative increased transmissibility of this infection, it is important to determine the incidence of this infection in Kuwait especially in children, the major high-risk age group. *Cryptosporidium* spp. were isolated from young children in Kuwait positive for cryptosporidiosis and were further characterized at the molecular level to understand the transmission of infection. Detailed socio-demographic data of all included in the study were collected to determine the risk factors for the transmission. **Methods:** This study was conducted over a period of two years and fecal specimens collected from 200 Kuwaiti children with persistent diarrhea found to be positive for *Cryptosporidium* spp. by microscopy were genotyped and sub-typed with a small subunit rRNA-based PCR-restriction fragment length polymorphism analysis. Socio-demographic data were obtained from all included in the study. **Results:** More than 85% of the children with cryptosporidiosis had only *Cryptosporidium* infection. Socio-demographic information did not reveal any particular mode of transmission of infection. Genotyping of the organisms isolated showed that ninety-two (95%) of the children had *C. parvum*, 4 (4%) had *C. hominis*, and 1 (1%) had both *C. parvum* and *C. hominis*. Altogether, 9 subtypes of *C. parvum* and *C. hominis* were observed. The analysis of the socio-demographic data revealed a close association of *C. parvum* 2a subtype, that showed increased symptoms, with decreased nutritional status (p<0.03), consumption of stored water rather than piped-water supply (p<0.05) and presence of an infected case in the family (p<0.05). **Conclusions:** This study concludes that the majority of cryptosporidiosis cases detected in Kuwait were in people who were immunocompetent, and we detected a very different distribution of *Cryptosporidium* genotypes in Kuwaiti children as compared to other tropical countries. The study also showed a close association with the use of stored water and decreased nutritional status, thus highlighting the importance of testing the water supply.

Board 182. *Acanthamoeba* Disease Associated with the Practice of Nasal Rinsing in Immunocompromised Patients

J. Cope, I. Ali, S. Roy
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The genus *Acanthamoeba* are free-living amebae (FLA) found worldwide in water, including tap water, and soil that can cause rare but severe infections of the eye, skin, and central nervous system. *Acanthamoeba* spp. generally cause disease in immunocompromised persons including those with HIV, hematologic malignancies, and solid organ transplants. The route of transmission and incubation period are not well known in humans but animal studies have shown that disease can be produced via the intranasal, intrathecal, and intravenous routes. We describe five cases of *Acanthamoeba* disease among immunocompromised patients who practiced nasal rinsing before illness onset. **Methods:** The Centers for Disease Control and Prevention (CDC) offers a clinical consultation service

for FLA infections and maintains a free-living ameba laboratory with confirmatory diagnostic testing capabilities. When an *Acanthamoeba* case is confirmed in the United States, details about the case are collected on a standardized case report form which includes questions about the case-patient's water and soil exposure before illness onset. Questions about nasal rinsing were added to the form in 2011. **Results:** Of 37 *Acanthamoeba* case-patients from 2011 to 2017, 5 in CDC's FLA database were reported to have performed nasal rinsing before illness onset. The median age was 60 years (range 36–73 years) and 3/5 patients were women. Two were solid organ transplant patients (heart and kidney), 2 had chronic lymphocytic leukemia, and 1 had HIV. Three patients presented only with encephalitis and died. The two organ transplant patients had a combination of rhinosinusitis, osteomyelitis, and skin lesions. One survived and the other died of a cause unrelated to *Acanthamoeba*. All reported using tap water to perform nasal rinsing, most for sinus congestion using a neti pot or similar device and one for religious purposes. **Conclusions:** *Acanthamoeba* is a common inhabitant of water, including tap water from public water systems. Immunocompromised patients, like those presented here, might be at risk for infections caused by *Acanthamoeba* when using tap water for nasal rinsing. Clinicians caring for immunocompromised patients should advise their patients not to use tap water for nasal rinsing unless it has been made safe (e.g., by boiling).

Antimicrobial Resistance

Board 183. Assessment of HAI/AR Outbreak Detection Data, Tools, and Barriers

W. Bamberg[1], M. Kainer[2], N. Bryan[3], M. Anderson[4]
[1]Colorado Department of Public Health and Environment, Denver, CO, USA, [2]Tennessee Department of Health, Nashville, TN, USA, [3]Gwinnett County Medical Center, Lawrenceville, GA, USA, [4]Council of State and Territorial Epidemiologists, Atlanta, GA, USA

Background: The Council for Outbreak Response: Healthcare-Associated Infections (HAI) and Antimicrobial Resistance (AR) (CORHA) is a multidisciplinary partnership consisting of public health and healthcare organizations charged with developing consistent and coordinated approaches to improve the detection, investigation, response, and prevention of HAI/AR outbreaks. CORHA developed an assessment to better understand how HAI programs at public health departments use technology to detect potential HAI/AR outbreaks. **Methods:** The assessment was launched in July 2017 and responses were collected electronically using Qualtrics. In addition to demographic information, recipients were asked to describe their HAI surveillance efforts regarding data sources and software tools used to detect outbreaks of HAI/AR pathogens. They were also asked to describe barriers they experienced using surveillance system data for outbreak detection. **Results:** A total of 89 responses were received. Fifty-two respondents were from state health departments, while 16 were from local health departments, 2 from regional health departments, and 1 other. Ninety-seven percent (69) of respondents indicated that they have some role in HAI outbreaks. Software tools used by public health to identify potential HAI/AR outbreaks included: SAS (17), Essence (9), SATScan (6), R (5), WHONet (3), and other tools (16). Thirty-one respondents indicated that they do not use any software tools. Data sources used to detect HAI/AR outbreaks included communicable disease surveillance (44), public health lab systems (15), NHSN HAI data (15), NHSN Lab ID events (14), syndromic surveillance data (14), and other data sources (7). Twenty respondents indicated that they do not use surveillance system data. Barriers to utilizing surveillance system data for outbreak detection included: insufficient resources (38), information not timely (26), lack of data access (23), lack of expertise (23), inaccurate data (18), and lack of simplicity (18). **Conclusions:** Public health and healthcare have important roles in HAI outbreak detection and surveillance, yet there are barriers to utilizing surveillance system data and tools to detect HAI/AR outbreaks. CORHA is working to develop resources to help public health improve HAI/AR outbreak detection.

Board 184. Year One of the Antimicrobial Resistance Laboratory Network (ARLN): A New Laboratory Network That Allows Early Identification of Emerging Resistance in Healthcare-Associated Infections—United States, 2017

J. Huang, S. Malik, A. Brown
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: In 2016, CDC began funding state and local public health laboratories (PHLs), including seven regional laboratories, to identify and characterize clinical isolates of carbapenem-resistant Enterobacteriaceae (CRE), *Pseudomonas aeruginosa* (CRPA), and *Acinetobacter* (CRAB) as part of the ARLN. Here we summarize testing data from the first year of ARLN to describe the characteristics of these isolates. **Methods:** Methods: State and local PHLs in the ARLN performed testing for organism identification, antimicrobial susceptibility (AST), carbapenemase production, and molecular detection of KPC, NDM, OXA-48-like, VIM, and IMP carbapenemase genes. ARLN labs submitted monthly testing reports to CDC. CDC conducted supplemental testing, including AST for additional drugs and PCR for additional carbapenemase genes and variants, on a small subset of isolates. Alert notifications about isolates of novel and emerging resistance were sent to the local HAI/AR coordinator and CDC within one day to support rapid containment and prevention activities. These alerts included less common carbapenemase-producing organisms (CPOs) and those suspected as being pan-resistant. **Results:** Results: In 2017, ARLN tested 10,292 isolates. Among 6,537 CRE tested, 35% (2,305) were CPOs and KPC was the most common carbapenemase identified. Fifty-eight CRE were positive for more than one carbapenemase, with KPC/NDM being the most common combination. Mechanism combination varied by organism and geographic region, with KPC/NDM highest in the Southeast and NDM/OXA-48-like highest in the Mid-Atlantic. Among 3,609 CRPA tested, 3.7% (130) were CPOs and VIM was the most common carbapenemase. Four isolates were positive for more than one carbapenemase: three were KPC/NDM and one was KPC/VIM. Among 228 CRAB tested, 24% (54/228) were CPOs and OXA-23 was the most common carbapenemase. No CRAB isolates had more than one carbapenemase gene. We received 422 alerts over 12 months from 38 PHLs. **Conclusions:** ARLN is a new laboratory network that provides frontline testing capacity to detect emerging resistance threats. With over 10,000 isolates tested in its first year, the data generated by ARLN is facilitating rapid public health responses and furthering our understanding of the biology and epidemiology of known and unknown carbapenemases.

Board 185. Architecture of an Extensively Drug-Resistant Organism (XDRO) Registry Utilizing the Existing Infrastructure of the State of Tennessee's NEDSS Base System (NBS)

M. Morrell[1], M. Kainer[1], S. Harney[1], P. Harris[2]
[1]Tennessee Department of Health, Nashville, TN, USA, [2]Vanderbilt University Medical Center, Nashville, TN, USA

Background: With the implementation of the Illinois Department of Public Health's XDRO Registry in 2013, the Tennessee (TN) Department of Health was inspired to create a similar infrastructure to facilitate more timely infection control of carbapenem-resistant Enterobacteriaceae (CRE) and other multidrug-resistant organisms (MDROs). The XDRO Registry would provide information to TN healthcare facilities on patients with any of the Tier One through Tier Three MDROs that may be entering their facilities, enabling healthcare providers to rapidly implement infection control practices and reduce the spread of these organisms. **Methods:** The XDRO Registry will be populated with an extract of data from NBS – a general communicable disease surveillance tool used by public health. These data will be output via Application Programming Interface (API) and input into Research Electronic Data Capture (REDCap), the foundational database for the registry. In TN, all CRE including non-big three genera (*Enterobacter* spp., *E. coli,* and *Klebsiella* spp.) are reportable. Therefore, antimicrobial susceptibility data are captured to ensure the organism meets the case definition. Authorized users at TN healthcare facilities will log into the registry and search for an admitting patient who may have tested positive for a MDRO. The external user interface for REDCap is under development by Vanderbilt University. Additionally, Infection Preventionists in the Healthcare Associated Infection program at TN are collaborating to aggregate and develop educational resources for inclusion in the registry. **Results:** In February 2018, a draft of the user interface was shared with multiple stakeholders including over 285 partners from the CSTE Healthcare Associated Infections Subcommittee, TN Multi-Disciplinary Advisory Group, and TN Users of the National Healthcare Safety Network. There has been significant enthusiasm from all involved, with over 15 members providing constructive feedback to formulate an optimally-designed XDRO Registry. **Conclusions:** The TN XDRO Registry will be an essential tool among healthcare providers. The registry will facilitate immediate MDRO detection and trigger appropriate infection control precautions, while also educating staff, ultimately reducing the spread of MDROs within TN healthcare facilities.

Board 186. External Validation of Surveillance and Reporting of Carbapenem-Resistant Enterobacteriaceae to the National Healthcare Safety Network—Wisconsin

M. Lasure[1], N. Shrivastwa[2]
[1]Wisconsin State Laboratory of Hygiene, Madison, WI, USA, [2]Wisconsin Department of Health, Madison, WI, USA

Background: In the United States, carbapenem-resistant *Enterobacteriaceae* (CREs) are emerging healthcare-associated pathogens that are associated with high mortality. Beginning December 2011, the Wisconsin Division of Public Health (DPH) required hospitals to report CRE laboratory-identified events using the National Healthcare Safety Network (NHSN) CRE definition and protocol. External validation was conducted to determine the accuracy of statewide CRE surveillance data. **Methods:** DPH reviewed reported CRE cases during 2015 and conducted standardized interviews with hospital infection preventionists. In accordance with the 2016 NHSN Data Validation toolkit, the sample consisted of 18 hospitals equally split between those with CRE prevalence rates (1) above the median, (2) below the median, and (3) equal to zero relative to 2015 NHSN data and 6 additional hospitals that were randomly selected. Microbiology laboratories provided line lists of cultures positive for *Escherichia coli*, *Klebsiella pneumoniae, Klebsiella oxytoca*, or *Enterobacter* species with antimicrobial sensitivity test results. During 2015, the NHSN definition of CRE laboratory-identified event was any *Escherichia coli*, *Klebsiella pneumoniae, Klebsiella oxytoca*, or *Enterobacter* species testing resistant to ertapenem, meropenem, imipenem or doripenem. **Results:** Among 37,336 culture results reviewed from 15 acute care hospitals, 156 met the NHSN CRE definition, of which 51 were reported to NHSN; resulting in a sensitivity of 34.5%, specificity of >99.9%; positive predictive value was 96.2%, and negative predictive value was 99.7%. Reporting errors included failure to report eligible isolates and failure to report CRE events when subsequent cultures yielded a different CRE organism. **Conclusions:** The validation study detected 65.5% underreporting of CRE laboratory-identified events associated with misapplication of the NHSN definition. Continued validation and training of infection preventionists are recommended to improve the accuracy of CRE reporting.

Board 187. Impact of Ertapenem on Detection of Carbapenemase-Producing Enterobacteriaceae in Tennessee, United States

A. Chan, R. Octaria, P. Talley, M. Kainer
Tennessee Department of Health, Nashville, TN, USA

Background: Carbapenem-resistant Enterobacteriaceae (CRE) are reportable in Tennessee; isolates must be sent to the State Public Health Laboratory (SPHL) for carbapenemase-production (CP-CRE) detection. In 2015, the Council of State and Territorial Epidemiologists changed the CRE case definition to include resistance to ertapenem. We aim to describe the role ertapenem plays in statewide surveillance. **Methods:** CRE were defined as *E.coli*, *Klebsiella*, and *Enterobacter spp.* isolated from any clinical specimen and resistant to doripenem, meropenem, imipenem (minimum inhibitory concentrations [MIC] of ≥4 μg/ml) or ertapenem (MIC ≥2 μg/ml), or demonstrated production of a carbapenemase. We aggregated CRE surveillance data from Jan. 1st, 2016 thru Nov. 30th, 2017. We grouped isolates into an 'ertapenem only' group, based on resistance to ertapenem alone, and an 'other carbapenems' group, based on resistance to at least one other carbapenem (i.e. meropenem, doripenem, imipenem) regardless of ertapenem resistance. **Results:** Among 1,410 cases reported, 1,043 cases (74%) had isolates submitted to the SPHL with susceptibilities. Out of these 1,043 cases, 401 (38%) were CP-CRE. There were 412 (40%) cases in the 'ertapenem only' group and 631 (60%) in the 'other carbapenems' group. Within each group, 22 (5%) of the ertapenem group were CP-CRE and 379 (60%) of the 'other carbapenem' group were CP-CRE. By univariate logistic regression, the odds of detecting a CP-CRE were 26 times higher when an isolate was resistant to at least one of meropenem, doripenem, or imipenem when compared to the isolates resistant to only ertapenem (OR=26.7, 95% CI 16.9—42.2). Within the 'ertapenem only' group, out of all the *Enterobacter*, *E. coli*, and *Klebsiella* sent to the SPHL, 5%, 2%, and 11% were CP-CRE compared to 67%, 21%, and 71% of the 'other carbapenems' group, respectively. **Conclusions:** Including ertapenem in the case definition detected ad-

ditional CP-CRE cases and may be important if ertapenem is the only carbapenem tested. However, the likelihood of detecting CP-CRE was much lower compared to other carbapenems. These findings should be considered if resources are limited (e.g., perform additional characterization of CRE or number of isolation rooms). We suggest including at least one non-ertapenem carbapenem when performing susceptibility testing.

Board 188. Impact of Human and Food Animal Wastes on Antimicrobial Gene Abundance and *E. coli* Susceptibility Patterns

W. Tanner, W. Brazelton, C. Thornton, C. Dangerfield, A. Hyer, B. Singh, J. VanDerslice
University of Utah, Salt Lake City, UT, USA

Background: Dissemination of antimicrobial-resistant organisms via water sources such as rivers, lakes, and streams, is a serious concern. Shotgun metagenomic analyses of surface water samples can reveal differences in resistance gene occurrence and relative abundances between sites within watersheds. Our objective was to characterize differences in occurrence and frequency of clinically-significant antimicrobial resistance genes (ARGs) and *E. coli* isolates in an urban and an agricultural watershed. **Methods:** Data on water source impairment, geographic locations of wastewater treatment plants (WWTPs), and agricultural land use were used in conjunction with data from the National Healthcare Safety Network on state prevalence of carbapenem- and 3rd generation-cephalosporin-resistant Enterobacteriaceae to select two watersheds for sampling: 1) a predominantly agricultural watershed in a rural location, and 2) a predominantly urban watershed with little to no agricultural influence. Water samples were collected at multiple sites along the rivers from the top of the watershed to discharge into a major waterway (approximately 30 to 60 miles downstream). *E. coli* isolates in samples were tested for susceptibility to various antibiotics by disk diffusion. **Results:** Preliminary shotgun metagenomic results indicate elevated numbers of ARGs associated with agricultural and wastewater impacts. In the urban watersheds, increased abundances of resistance genes were seen immediately downstream of WWTPs. Overall, raw counts of ARGs were higher in samples from the agricultural watershed. *E. coli* susceptibility testing showed increased prevalence of tetracycline-resistant *E. coli* in the agricultural watershed. Tetracycline and cefazolin were the most common resistance phenotypes in the agricultural watershed, with ampicillin and cefazolin resistance being most common in the urban watershed. **Conclusions:** Frequency of specific ARGs differ based on inputs within each watershed, and *E. coli* isolate phenotypes often reflect the ARGs that are present. Waste inputs in watersheds may contribute to the dissemination of ARGs within the natural environment. Further research is needed to determine the public health implications of the presence of ARGs in watersheds serving as downstream drinking water sources,

Board 189. Characterization of Multidrug-Resistant Gram-Negative Bacilli from Human Infections, Nicaragua

A. Dretler[1], L. Sandoval[2], J. Avila[2], M. Rener[3], R. Burger-Calderon[4], M. Hargita[1], A. Page[5], J. Thonkulpitak[5], J. Waggoner[1], S. Satola[1]
[1]Emory University School of Medicine, Atlanta, GA, USA, [2]Bacteriology Department, Centro Nacional de Diagnóstic y Referencia, Ministerio de Salud, Managua, Nicaragua, [3]Sustainable Sciences Institute, Managua, Nicaragua, [4]University of California, Berkeley, Berkeley, CA, USA, [5]Atlanta Research and Education Foundation, Veterans Affairs Medical Center, Atlanta, GA, USA

Background: Antimicrobial resistance (AMR) represents a global public health crisis. Much of the burden of AMR in limited resourced settings remains unknown. In Nicaragua, no studies have characterized AMR among clinical isolates. At a national pediatric reference hospital in Managua, high rates of AMR among gram-negative rods (GNRs) have been observed;in 2013, 70% of *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* isolates and 10% of *Acinetobacter baumannii* isolates were susceptible to meropenem. The aim of this pilot study was to better characterize 100 isolates of multidrug resistant (MDR) GNRs from Nicaragua. **Methods:** Isolates, collected from 2014-2017 from medical facilities throughout Nicaragua, were originally sent to the Centro Nacional de Diagnóstico y Referencia in Managua. Isolates with resistance to > 1 class of antibiotics, identified by E-test, were stored in media supplemented with 25% glycerol. 100 suspected MDR-GNRs cultured from sterile body sides representing the most common species (*E. coli*, *K. pneumoniae*, *A. baumannii*, and *P. aeruginosa*) were shipped to Emory University for molecular testing for the presence of carbapenemase by qPCR. **Results:** Of the 100 total isolates, 16% were *P. aeruginosa,* 30% were *A. baumannii*, and 54% were *Enterobacteriaceae*. Metallo-β-lactamase production was suspected as the primary mechanism of resistance in these isolates based on imipenem-EDTA synergy disk testing. New Delhi Metallo-β-lactamase (NDM) carbapenemase genes were detected in 62% of these bacterial isolates. The *Enterobacteriaceae* had the highest rates of NDM detection, with 92% (50/54 isolates) positive by PCR. Further analysis of the isolates is ongoing. **Conclusions:** This study reveals very high rates of NDM- carbapenemase genes in MDR-GNRs from hospitals throughout Nicaragua. Prior studies have shown the presence of NDM-1 in Latin and Central America[1] but there is limited evidence regarding the prevalence of this resistance mechanism in most of Central America, and particularly Nicaragua. Further research is needed to determine the burden of highly resistant bacteria in Nicaragua and to guide interventions to limit further spread.

Board 190. The Epidemiology of Antibiotic Resistance in Clinical Non-Typhoidal *Salmonella* (NTS) Isolates in Michigan

S. Mukherjee[1], C. Anderson[1], R. Mosci[1], J. Rudrik[2], S. Manning[1]
[1]Michigan State University, East Lansing, MI, USA, [2]Michigan Department of Health and Human Services, Lansing, MI, USA

Background: NTS is a serious public health threat resulting in 1.2 million infections every year in the United States. Additionally, the emergence of resistance to important antimicrobials used in human medicine complicates the treatment of NTS infections. Since Michigan is not part of the FoodNet surveillance network, data about the frequencies of antimicrobial resistance and resistance genes (ARGs) is lacking. **Methods:** Clinical NTS (n= 198) isolates were collected by the MDHHS between 2011-2014 and were examined for resistance to 24 antibiotics using broth microdilution. Case information and epidemiological data were extracted from the Michigan Disease Surveillance System (MDSS) and associations with resistant infections were identified using multivariate logistic regression analysis. Whole genome sequencing was performed on 148 isolates and bioinformatic scripts were developed to extract antibiotic resistance using the ResFinder 3.0 database. **Results:** Thirty (15.2%) isolates were resistant to ≥1 antibiotic and 15 (7.5%) were resistant to ≥3 antimicrobial classes. Frequencies of resistance in Enteritidis serovars (5.6%, n=4) were

significantly lower than frequencies in other serovars (21.1%, n=26), while resistance was higher in winter, spring and fall (19.8%, n=20) compared to summer months (10.5%, n=10). Multivariate logistic regression analysis identified serovar Enteritidis (Odds Ratio (OR): 0.2, 95% Confidence Interval (CI): 0.07, 0.90) and summer season (OR: 0.3; 95% CI: 0.11, 0.89) to be independently associated with resistance. Preliminary genomic analyses (n=45) revealed the presence of 15 unique ARGs, 60% of which result in antibiotic inactivation. An additional 20% of ARGs encode efflux pumps and 20% encode enzymes that result in drug target replacement. **Conclusions:** These data indicate a high frequency of resistance in NTS strains in Michigan and highlight important risk factors for resistance. Our findings also demonstrate the importance of continued surveillance of both NTS and resistance mechanisms in strains linked to clinical infections to develop revised strategies that minimize the impact of resistant infections. Future work will focus on identifying relationships between certain phylogenetic lineages and antibiotic resistance.

Board 191. Decreased Susceptibility to Azithromycin among Nontyphoidal *Salmonella* Isolates in the United States, 2011–2017

L. Francois Watkins, J. Chen, B. Karp, J. Folster, H. Caidi, C. Friedman
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Antimicrobial resistance among nontyphoidal *Salmonella* (NTS) is a serious public health threat. Decreased susceptibility to azithromycin (DSA), a clinically important antimicrobial, is often plasmid mediated but has historically been rare in NTS in the US. We evaluated trends and assessed characteristics of nationally representative NTS isolates with DSA. **Methods:** In 2011–2017, US health departments submitted every 20th NTS isolate for surveillance and additional outbreak isolates to CDC, where they were tested for antimicrobial susceptibility by broth microdilution (Sensititre™) to 14 drugs, including azithromycin. For this analysis, we defined DSA as a minimum inhibitory concentration of ≥32 µg/mL based on the current Clinical and Laboratory Standards Institute's investigational breakpoint for *Salmonella* Typhi (breakpoints have not been established for NTS). A subset of isolates underwent whole genome sequencing; sequences were screened for the presence of resistance determinants. Patients' epidemiological characteristics were reviewed when available. **Results:** We identified DSA in 44 NTS isolates comprising 22 serotypes from patients in 23 states. The prevalence of DSA increased from 1.4 per 1000 surveillance isolates tested in 2011–2014 to 5.1 in 2015–2017 (P <0.001). Most of these isolates were multidrug resistant; 20 (45%) were resistant to agents from ≥5 antimicrobial classes. Of 20 sequenced isolates with an azithromycin resistance mechanism detected, 18 (90%) had *mphA* and 2 (10%) had *mphE*. Median patient age was 37 years (interquartile range 15.5–60); 21 (48%) were male. Of 26 patients with travel histories, 6 (23%) traveled to Asia, 3 (12%) to Latin America, and 2 (8%) to Europe before illness began. **Conclusions:** DSA among NTS is increasing in the United States, though it remains rare. The rise is associated with the emergence of macrolide resistance genes *mphA* and *mphE*, typically carried on plasmids, raising concern for horizontal spread of resistance among bacteria. Resistance determinants may enter the US via international travelers, and frequent clinical use of azithromycin may contribute to selective pressure domestically. Patient outcome data are needed to determine clinical breakpoints for NTS.

Board 192. Antimicrobial Resistance of *Salmonella* and *Staphylococcus* Species Isolated from Free-Ranging Rhesus Macaques (*Macaca mulatta*): Eco-epidemiological Assessment at a Human-Animal Interface in Bangladesh

M. Rahman[1], A. Islam[1], M. Samad[2], S. Islam[1], M. Uddin[3], M. Rostal[1], E. Hagan[1], M. Hassan[3], M. Flora[4], J. Epstein[1]
[1]EcoHealth Alliance, New York, NY, USA, [2]Bangladesh Livestock Research Institute (BLRI), Dhaka, Bangladesh, [3]Chittagong Veterinary and Animal Sciences University (CVASU), Chittagong, Bangladesh, [4]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh

Background: Antimicrobial resistance (AMR) is a growing global health threat. Environmental pollution of antimicrobials from human and animal waste has been linked to AMR within wildlife populations, including rhesus macaques. This study aims to better describe the eco-epidemiology of AMR in *Salmonella* and *Staphylococcus* spp. from rhesus macaques. **Methods:** Fecal samples were collected from the macaques, cultured and an antimicrobial susceptibility test (AST) for 12 antimicrobials was conducted using the Kirby-Bauer Disc diffusion method on selective media. Isolates were confirmed by biochemical characteristics and PCR. **Results:** Results yielded 5% (18/399; 95%CI: 3-7) of samples were positive for *Salmonella* spp. and significantly more common among macaque from urban areas (8%; 11/140) than those from rural (2/149) and peri-urban (5/110) areas (p<0.05). AST profiling of *Salmonella* spp. detected resistance to tetracycline (89%), azithromycin (83%), sulfamethoxazole-trimethoprim (50%), nalidixic acid (44%) among others. Of 18 samples, 56% of the *Salmonella* spp. were resistant to at least five common antibiotics. Fifteen percent of the macaque fecal samples (61/399; 95%CI: 12-19) were positive for *Staphylococcus* spp. though no significant difference between sites was noted. *Staphylococcus* spp. had the highest resistance to ampicillin (93%), methicillin (31%) and clindamycin (26%) and less resistant to rifampicin (18%), streptomycin (15%) and tetracycline (13%). Only six of the 61 samples were resistant to at least five common antibiotics. **Conclusions:** Resistant bacteria were identified in macaques. While only 5% of macaque samples cultured *Salmonella,* those that were infected may be at greater risk for AMR. As *Salmonella* is shed in feces, a further study investigating the types of contact between macaques and livestock and people are indicated, as are further genetic analysis to better understand the virulence of the cultured *Salmonella*.

Board 193. Etiology and Antimicrobial Resistance Patterns of *Salmonella* Bacteremia in Hospitalized Children with Acute Febrile Illness—Uganda, 2016–2017

A. Winstead[1], A. Mpimbaza[2], A. Sserwanga[2], J. Kapisi[2], C. Maiteki[2], M. Kamya[2], M. Lamorde[3], R. Walwema[3], F. Kizito[3], H. Tasimwa[4], A. Kusemererwa[2], Y. Manabe[5], G. Odongo[1], R. Ransom[1], J. Borchert[1], P. Mead[6], K. Kugeler[6], M. Mikoleit[1], M. Freeman[1], E. Mintz[1], G. Appiah[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Infectious Disease Research Collaboration, Kampala, Uganda, [3]Infectious Disease Institute, Kampala, Uganda, [4]Makerere University, Kampala, Uganda, [5]Johns Hopkins Center for Global

Health, Baltimore, MD, USA, [6]Centers for Disease Control and Prevention, Fort Collins, CO, USA

Background: Typhoid fever, paratyphoid fever, and invasive non-typhoidal *Salmonella* cause an estimated 30.4 million illnesses and >1 million deaths annually worldwide. In a systematic review, *Salmonella enterica* was found to cause 29% of community-acquired bacterial bloodstream infections in Africa (58.4% of which were non-typhoidal *Salmonella*). However, data from sub-Saharan Africa are scarce because of limited laboratory capacity. To characterize invasive salmonellosis in hospitalized Ugandan children, we evaluated data from six hospitals participating in the Uganda Acute Febrile Illness (AFI) Project. **Methods:** The Uganda AFI Project recommends a blood culture for any febrile child aged ≤14 years admitted to a hospital surveillance site with a negative test for malaria. We evaluated demographic information, blood culture results, and antimicrobial susceptibility results from all six participating hospitals from July 1, 2016 to November 16, 2017. **Results:** Over a combined total of 2,146 days across all sites, blood cultures were performed and results were available for 4,257 (19%) of 22,533 hospitalized children. Overall, 3,894 (91%) yielded no growth, 220 (5%) yielded a likely contaminant, and 143 (3%) yielded a pathogen. *Salmonella* was the most commonly detected pathogen, found in 57 (38%) positive samples, including 21 identified as *Salmonella* Enteritidis, 14 as *Salmonella* Typhi, 12 as *Salmonella* Typhimurium, 1 as Salmonella 4,5,12:i:-, and 9 whose serotypes are unconfirmed. Among patients with *Salmonella* bacteremia, the median age was 36 months (range: 2 days to 12 years), 70% were male, and 3 (6%) died. The median length of stay for patients with *Salmonella* bacteremia was 6 days, compared to 3 days for those without *Salmonella* bacteremia (P<.0001). *Salmonella* isolates were resistant to ampicillin (61%), cotrimoxazole (60%), ciprofloxacin (11%), and ceftriaxone (4%). Additionally, decreased susceptibility was noted to ciprofloxacin (38%) and ceftriaxone (4%). **Conclusions:** *Salmonella* is a key cause of bacterial bloodstream infections in Ugandan children. Data from this ongoing project document the threat of emerging antimicrobial resistance, notably to fluoroquinolones and ceftriaxone, which are often used for *Salmonella* infections.

Board 194. Evolution of Antimicrobial Resistance among *Shigella* Isolates in Argentina from 2007-2016

R. Pellegrino[1], H. Sati[2], M. Galas[2], N. Bruinsma[2], A. WHONET Network[3], C. Lucero[3], F. Pasteran[3], E. Tuduri[3], A. Corso[3]
[1]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [2]Pan American Health Organization, Washington, DC, USA, [3]Dr. Carlos G. Malbran National Institute of Infectious Diseases, Buenos Aires, Argentina

Background: Infection from *Shigella* is the second leading cause of diarrheal death in Argentina, and treatment worldwide has been complicated by the emergence of antimicrobial resistance. This study aims to highlight the patterns of resistance and species distribution over 10 years in Argentina. **Methods:** Surveillance data was acquired from WHONET-Argentina, a network through the National Reference Laboratory (NRL) that collects antimicrobial resistance data from 95 clinical laboratories representing all geographic regions of the country. Data on resistance, species type, and patient demographics of *Shigella* isolates were analyzed for geographic and temporal trends. **Results:** From 2007 to 2016, 28,063 *Shigella* isolates were reported to the NRL, mostly from patients under 5 years of age (56%). *S. flexneri* was the most frequent species of *Shigella* isolated (70.4%), followed by *S. sonnei* (23.7%), and the proportion of *S. sonnei* has increased over the past 10 years. Overall, *Shigella* in Argentina has a high resistance to ampicillin (70.8%) and trimethoprim/sulfamethoxazole (51.6%). Resistance to third generation cephalosporins, ciprofloxacin, nalidixic acid and nitrofurantoin remains under 2.5%. Increasing trends in resistance have been seen regionally to ampicillin, trimethoprim/sulfamethoxazole and nalidixic acid. Regional differences are seen in distribution of species and resistance. Resistance to ampicillin and trimethoprim/sulfamethoxazole in *S. sonnei* has increased at a higher rate than the resistance to these antibiotics in *S. flexneri*. *S. sonnei* isolates were also found to have more seasonal variation then *S. flexneri* isolates. **Conclusions:** *S. flexneri* remains the predominant species of *Shigella* in Argentina, but the proportion of *S. sonnei* is increasing. While *Shigella* in Argentina remains largely susceptible to first line treatments, such as ciprofloxacin and third generation cephalosporins, there has been a significant increase in *Shigella* resistance to ampicillin and trimethoprim/sulfamethoxazole. Though resistance to nalidixic acid remains low, the increasing trend is concerning given the global emergence of quinolone resistant *Shigella*. These trends support the need for continued surveillance and the need for monitoring of antibiotic use.

Board 195. Emerging Quinolone Resistance Mechanisms among *Shigella* in the United States

B. Karp[1], L. Francois Watkins[1], J. Chen[2], M. Birhane[3], C. Friedman[1], J. Whichard[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]IHRC, Inc., Atlanta, GA, USA, [3]Atlanta Research and Education Foundation, Inc., Atlanta, GA, USA

Background: *Shigella* causes an estimated 500,000 illnesses in the US annually. Most infections are self-limited and can be managed without antibiotics. Treatment is recommended for patients with severe disease or immunosuppression. In adults, fluoroquinolones (FQ) such as ciprofloxacin (CIP) are commonly used to treat shigellosis. In 2017, isolates from a *Shigella* outbreak were found to have an emerging plasmid-mediated quinolone resistance (PMQR) mechanism. It conferred an elevated CIP minimum inhibitory concentration (MIC) of 0.25 µg/mL, raising concerns about response to treatment, even though the MIC falls into the "susceptible" (MIC ≤1 µg/mL) category according to current Clinical and Laboratory Standards Institute (CLSI) criteria. **Methods:** We reviewed CIP MIC data, phenotypic-genotypic correlation data, and quinolone resistance trends for *Shigella* isolates submitted to the National Antimicrobial Resistance Monitoring System (NARMS) at the Centers for Disease Control and Prevention. Antimicrobial susceptibility testing for CIP and the quinolone nalidixic acid was performed using broth microdilution (Sensititre™). Quinolone resistance mechanisms were determined for a subset of isolates using whole genome sequencing. **Results:** CIP MIC distributions for *Shigella* surveillance isolates were trimodal. The percentage of isolates with CIP MIC ≥0.12 µg/mL more than doubled from 5.5% in 2013 to 13.4% (preliminary data) in 2016; most had CIP MICs of 0.12–0.5 µg/mL. Among sequenced surveillance and outbreak isolates, CIP and nalidixic acid MICs varied based on the presence, type, and number of quinolone resistance mechanisms. Almost all isolates lacking quinolone resistance mechanisms had CIP MICs ≤0.015 µg/mL. Isolates with CIP MICs 0.12–0.5 µg/mL had PMQR or 1–2 chromosomal mutations in the quinolone resistance-determining region (QRDR). Isolates with ≥3 quinolone resistance mechanisms had CIP MICs ≥4 µg/mL. **Conclusions:** The increase in the percentage of *Shigella* with elevated CIP MICs, their association with PMQR and QRDR mutations, and their placement in the "susceptible" category, raise concerns about

the spread of quinolone resistance mechanisms and treatment effectiveness. Clinical outcome data for patients who had FQ treatment and whose isolates show CIP MICs of 0.12–1 µg/mL are needed.

Board 196. Characterizing *Shigella* Species Distribution and Antimicrobial Susceptibility to Ciprofloxacin and Nalidixic Acid in Latin America between 2000-2015, Using Data from the Latin American Antimicrobial Resistance Surveillance Network (ReLAVRA)

H. Sati[1], N. Bruinsma[1], M. Galas[1], P. Ramon Pardo[1], M. Espinal[2]
[1]Antimicrobial Resistance Program, Communicable Diseases and Environmental Determinants of Health, Pan American Health Organization, Washington DC, USA, [2]Communicable Diseases and Environmental Determinants of Health, Pan American Health Organization, Washington, DC, USA

Background: Shigellosis is the second leading cause of diarrheal death globally, and one of three leading causes of diarrheal deaths in children under 5 years. The global burden has been complicated by the emergence of *Shigella* strains resistant to first line antibiotic treatments such as ciprofloxacin. This study aims to describe the epidemiologic distribution of the most common *Shigella* species, and their antimicrobial susceptibility patterns to the quinolones ciprofloxacin and nalidixic acid in Latin America. **Methods:** Laboratory data from 2000-2015 were obtained through the ReLAVRA network from 19 countries in Latin America. Negative binominal regression was used to analyze longitudinal trends of *Shigella* isolates antimicrobial susceptibility. **Results:** Overall 79,548 *Shigella* isolates were tested and reported between 2000-2015. The most common isolated *Shigella* species were *S. flexneri* (49%), and *S. sonnei* (28%). The average annual percentage increase (AAPI) in nonsusceptibility was 18.4 %(95% CI:10.8%-26.6%,p<0.001) for ciprofloxacin and 13.2%(95% CI:7.8%-18.9%, p<0.001) for nalidixic acid. When stratified by common species, a similar increasing trend in the percentage nonsusceptibility to both drugs was found. AAPI in ciprofloxacin nonsusceptibility was 13.3% for *S. flexneri* (95%CI: 0.4%-27.9%;p=0.0425), and 39.9% for *S.sonnei* (95%CI:60.5%-22.1%,p<0.001). AAPI in nalidixic acid nonsusceptibility was 1.5% (95% CI:6.1%-9.8%; p=0.7026) for *S.flexneri*, and 31.7%(95%CI:44.8%19.7%,p<0.001) for *S.sonnei*. Nonsusceptibility to ciprofloxacin varied between reporting countries, with the highest average in Honduras, Bolivia, and the lowest in Argentina and Panama. No resistance was reported in Costa Rica and Uruguay. **Conclusions:** The increase in *Shigella* nonsusceptibility to ciprofloxacin and nalidixic acid threatens effective prevention, control, and management of shigellosis in Latin America. Improving countries capacity for data collection and reporting, including demographic and clinical outcome data, is needed to understand epidemiological changes, species distribution and risk groups. Utilization of AMR surveillance platforms should be used to inform treatment guidelines, control measures, and mitigation of further development of AMR at country and regional level.

Board 197. Colistin-Resistant *Klebsiella pneumoniae* Bloodstream Infection: Old Drug, Bad Bug

E. Ben-Chetrit[1], P. Mc Gann[2], R. Maybank[2], J. Stam[2], D. Katz[1]
[1]Shaare Zedek Medical Center, Jerusalem, Israel, [2]Walter Reed Army Institute of Research, Silver Spring, MD, USA

Background: Multidrug-resistant (MDR) *Enterobacteriaceae* pose a global threat to hospitalized patients. We report a series of colistin-resistant *Klebsiella pneumoniae* blood isolates from Israel, and explore their resistance mechanisms using whole genome sequencing (WGS). **Methods:** Patients with colistin-resistant *Klebsiella pneumoniae* bloodstream infection (BSI) were identified over a 10-year period (2006-2016) utilizing the electronic medical record at the Shaare Zedek Medical Center in Jerusalem, Israel. Patient demographic and clinical data were collected and antibiotic susceptibility testing (AST) performed using three commercial platforms. Long and short read sequencing were performed on a PacBio RS II (Pacific Biosciences) and an Illumina Miseq (Illumina), respectively. **Results:** Thirteen patients with colistin-resistant *Klebsiella pneumoniae* BSI were identified, and seven isolates from seven different patients were successfully revived. Patient records indicated that five of the patients were previously treated with colistin. AST indicated that six of the seven isolates were colistin resistant and four isolates were resistant to carbapenems. WGS assigned the isolates to four distinct clusters that corresponded to *in silico*-derived multi-locus sequence types (MLST). Two isolates were genetically identical, but all other isolates, even those within the same sequence type (ST), contained sufficient single nucleotide polymorphism (SNPs) to assign them to different strains. Three isolates carried bla_{KPC-3} on two different plasmids and one isolate carried bla_{OXA-48} on a novel IncL/M plasmid. *Mcr* was not detected in any isolate, but all colistin resistant isolates carried a variety of different mutations that inactivated the *mgrB* gene. **Conclusions:** We report the first comprehensive analysis of a large series of colistin-resistant *Klebsiella pneumoniae* from Israel. A diverse set of isolates were obtained and colistin resistance was found to be attributed to different mechanisms that ablated the *mgrB* gene. Notably, carbapenemase genes were identified in four isolates and were carried on novel plasmids.

Board 198. In Vitro Antimicrobial Activity of Fosfomycin Tromethamine against Urinary Extended Spectrum Beta-Lactamase-Producing *Escherichia coli* and *Klebsiella pneumoniae*

M. Khan
Abbas Institute of Medical Sciences, Muzaffarabad, Pakistan

Background: Urinary tract infections (UTIs) are common infectious diseases in clinical practice. *Escherichia coli* and *Klebsiella pneumoniae* are the most common infecting organisms in patients with uncomplicated UTI. Resistance against most of the commonly used antibiotics used for treating these infections is increasing. Fosfomycin tromethamine is one of the antibiotics which are effective against most of the bacteria causing UTIs especially extended spectrum beta lactamase (ESBL) producing bacteria. These bacteria are resistant to most of the other commonly prescribed antibiotics used to treat these infections. The objective of this study was to determine the in vitro antimicrobial activity of fosfomycin tromethamine in ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* causing urinary tract infections. **Methods:** This descriptive study was carried out at Abbas Institute of Medical Sciences, Muzaffarabad from January, 2017 to December, 2017. Urine specimens were inoculated on cysteine lactose electrolyte

deficient (CLED) agar and incubated at 37°C for 18-24 hours. After identification; the isolates were screened for ESBL with cefotaxime 30 µg disc by Kirby-Bauer disc diffusion technique. The isolates with cefotaxime zone diameter ≤ 27 mm were further confirmed for ESBL by phenotypic confirmatory test by applying cefotaxime clavulanic acid 30/10 µg combination disc. The inoculums of bacterial suspensions were plated on Mueller-Hinton agar with subsequent application of Fosfomycin tromethamine disc 200 µg. Plates were incubated overnight aerobically and zone diameters were interpreted. **Results:** Out of 84 ESBL producing gram-negative isolates, 81% (*n=68*) were identified as *E. coli* and 19% *(n=16*) as *Klebsiella pneumoniae.* The age of the patients in ESBL producing urinary isolates ranged from 1 to 80 years, with larger numbers around 60 years of age. According to the study results, 65% (*n=44*) of *Escherichia coli* and 75% (*n =12*) of *Klebsiella pneumoniae* were susceptible to Fosfomycin tromethamine, while 11.76 % (*n=8*) of *Escherichia coli* were sensitive intermediately. **Conclusions:** Fosfomycin has shown good activity against ESBL producing *E coli* and *Klebsiella pneumoniae* emphasizing its role to be used in empirical therapy for uncomplicated lower urinary tract infections caused by these uropathogens.

Board 199. KPC Carbapenemase Is Common among Carbapenem-Resistant Enterobacteriaceae in Connecticut, but Other Mechanisms Have Been Detected, 2017

B. Macierowski, MS, M(ASCP)[1], A. Durante Ph.D., M.Sc.[2], M. Maloney, MPH[3], J. Razeq, Ph.D., HCLD (ABB)[1]
[1]Connecticut Department of Public Health, Dr. Katherine A. Kelley Public Health Laboratory, Rocky Hill, CT, USA, [2]UConn Health, Farmington, CT, USA, [3]Connecticut Department of Public Health Healthcare Associated Infections/Antimicrobial Resistance Program, Hartford, CT, USA

Background: Carbapenem-resistant *Enterobacteriaceae* (CRE) of all genus and species isolated from sterile sites, sputum, and urine are laboratory-reportable in Connecticut. *Enterobacteriaceae* are considered CRE if they are resistant to at least one carbapenem. Beginning in 2017, clinical laboratories are required to submit CRE isolates to the state public health laboratory (SPHL) facilitating routine characterization testing. **Methods:** Starting in 2017, the CT SPHL collected CRE isolates submitted by clinical laboratories statewide for characterization. All isolates submitted for testing underwent species confirmation using bioMérieux's API 20E. Isolates were then screened for carbapenemase activity using the modified Carbapenem Inactivation Method (mCIM). Finally, CDC protocols for multiplex real-time PCR were used to identify bla_{KPC}, bla_{NDM}, Oxa-48-like, and bla_{VIM} gene targets. Those isolates that tested positive on the mCIM but did not test PCR-positive at the CT SPHL were forwarded to the Antibiotic Resistance Laboratory Network (ARLN) regional laboratory at Wadsworth Center (Albany, NY) and the Centers for Disease Control and Prevention (CDC) (Atlanta, GA) for further testing. **Results:** During 2017, the CT SPHL received 198 isolates for CRE testing. The most common organisms were *Enterobacter cloacae* (40%), *Klebsiella pneumoniae* (36%), and *Escherichia coli* (13%). Of these isolates, 58 (29%) were characterized as carbapenemase-producing CRE (CP-CRE). The percentage of isolates that were CP-CRE varied by organism at 10% for *Enterobacter cloacae*, 72% for *Klebsiella pneumoniae*, and 13% for *Escherichia coli.* Of the CP-CRE: 50 (86%) were positive for bla_{KPC}, 4 (7%) were positive for bla_{NDM}, 2 (3%) were positive for OXA-48, and 2 (3%) were PCR-negative at CT SPHL. The two PCR negative, *Enterobacter cloacae* isolates, collected from a single patient, tested positive on a multiplex PCR targeting bla_{NMC-A} and bla_{IMI} at the Centers for Disease Control and Prevention. **Conclusions:** Connecticut surveillance data show that the most common mechanism for carbapenem resistance among CP-CRE statewide was bla_{KPC}; however, other carbapenemase mechanisms (i.e., bla_{NDM}, and OXA-48,) are beginning to emerge.

Board 200. Molecular Characterization of Carbapenem-Resistant *Acinetobacter baumannii* in the United States, 2013-2015

J. Daniels, V. Albrecht, N. Vlachos, V. Stevens, J. Rasheed, M. Karlsson, A. Halpin
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: *Acinetobacter baumannii* is an opportunistic healthcare-associated pathogen. The Centers for Disease Control and Prevention (CDC) has designated multidrug-resistant (MDR) *A. baumannii* as a serious threat. While carbapenems are the drugs of choice for treating MDR *Acinetobacter*, carbapenem resistance is increasing. Carbapenem resistance in *Acinetobacter* may be due to a variety of mechanisms, including OXA-type carbapenemases, which may be either intrinsic or acquired. Genes encoding OXA-23, -24/40, and -58-like enzymes are most clinically relevant since they commonly are carried on mobile genetic elements that can spread rapidly. Our objective was to describe the molecular epidemiology of carbapenem-resistant *A. baumannii* (CR-AB) in the United States, specifically those harboring OXA-23, a globally successful carbapenemase in CR-AB. **Methods:** During 2013-2015, *A. baumannii* isolates were obtained from 16 geographically diverse US sites through CDC's surveillance and reference activities. Each isolate underwent species identification by MALDI-TOF MS, reference antimicrobial susceptibility testing (AST), and whole genome sequencing (WGS). Isolates were sequenced on a MiSeq benchtop sequencer (Illumina, San Diego, CA) and data were processed and analyzed with in-house pipelines for quality, species identity, antimicrobial resistance genes, and multilocus sequence type. **Results:** In total, 106 CR-AB isolates were confirmed. Sequence analysis revealed that while 104/106 (98%) harbored at least one bla_{OXA} gene, 72% (76/106) harbored two bla_{OXA} carbapenemase genes. Half (n=53) harbored a bla_{OXA-23} gene; 33 (63%) of these were sequence type (ST) 2. Eleven (69%) of 16 sites submitted at least one bla_{OXA-23}-harboring ST2 CR-AB. Although resistant to carbapenems, the majority of the bla_{OXA-23}-positive isolates remained susceptible to colistin (74%) and minocycline (88%). **Conclusions:** The bla_{OXA-23} gene is frequently associated with carbapenem resistance among *A. baumannii* in the United States. Of concern, the majority of the bla_{OXA-23}-harboring isolates belonged to ST2, a highly successful clone reported worldwide. The distribution of OXA-23 ST2 CR-AB across the US may have important implications for infection control and containment. In addition, since treatment options for CR-AB are limited, this further underscores the importance of antibiotic stewardship.

Board 201. Pharmacoeconomic Evaluation of Meropenem Versus Imipenem/Cilastatin in Hospital and Ventilator-Acquired Pneumonia (HAP/VAP), Alexandria, Egypt, 2017

M. Abdel-Aty[1], E. Mohamed[2], S. Abdelmoneim[3], I. Momtaz[4], E. Mohammed Ahmed Hassan[5]
[1]Ministry of Health, Mansoura, Egypt, [2]Alexandria directorate of Health Affairs,Ministry of Health, Alexandria, Egypt, [3]Ras El-Teen General Hospital,Minstry of Health, Alexandria, Egypt, [4]Andalusia Hospital, Alexandria, Egypt, [5]Mabaret Al-Asafra Hospital,Ministry of Health, Alexandria, Egypt

Background: Hospital and Ventilator-Acquired Pneumonia (HAP/VAP) are a leading cause of mortality among patients with hospital-acquired infections (20-50%). Besides, antibiotic misuse and resistance are major worldwide public health problems especially in Egypt where consuming of carbapenems is increasing. This imposes increased economic burden on the Egyptian health care budget (Egypt/USA: 5.6/17.1 of % GDP, 2014). The aim of this retrospective study was to evaluate the cost-effectiveness and cost-benefit of imipenem/cilastatin vs. meropenem (2 g vs. 3 g daily) in the management of HAP/VAP in Alexandria hospitals, Egypt, 2017. **Methods:** Data were collected from five hospitals (Alexandria University Hospital, Raselteen General Hospital, Andalusia Smoha Hospital, Andalusia El-Shlalat Hospital and Mabaret El-Asafra Hospital). All patients, admitted between November 2016 & April 2017 and fullfiling eligibility criteria according to *IDSA* guidelines, were enrolled in this study. Fifty and Sixty-Four patients were assigned for imipenem/cilastatin and meropenam arms, respectively. Statistical and economic analyses were performed using *SPSS (v.20)*. Cost-effectiveness and cost-benefit analyses were evaluated from healthcare provider and governmental perspectives, respectively. Direct costs and net benefits were expressed in *Egyptian Pounds (EGP).* A decision tree was modeled to estimate the clinical outcomes (Length of Stay (LOS) & Mechanical Ventilation (MV) days) and direct costs for both arms. One-way sensitivity analysis was performed. The Average Cost-Effectiveness Ratio (ACER), Benefit/Cost (B/C) ratio and net benefit were calculated. **Results:** Although there was no statistically significant difference between both carbapenems in LOS ($P>0.05$) and MV days ($P>0.05$) using Mann–Whitney U test, it was estimated that LOS for imipenem/cilastatin vs. meropenem was economically different with additional cost. For Cost-effectiveness analysis, the total costs of therapy were estimated as 16524 & 15795 EGP and ACERs were 289.8 & 254.75 EGP for imipenem/cilastatin and meropenam, respectively. For cost-benefit analysis, B/C ratio was 70 & 72 EGP for imipenem/cilastatin and meropenem, respectively and the net benefit was 773 EGP. **Conclusions:** The management of pneumonia (HAP/VAP) with meropenam has been shown to be more both cost-effective and cost-benefit if compared with imipenem/cilastatin.

Board 202. Identifying the Misidentified: Detecting *Candida auris* through the Antibiotic Resistance Laboratory Network, United States, 2017

K. Forsberg[1,2], E. Berkow[1], S. Lockhart[1], S. Chaturvedi[3], J. Fischer[4], P. Snippes Vagnone[4], S. Hun[5], R. Ruiz[5], E. Holodnick[6], N. Smith[6], T. Henning[1], S. Gumbis[1], J. Patel[1], B. Jackson[1], S. Vallabhaneni[1]
[1]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [2]IHRC, Inc., Atlanta, GA, USA, [3]Wadsworth Center, New York State Department of Health, Albany, NY, USA, [4]Minnesota Department of Health, St. Paul, MN, USA, [5]Washington State Department of Health, Shoreline, WA, USA, [6]Tennessee Department of Health, Nashville, TN, USA

Background: *Candida auris* is an emerging multidrug-resistant yeast that spreads in healthcare settings. Infection control interventions are needed to prevent its transmission. *C. auris* can be misidentified as other yeasts (most frequently as *Candida haemulonii*) by identification methods commonly used in clinical laboratories. The CDC Antibiotic Resistance Laboratory Network (AR Lab Network) which funds seven regional public health laboratories was initiated in 2016 to provide advanced laboratory capacity to detect and control drug-resistant organisms. We report on detection of *C. auris* through the AR Lab Network in the United States in 2017. **Methods:** Through extensive outreach, clinical laboratories were asked to submit confirmed or suspected *C. auris* isolates, including local species identification, from any specimen source to their regional laboratory for definitive identification. Four of seven regional laboratories (MN, NY, TN, and WA) began *Candida* species identification in 2017; species identification was performed using matrix assisted light desorption/ionization-time of flight. **Results:** The AR Lab Network performed species identification on 401 isolates from 335 patients. *C. auris* was confirmed for 169 (42.1%) isolates. These 169 isolates had been identified at clinical laboratories as *C. auris* (43.8%), *C. haemulonii* (22.5%), suspected *C. auris* without species specified (15.4%), unspecified yeast (14.8%), *Candida famata* (0.6%), and other species (1.8%). Of isolates submitted as *C. auris,* 94.9% were confirmed to be *C. auris.* Of isolates originally identified as *C. haemulonii*, 60.3% were confirmed as *C. auris* (94.1% of blood isolates and 85.7% of urine isolates). The NY regional laboratory identified 109 patients with *C. auris*, MN identified ten, and TN identified one. **Conclusions:** The AR Lab Network is able to help identify *C. auris* cases. Over half of *C. haemulonii* isolates were confirmed as *C. auris*, highlighting the importance of confirmatory testing for such isolates. Most *C. auris* cases were identified in NY, where an outbreak of *C. auris* has been documented; however, isolated cases were identified by other AR Lab Network regional laboratories, enabling rapid implementation of containment measures. The AR Lab Network should continue to be leveraged to detect this emerging fungal pathogen.

Board 203. Characterizing *Candida* Species Identification Isolate Submission to the Southeast Regional Laboratory for the US Antibiotic Resistance Laboratory Network (ARLN)

N. Smith[1], D. Baynham[2], N. Lindhal[2], P. Gibbs[2], M. Kainer[1]
[1]TN Department of Health, Nashville, TN, USA, [2]TN Department of Health Laboratory Services, Nashville, TN, USA

Background: *Candida auris*, an emerging multi-drug resistant fungal pathogen found in healthcare settings, is unlike other fungal species found in healthcare settings because it persists in the environment and spreads easily from patient to patient. Identification of *Candida auris* in a timely manner is critical to prevent the spread of this organism. Timely identification in clinical laboratories is hindered by misidentification of *Candida auris* as other *Candida* species by commercial systems. Characterizing *Candida* isolates submitted to the Southeast ARLN regional laboratory helps inform guidance to laboratories and provides situational awareness of common machine misidentifications in the region. **Methods:** *Candida* isolates submitted to the Southeast ARLN regional laboratory from February through December of 2017 were included for analysis. Species identification of isolates submitted was confirmed by Bruker Biotyper brand matrix assisted laser de-

sorption-ionization time of flight (MALDI-TOF) software version 4.1. Data were obtained from the laboratory information management system (STARLIMs) and cleaned and aggregated into a comma separated values (.csv) file using R. Data was visualized and summarized using Tableau. **Results:** 43 *Candida* isolates were submitted to the Southeast ARLN. Isolates were predominately submitted by Tennessee (49%) and Florida (44%) facilities. Regional isolate submission was visualized using maps of isolate submission by public health laboratory and patient state of origin. Vitek-2 and MALDI-TOF were the two most frequently used identification methods characterizing 57.1 and 26.2 percent of isolates, respectively. Of the 11 isolates tested by clinical laboratories using MALDI-TOF 4 (36%) clinical species did not match the ARLN species. For Vitek-2, of 25 isolates tested 22 (83%) did not match the ARLN species including 5 isolates from one patient identified by the clinical laboratory as *Candida haemulonii* but confirmed at the ARLN as *Candida auris*. **Conclusions:** Situational awareness of *Candida* identification methods used in clinical laboratories can help identify gaps and improve recommendations to rapidly identify and prevent the spread of *C. auris*. Laboratory instruments should use up to date software and associated databases should include *Candida auris*.

Board 204. Antibiotic Use and Drug-Resistant Late-Onset Infections among Neonates Admitted to Neonatal Intensive Care Units in Pune, India

M. Robinson[1], S. Agarkhedka[2], D. Armstrong[1], R. Bharadwaj[3], S. Cox[4], V. Dohe[3], A. Gupta[1], N. Gupte[1], J. Johnson[1], A. Kadam[5], A. Kinikar[3], S. Malwade[2], Y. Manabe[1], V. Mave[1], A. Milstone[1], T. Parikh[6], U. Rajput[3], B. Randive[5], R. Smith[7], N. Suryavanshi[5], U. Vaidya[6], M. Westercamp[7]
[1]Johns Hopkins School of Medicine, Baltimore, MD, USA, [2]D. Y. Patil Medical College, Pune, India, [3]Byramjee-Jeejeebhoy Government Medical College, Pune, India, [4]Johns Hopkins University School of Medicine, Baltimore, MD, USA, [5]Byramjee-Jeejeebhoy Government Medical College-Johns Hopkins University Clinical Research Site, Pune, India, [6]K. E. M. Hospital, Pune, India, [7]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Late-onset infections are common among neonates admitted to the neonatal intensive care unit (NICU) in low- and middle-income countries. Rising antimicrobial resistance has been reported in Indian NICUs, but has not been described in the context of antibiotic use. **Methods:** Neonates admitted to NICUs in 3 hospitals in Pune, India were prospectively observed from May 1, 2017 through January 10, 2018. Clinical characteristics, antibiotic use, and microbiology results were obtained prospectively from the medical record. Early antibiotic use was defined as antibiotic use in the first 3 days of life. **Results:** During the study period, 3,275 neonates were admitted to NICUs. Median gestational age was 36 weeks (interquartile range [IQR], 33-38); median birth weight was 2 kg (IQR, 1.6-2.6 kg); 2833 (87%) neonates were inborn. Sources of culture for neonates suspected of sepsis included blood (n = 834, 26%), cerebrospinal fluid (CSF) (n = 252, 8%), and urine (n = 44, 1%). Early onset bacteremia was detected in 38 (1%) neonates. Late onset Gram negative (GN) infections were detected in 84 (3%) neonates; 73 had bacteremia, 11 had positive CSF cultures, and 1 had a positive urine culture. The most common GN isolates were *Klebsiella* (n = 40, 48%), *Acinetobacter* (n = 24, 29%), and *Citrobacter* (n =7, 8%). Late onset Gram positive infections occurred in 44 (1%) neonates, and late onset candidemia occurred in 20 (1%) neonates. Among patients with late-onset GN infections, 89% were resistant to third generation cephalosporins and 49% were resistant to carbapenems. Early antibiotics use was recorded for 907 (29%) neonates, most commonly amikacin (28%) and piperacillin/tazobactam (14%). Among neonates with late-onset GN infections, early antibiotic use was associated with resistance to third generation cephalosporins (odds ratio [OR] 7.4, 95% confidence interval [CI], 1.2-81.6) and carbapenems (OR 3.5, 95% CI 1.2-11.7). Among all neonates, early antibiotic use was associated with candidemia (OR 3.7, 95% CI 1.4-10.6). **Conclusions:** Candidemia and carbapenem-resistant organisms were common among neonates with late-onset infections and were associated with early antibiotic use. Further research on the potential for antibiotic stewardship to impact antimicrobial resistance in NICUs in India is warranted.

Board 205. Predicting Bacteria Detection in Pediatric Acute Gastroenteritis to Encourage Appropriate Treatment

G. Tarr, S. Freedman
University of Calgary, Calgary, AB, Canada

Background: Acute gastroenteritis (AGE) caused by several established and emerging pathogens is one of the largest causes of morbidity in children worldwide. In high income settings, clinical management of AGE is often guided by knowledge about the causative agent. However, routine etiologic testing is not recommended for AGE, and guidelines suggesting when to test are inconsistent, leaving many infections unrecognized. In the absence of knowledge about the causative agent, empiric treatment can result in unnecessary interventions, including inappropriate antimicrobial use. **Methods:** We developed a predictive model to distinguish between children with diarrhea likely to test positive for a bacteria and those not. We used data from the Alberta Provincial Pediatric EnTeric Infection TEam (APPETITE) study, a prospective cohort of children <18 years-old with ≥3 episodes diarrhea in 24 hours presenting in the emergency departments of two large Alberta children's hospitals, Dec. 2014-Jan. 2018. All APPETITE participants were tested for 18 pathogens. We used lasso penalized regression to identify a model with the minimum number of characteristics out of 19 potential predictors to best predict bacteria test positivity and bootstrapped our dataset to determine the stability of our estimates. *C. difficile* (only in children ≥2 years-old) and non-*C. difficile* (NCD) bacteria were analyzed separately. We summarized model performance using sensitivity and number of children who would need to be tested to identify one positive for a bacteria (NNT). **Results:** Of 1,159 children with diarrhea, 121 were positive for a bacteria when tested, including 15 with *C. difficile* and 109 with NCD bacteria. Maximizing area under the curve, the most predictive model for both outcomes included all 19 variables. The model for *C. difficile* had NNT = 2 and sensitivity = 14%. The model for NCD bacteria had NNT = 2 and sensitivity = 10%. By changing the discrimination threshold, sensitivity can be increased (e.g. to 79% for NCD bacteria), with a corresponding increase in the NNT (e.g. to 5). **Conclusions:** By predicting which children with diarrhea are most likely to test positive for a bacteria, clinicians can target their testing to improve resource use and increase case ascertainment. Better knowledge of the causative agent supports the use of appropriate interventions, such as antimicrobials.

Board 206. Parental Knowledge, Attitude and Practices Regarding Antibiotic Usage among Children under Five in Pakistan

M. Ranjha, M. Khan, M. Salman, J. Ansari
National Institute of Health, Islamabad, Pakistan

Background: The emergence of anti-microbial resistance (AMR) is a serious public health threat globally. The blame falls on both the general public as well as medical practitioners. The study was designed to determine the knowledge, attitudes and practices among parents towards antibiotic use for under-5 children in Pakistan. **Methods:** A cross-sectional survey using pre-tested, structured questionnaire was conducted during July-October 2016. A total of 270 parents of <5 years age children who presented in outpatient pediatric department of PIMS, Islamabad were randomly enrolled. Information regarding demographics, antibiotic usage, side effects and resistance was taken. Lickert scale was used to score responses (1=Strongly Disagree, 2=Disagree, 3=Neutral, 4=Agree, 5=Strongly Agree). Knowledge was graded as low (0-5 correct responses), moderate (6-7 correct responses) and high (8-11 correct responses). Attitude was classified as negative (0-3 correct responses) and positive (4-7 correct responses). Median score with inter quartile range (IQR), correlation-coefficient (r) and Pearson Chi-square test was calculated. **Results:** 60.7% (n=164,) of the respondents had low 27.8% (n=75,) 27.8% (n=75) had moderate and 11.5% (n=31) showed high level knowledge regarding antibiotic usage. Median score for knowledge remained 05 (IQR 5-4). 74% (n=200) thought antibiotics are effective for cough. 70% (n=189) respondents used antibiotics as self-medication. 61% (n=162) has used leftover medicines and 30% (n=81) shared other siblings medicine. Knowledge remained a predictor for positive attitude ($r=0.07$, $p<0.05$). 21.9% (n=60) of the respondents showed positive attitude towards antibiotics usage. The median score for attitude was 02 (IQR 3-2). Agreement that doctors often prescribe antibiotics to meet the patient's expectation remained 36% (n=97). Low education levels, non-medic families and low socioeconomic status had low knowledge and a negative attitude ($p<0.05$). **Conclusions:** There is a dire need to initiate public educational awareness campaigns and wide range interventions across all health sectors to overcome irrational use of antibiotics and the emergence of resistance in Pakistan.

Board 207. Developing and Implementing Antibiotic Stewardship in ICU Setting: Prospective Interventional Pilot Study, Cairo, Egypt, 2016

M. Abdel-Aty[1], S. Mesriga[2], A. Abo-Almagd[2]
[1]Ministry of Health, Mansoura, Egypt, [2]Ministry Of Health, Cairo, Egypt

Background: Antibiotic resistance is an emerging global health problem. Besides, antibiotic misuse is a major worldwide public health problem especially in Egypt where consuming of antibiotics is increasing without adopted national antibiotic stewardship. This imposes increased economic burden on the health care systems with limited budget (e.g. Egypt/USA: 5.6/17.1 of % GDP, 2014).The aims of this prospective interventional study were to develop and implement a local antibiotic policy by applying antibiotic stewardship strategies at ICU setting and evaluating the adherence to the implemented policy. **Methods:** All patients admitted to ICU of Ahmed Maher Teaching hospital, Cairo (August- October 2016) were included in this study. An antibiogram was developed based on culture sensitivity from isolates of urine, sputum, blood and swab, one year earlier. Local antibiotic policy was approved based on a harmony between the antibiogram and the updated international antimicrobial guidelines (e.g. IDSA and Sanford). Daily interventions and recommendations for antibiotic selection, dose, duration and route of administration were documented by clinical pharmacists. Statistical analysis was performed using SPSS (v.20). **Results:** During three months' interventional period, seventy-seven cases were reviewed, 55 % were females and the average age and weight were (64±12.66, 76.5±10.33) respectively. The most frequent co-morbidities were cardiovascular, renal, diabetes and hepatic diseases. The most commonly prevalent infections were community, hospital and aspiration pneumonia and line infections. Sixty drug-related problems were collected including: violation of protocol (68.3%), inappropriate dose (25%), inappropriate duration (3.3%) and inappropriate route (3.3%). Interventions recommended by clinical pharmacists were sixty including: implementing antibiotic policy (65.6 %), optimizing dose (23.3%), de-escalation (11.6%) optimizing duration (5%) and switching to oral route (3.3 %). Total number of accepted interventions was Fifty (83%) including: Implementing antibiotic policy (54%), optimizing dose (26%), de-escalation (10%) optimizing duration (6%) and switching to oral route (4%). **Conclusions:** Developing and implementing the Egyptian antibiotic stewardship is an inevitable issue for enhancing rational antibiotic use and minimizing antibiotic resistance at the national level.

Board 208. Implementation of Antimicrobial Stewardship and Infection Control and Prevention Practices in Long-Term Care Facilities—Pennsylvania, 2017

N. M'ikanatha[1], S. Boktor[1], A. Seid[1], A. Kunselman[2], J. Han[3]
[1]Pennsylvania Department of Health, Harrisburg, PA, USA, [2]Division of Biostatistics and Bioinformatics, Department of Public Health Sciences, Penn State College of Medicine, Hershey, PA, USA, [3]Division of Infectious Diseases, Department of Medicine, Center for Clinical Epidemiology and Biostatistics, and Department of Biostatistics and Epidemiology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA

Background: Given the increasing emergence of multidrug-resistant organisms (MDROs) in long-term care facilities (LTCFs), there is an urgent need for effective antimicrobial stewardship (AS) and infection prevention and control (IPC) programs in this setting. The objective of our study was to evaluate the scope of AS and IPC programs in Pennsylvania (PA) LTCFs. **Methods:** In 2017, an electronic survey was sent to representatives of all 702 LTCFs licensed by the PA Department of Health. The survey included questions on the status of AS and IPC programs, as well as existing surveillance and precaution practices for MDROs. Facilities were also asked about challenges to implementing effective AS and IPC programs. **Results:** Responses were obtained from 244 (35%) of all LTCFs, located in 85% of PA counties. Forty percent of facilities were free-standing; median capacity was 111 beds. While nearly 90% of LTCFs had an existing IPC program, only 47% had a formal AS program (84 of 179 LTCFs with a non-missing response). Staffing of AS programs varied: 94% included nurses, 85% included a pharmacist, 16% included an infectious diseases (ID) physician, and 2% had clinical microbiology involvement. The majority (75%) of programs were led by registered nurses. Regarding AS practices, 145 (80%) had pharmacist management of antibiotic orders, 43 (24%) utilized an ID consult service, and 23 (13%) used formulary restriction with preauthorization. A total of 115 (63%) of 183 reporting LTCFs used prospective audit and feedback and 67

(37%) of 179 reporting facilities used antibiotic de-escalation. Of 193 responding LTCFs, 105 (54%) reported performing surveillance for MDROs. Ninety percent of these LTCFs reported implementing contact precautions for any MDROs; 156 (90%) and 125 (72%) required them for MRSA and CRE respectively. Challenges to implementing effective AS programs included staffing constraints (28%), inadequate education (26%), insufficient microbiology resources (16%), and lack of leadership support (9%). **Conclusions:** Our survey found that less than half of Pennsylvania LTCFs had formal AS programs. There was also considerable variation in both AS and IPC practices across facilities. Effective strategies and targeted resources are needed to improve AS and IPC programs and reduce the further emergence of MDROs in LTCFs.

Board 209. Policy Writing Tools and Workshops as a Way to Advance Antibiotic Stewardship in Long-Term Care

A. Beaudoin[1], P. Gahr[1], T. Hale[1], C. Parker[2], J. Lilleberg[1], J. Walters[1], R. Lynfield[1]
[1]Minnesota Department of Health, Saint Paul, MN, USA, [2]University of Minnesota School of Nursing, Minneapolis, MN, USA

Background: To a greater degree than other healthcare settings, professionals in long-term care (LTC) facilities have significant constraints on human and material resources for antibiotic stewardship (AS). AS leaders in LTC often have several concomitant responsibilities, low levels of AS expertise, and few opportunities for content-specific training. However, to comply with US Centers for Medicaid and Medicare Services conditions of reimbursement, LTC facilities must have AS protocols and be tracking antibiotic use. **Methods:** With a multi-step approach, Minnesota Department of Health (MDH) supported LTC AS protocol needs. First, a sample antibiotic stewardship policy was developed to outline a LTC facility's documented commitment and operational approach to AS. The sample policy aligns with Center for Disease Control and Prevention's (CDC) Core Elements of AS for Nursing Homes. A "companion guide" was developed to accompany the sample policy and walk LTC facilities through the policy-writing process. Both documents were reviewed, co-branded, and cross-promoted by Minnesota LTC industry partners and the state's hospital association and quality improvement organization. Second, MDH piloted a structured half-day policy writing workshop. Workshop facilitators provided section-by-section support for document development, with explanation of CDC's AS Core Elements, considerations for translating actions into written protocols, and experience sharing. Participating facilities were encouraged to involve multiple staff and complete a pre-workshop worksheet with information needed for policy writing. **Results:** Feedback from LTC facilities in Minnesota and beyond has been positive for the sample policy. Partner co-branding and promotion prevented resource duplication and enhanced confidence in document content. Multiple facilities used the resource to meet minimum state AS honor roll requirements. Twelve LTC staff from 8 facilities attended the pilot workshop. In a post-survey, all respondents (n=11) agreed that the workshop helped them understand AS concepts and led to a completed or improved policy. **Conclusions:** MDH's AS sample policy for LTC has been easy for facilities to understand and adapt, despite limited staff time and resources. Workshops focused on tangible AS deliverables could be a way to make time spent receiving AS education more valuable.

Board 210. Using Web-based Seminars for Healthcare and Public Health Professionals to Increase Knowledge on Emerging Antimicrobial Resistance in Latin America

H. Maldonado[1], L. Castillo[2], C. Valenzuela[2], A. Espinosa[3], J. Bryan[3]
[1]Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Unidad Central de Referencia para la Vigilancia Epidemiologica, Laboratorio Nacional de Salud, Guatemala, Guatemala, [3]Division of Global Health Protection, Central American Regional Office Centers for Disease Control and Prevention, Guatemala, Guatemala

Background: Antimicrobial resistance (AMR), including multi-drug-resistance in healthcare settings, is a growing problem in Latin America. To expand knowledge on emerging AMR among Latin American health professionals and strengthen detection of resistance, we coordinated no cost webinars for healthcare providers, public health institutions and health research centers in Latin America. **Methods:** Topics and speakers were determined in collaboration with the Guatemalan National Antimicrobial Resistance Technical Working Group, the Pan American Health Organization (WHO/PAHO), and the Centers for Disease Control and Prevention. From February 2017 to January 2018, 15 one-hour, Spanish-language, webinars were held. Thematic areas included the WHO Global Action Plan on AMR, drug-resistant organisms, AMR mechanisms, drug susceptibility testing, rational use of antimicrobials, and strategies to combat AMR. **Results:** Registrants included 88 professionals from Belize, Guatemala and Mexico representing microbiologists (56%), physicians (30%), laboratory technicians (5%), and other (8%). Sixty-one percent of registrants were from public institutions. The top drug-resistant threats emphasized included *Salmonella* and *Shigella,* carbapenem-resistant and extended spectrum beta-lactamase producing Enterobacteriacea, non-fermentative gram-negative bacilli, methicillin-resistant *Staphylococcus aureus*, vancomycin-resistant enterococci, group A and B streptococci and *Streptococcus pneumoniae*. Detection of emerging antifungal resistant pathogens such as *Candida auris* was also addressed. **Conclusions:** This effort offered updated information on diagnostic methods to detect and report AMR appropriate for middle-income countries and reference centers; increased awareness of the emergence of new resistant organisms; discussion on the changes in drug susceptibility patterns; improved AMR surveillance information exchange among local, national, regional, and global health institutions; and dissemination of the latest national and global policies to combat AMR. We plan to expand this initiative to detect, prevent, and respond to other priority organisms such as *Neisseria gonorrhoeae* and *Campylobacter* as well as advance AMR surveillance and antimicrobial stewardship programs in the region.

Hepatitis / HIV / STDs / TB

Board 211. Assessment of Risk Behaviors and Sex-Seeking Practices among Male Active Duty Sailors and Marines Infected with HIV, 2010-2016

R. Payne[1], V. Paul[2], G. Nowak[3]
[1]Battelle Memorial Institute, Hampton, VA, USA, [2]Booz Allen Hamilton, Norfolk, VA, USA, [3]Navy and Marine Corps Public Health Center, Portsmouth, VA, USA

Background: Department of Defense (DOD) policy requires the screening of active and reserve components of the US military for HIV

every two years. To help better understand risk behaviors unique to the military, a behavioral reporting process was proposed by the Navy and Marine Corps Public Health Center's (NMCPHC) Sexual Health and Responsibility Program and adopted in 2010. The process provides data on HIV-related risk behaviors and sex-seeking practices among recently diagnosed individuals. Since 2014, the data gathered from this process has been analyzed by the NMCPHC's EpiData Center, providing relevant information used to inform Department of the Navy (DON) HIV prevention and policy efforts. **Methods:** Anonymous cases reports were entered into a secure database encompassing a timeframe from 2010 to 2016 and are analyzed on a yearly basis. Only reports from male active duty Sailors and Marines were included in analysis as very few female reports are received. Descriptive analyses of demographics and risk behaviors were conducted to review population differences, as well as identify key factors that could be addressed in training or prevention efforts. Relationships between sexual orientation and demographics, select risk behaviors, and locations where personnel met or had sex with partners were also assessed. Analyses were conducted utilizing SAS software version 9.4 (Cary, North Carolina). **Results:** Cases most frequently identified as Black (41.0%) or White (38.9%) race, were between the ages of 17 to 24 years, and had a marital status of single. During the twelve months prior to diagnosis, the most frequently identified risk behaviors included sex with a male (66.3%), sex with an anonymous partner (54.2%), sex with a female (45.6%), and sex while intoxicated and/or high on drugs (34.5%). No significant associations between men who have sex with men (MSM) status and risk behaviors were identified. The most common sex-seeking practice was meeting sexual partners on the internet (49.4%). Analysis showed that MSM were about twice as likely to meet their partners online as heterosexual men. **Conclusions:** This analysis provides a systematic and comprehensive description of risk behaviors for male DON service members recently diagnosed with HIV infection, utilizing an established behavioral reporting system in the DON.

Board 212. Co-Occurrence of HIV, HBV, and HCV Infections in Tennessee by Region

H. Wingate, L. Sizemore, M. Brantley, J. Black, S. Mathieson, R. Octaria, K. Thure, T. Sondgerath, C. Wester
Tennessee Department of Health, Nashville, TN, USA

Background: Tennessee (TN) had the 17th highest rate of newly diagnosed Human Immunodeficiency Virus (HIV) in the nation in 2015, and the 2nd highest and 4th highest case rates nationally for acute hepatitis B (HBV) and acute hepatitis C (HCV) in 2015, respectively. The extent to which these infections overlap is unknown. The objectives of this analysis are to estimate the overlap between HIV, HBV, and HCV infections among Tennesseans and characterize geographic variations. **Methods:** A unique dataset of HIV, HBV, and HCV cases was generated at the end of 2016 using TN's Enhanced HIV/AIDS Reporting System (eHARS) and the National Electronic Disease Surveillance System (NEDSS) Based System (NBS). Using a three-step matching algorithm, NBS cases were matched to eHARS cases to determine number of HIV, HBV, and/or HCV co-infections that occurred statewide and regionally. **Results:** As of 12/31/2016, 17,489 persons were living with diagnosed HIV with the preponderance in West and Middle TN (12.7% in East, 42.3% in Middle, and 45.0% in West). In contrast, reported acute/chronic HBV (n=17,597) and reported acute/chronic HCV (n=64,661) infections were more evenly distributed across the state. Of persons co-infected, 889 were HIV/HCV (20.5% in East, 40.6% in Middle, 38.9% in West), 743 were HIV/HBV (8.5% in East, 45.2% in Middle, and 46.3% in West), and 2,212 were HBV/HCV (49.6% in East, 30.7% in Middle, and 19.7% in West). Co-infection proportions were highest in Middle and West TN with the exception of HCV/HBV, which was predominantly found in East. Tri-infections were relatively rare (n=71) and were predominately in Middle and West TN as compared to East TN (15.5% in East, 47.9% in Middle, and 36.6% in West). **Conclusions:** Co-infection rates in TN were lower than national estimates, which could be the result of limited chronic HBV and HCV reporting in TN, and/or the fact that people living with HIV may not be engaged in care and subsequently, may not be screened for HBV or HCV. This new surveillance strategy has enabled the TN Department of Health to quantify HIV/VH co-infections retrospectively to determine disproportionately affected regions. Future efforts will include prospective application of this analysis to identify outbreak vulnerability and determine sites for outbreak response planning activities.

Board 213. Building HIV/HCV Outbreak Response Capacity in Tennessee

S. Mathieson, L. Sizemore, M. Brantley, C. Davis, C. Wester
Tennessee Department of Health, Nashville, TN, USA

Background: In 2016, the Centers for Disease Control and Prevention (CDC) developed a ranking of the top 5% (n=220) US counties vulnerable to an HIV/hepatitis C (HCV) outbreak among people who inject drugs. Nearly half of Tennessee's counties were identified, highlighting the need for the early detection and rapid response to an HIV/HCV outbreak. We describe the process and lessons learned during the development and piloting of an HIV/HCV outbreak response plan (OBRP). **Methods:** In September 2015, TDH convened an interdisciplinary workgroup (HIV/STD/Viral Hepatitis (VH), Emergency Preparedness (EP) programs) to create an OBRP; establish routine and enhanced HIV/HCV surveillance practices; assign responsibilities; and develop associated tools (e.g., specimen collection guidance, outbreak response form [OBRF], REDCap database, and network visualization R program). In August 2016, stakeholders (STD/HIV supervisors, EP staff, and Disease Intervention Specialists [DIS]) convened for a one-day OBRP pilot at the Nashville Metro Public Health Department (NMPHD). TDH HIV/STD/VH leadership facilitated review of the OBRP and incident command systems (ICS), and observed mock interviews. Participants provided feedback throughout the exercise and via formal evaluation tools. **Results:** The classroom exercise revealed several opportunities for improvement: OBRF organization, interview team composition, and optimal ICS structure. Participants called for a natural flow to the OBRF and to decrease the amount of information collected. Feedback enlightened TDH to consider pairing DIS with epidemiologists for interview teams, to maximize skills and experience. Participants identified a need for parallel ICS centers with embedded agency liaisons. **Conclusions:** Tennessee continues to spearhead HIV/HCV outbreak response preparedness for vulnerable communities. This exercise demonstrated the importance of soliciting and incorporating feedback from local stakeholders when developing statewide resources. Discussions are ongoing to conduct additional classroom exercises throughout the state, specifically in regions with vulnerable counties. The OBRP can be adapted for use in other states looking to expand HIV/HCV outbreak response capacity.

Board 214. Hepatitis C Infection in Pregnant American Indian and Alaska Native Women, 2003-2015

L. Nolen[1], J. O'Malley[2], S. Seeman[1], D. Bruden[1], A. Apostolou[3], B. McMahon[4], M. Bruce[1]
[1]Centers for Disease Control and Prevention, Anchorage, AK, USA, [2]WWAMI University of Alaska Anchorage, Anchorage, AK, USA, [3]Indian Health Service, Rockville, MD, USA, [4]Alaska Native Tribal Health Consortium, Anchorage, AK, USA

Background: Hepatitis C (HCV) infection was historically thought to occur predominately in individuals born during the baby boom years (1945-1965), however recent data show an increasing number of younger HCV-infected individuals. One population of specific concern is pregnant women, as HCV can be passed to the infant during pregnancy and delivery. Recent reports have found a rise in infection in women of reproductive age in the general population and greater increases in specific subpopulations within the United States. Data from the Centers for Disease Control and Prevention's surveillance system suggests one group that is at increased risk of HCV infection is the American Indian and Alaska Native population (AI/AN). **Methods:** Using the National Center for Health Statistics (NCHS) birth certificate database and the Indian Health Services, Tribal, and Urban Indian (IHS) inpatient and outpatient database, we evaluated the number of reported cases of HCV infection in women who gave birth or were pregnant between 2003 and 2015. Within the IHS dataset, a woman was considered pregnant if she had two pregnancy-related ICD codes within an eight-month span. A woman was considered HCV infected if it was recorded in the birth certificate database or if two ICD codes for HCV infection were recorded in the IHS dataset. AI/AN women were identified within the NCHS database using the mother's self-reported race. **Results:** Based on the NCHS database, the number and percentage of mothers who were known to have HCV infection increased between 2011 and 2015 in both the AI/AN population (194 [0.57%] to 298 [1.19%], $p<0.001$) and the non-native population (6,706 [0.21%] to 11,660 [0.36%], $p<0.001$). The IHS database confirmed these results and showed an increase from 86 (0.38%) to 214 (0.92%) between 2003 and 2014 ($p<0.001$) in pregnant AI/AN women. **Conclusions:** This study demonstrates a significant increase in the proportion of pregnant women in the US infected with HCV between 2003 and 2015. In addition, a higher proportion of pregnant AI/AN women were detected to have HCV compared to pregnant non-native women. These data highlight the need for HCV screening and prevention programs in pregnant AI/AN women.

Board 215. Withdrawn

Board 216. National Prevalence Survey of Viral Hepatitis B and C in Tunisia, 2015

H. Bouguerra[1], S. Chelly[1], M. Ben Hadj[1], H. Letaief[1], A. Hechaichi[1], F. Saffar[1], A. Cherif[1], K. Talmoudi[1], A. Bahrini[1], T. Chouki[1], O. Bahri[2], N. Ben Alaya[1]
[1]National Observatory of New and Emerging Diseases, Tunis, Tunisia, [2]Aziza Othmana Laboratory, Tunis, Tunisia

Background: In the Eastern Mediterranean region, hepatitis B and C virus (HBV and HCV) remain a significant burden with more than 75% attributable cirrhosis and hepatocellular carcinoma. WHO aims to eliminate viral hepatitis by 2030 and recommends countries to identify their most affected populations and set actions accordingly. In the Tunisian context of lack of national and recent data, our study aimed to estimate the national prevalence of HBV and HCV infection in the general population and to assess their distribution. **Methods:** We conducted a cross-sectional household-based survey in the general population from January to December 2015. We used a two-stage cluster sampling based on 2014 national census and data provided by the National Institute of Statistics. The expected sample size was 22 275 individuals. Data collection was through standardized questionnaires and blood samples testing anti-HCV antibodies IgG and HBsAg (electrochemiluminescence) in a reference laboratory. We used EpiData and SPSS-20 for data entry and analysis. Results were adjusted to the 2015 population. Ethical considerations were respected. **Results:** A total of 21 720 household members participated to the study. Response rate was 97.5%. Overall prevalence of Anti-HCV antibodies was 0.88% CI 95% [0.78-1.01%], estimating 88130 persons in Tunisia. It increased with age ($p<10^{-3}$) but was not related to sex. Anti-HCV prevalence ranged from 0.13% in the south-east to 2.57% in the north-west region ($p<10^{-3}$). Prevalence of HBsAg was 1.70% [1.55-1.85%] representing 169564 [154077-185050] individuals. HBsAg prevalence was significantly higher in men (2.1%), in the age group more than 20 years (2.14%) and in the Central region (2.3%). **Conclusions:** Within its limits, our study provide important insights into HBV and HCV prevalence in Tunisia. Despite low national rates, some regions remain of intermediate and high endemicity (central region for HBV and north region for HCV). Further steps of our study will assess the associated risk factors in each region in order to implement appropriate control measures.

Board 217. Next Generation Sequencing of the Hepatitis A Virus Outbreak in San Diego County

T. Basler, S. Steele
San Diego County Public Health Laboratory, San Diego, CA, USA

Background: In San Diego County, California, a hepatitis A virus (HAV) outbreak developed, affecting over 575 people. The first case was identified in November of 2016. Unlike other HAV outbreaks, the nature and size of this particular outbreak was unique as it had circulated in the homeless and illicit drug user population. The County of San Diego declared a local public health emergency from September 1, 2017 to January 23, 2018. The declaration significantly increased the involvement of the San Diego Public Health Laboratory (SDPHL) for diagnostic testing. Collaborating with public health partners, such as the California Department of Public Health Viral and Rickettsial Disease Laboratory (VRDL) and the Centers for Disease Control and Prevention (CDC), allowed SDPHL to implement both PCR screening and sequencing to increase the testing capacity, improve detection, and focus on prevention efforts for HAV in San Diego County. **Methods:** SDPHL created a testing workflow that first screens suspect patient specimens with a laboratory developed TaqMan assay to determine if the HAV RNA is present. If detected, the virus is sequenced using Sanger sequencing of the VP1/P2B region of the HAV genome, which demonstrates high sequence variability compared to other regions in the genome. SDPHL will also use the CDC's recently developed Global Hepatitis Outbreak and Surveillance Technology (GHOST) next generation sequencing (NGS) protocol for HAV to re-characterize all (>575) of the locally identified HAV infections. **Results:** Of the 511 hepatitis A positive specimens tested so far in this study, 16 were identified as genotype 1A; 411 were 1B and grouped as Cluster A, 13 were 1B and grouped as Cluster B, 34 were 1B and grouped as Cluster D, and 37 were 1B and have not yet been categorized to a cluster. **Conclusions:** Genotyping and cluster identification by sequencing the VP1/2PB region showed that the outbreak was caused by HAV gen-

otype IB, with the majority in one main group called Cluster A. Additional clusters were identified and some genotype 1B strains remain outside a named cluster. In this continuing study, SDPHL will pilot the use of the GHOST protocol for HAV to demonstrate and compare the NGS data to the Sanger sequence data for a HAV outbreak. We hope to determine if NGS provides a better picture of the viral transmission in the community during the outbreak.

Board 218. Withdrawn

Board 219. Prevalence of Anal and Oral HPV DNA and HPV Seroprevalence among Transgender Women in Two Cities, United States, 2012–2014

V. Singh[1], B. Gratzer[2], P. Gorbach[3], R. Crosby[4], G. Panicker[1], M. Steinau[1], E. Unger[1], L. Markowitz[1], E. Meites[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Howard Brown Health, Chicago, IL, USA, [3]Department of Epidemiology, Fielding School of Public Health, University of California at Los Angeles, Los Angeles, CA, USA, [4]College of Public Health, University of Kentucky at Lexington, Lexington, KY, USA

Background: Human papillomavirus (HPV) is the most common sexually transmitted infection; prevalence is particularly high among men who have sex with men (MSM), yet little is known about prevalence among transgender women (TW). We assessed evidence of HPV among a convenience sample of TW. **Methods:** During 2012–2014 at clinics in Chicago and Los Angeles, we enrolled 1033 young (≤26 years) gay, bisexual, and other MSM assigned male sex at birth. Participants self-reported gender identity (TW or cisgender males (CM)), vaccinations, and HIV status. Self-collected anal and oral specimens were tested for HPV DNA (37 types); serum was tested for HPV antibodies (quadrivalent vaccine types 6, 11, 16, 18). For unvaccinated participants, HPV was assessed among TW compared to CM using prevalence ratios (PRs) and 95% confidence intervals (CIs). Participants with no DNA or serologic evidence of HPV were considered naïve. **Results:** HPV prevalence was compared for 44 TW and 855 CM. In anal specimens, any HPV DNA was detected among 39 (88.6%) TW and 606 (70.9%) CM, PR:1.3 (CI:1.2–1.4), and ≥1 vaccine type among 22 (50.0%) TW and 311 (36.4%) CM, PR:1.4 (CI:1.01–1.9). In oral specimens, any HPV DNA was detected among 4 (9.1%) TW and 81 (9.5%) CM, PR:1.0 (CI:0.4–2.5). Serum antibodies to ≥1 vaccine type were detected among 37 (84.1%) TW and 467 (54.6%) CM, PR:1.5 (CI:1.3–1.8). Most (65.9% TW and 90.6% CM) were naïve to ≥1 vaccine type. Differences were maintained in analyses limited to HIV-negative TW and CM. **Conclusions:** HPV was common among TW; anal prevalence and seroprevalence were significantly higher than among CM in this study. Nevertheless, participants were not previously exposed to all vaccine types. Although vaccination ideally occurs prior to HPV exposure, these findings support current national recommendations to vaccinate transgender people and MSM through age 26 years.

Board 220. Surveillance for Disseminated Gonococcal Infections, Active Bacterial Core Surveillance (ABCs)–United States, 2015–2017

E. Weston[1], G. Lee[2], M. Tobin-D'Angelo[3], A. Tunali[4], M. Farley[4], A. Abrams McLean[1], K. Workowski[1,5], E. Torrone[1], H. Weinstock[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]California Emerging Infections Program, Oakland, CA, USA, [3]Georgia Department of Public Health, Atlanta, GA, USA, [4]Emory University School of Medicine, Georgia Emerging Infections Program, Veterans Affairs Medical Center, Atlanta, GA, USA, [5]Emory University, Department of Medicine, Atlanta, GA, USA

Background: *Neisseria gonorrhoeae* (GC) is the second most commonly reported infection in the United States. Disseminated gonococcal infections (DGI), however, are uncommon and thought to occur in 0.5–3% of GC cases. Surveillance for DGI is limited and case reports are often analyzed retrospectively or in case clusters. We describe the population-level burden of reported DGI using an established surveillance infrastructure, the Active Bacterial Core surveillance (ABCs) system of CDC's Emerging Infections Program. **Methods:** Active, laboratory, population-based surveillance for DGI cases included 2 components: a) prospective surveillance for 2017, and b) retrospective review for 2015 – 2016. A DGI case was defined as isolation of GC from a normally sterile site in a resident of 2 ABCs areas in 2015 – 2017: 3-counties in the Bay Area in CA and the 20-county Atlanta metropolitan area (GA-MSA) or of 1 surveillance area in 2017: GA outside the 20-county metropolitan area (GA-DPH). A case report form, including clinical and demographic information, was completed for cases for all years. **Results:** During 2015–2017, 26 DGI cases were identified (2 in CA, 3 in GA-DPH, and 21 in GA-MSA). The DGI rate ranged by site (0.02 in CA to 0.13 cases per 100,000 population in GA-MSA). DGI cases accounted for 0.04% of all reported cases of GC in the 3 ABCs surveillance areas. Similar to reported GC cases in these areas, most DGI cases were male (58%), between 15-29 years of age (38%), and were among Black, non-Hispanics (58%). A majority of DGI cases had either bacteremia alone (31%) or septic arthritis alone (35%). Most cases (54%) received the CDC recommended dual therapy (duration of therapy ranged from 1-14 days), 8% of cases had no treatment documented. **Conclusions:** Based on these preliminary data, DGI remains an infrequent complication of GC and the epidemiology appears to be consistent with that of non-DGI GC. The ABCs infrastructure is a viable platform to perform enhanced surveillance for cases of DGI. As GC can quickly develop antimicrobial resistance to recommended treatments, continued surveillance, including monitoring trends in antimicrobial susceptibility of DGI isolates and molecular epidemiology, could help inform DGI treatment recommendations.

Board 221. Characterizing *Neisseria gonorrhoeae* Susceptibilities for Isolates Submitted to the Southeast Regional Laboratory for the US Antibiotic Resistance Laboratory Network (ARLN)

N. Smith[1], H. Hardin[2], R. Rasnic[2], P. Gibbs[2], M. Kainer[1]
[1]TN Department of Health, Nashville, TN, USA, [2]TN Department of Health Laboratory Services, Nashville, TN, USA

Background: Emerging antibiotic resistance in *Neisseria gonorrhoeae* was identified as a public health threat by the National Action Plan for Combating Antibiotic Resistant Bacteria (CARB). CDC's Antibiotic Resistance Laboratory Network (ARLN), a system of laboratories used to characterize antibiotic threats identified by the National Action Plan for CARB, currently tests *Neisseria gonorrhoeae* isolates in four regional laboratories including the Southeast regional laboratory. **Methods:** *Neisseria gonorrhoeae* isolates submitted to the Southeast ARLN regional laboratory from April to December (n=1676) from sentinel Gonococcal Isolate Surveillance Project (GISP) and (Strengthening the United States Response to Resistant Gonorrhea) SURRG sites were included for analysis in WHONET. Confirmatory species identification was done using matrix assisted laser desorption-ionization time of flight (MALDI-TOF). Minimum inhibitory concen-

trations were obtained using agar dilution. Data from the Southeast ARLN laboratory information management system (STARLIMs) was cleaned using R and converted to WHONET files. WHONET analysis included determining the percent of isolates resistant, susceptible or intermediate to antibiotics tested, MIC distributions of each antibiotic used and scatterplots to determine interactions of key drugs used for treatment of *Neisseria gonorrhoeae*. 75 isolates met ARLN alert criteria: azithromycin MIC >=2.0 ug/mL (n=69), cefixime MIC >=0.25 ug/mL (n=2), and ceftriaxone MIC >=0.125 ug/mL (n=4). Azithromycin alert organisms were subset for scatterplot analysis. **Results:** Isolates had the highest percentage of resistance to ciprofloxacin (28%) and tetracycline (21%). 100% of isolates were sensitive to ceftriaxone and cefixime. Most isolates were susceptible to azithromycin (98%) and ciprofloxacin (70%). Scatterplot analysis identified that 99% of isolates were susceptible to both ceftriaxone and azithromycin and both cefixime and azithromycin. 69% were susceptible to both ciprofloxacin and azithromycin. Of 69 isolates meeting the azithromycin alert value, no isolates also had resistance to cefixime or ceftriaxone. **Conclusions:** *Neisseria gonorrhoeae* susceptibility testing assists in identifying emerging resistance and provides valuable information to develop treatment guidelines.

Board 222. Testing and Utilization of Preventive Services for Sexually Transmitted Infections (STI) among Men Who Have Sex with Men (MSM) in the Boston National HIV Behavioral Surveillance (NHBS) Survey

M. Klevens[1], B. Martin[2], R. Doherty[1], H. Fukuda[1], K. Hsu[1], A. DeMaria[1]
[1]Massachusetts Department of Public Health, Boston, MA, USA, [2]Boston University Biostatistics and Epidemiology Data Analytics Center (BEDAC), Boston, MA, USA

Background: The syphilis incidence rate among men in Massachusetts soared from 7.8 in 2007 to 28.9 per 100,000 in 2016. We analyzed data from the Boston NHBS to evaluate factors associated with STI testing and utilization of prevention services among MSM. **Methods:** The NHBS uses a standardized protocol for survey and HIV testing of persons with high risk behaviors. In 3-year cycles, data collection rotates among three populations: MSM, persons who inject drugs, and high risk heterosexuals. We analyzed data from the 2011 (MSM cycle 3) and 2014 (MSM cycle 4) of the Boston NHBS. Recruitment was anonymous and venue-based; potential participants were first screened to determine whether they were aged ≥18 years, ever had sex with another man, resided in the Boston metro area, could complete an interview in English or Spanish, and could provide informed consent. In separate questions, respondents were asked whether they were tested for an STI (gonorrhea, chlamydia, or syphilis) within the previous 12 months. We compared results over the two cycles and evaluated predictors of testing from the 2 cycles combined. **Results:** In 2011, 440 MSM and in 2014, 316 MSM participated in the Boston NHBS. Samples were not different by race/ethnicity, but the 2014 participants were more frequently 18-29 years of age (p=0.01) and had college or higher education degree (p=0.004). The mean number of partners was not different in 2011 and 2014 (11 and 13; p=0.3). The proportion of MSM reporting receipt of free condoms decreased from 82.3% in 2011 to 69.8% in 2014 (p<.0001), but there was no significant difference in participation in discussions of HIV prevention. Testing for any STI increased from 43.9% in 2011 to 56.1% in 2014 (p=0.001). Compared to MSM who were tested, those not tested for an STI within the previous 12 months were more frequently ≥40 years of age (26.2% vs 13.1%, p<0.0001), white non-Hispanic (72.6% vs 55.1%, p<0.0001) and less frequently reported a usual source of medical care (85.3% vs 91.3%, p=0.01). **Conclusions:** Over half of MSM in Boston reported being tested for an STI in 2014, an improvement over 2011; however, testing needs to increase given the context of increasing syphilis incidence. Ensuring that MSM at risk, especially those who are older or white, have greater testing access, may improve testing frequency to levels necessary to drive down population levels of syphilis.

Board 223. Developing Messaging to Prevent Multidrug-Resistant *Shigella* Infections among Men Who Have Sex with Men

A. Peschard
Sensis ATL, Atlanta, GA, USA

Background: Recently, there has been an increase of outbreaks of shigellosis among men who have sex with men (MSM). Researchers estimate MSM are at least three times more likely to have a resistant infection. However, there is no effective health messaging for this group. **Methods:** The Centers for Disease Control and Prevention's National Center for Emerging and Zoonotic Infectious Diseases engaged Sensis, the behavior change agency, to develop evidence-based health promotion materials for shigellosis prevention among MSM. Sensis transcribed and analyzed feedback from six focus groups to identify insights to better inform creative development of the materials. These materials will be placed on the CDC's shigellosis website and further tested in focus groups for effectiveness. **Results:** Sensis has analyzed qualitative data gleaned from transcribing remarkable stories from the MSM community, gathered through focus groups conducted by the CDC in partnership with Georgia State University. This focus group data revealed four key insights about the MSM community: 1) They are weary of messaging due to HIV/AIDS fatigue. 2) They don't view shigellosis as a serious disease. 3) Symptoms are uncomfortable to discuss with peers. 4) They are concerned about stigmatization. **Conclusions:** While messaging is still under development, it has been determined that several key elements must be included for a prevention campaign to be successful. Messages must 1) be inclusive, 2) be brief, 3) be clever, 4) reflect culture, 5) be informative, and 6) be actionable to encourage prevention. Evidence-based prevention materials using these elements could help promote behavior change and reduce the incidence of shigellosis among MSM.

Board 224. Determinants of Health Care-Seeking Delay among Tuberculosis Patients in a Rural Area of Central China: A Multicenter Study

Y. Tong[1], X. Guan[1], L. Wang[1], Y. Wu[1], S. Wei[2], J. Huang[2]
[1]Institute of Infectious Diseases, Hubei Center for Disease Control and Prevention, Wuhan, China, [2]School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background: The prevalence of tuberculosis (TB) in low and middle income countries is high and a significant public health and social concerns. TB is a common infectious disease caused by the *Mycobacterium tuberculosis* infection, which has a widespread infection rate. Health care-seeking delay maybe one of the most important neglected risk factors for the spread of TB. The aim of this study was to understand the situation of health care-seeking delay among rural tuberculosis patients in Hubei Province and explore its risk factors. **Methods:** 1408 rural

tuberculosis patients were surveyed using a self-designed questionnaire in three cities in Hubei Province during the past two years. **Results:** For the 1408 cases of pulmonary tuberculosis, 39.56% of them were health care-seeking delayed. Logistic regressions indicates that the Han nationality, farming career, monthly income less than 800 Yuan, and the time of walking to the township's hospital more than 45 minutes, were significantly associated with higher odds of delay in care seeking. **Conclusions:** The prevalence of care-seeking delay among tuberculosis patients was high in rural areas. It is essential to take comprehensive targeted interventions to reduce care-seeking delay.

Board 225. Risk Factors of Multidrug-Resistant Tuberculosis among Pediatric Patients: A Retrospective Cohort Study

R. Espino
East Avenue Medical Center, Quezon City, Philippines

Background: Multidrug-resistant tuberculosis (MDR–TB) is a form of TB caused by bacteria that do not respond to at least isoniazid and rifampicin. The primary cause of developing MDR–TB is inappropriate treatment. Investigation of MDR–TB in children is limited, largely due to the well-known difficulties of isolating *M. tuberculosis* from pediatric specimens. **Objective:** To determine the risk factors of pediatric patients diagnosed with multidrug-resistant tuberculosis. **Methods:** A Retrospective Cohort study conducted in a tertiary hospital in Quezon City TB DOTS, Batasan Super Health Center and Payatas Health Center from January 2011 to December 2016. A minimum cohort of 156 patients 0 – 18 years old, either bacteriologically confirmed or clinically diagnosed tuberculosis were included in the study. Patients whose significant portions/data of their charts went missing were excluded in the analysis of the study. The following information was gathered: a.) demographic profile: age, gender, nutritional status, socioeconomic status, district from which the patient came from b.) clinical profile, history of exposure, results of laboratories, clinical presentation, delay in treatment, and previous treatment with tuberculosis and outcome. **Results:** Results: 162 patients were analyzed, 12/162 had MDR–TB and 150/162 had Non MDR–TB. Results of univariate analysis showed that age and symptoms of weight loss, back pain, night sweats, and fever had significant association with MDR–TB. Of these factors, back pain (p=0.001; RR: 31.771; 95% CI: 3.801, 265.554) and fever (p=0.020; RR: 7.6587; 95% CI: 1.380, 42.494) were independent factors significantly related with MDR–TB. **Conclusions:** Age, weight loss, back pain, night sweats, and fever had significant association with MDR–TB. Larger sample population and a prospective study is recommended to assess the epidemiologic data and further identify other possible risk factors for resistance.

Board 226. Cerebral and Cerebellar Toxoplasmosis Presenting with Disseminated Mycobacterium Co-infection in a Patient with HIV/AIDS: A Case Report

J. Tuan
University of Connecticut, Farmington, CT, USA

Background: Central nervous system toxoplasmosis is a disease caused by the intracellular protozoan parasite *Toxoplasma gondii*, commonly seen in HIV/AIDS patients with CD4 count <100 cells/µL. Presumptive diagnosis is made by positive *Toxoplasma gondii* IgG serology, ring-enhancing lesions on brain imaging, and clinical syndrome and response to treatment. Patients with disseminated *Mycobacterium avium* complex (MAC) infection may present with fever and nonspecific symptoms, with MAC-positive blood cultures in HIV/AIDS patients with CD4 count <50 cells/µL. **Methods:** A 49-year-old Puerto Rican woman with chronic HIV/AIDS noncompliant with HAART (CD4 count 11 cells/µL, viral load 93,000 copies/mL), hepatitis C, ESRD noncompliant with hemodialysis, presented with lethargy, fever, and shortness of breath. Over one month, she was noted to be progressively more lethargic and confused, with increased falls. She was febrile to 102 °F. Physical exam demonstrated cachexia, bilateral crackles and ronchi, and altered mentation. She presented with pancytopenia and severe renal dysfunction. *Toxoplasma* IgG was >400 IU/mL and IgM <3 AU/mL. MRI brain showed an 18 mm multilobulated enhancing mass in the left lentiform nucleus and corona radiata with vasogenic edema and 5 mm right midline shift. Also noted were 10 mm left cerebellar, 11 mm right cerebellar, and 7 mm right occipital lesions with vasogenic edema. Blood AFB culture collected from hospital day seven grew *Mycobacterium* species preliminarily, on hospital day 18. **Results:** She was treated with two weeks of sulfamethoxazole-trimethoprim for toxoplasmosis and clinically responded, as her mentation improved and fever defervesced rapidly. Two weeks later, MRI brain showed reduced size of the left basal ganglia lesion, white matter edema, and resolved midline shift. The left cerebellar lesion was minimally noted and the prior right occipital and right cerebellar lesions were undetected. She was started on treatment for disseminated mycobacterium infection (presumed *Mycobacterium avium* complex) with azithromycin, ethambutol, and rifabutin. **Conclusions:** Cerebral and cerebellar toxoplasmosis and disseminated mycobacterium co-infection developed in this nonadherent HIV/AIDS patient, highlighting the importance of compliance with HAART and prophylaxis medications. Either infection can be seen with HIV/AIDS, however fewer cases of co-infection have been reported.

Influenza Burden

Board 227. Comparison of Incidence and Cost of Influenza in Healthy and High-Risk Children <5 Years Old in Thailand, 2011-2015

W. Kittikraisak[1], P. Suntarattiwong[2], W. Kanjanapattanakul[2], D. Ditsungnoen[1], C. Klungthong[3], K. Lindblade[4], S. Fernandez[3], F. Dawood[4], T. Chotpitayasunondh[2], S. Olsen[4]
[1]Thailand Ministry of Public Health – US Centers for Disease Control and Prevention Collaboration, Nonthaburi, Thailand, [2]Queen Sirikit National Institute of Child Health, Bangkok, Thailand, [3]Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Thailand recommends influenza vaccination for children aged 6 month-2 years, but investment in vaccine purchase is limited. To explore the investment case, we conducted a prospective cohort study of children in Bangkok hospital to estimate and compare influenza incidence and cost between healthy and high-risk children. **Methods:** Caregivers of healthy children and children with medical conditions ('high-risk') aged <36 months were called weekly for two years to identify acute respiratory illness (ARI) episodes and collect illness-associated costs. Children with ARI were tested for influenza viruses by polymerase chain reaction. Illnesses were categorized as mild or severe depending on whether children were hospitalized. Population-averaged Poisson models were used to compare influenza incidence by risk group. Quantile regression was used to examine differences in the median illness expenses. **Results:** From August 2011-September 2015, 659 healthy and 490 high-risk children were enrolled; median age was 10

months. Incidence of mild influenza-associated ARI was higher among healthy than high-risk children (incidence rate ratio [IRR]: 1.67; 95% confidence interval [CI]: 1.13-2.48). Incidence of severe influenza-associated ARI did not differ (IRR: 0.40; 95% CI: 0.11-1.38). The median cost per mild influenza-associated ARI episode was $22 among healthy and $25 among high-risk children (3-4% of monthly household income; p-value for difference in medians =0.78). The median cost per severe influenza-associated ARI episode was $232 among healthy and $318 among high-risk children (26-40% and 36-54% of monthly household income, respectively; p-value for difference in medians=0.62). **Conclusions:** Compared with high-risk children, healthy children had higher incidence of mild influenza-associated ARI but not severe influenza-associated ARI. Costs of severe influenza-associated ARI were substantial.

Board 228. Estimating Annual Direct Medical Costs from Seasonal Influenza in China

S. Zhou[1], S. Situ[2], M. Biggerstaff[2], T. Chen[3], J. Yang[3], R. Zhang[1], D. Wang[3], C. Greene[1]
[1]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Chinese National Influenza Center, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China

Background: China, the most populous country in the world, has limited data on its annual rate and economic burden of seasonal influenza illness. **Methods:** We used keywords "China," "influenza," and "annual rate" to search PubMed and China Knowledge Resource Integrated Database (CNKI) from January 1, 2007 – December 31, 2017 for articles with laboratory-confirmed seasonal influenza disease rate estimates for China. We also reviewed unpublished data from a US Centers for Disease Control and Prevention (CDC) supported 2016 study on influenza disease burden in Changsha, China. We abstracted age-specific data on annual rates of influenza-associated outpatient visits and hospitalizations. For multiple data sources for the same age group across years, we calculated average rates per year across sources. Direct medical cost estimates based on medical out-of-pocket expenses and payments by insurers were from findings of a 2015 national survey. Population estimates were from the 2010 national census. We estimated total number of influenza outpatient visits, hospitalizations, and direct medical costs by age group and for the total population. **Results:** From 2007-2017, we identified 47 PubMed English and 91 CNKI Chinese citations. We abstracted data from the two published articles with estimates of laboratory-confirmed influenza rates for China: one estimating influenza hospitalizations in 2010-2012 and one estimating influenza outpatient visits in 2011-2014. We also used unpublished estimates of influenza outpatient visits from the 2016 CDC study. The attack (20%, range 10-31%) and hospitalization rates (2.4%, range 2.3-2.4%) were highest in children <5 years of age. On average, each year 65 (range 57-74) million persons sought medical care for influenza and 2.7 (range 2.6-2.8) million were hospitalized. Average direct medical costs were: per outpatient visit, 70 USD (range: 61 USD in adults >60 years - 85 in children <5 years); per hospitalization 1072 USD (range: 980 USD in children <5 years -2300 in adults >60 years). The average total direct medical cost of influenza was $7.4 (range 6.6-8.3) billion per year. **Conclusions:** Although data are limited, in 2010-2016 seasonal influenza caused substantial outpatient and hospitalization burden in China, and significant economic loss from direct medical costs alone. Findings suggest value of enhancing influenza prevention in China, especially in young children and older adults.

Board 229. Withdrawn

Board 230. Burden of Hospitalized Influenza in Vietnam: Hospitalization Admission Survey in Quang Ninh Province

C. Nguyen[1], D. Ngu[1], N. Tran[1], H. Ngo[1], A. Tran[1], J. McFarland[2], T. Nguyen[2], A. Fowlkes[2], A. Iuliano[2], T. Nguyen[3], D. Dang[1]
[1]National Institute of Hygiene and Epidemiology, Ha Noi, Viet Nam, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Quang Ninh Provincial Preventive Medicine Center, Quang Ninh, Viet Nam

Background: Annually influenza causes millions of severe acute respiratory infections (SARI) worldwide. Since 2011, Vietnam has conducted surveillance for SARI and laboratory-confirmed influenza in sentinel hospitals. To estimate population-based rates of influenza-associated SARI hospitalizations, we conducted a hospitalization admission survey (HAS) in four provinces. We present the preliminary results from the first province, Quang Ninh. **Methods:** From January 2014–December 2016, we identified all admissions in 12 district and 2 provincial hospitals in Quang Ninh with admission ICD-10 codes J06, J09-J18, and J20-J22. We randomly selected 80 medical charts at each hospital to determine the proportion of patients with a J-code that met the WHO SARI case definition. We multiplied the total number of all J-code admissions by the SARI proportion to estimate the total number of SARI hospitalizations. Using data from the existing SARI surveillance platform, the number of influenza-associated SARI hospitalizations was extrapolated using the proportion of influenza test-positive SARI cases. Since all hospitals in the province participated in the HAS, provincial census data were used to calculate rates by age and year; non-resident patients were censored. **Results:** Of 1,220 requested medical charts, 1,092 (89%) were reviewed, representing 3% of 35,479 J-code admissions. Overall, 618 (57%) patients with J-code admissions met the SARI case definition, varying by hospital from 15–75%. At the two sentinel sites routinely conducting SARI surveillance, 65% (53/82) and 71% (56/79) of patients met SARI criteria. The most common reason for discordance was no measured or recorded fever (n=447). We estimated an adjusted influenza-associated SARI hospitalization rate of 131, 304 and 138 per 100,000 persons in 2014, 2015, 2016, respectively. Children <5 years had the highest influenza-associated SARI incidence (annual range 452-877 per 100,000 persons), followed by adults aged ≥65 years (annual range 138-244 per 100,000 persons). **Conclusions:** Influenza-associated SARI hospitalization represented a significant burden in Quang Ninh Province, Vietnam, from 2014-2016. Rates were highest among young children and older adults, highlighting the potential benefit of vaccination to reduce burden in these age groups.

Board 231. Heterogeneity in Rates of Influenza-Associated Hospitalizations: A Systematic Review, 2007-2016

K. Roguski[1,2], J. Reich[1], M. Rolfes[1], Z. Owens[3], J. Fitzner[4], V. Cozza[4], K. Lafond[1], E. Azziz-Baumgartner[1], A. Iuliano[1]
[1]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Atlanta Research and Education Foundation, Inc., Atlanta, GA, USA, [3]Department of Epidemiology, Rollins School of Public Health, Emory University, Atlanta, GA, USA,

[4]Global Influenza Programme, World Health Organization, Geneva, Switzerland

Background: While the majority of countries in the world have influenza vaccine polices, few routinely vaccinate due to insufficient quality burden data to substantiate an investment case. We reviewed the current literature on influenza-associated hospitalization rates. **Methods:** We systematically searched peer-reviewed literature, published from 2007-2016, to extract results and methods used in articles that estimated influenza-associated hospitalization rates from at least one non-pandemic influenza season, accounted for influenza laboratory testing, and had specified catchment areas. We conducted meta-regressions to assess and identify study characteristics associated with heterogeneity in these rate estimates. **Results:** Of 5,174 articles identified, 72 met criteria and 43% (n=31) were from the United States. Articles presented rates from 18 high, six upper-middle, five lower-middle, and two low income countries as defined by the World Bank. A median of three years of data were presented (IQR: 2-6 years), ranging from 1991-2015. Thirteen articles (18%) used regression modeling while 59 (82%) used a multiplier approach. The interquartile range of published influenza-associated hospitalization rates was 7-54/100,000 for all ages, 16-161/100,000 for children <5 years, and 28-203/100,000 for adults ≥65 years. We observed large heterogeneity among extracted rate estimates ($Q = 1x10^7$, $p < 0.001$, $I^2 = 99.9\%$). Age group, analytic method, case definition, and World Bank region accounted for 22%, 3%, 7%, and 13% of this heterogeneity respectively. We observed complete correlation between analytic method and case definition and between World Bank region and analytic method. **Conclusions:** We observed large variability in currently published rates of influenza-associated hospitalization, even after we stratified by key study characteristics. Due to strong correlation between study characteristics, we were unable to determine the specific impact of different methodologies or other factors on rate estimates. We suggest future analyses use standardized methods across different populations or applying different methods in the same study population to better understand the contribution of epidemiologic methods to differences in rates of influenza-associated hospitalization seen globally.

Board 232. Evaluation of Hospital Discharge Diagnoses as a Surrogate for the World Health Organization Severe Acute Respiratory Illness Case Definition for Influenza Surveillance

O. de León[1], R. Chacón[1], M. López[1], A. Paredes[2], C. Arriola[3], J. Bryan[4], S. Kaydos-Daniels[4], J. McCracken[1]
[1]Centro de Estudios en Salud, Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Epidemiology Department, Guatemalan Ministry of Health, Guatemala, Guatemala, [3]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]CDC-CAR, Guatemala, Guatemala

Background: WHO recommends the severe acute respiratory illness (SARI) case definition for influenza surveillance to allow comparisons across regions and over time. This case definition is not universally used, and ICD10 discharge codes J09-18 (Influenza, bacterial and non-specific pneumonia) are proposed as an alternative. We evaluated ICD10 discharge codes as a surrogate for the WHO SARI definition for influenza surveillance in Guatemala. **Methods:** We conducted surveillance in two regional public hospitals (Santa Rosa and Quetzaltenango) during 2010-2017. We screened hospitalized patients with acute illness and residing in predefined catchment areas for respiratory tract infections upon admission. We defined acute respiratory illness (ARI) hospitalization as ≥1 sign or symptom of respiratory illness and a predetermined set of clinical and laboratory criteria. We defined SARI as reported or measured temperature ≥38°C and cough, with onset ≤10 days. We assigned ICD10 J09-18 codes based on discharge diagnoses from patient records. We collected oropharyngeal and nasopharyngeal swab samples upon patient enrollment and tested for influenza virus using real-time RT-PCR. We adjusted incidence rates for the proportion of enrolled cases who were not tested, and health utilization surveys. **Results:** We enrolled 7031 hospitalized patients with ARI and tested 97% (n=6870) for influenza A and B over 5,421,087 person-years. We found 465 (7%) lab-proven influenza cases, resulting in an adjusted incidence of 17 per 100,000 person-years for all ages. The most common diagnosis (66%) was J18.9 (Pneumonia, unspecified organism). The proportions of the total influenza cases captured by SARI definition and the ICD10 J09-18 were 32% (n=148) and 64% (n=296), respectively. SARI definition resulted in a sensitivity of 35% (30-40) and a specificity 68% (67-70). ICD resulted in a sensitivity of 69% (64 -73) and a specificity of 30% (29-31) compared with PCR confirmed influenza. **Conclusions:** Use of ICD10 J09-18 rather than SARI definition may double the influenza incidence estimate due to its low specificity. These differences should be considered when interpreting influenza surveillance results based on either SARI or hospital discharge diagnoses. Both ICD and SARI definition methods underestimate the incidence of influenza compared with sensitive lab diagnosis.

Board 233. Estimating the National Burden of Hospitalized Influenza in Lao People's Democratic Republic, 2016

B. Khamphaphongphane, O. Keosavanh
National Center for Laboratory and Epidemiology, Vientiane, Lao People's Democratic Republic

Background: Reliable burden estimates for influenza are needed in Lao PDR to target influenza vaccine distribution. Using the WHO Manual for Estimating Disease Burden, we used sentinel surveillance data to estimate national influenza-associated SARI hospitalization incidence rates. **Methods:** SARI was defined as history of fever or measured temperature ≥38°C and cough, and onset within the last 7 days, requiring hospitalization. Sentinel surveillance data, requiring systematic testing of SARI patients by RT-PCR for influenza virus, were obtained from Champasack and Luangprabang Provincial Hospitals. Data from January to December 2016 were used to estimate influenza-associated SARI incidence. The catchment area for both hospitals was determined by the district of residence of SARI patients in 2014. For the calendar year 2016, hospital admission reviews were conducted in health facilities within the two catchment areas of these hospitals and SARI cases were identified using hospital admission logbooks documenting date of onset, fever and cough. We then applied the percent of specimens testing positive for influenza from the sentinel surveillance data by the age group to the SARI patients identified in the record review. SARI cases from both catchment areas were then pooled and applied to national population estimates using 2015 Census data, by age group. **Results:** From January to December 2016, in the two catchment areas a total of 870 SARI patients were identified of which 140 (16%) were estimated to be influenza-associated. Of these 870 SARI patients 376 (43%), 100 (12%), 245 (28%) and 149 (17%) were in the age groups <5, 5-<15, 15-<65, and 65+ years, respectively. Following record review and extrapolation to national census data we estimated a national total of 13,604 SARI cases, with 2,170 influen-

za-associated SARI cases in 2016. The estimated annual national influenza-associated SARI hospitalization rates per 100,000 were 155.7, 44.5, 8.9 and 42.2 in the age groups <5, 5-<15, 15-<65, and 65+ years, respectively. **Conclusions:** Influenza exerts a considerable burden of hospitalization in Lao PDR, especially among the <5 year age group. These estimates were comparable to neighboring countries and will assist Lao PDR target influenza vaccination efforts in the future.

Board 234. Active Surveillance of Influenza-Associated Hospitalizations among Persons Aged 16 Years and Older in Shanghai, China, April 2017-March 2018

J. Chen[1], Y. Zheng[1], H. Wu[1], C. Jiang[1], R. Zhang[2], D. Yuan[1], S. Lin[1], D. Kong[1], T. Tan[1], S. Mao[1], Y. Song[2], C. Greene[2], Z. Yuan[1], F. Wu[1]
[1]Shanghai Municipal Center for Disease Control and Prevention, Shanghai, China, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: As local data on influenza-associated hospitalizations are limited, we conducted active, hospital-based severe acute respiratory infection (SARI) surveillance in 11 sentinel hospitals in Shanghai, China. Collecting data on influenza vaccination and empiric antivirals received among patients hospitalized with influenza infection will inform local influenza prevention and control. **Methods:** From April 2017-March 2018, we used the electronic Hospital Information System (HIS) in 8 tertiary and secondary hospitals and manual review in 3 community-level hospitals to screen all newly admitted patients >=16 years of age for SARI using the 2014 WHO SARI definition. For SARI patients providing written consent, we completed a standardized case report form and collected a throat swab. Specimens were tested in national influenza surveillance network laboratories in Shanghai. **Results:** From April 1 to December 31 2017, we enrolled 1984 SARI case-patients aged 16–103 years, median age 74 years (IQR=62-84). 71% had underlying medical conditions and 12 were pregnant. 13% were current smokers. Only 0.2% (95%CI: 0%-0.3%) reported receiving influenza vaccination in the past year. SARI cases were distributed throughout numerous wards including the respiratory department (42%), emergency department (22%), general medicine ward (20%), geriatric department (4%), respiratory intensive care unit (ICU) (4%), and 12 other wards (8%). Among 1084 cases with completed chart reviews, 56% (95%CI: 54%-59%) received antibiotic treatment during hospitalization, while 2.0% (95%CI: 1.3%-2.6%) received antiviral treatment. Among all SARI cases, 11% tested positive for influenza viruses, 81% were type A and 19% were type B. Among influenza positive cases, 61% were identified during the summer peak (July-September), and 19% during the first month of the winter peak (December). **Conclusions:** Preliminary data from this first active SARI surveillance system in Shanghai suggest that <50% SARI cases in Shanghai were admitted to respiratory wards. Although the majority of SARI patients were adults >=60 years of age and persons with underlying medical conditions, <1% had received influenza vaccination and only 2% received antiviral treatment. Findings suggest the need to promote influenza vaccination and empiric antiviral treatment for high risk groups in Shanghai.

Board 235. Incidence of Hospitalization Due to Influenza-Associated Acute Respiratory Infection in Bangladesh, 2009-2016

M. Aleem[1], K. Roguski[2], M. Ahmed[3], M. Islam[1], M. Rahman[1], M. Rahman[1], M. Flora[4], A. Alamgir[4], E. Gurley[5], K. Sturm-Ramirez[2], F. Chowdhury[1], E. Azziz-Baumgartner[2], A Iuliano[2]
[1]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [3]The University of Texas MD Anderson Cancer Center, Houston, TX, USA, [4]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh, [5]Johns Hopkins University, Baltimore, MD, USA

Background: Robust estimates of influenza-associated burden are useful to prioritize preventive measures such as influenza vaccination among vulnerable age groups. We analyzed hospital-based influenza surveillance and community survey data to estimate influenza-associated hospitalization rates during 2009-2016 in Bangladesh. **Methods:** Eleven hospitals across Bangladesh enrolled and collected specimens from all hospitalized patients with severe acute respiratory infections (SARI) or severe pneumonia (SP) and tested specimens for influenza viruses using real time RT-PCR. We defined hospital catchment areas as the districts surrounding each hospital where ≥75% of enrolled patients lived. We conducted community surveys within the catchment areas to identify the proportion of all-cause hospitalizations in the past year that occurred at the surveillance hospital compared to other hospitals in the area. We estimated annual influenza-associated hospitalization rates for persons aged<5, 5-15, 15-50, 50-65 and ≥65 years by dividing the number of influenza confirmed SARI and SP patients from the catchment area by the age-specific catchment area census population, adjusting for the site-specific proportion of hospitalizations at the surveillance hospital from all hospitalizations in the catchment area. **Results:** Among 12,517 SARI and SP patients enrolled from 2009-2016, 1,775 (14%) had laboratory-confirmed influenza. The annual percent of samples testing positive for influenza ranged from 11-17%. Of the 915 persons reporting a hospitalization in the past year, 243 or 27% (95% CI: 23.7%-29.4%) were hospitalized at a surveillance hospital. The highest annual influenza-associated respiratory hospitalization rates per 100,000 population were among children <5 years, ranging from 13 (95% CI: 10-16) in 2009 to 69 (95% CI: 62-76) in 2012, when A/H3N2 and A/H1N1pdm09 were the predominant subtypes. Rates among persons ≥65 years ranged from 7 (95% CI: 3-10) in 2009 and 2012 to 17 (95% CI: 13-22) in 2016, when A/H3N2, B and A/H3N2 were predominant, respectively. **Conclusions:** Children aged <5 years and adults ≥65 years had the highest rates of influenza-associated hospitalization. These findings could be used to inform possible prevention strategies and programs, such as seasonal influenza vaccination.

Board 236. Estimation of Influenza-Associated Hospitalization in the United States Using a Rate Difference Method, 2011 to 2015

J. Chen[1], I. Foppa[1], A. Fowlkes[2], C. Reed[2]
[1]Battelle Institute, US CDC contractor, Atlanta, GA, USA, [2]US CDC, Atlanta, GA, USA

Background: Estimation of influenza-associated disease burden can provide support for influenza-associated disease prevention and control. Several statistical methods often involving complex mathematical

modeling have been used to estimate influenza hospitalization rates; we explored the use of a simple rate difference method to estimate excess hospitalizations and compared with other published estimates. **Methods:** We estimated influenza hospitalization rates in 10 regions of the United States with 7 age groups (<1, 1-4, 5-17, 18-49, 50-64 and >= 65 years) during the 2011-12 through 2014-15 influenza seasons using insurance claims and population enrollment data from Marketscan databases. Influenza predominant and peri-weeks during October through May of each year were determined from CDC's influenza virologic surveillance. Influenza predominant weeks were those with >10% of specimens testing positive for influenza while peri-weeks were those with <=10%of specimens testing positive for influenza. The analysis was done by region to account for geographic differences in the timing of influenza activity. For each region and age group, we estimated influenza-associated hospitalizations by subtracting hospitalization rates during peri-weeks from influenza predominant-weeks. **Results:** The population-weighted average rates of influenza-associated-respiratory and circulatory hospitalizations across the 10 regions and seasons was 53.7 (95% CI 39.3-68.0) per 100,000 person-seasons. The highest rate for influenza hospitalization was among those aged < 1 year (445.1; 95% CI 403.7-486.4) followed by those aged >=65 years (299.6; 95% CI 265.6-333.5) per 100,000 person-seasons. Among the 10 geographic regions, influenza-associated hospitalization rates varied from 34 to 84 per 100,000 person-seasons. The annual estimations of influenza associated-respiratory and circulatory hospitalizations from the previous studies using different statistical methods ranged from 63.5 (1993-2008) to 88.4 (1980-2000) per 100,000 person-years. **Conclusions:** A simple rate-difference method produced influenza-associated hospitalization rates and trends consistent with other more complex methods and may be a useful tool to generate influenza burden estimates when other data or statistical resources are limited.

Board 237. Regional Estimates of Influenza-Associated Mortality in India, 2007–2013

V. Narayan[1], A. Iuliano[2], K Roguski[2], M. Chadha[3], P Haldar[1], V Sreenivas[1], S Kant[1], S Saha[4], A Krishnan[1]
[1]All India Institute of Medical Sciences, New Delhi, India, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]National Institute of Virology, Pune, India, [4]Influenza Division, Centers for Disease Control and Prevention, New Delhi, India

Background: In India, mortality and influenza virus circulation patterns vary by geographic region. Policy decisions are often made at the state level, thus regional influenza death estimates could inform resource allocation and decision making for influenza control. We quantified influenza-associated excess respiratory mortality for Indian regions using 2007-2013 nationally representative influenza virus circulation and mortality data. **Methods:** We obtained virological data from the National Institute of Virology's Influenza Surveillance Network. Swabs were collected from 10 sentinel sites among both inpatients and outpatients with acute respiratory illness. We calculated monthly influenza percent positive for three regions and virus type and subtype. We obtained monthly counts of International Classification of Diseases (ICD)-10 coded respiratory (J00-J99) deaths for all ages from the Sample Registration System (SRS), which is a nationally representative survey of deaths coded using a standardized verbal autopsy tool. SRS divides India into six regions; for this analysis, the northern and southeastern regions were split due to different influenza seasonality, resulting in eight regions. We used a negative binomial model with viral surveillance terms to estimate influenza-associated excess respiratory deaths. For each region, we divided excess deaths by the SRS surveyed population to obtain rates. **Results:** The all-age excess influenza-associated respiratory mortality adjusted rate across regions and averaged across years ranged from 1–6/100,000 population and the annual rates by region ranged from 0–14/100,000 population. The highest annual rates occurred in 2009 in five regions (range 5–14/100,000); the lowest in 2012 in three regions (0–2/100,000). The southeastern region had the lowest annual rates (0–3/100,000) out of all regions for five of seven years. The northern region, including Delhi, had the highest annual rates out of all regions for three of seven years (5–14/100,000). **Conclusions:** We observed variability in influenza deaths by region, implying that regional estimates may be important for large countries, such as India. These findings may inform strategies for regional influenza prevention and control, including seasonal influenza vaccine and antiviral treatment.

Board 238. Characterization of Influenza-Related Lethal Cases in Georgia, 2014-2017 Seasons

A. Machablishvili, O. Tarkhan-Mouravi, P. Imnadze
L. Sakvarelidze National Center for Disease Control and Public Health, Tbilisi, Georgia

Background: Seasonal influenza-related deaths occur in people of all ages worldwide. In this study we describe epidemiological characteristics of patients who died from influenza-associated SARI in three consecutive influenza seasons in Georgia. **Methods:** Standardized questionnaires were used to obtain patients' information (demographic, underlying conditions, antiviral treatment, etc.) from SARI sentinel surveillance sites of 2014-2017 seasons. Data were analyzed using EpiInfo 7. **Results:** 27 (4.6%) out of 581 laboratory-confirmed influenza SARI case-patients died during three influenza seasons. Influenza A/H1N1pdm09 accounted 74.1% (20/27) deaths followed by 18.5% (5/27) A/H3N2 and 7.4% (2/27) B. 48% (13/27) deaths occurred during 2015-2016 season when dominant virus was A/H1N1pdm09. Patients infected with A/H1N1pdm09 had higher risk for lethal outcome compared to A/H3N2 and B infection (p=0.00, OR 4.3, CI 1.8-10.4). Age ranged from 1-84 years (median 55 years, IQR 52-64). 67% (18/27) cases represented 30-64 years age group with higher odd of lethal outcome (p=0.00, OR 10.2, CI 4.4-23.4). 25 (93%) out of 27 lethal cases suffered with at least one underlying condition; leading comorbidities were cardiovascular (12/27; 44%) and neurological disorders (7/27; 26%). Median time between symptom onset and hospitalization was 4 days (range 0-12 days, IQR 3-6 days). Oseltamivir was administered to all patients except one; however, only three patients were treated with antivirals within 48 hours after showing clinical signs. Median time between illness onset and influenza-associated death was 6 days (range 3-44, IQR 1-13 days). Only one was vaccinated with seasonal vaccine. **Conclusions:** We observed that SARI case-patients who were 30-64 years old and had confirmed influenza had higher risk of lethal outcome, especially in cases of A/H1N1pdm09 infection. Since cardiovascular and neurological disorders were major comorbidities among fatal cases, promotion of influenza vaccination among mentioned risk groups might lead to decreased number of influenza associated deaths.

Board 239. Mortality-Associated Risk Factors among Patients with Influenza A(H1N1)pdm09 Infections, Pakistan, 2009-2016

M. Ranjha, M. Salman, N. Badar, M. Khan, J. Ansari
National Institute of Health, Islamabad, Pakistan

Background: In April 2009, human infections with a novel influenza A(H1N1)pdm virus were identified, resulting in a subsequent worldwide pandemic. This viral subtype is presently circulating in Pakistan with peak infections every winter season causing a high death toll. **Purpose:** To identify mortality-associated risk factors among patients with influenza A(H1N1)pdm09 infections in Pakistan. **Methods:** A case-control study was conducted of laboratory-confirmed fatal cases of influenza-A(H1N1) reported from 2009 to 2016 to the National Institute of Health, Islamabad. Controls were randomly selected from the Influenza-A(H1N1)pdm09 positive non-fatal cases with 1:3 ratio. Fatal cases were defined as, "mortality associated with influenza-A(H1N1)pdm09 laboratory confirmation before or after a patient's death." Analyses were performed using Epi Info-7. **Results:** A total of 1034 positive cases of influenza A (H1N1)pdm09 were recorded including 46 deaths (CRF=4%). Median age of patients who died was 40 years (range=2-75 years). Males were more frequent 54% (n=25). A total of 61% (n=28) deaths occurred in patients 15-60 years of age, 26% (n=12) occurred in >60 years, 09%(n=04) in children <5 years and 04% (n=02) occurred among children 5-<15 years. Smoking was significantly associated with fatal cases [OR=4.5; 95%CI= 1.7-11, p<0.05]. Other factors were underlying respiratory diseases [OR=2.9; 95%CI=1.3-6.5 p<0.05], allergies [OR=2.5; 95%CI=1.2-5.3, p<0.05] and metabolic diseases [OR=2.3; 95%CI=1.2-4.9, p<0.05]. Eleven percent (n=5) of deaths were among healthcare workers, and chances of deaths among healthcare workers were higher than other professions [OR=4.1, 95% CI= 1.1-16, p<0.05]. **Conclusions:** More deaths were recorded in young age group, people 15-60 years old. Smokers and case-patients with underlying respiratory diseases, allergies, and metabolic diseases were at high risk for mortality. We recommend that clinicians identify high risk populations and vaccination including health care workers before the peak season. Implementation of infection control measures in the clinical settings is essential for the safety of healthcare professionals.

Board 240. Genomic Variability and Neuraminidase Inhibitor Drug Susceptibility Profile of Influenza A/H1N1pdm09 Strains Circulating in Morocco during 2015-2016 Season

F. Elfalaki[1], H. Ihazzmad[1], A. Bimouhen[1], Z. Regragui[1], S. Benkerroum[1], Y. Bakri[2], A. Barakkat[3], H. Oumzil[1]
[1]National Institute of Hygiene, Rabat, Morocco, [2]Biochemistry Laboratory Faculty of Sciences, Rabat, Morocco, [3]World Health Organization. Regional Office for the Eastern Mediterranean (EMRO), Cairo, Egypt

Background: In Morocco, information regarding genomic variability, molecular characteristics, and susceptibility profile to antiviral drug are scarce for influenza A/H1N1pdm09 viruses. The aims of the present study were to monitor genetic alterations in the Hemagglutinin (HA) and Neuraminidase(NA) genes, in addition to evaluation of the susceptibility profile to neuraminidases inhibitors(NAIs) Drug particularly oseltamivir and zanamivir of A/H1N1pdm09 viruses circulating in Morocco during 2015-2016 season. **Methods:** Respiratory specimens were collected from influenza-like illness (ILI) and severe acute respiratory illness (SARI) cases. PCR positive A/H1N1pdm09 viruses were inoculated to MDCK cell line for virus isolation. Sequencing and phylogenetic analysis of HA and NA were done to evaluate the genetic diversity of Moroccan A/H1N1pdm09 strains. The phenotyping evaluation to oseltamivir and zanamivir was performed with the use of a fluorescent assay. **Results:** The season was characterized by dominant circulation of A/H1N1pdm09 viruses accounting for (67%), followed by A/H3N2 (22%) and influenza B (11%). All sequenced A/H1N1pdm09 isolates clustered with the strains of antigenic group 6B.1. In respect to prototype A/California/7/2009, the amino acid analysis of 10 A/H1N1pdm09 viruses revealed the presence of significant amino-acid changes in the hemagglutinin(HA) located in antigenic site (S203T,S189T, K163Q,S162N) and in receptor binding domain (S185T). May have contributed towards enhanced virulence. The amino-acid sequences of NA showed any oseltamivir or zanamivir resistant marker. The phenotypic analyses of 96 isolates revealed normal inhibition to the both drugs. **Conclusions:** This study confirms the genetic variability and dynamic evolution of A/H1N1pdm09.As recommended by WHO, monitoring of the specific mutations and genetic evolution in influenza viral genes is crucial for assessing emergent strains.

Board 241. Efficacy of FLU-IGIV in Ferrets and Mice Infected with H1N1pdm09 Influenza Virus

H. Qiu[1], A. Simon[1], H. Andersen[2], L. Pessaint[2], B. Tarbet[3], S. Kodihalli[1]
[1]Preclinical Study, R&D, Emergent BioSolutions Canada Inc, Winnipeg, MB, Canada, [2]BIOQUAL Inc, Rockville, MD, USA, [3]Department of Animal, Dairy and Veterinary Sciences, School of Veterinary Medicine, Utah State University, Logan, UT, USA

Background: Severe influenza virus infections cause about 34,000 to 49,000 annual deaths in the United States alone even with the use of vaccines and antivirals. There is a need for more effective treatments for severe cases of influenza and influenza patients who are hospitalized. To address this unmet need, Emergent has developed a human polyclonal Influenza Immune Globulin Intravenous (FLU-IGIV) product for the treatment of serious influenza infection in hospitalized patients. FLU-IGIV was evaluated for its efficacy in both mouse and ferret models of influenza infection. **Methods:** The pharmacodynamic studies of FLU-IGIV against influenza H1N1 have been conducted in mice and ferrets to support clinical trials. FLU-IGIV was evaluated in a lethal mouse model using an adapted A/California/04/09 (H1N1) virus. Mice were exposed to lethal doses of influenzas virus and administered with various dose levels (50-400mg/kg) of FLU-IGIV or saline (placebo control) at 4 hours post-exposure. Animals were monitored for body weight loss and mortality for 21 days. Ferrets were exposed to A/California/ 076/2009 virus and treated with FLU-IGIV at one-day post infection. Ferrets were monitored daily for clinical signs and body weight loss. Lung and nasal wash samples were assessed for virus load. **Results:** The FLU-IGIV protected mice against lethal influenza in a dose-dependent manner. The higher dose level (200 and 400 mg/kg) provided a significant survival benefit (70-100%, p<0.001) compared to placebo control. Also, the survival with the higher dose levels was equal or better than the survival observed for Oseltamivir (60%, p<0.001 compared to placebo control), a positive control. In ferrets, there was a significant reduction in the quantity of virus in lungs of treated ferrets at 400mg/kg group (mean virus titer $Log_{10}TCID_{50}$/gram: 3.88 vs. 4.80, p<0.01) compared to the controls suggesting a systemic

treatment effect. Based on these results, a dose range of 200-400mg/kg is proposed for human clinical trials. **Conclusions:** The results of these studies demonstrate the efficacy of FLU-IGIV in both animal models of influenza virus infection and help define the dose for clinical trials.

Board 242. Cytokine Profile in Pregnant Ferrets Infected with 2009 Pandemic Influenza A(H1N1) Virus

S. Yoon[1], S. Wong[2], H. Zhu[3], Y. Guan[3], R. Webby[2]
[1]Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea, [2]St. Jude Children's Research Hospital, Memphis, TN, USA, [3]The University of Hong Kong, Hong Kong, Hong Kong

Background: Pregnancy has been associated with severe influenza, an association highlighted during the 2009 pandemic of influenza A(H1N1) virus (A[H1N1]pdm09) infection. The mechanisms that affect influenza virus infection outcome in this population, however, are not well defined. In the present study, we investigated the consequence of A(H1N1)pdm09 infection during pregnancy using the ferret model. **Methods:** In this study, we used 10 pregnant ferrets (6 infected with A[H1N1]pdm09 and 4 uninfected) and 8 nonpregnant ferrets (4 infected with A[H1N1]pdm09 and 4 uninfected). All ferrets were serologically negative for A(H1N1) pdm09 and seasonal influenza A(H3N2) virus as determined by hemagglutination inhibition assays. All virus titers were expressed as TCID50 in Madin-Darby canine kidney cells. For histopathologic analysis, tissue specimens were processed for hematoxylin and eosin staining and stained with a mouse anti–nucleoprotein (NP) monoclonal antibody. For quantification of peripheral CD8+ cells, PBMCs were stained with allophycocyanin-labeled CD8 antibody and data acquired on a BD FACSAria II. Cytokine and chemokine expression levels were measured using quantitative real-time polymerase chain reaction analysis. **Results:** To assess the underlying mechanism, we infected pregnant and non-pregnant ferrets with A(H1N1) pdm09 virus. A(H1N1)pdm09-infected pregnant ferrets also had higher levels of inflammatory cytokines in their pulmonary tracts. Systemically, total CD8+ T cell counts and A(H1N1)pdm09-specific B-cell responses in blood were significantly lower in pregnant ferrets. **Conclusions:** In our combined virologic and immunologic analyses, we showed that A(H1N1)pdm09 infection during pregnancy induces more-severe disease as a consequence of elevated viral loads and innate responses, combined with a diminished adaptive response. These factors likely contributed to the increased morbidity and mortality rates observed during the 2009 influenza pandemic in pregnant women.

Board 243. Obesity Increases the Duration of Influenza A Shedding in Adults

H. Maier[1], R. Lopez[2], N. Sanchez[3], S. Ng[1], L. Gresh[3], S. Ojeda[3], R. Burger-Calderon[3], G. Kuan[4], E. Harris[5], A. Balmaseda[2], A. Gordon[1]
[1]University of Michigan, Epidemiology, Ann Arbor, MI, USA, [2]Ministry of Health, Centro Nacional de Diagnósico y Referencis, Managua, Nicaragua, [3]Sustainable Sciences Institute, Managua, Nicaragua, [4]Ministry of Health, Centro de Salud Sócrates Flores Vivas Health Center, Managua, Nicaragua, [5]University of California, Berkeley, Division of Infectious Diseases and Vaccinology, Berkeley, CA, USA

Background: Many epidemiologic studies since the 2009 H1N1 influenza pandemic suggest that obesity increases the risk of severe complications and death from influenza infections, especially in the elderly. However, obesity's effect on influenza transmission dynamics has not been as well studied. **Methods:** This work uses data from households in the catchment area of the Health Center Sócrates Flores Vivas in District II of the capital Managua, Nicaragua. Household members were intensively monitored for 10-13 days once a symptomatic influenza index case was identified over three seasons between October 2015 and November 2017. Daily symptoms were recorded and up to five nasal/oropharyngeal swabs collected for influenza testing by RT-PCR during follow up. Shedding duration was defined as time from symptom onset to shedding cessation, and models accounted for censoring. The non-obese reference group was defined as normal weight and overweight, excluding underweight. Accelerated failure time models, adjusted for age and sex, were used to calculate event time ratios (ETRs) comparing shedding duration in obese vs non-obese participants. **Results:** Of 1,783 people enrolled during the study period with intense monitoring periods (587 households), influenza shedding was detected by RT-PCR in 758 people (42.5%). The obesity prevalence varied significantly by age with 2% (n=4), 8% (n=24), and 40% (n=83) in the age groups 0-4, 5-17, and 18-92 years, respectively. Of the 758 influenza cases, 20% were H1N1, 45% H3N2, and 35% influenza B positive. Obese adults shed influenza virus 50% longer (adjusted ETR 1.50; 95%CI: 1.10, 2.07) than non-obese adults; predicted mean shedding times 4.5 days vs 2.99 days. Obesity was not associated with longer shedding duration in children. The effect of obesity on influenza shedding duration was type specific, with influenza A positive obese adults shedding virus for 81% (adjusted ETR 1.81; 95%CI: 1.24, 2.65) longer than non-obese adults, while there was no association between shedding duration and obesity in adults infected with influenza B. **Conclusions:** We found that obesity significantly increased the duration of influenza A shedding in adults. Further analyses are underway to examine the effect of obesity on influenza transmission in households.

Board 244. Absolute Humidity and Influenza Transmissibility in Subtropical Hong Kong

S. Ali[1], P. Wu[1], D. He[2], V. Fang[1], E. Lau[1], S. Cauchemez[3], B. Cowling[1]
[1]The University of Hong Kong, Hong Kong, China, [2]Hong Kong Polytechnic University, Hong Kong, China, [3]Institut Pasteur, Paris, France

Background: The seasonality of influenza virus transmission in humans largely determines the timing and frequency of annual influenza vaccination programs worldwide. However the mechanisms underlying influenza seasonality remain difficult to disentangle, particularly in temperate locations where many possible driving factors occur simultaneously in the winter. **Methods:** We analyzed surveillance data on influenza virus activity in a subtropical city Hong Kong during the period 1998-2013. The time varying transmissibility of influenza at the start of an epidemic and then during an epidemic was characterized by the effective (or instantaneous) reproduction number, R_t, defined as the average number of secondary infections caused by a typical single infectious individual at time t. We used mechanistic models to quantify the influence of intrinsic and extrinsic factors on the effective reproduction number. **Results:** Point estimates of the effective reproductive numbers at the start of each influenza epidemic fell in the range 1.2 to 1.5. We found that a large part of the variance in transmissibility (24%-55%) was explained by the depletion of susceptibles during epidemics, while 4%-7% was explained by inter-seasonal effects, 1%-3% by absolute humidity, and 2%-5% by school holidays. A strong U-shaped effect of absolute humidity was identified on influenza transmissibility although the overall association between absolute humidity and

influenza transmission was comparatively small. **Conclusions:** The U-shaped effect of humidity on influenza transmission may contribute to the distinct irregular patterns of influenza seasonality observed in subtropical areas, including the occurrence of summer epidemics.

Board 245. Withdrawn

Board 246. Laboratory-Confirmed Influenza among Family Caregivers in District Hospitals in Bangladesh—2015–2017

K. Islam[1], M. Islam[1], M. Rahman[1], M. Islam[1], M. Kafi[1], S. Chai[2]
[1]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: In Bangladesh hospitals, most of a patient's care is provided by family and friends, collectively referred to as family caregivers (FCGs). Illness combined with poor infection control among healthcare providers can place patients at increased risk for hospital-acquired infections. With an average of two FCGs per patient, FCGs represent the largest group of healthcare providers in Bangladesh hospitals. We seek to assess the potential for transmission of influenza by FCGs in Bangladeshi hospitals. **Methods:** From December 2015–December 2017, we collected two nasopharyngeal and oropharyngeal swabs from each consenting FCG who reported symptoms of influenza-like illness (ILI) in four district hospitals in Bangladesh with ongoing influenza surveillance among patients. We tested one swab using a rapid point-of-care test (Sofia Influenza A+B FIA) at bedside and another swab by real-time RT-PCR for influenza in a reference laboratory. We compared results with national inpatient and outpatient influenza surveillance data. We assessed for influenza virus in the air by passing air within one meter of an FCG testing positive by the rapid test through a filter for eight hours and tested the filter by RT-PCR for influenza. **Results:** Among 389 participating FCGs, the median age was 30 years and 318 (82%) were female. One in six (16%) FCGs were positive for influenza by RT-PCR; of these, 10% were influenza A and 6% were influenza B. Among the influenza A strains, H1pdm09 and H3 were similarly common. Influenza among FCGs had similar trends and subtypes compared with Bangladesh national influenza surveillance. Of 30 filters from air collected next to FCGs positive for influenza by RT-PCR, four (13%) were positive for influenza virus RNA; each matched the subtype obtained from the corresponding FCG. **Conclusions:** FCGs are a potential source of influenza transmission in Bangladeshi hospitals. Although influenza trends and subtypes among FCGs reflect those of the community, infected FCGs' close contact with ill patients pose a risk for influenza transmission and subsequent serious complications to patients. Hospitals in Bangladesh should consider screening FCGs for ILI before permitting them to stay on inpatient wards and requiring FCGs with ILI to wear masks to prevent disease transmission.

Respiratory Infections

Board 247. Differences in Legionnaires' Disease Incidence among Large Counties—United States, 2012–2016

J. Smith, A. Barskey, C. Edens, S. Lee, P. Shah, N. Shang, L. Cooley
CDC, Atlanta, GA, USA

Background: Geographic distribution of Legionnaires' disease (LD) in the United States is typically described by census division or state, with reported rates of LD cases usually highest for the Middle Atlantic and East North Central census divisions. We used county-level national surveillance data to determine if areas with high LD burden could be more clearly identified. **Methods:** We obtained annual reported confirmed cases of LD per county from the National Notifiable Diseases Surveillance System for 2012–2016. The county-level five-year average annual incidence of LD (cases per 100,000) was calculated using corresponding population estimates from the US Census Bureau. To stabilize incidence rates for small population size, only counties with 5-year average populations of at least 500,000 ("large counties") were included. Because county-level case counts were not available for 2016, Minnesota data were excluded. **Results:** The average national LD incidence was 1.66 per 100,000 population from 2012–2016. Average rates by census division ranged from 0.89 in the Pacific and West South Central divisions to 3.06 in the Middle Atlantic division; three divisions (Middle Atlantic, East North Central, New England) had average incidences greater than the US rate (3.06, 2.62, and 2.13, respectively). Average annual incidences ranged from 0.21 to 7.71 among the 133 (4% of 3,055) US counties included in this analysis. Two census divisions (East North Central and Middle Atlantic) included 20 (74%) of the 27 large counties in the top quintile (2.55 or greater) of LD incidence rates. Among the remaining seven census divisions, five either had counties with rates at least double the average census division rate (N=4 divisions) or in the top quintile for rates (N=3 divisions). **Conclusions:** While many of the counties with highest rates were located in the previously-known '*Legionella* belt' census divisions, most regions had counties with rates well above the average for the region. Factors such as population or large building density and variations in testing practices may drive differences among counties. Further analyses are needed to understand these differences and support health departments in their prioritization of LD prevention efforts in jurisdictions with highest LD incidence.

Board 248. Cases of Legionnaires' Disease with Travel Exposures—United States, 2015–2016

A. Barskey, P. Shah, C. Edens
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Reported incidence of Legionnaires' disease (LD), a severe pneumonia, has increased by 4.5 times in the United States since 2000. Travel away from home, particularly stays in hotels with poorly maintained water systems, is a known risk factor for LD. We used national reporting data to describe cases and clusters of LD with travel exposure. **Methods:** We defined LD cases according to Council of State and Territorial Epidemiologists criteria. Our analysis examined reported travel exposure among US residents with confirmed LD during 2015-16. A travel-related LD case was defined as one in which the patient stayed away from home for ≥1 night in the 10 days preceding symptom onset; jurisdictions of travel were those in which the patient stayed for ≥1 of these nights. A travel cluster was defined as ≥2

travel-related cases associated with the same accommodation within 12 months. **Results:** A total of 12,220 LD cases was reported, of which 1,532 (12.5%) were travel-related. At least one stay in a commercial (e.g., hotel, resort, or cruise ship) or unknown accommodation was reported for 72.4% of travel-related cases. Travel-related cases with exposure to a commercial or unknown lodging type were linked to all US jurisdictions except Delaware. Median number of visits by patients with travel-related LD per jurisdiction was 16 (range 1 – 149). Additionally, there were 4 visits to US territories, 190 to non-US countries, and 36 cruises. In 2015-16, 80 travel clusters were identified, with a median number of 2 cases per cluster (range 2 – 55). Clusters were identified in 34 US jurisdictions, 3 foreign countries, and on 6 cruises. Number of clusters per US jurisdiction ranged from 1 – 10. **Conclusions:** Travel-associated cases and clusters of LD with geographically diverse potential exposure sources were identified. Prompt reporting to CDC of cases with travel exposure could facilitate timely identification of clusters, lead to a more effective public health response, and prevent new cases. Lodging management can reduce risk to visitors and employees by implementing effective water management programs.

Board 249. Outbreak of *Kingella kingae* Infections in a North Dakota Child-Care Facility

L. Cronquist, M. Feist, J. Schmidt, M. Howell, B. Nesemeier, K. Kruger
North Dakota Department of Health, Bismarck, ND, USA

Background: *Kingella kingae* is a member of the *Neisseriaceae* family that colonizes the upper respiratory tract of humans. Rarely, colonized bacteria can enter the bloodstream and cause serious invasive infections. Outbreaks of severe *K. kingae* infections among children ages 6 to 36 months have been associated with child care facilities. In December 2017, the North Dakota Department of Health (NDDoH) was notified of a possible outbreak of *K. kingae* infections among children in a child care facility. Two children who attend child care at the facility had been recently diagnosed with bone and joint infections. *K. kingae* was isolated from a clinical specimen collected from one of the children. **Methods:** The NDDoH recommended that all children who attended child care at the same facility as the two case-patients receive chemoprophylaxis with rifampin and amoxicillin. Parents or guardians of the children were advised to consult with their child's primary healthcare provider for appropriate antimicrobial prophylaxis. Child care providers were advised to thoroughly clean and disinfect all toys and surfaces in the facility and encourage good hand hygiene. Two epidemiologists from the NDDoH and the director of the local public health unit met with parents and guardians at the child care facility to address questions and concerns. A Health Advisory regarding the *K. kingae* outbreak was sent to all healthcare providers in the state via the North Dakota Health Alert Network (HAN). Parents or guardians of children who attended child care at the facility were asked to participate in a voluntary online survey to gather data on compliance with prophylaxis recommendations. **Results:** Survey responses were received for 45 (49%) of the 91 children at the childcare facility. Thirty-five (78%) of the 45 survey respondents reported completing the chemoprophylaxis as recommended. As of March 1, 2018, no additional cases have been reported. **Conclusions:** One possible limitation to the reported data is that parents or guardians who were compliant with recommendations were more likely to respond to a survey. Limited guidance exists on the public health response to *K. kingae* infection outbreaks in child care facilities. Additional research on transmission routes of *K. kingae* and infection control measures is warranted.

Board 250. Severe Acute Respiratory Infection (SARI) Surveillance: Building on an Existing Influenza Platform to Test for Non-Influenza Respiratory Viruses

K. Alroy[1], T. Do[2], P. Tran[3], T. Dang[3], L. Vu[4], N. Le[4], T. Do[2], P. Dao[2], B. Whitaker[1], J. McFarland[5], A. Mounts[2], S. Balajee[1]
[1]Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Division of Global Health Protection, Center for Global Health, Centers for Disease Control and Prevention, Hanoi, Viet Nam, [3]General Department of Preventive Medicine, Ministry of Health, Hanoi, Viet Nam, [4]General Department of Preventive Medicine, Hanoi, Viet Nam, [5]Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Hanoi, Viet Nam

Background: In 2016, Vietnam's Ministry of Health expanded its existing influenza sentinel surveillance for severe acute respiratory infection (SARI) to include testing for 7 additional respiratory viral pathogens: respiratory syncytial virus (RSV); human metapneumovirus (hMPV); human parainfluenza viruses 1 (PIV1), 2 (PIV2) and 3 (PIV3); human rhinovirus (RV); and human adenovirus (AdV). **Methods:** This multi-step process of expanding SARI surveillance entailed developing a new laboratory-testing algorithm for real-time reverse transcriptase–polymerase chain reactions (rRT-PCR), conducting laboratory trainings, as well as the procurement/distribution of quality reagents. Expansion also involved strengthening and aligning SARI surveillance epidemiological practices at sentinel sites and at the four regional institutes overseeing SARI surveillance in Vietnam. **Results:** From January 2016 until May 2017, 4,003 SARI specimens were tested by the regional institute laboratories and 20.2% (n = 810) were positive for influenza virus. Of the 3,193 influenza-negative specimens, 41.8% (n = 1,337) were positive for at least 1 non-influenza respiratory virus, of which 16.2% (n = 518), 13.4% (n = 428), and 9.6% (n = 308) tested positive for RSV, RV, and AdV, respectively. Of all of the samples tested for non-influenza viruses, 11% were positive for more than 1 virus. Almost half of the SARI specimens were negative for all viruses tested (46.4%, n=1,856). **Conclusions:** The Government of Vietnam demonstrated that expanding respiratory viral surveillance by strengthening and building upon an influenza platform is feasible, efficient, and practical. While influenza viruses remain a significant burden of SARI cases in Vietnam, in this study, non-influenza positive specimens were more than twice as prevalent with other respiratory viruses. These data provide valuable initial insight; however, the real value will only be realized over time as data is collected and analyzed over multiple years to help understand seasonality, disease burden, and the risk groups for these non-influenza respiratory viral pathogens in Vietnam. Disclaimer: The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Board 251. Adenoviruses Associated with Influenza-Like Illness among College Students—Pennsylvania, 2016–2017

H. Biggs[1], X. Lu[1], L. Dettinger[2], S. Sakthivel[3], J. Watson[1], S. Boktor[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Pennsylvania Department of Health, Harrisburg, PA, USA, [3]Batelle,

contracting agency to Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Human adenoviruses (HAdV) have caused outbreaks of acute respiratory illness in the community, in civilian congregate settings, and among military recruits. The substantial burden of HAdV illness among military trainees led to development of a vaccine against HAdV-4 and HAdV-7 for use in this population. Little is known about the contribution of HAdVs to respiratory illness in college student populations. We describe HAdVs associated with influenza-like illness (ILI) among students who sought care at a student health center (SHC) on a large college campus in Pennsylvania during August 28, 2016 – August 26, 2017. **Methods:** Students who presented at SHC with ILI, defined as a temperature ≥37.8°C, plus cough or sore throat, had basic demographic information recorded, and, from a convenience sample, a nasopharyngeal (NP) swab was collected. NP swabs were tested at the Pennsylvania Department of Health Laboratory (PDHL) using a respiratory virus panel, and specimens identified as HAdV-positive were sent to CDC for confirmation and to determine HAdV species and type. Typing was performed by PCR and sequencing of the hexon hypervariable regions 1-6. **Results:** During August 28, 2016 – August 26, 2017, 1149 ILI cases were reported from SHC, and 288 (25%) had an NP specimen tested. Forty-four (15%) of 288 specimens tested were positive for HAdV. Three HAdV species and four HAdV types were identified: species B HAdV-3 in 21 (48%), species B HAdV-7 in 16 (36%), species E HAdV-4 in five (11%), and species C HAdV-1 in two (5%). HAdV-3 was detected during September – December 2016, and HAdV-4 and HAdV-7 during December 2016 – May 2017. The median age of HAdV-positive students was 19 years (range 18 to 27), 13 (30%) were female, and 31 (70%) male. **Conclusions:** HAdVs were associated with 15% of ILI cases among young adults presenting at a student health center surveillance site during the 2016-2017 academic year. HAdV-3, HAdV-7 and HAdV-4 were predominant, and temporal clustering of types was observed. HAdVs are likely an under-recognized contributor to ILI on college campuses.

Board 252. Viral Growth Characteristics of Clinical Isolates Identified as Human Adenovirus Type 1 (HAdV-1) with Molecular Homology to Feline Adenovirus

B. Anderson[1], D. Zhang[2], M. Yondon[2], G. Gray[2]
[1]Global Health, Duke Kunshan University, Kunshan, China, [2]Division of Infectious Disease, School of Medicine, Global Health Institute, Duke University, Durham, NC, USA

Background: Human adenovirus type 1 (HAdV-1) is a species C adenovirus commonly associated with acute respiratory illness. In 2006 and 2010, two studies reported that clinically obtained HAdV-1 isolates were genetically similar to the hexon gene sequence of a feline adenovirus deposited in GenBank (accession number AY512566), suggesting possible feline-to-human transmission. While conducting a molecular typing study of HAdV isolates collected from a large US tertiary hospital, we identified eleven samples that were also typed as HAdV-1 and similarly shared genetic identity with the hexon and fiber gene sequences of feline adenovirus in GenBank. As the virological data for the previously reported HAdV-1 isolates genetically similar to feline adenovirus is limited, we sought to characterize the growth kinetics of our eleven isolates in a human (A549) and feline (CRFK) cell line and compare them to the prototypic HadV-1 strain. **Methods:** All HAdV-1 isolates were diluted to 1.0×10^4pfu/ml and inoculated in duplicate onto A549 and CRFK cells seeded in 12-well tissue culture plates. Culture supernatant and cells were collected at 0, 24, 48, 72, 96, 120 h post-infection. Viral DNA was extracted from culture supernatant and cells and viral concentration quantified using qPCR with previously derived standard curves. **Results:** All eleven clinical HAdV-1 isolates grew in both the A549 and CRFK cell lines and reached an overall higher titer in A549 cells compared to CRFK cells. The prototypic HAdV-1 strain exhibited similar growth kinetics in both cell lines. **Conclusions:** The eleven HAdV-1 clinical isolates we evaluated had the same growth kinetics in A549 human and CRFK feline cell lines as compared to the prototypic HAdV-1 strain. Though additional study is needed, our findings demonstrate that HAdV-1 is at least permissive in both human and feline cells.

Board 253. A Retrospective Examination of a Human Rhinovirus-Associated Pneumonia Outbreak at a Long-Term Care Facility in Georgia Using McGreer's Criteria

S. Smith[1], J. Wagner[2], A. Erickson[1]
[1]North Central Health District, Macon, GA, USA, [2]Georgia Department of Public Health, Atlanta, GA, USA

Background: Respiratory tract infections such as human rhinovirus (HRV) have a high transmission rate, and outbreaks have been linked to illness and death in elderly residents and immunosuppressed adults in long-term care facilities (LTCFs). HRV outbreaks can be challenging to control due to the lack of infection control education on disease surveillance by LTCFs. McGreer's criteria is a set of infection surveillance definitions created for LTCFs. This surveillance tool can be used track disease and possibly detect the development of an infectious disease outbreak. In a recent pneumonia outbreak at a LTCF (Facility X) in Georgia, McGreer's criteria were not used by the facility for disease surveillance. **Methods:** The North Central Health District Epidemiology Program requested medical charts from the county hospital on residents from Facility X, to identify and confirm cases associated with the outbreak using McGreer's criteria. The Georgia Department of Public Health's (GDPH) Acute Epidemiology Program requested testing for viral respiratory illness for Facility X residents that were hospitalized and symptomatic. The Centers for Disease Control and Prevention's Infection Control Assessment and Response (ICAR) questionnaire was used to identify gaps and provide recommendations for Facility X. **Results:** Two out of five symptomatic residents were positive for HRVs. After completing the chart review, 26 residents at Facility X met McGreer's criteria with interpretation of chest-ray, one pneumonia specific symptoms criteria present and one constitution criteria present (i.e., fever, acute change in mental status, acute functional decline). 65% (n=17) of the residents had respiratory co-morbidity listed in their medical record. **Conclusions:** HRV is the main causative organism for this outbreak investigation due to confirmed laboratory evidence; however, multiple etiologies could have contributed to the severity of respiratory illness. It is possible the severity of the outbreak could have been alleviated if the facility reported the cases earlier and were following proper infection control protocols.

Board 254. Whole Genomes of Rhinovirus C47 and a Newly Discovered Genotype, C56, Characterized Using Advanced Molecular Detection

C. Pan[1], T. Padilla[1], S. Yagi[1], T. Huynh[1], T. Ng[2], R. Marine[2], W. Nix[2], D. Wadford[1]
[1]Viral and Rickettsial Disease Laboratory, California Department of Public Health, Richmond, CA, USA, [2]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Rhinovirus C (RV-C) respiratory infections are very common, and sometimes cause severe illness requiring hospitalization, particularly in pediatric patients with comorbidities. Rhinoviruses are detectable by qualitative diagnostic assays; however, discriminating between rhinovirus species A, B and C (163 total types) is possible only through sequencing. For many years, the Viral and Rickettsial Diseases Laboratory (VRDL) of the California Department of Public Health has used Sanger sequencing of the VP1 capsid gene to characterize rhinoviruses. With the advent of advanced molecular detection (AMD) technologies such as next-generation sequencing (NGS), it is possible to obtain whole genome sequences which provide increased resolution for identifying novel rhinoviruses. Using NGS, we have characterized the first complete genomes of RV-C47 and identified a new RV-C type (RV-C56). **Methods:** Human respiratory specimens were first screened for enterovirus (EV) and rhinovirus (RV) by real time RT-PCR. Samples with indeterminate results (i.e., positive for both EV and RV) were typed by Sanger sequence analysis. Samples typed as RV-C were subsequently sequenced using NGS to further characterize the viruses. The resulting data were filtered and assembled using the CDC Division of Viral Diseases Bioinformatics Pipeline (VPipe). **Results:** Complete genomes of RV-C from three independent cases/outbreaks were obtained by NGS. An RV-C isolate from an outbreak at a long-term care facility in Butte County, California was identified as RV-C47 (Genbank Accession MF806525). A newly recognized genotype (RV-C56) was sequenced from two separate patient cases: a 31-year old patient who had recently returned from Hong Kong, and from a one-year old female. While the VP1 capsid sequence shared less than 82% nucleotide identity with other RV-C prototypes, the amino acid sequence shared 91% identity with RV-C18 (Genbank Accession HM236918). **Conclusions:** AMD methods enabled us to characterize the genomes of two RV-C genotypes. Our findings add to the current knowledge for rhinovirus diversity in the US, and may help to better understand the pathogenesis and evolution of rhinoviruses. Going forward, the increased molecular resolution provided by NGS will be useful for studying the epidemiology of RV-C infections during outbreak investigations.

Board 255. Development of a Duplex Real-Time RT-PCR Assay for Detection and Subgroup-Specific Identification of Human Respiratory Syncytial Virus (HRSV)

L. Wang[1,2], N. Thornburg[2], T. Peret[2]
[1]IHRC Inc. contracting agency to the Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Respiratory Viruses Branch, Division of Viral Diseases, Centers for Diseases Control and Prevention, Atlanta, GA, USA

Background: Human respiratory syncytial virus (HRSV) is a leading cause of acute respiratory illness in young children worldwide. Reliable detection and identification of HRSV subgroup A and B infections are essential for accurate disease burden estimates in anticipation of licensure of novel HRSV vaccines and immunotherapies. To insure continued reliability, molecular assays must remain current with evolving virus strains. A HRSV subgroup-specific real-time RT-PCR (rRT-PCR) assay was designed using genome sequence data currently available in public domain. **Methods:** A HRSV rRT-PCR assay for detection and subgroup identification using primers and subgroup-specific probes targeting a conserved region of the nucleoprotein gene combined in a single duplex reaction was developed. The assay was validated for sensitivity, specificity, reproducibility and clinical performance with a geographically diverse collection of respiratory specimens in direct comparison with an established pan-HRSV rRT-PCR reference assay. **Results:** The assay was sensitive, detecting 5 to 10 copies/reaction of target RNA transcripts with a linear dynamic range of 10 log units ($5x10^0$ - $5x10^7$). The assay was specific, showing no amplification with a panel of 16 other common respiratory pathogens or predicted by *in silico* primer/probe analysis. A total of 15 HRSV field isolates and 325 positive clinical specimens were correctly identified to subgroup A or B, including 3 specimens with mixed A and B viruses that were confirmed by targeted sequencing. **Conclusions:** The duplex rRT-PCR assay permits rapid, sensitive, and specific detection and identification of HRSV subgroups.

Board 256. Estimating Age- and Region-Specific Excess Mortality Caused by Influenza and Respiratory Syncytial Viruses in Japan, 2006-2014

K. Mizumoto[1], G. Chowell[1], L. Simonsen[2], H. Nishiura[3]
[1]Georgia State University, Atlanta, GA, USA, [2]Roskilde University, Trekroner, Denmark, [3]Hokkaido University, Sapporo, Japan

Background: The morbidity and mortality impact of influenza and respiratory syncytial virus (RSV) infections on a population can be substantial. In this paper we estimate winter-seasonal excess mortality rates from influenza- and RSV-related in Japan from 2006 to 2014. **Methods:** We used a non-parametric method that captures seasonal and long-term trends and stratified the mortality time series by 6 age groups and prefecture. **Results:** Across the 8 seasons influenza was on average associated with 24,576 annual deaths in Japan, or 19.2per 100,000 population (and only 6.4/100,000 in the 2009 influenza pandemic). RSV was annually associated with 33,982 annual deaths (26.6 per 100,000 population) across the 8 seasons studied. For both infectious diseases, excess mortality rates were highest among those aged ≥ 80 years and substantially higher in more populated (urbanized) prefectures. Respiratory and circulatory disease mortality was found to be the most associated with influenza, accounting for 89% of influenza-related deaths and 85% of RSV-related deaths, respectively. **Conclusions:** Our study reveals that the mortality burden attributable to RSV is comparable to that of influenza. For comparison, the number of notified laboratory-confirmed deaths during the 2009 pandemic were 41 times smaller than our estimate of the actual number of excess deaths associated with the 2009 A/H1N1 influenza pandemic in Japan. Our findings clarify the substantial mortality impact of two major respiratory infections in Japan: influenza and RSV and emphasize the need to continue monitoring their effects on mortality across geographic areas and age groups in order to protect the vulnerable population.

Board 257. Surveillance for Respiratory Syncytial Virus and Parainfluenza Virus among Patients Hospitalized with Pneumonia in Sarawak, Malaysia

J. Fieldhouse[1], T. Toh[2], W. Lim[2], J. Ting[2], S. Ha[2], C. Kong[3], K. Hii[3], T. Wong[4], S. Wong[4], T. Warkentien[5], G. Gray[1]
[1]Duke University School of Medicine, Division of Infectious Diseases, Durham, NC, USA, [2]Clinical Research Center, Sibu Hospital, Sibu, Malaysia, [3]Kapit Hospital, Kapit, Malaysia, [4]Sibu Hospital Department of Paediatrics, Sibu, Malaysia, [5]US Naval Medical Research Center- Asia, Singapore, Singapore

BBackground: Pneumonia remains a leading cause of morbidity and mortality among children under five worldwide, and is responsible for nearly 16% of all childhood deaths. Respiratory syncytial virus (RSV) and parainfluenza virus (PIV) are two respiratory pathogens known to cause pneumonia among children in Sibu and Kapit Hospitals in Sarawak, Malaysia. Despite increasing pneumonia admissions in recent years, diagnostic capability for these viruses remained lacking. The primary objective of this study was to determine the prevalence of RSV subtypes A and B and PIV types 1- 4 among patients hospitalized with pneumonia in Sibu and Kapit hospitals, and to assess potential risk factors for infection. **Methods:** Patients hospitalized with pneumonia were enrolled in a cross-sectional pilot study over six weeks in these two hospitals. Nasopharyngeal swabs were collected and studied with real-time reverse transcription polymerase chain reaction assays at Sibu Hospital's Clinical Research Center Laboratory. Patient characteristics were analyzed for association with viral positivity. **Results:** Of 129 specimens collected, 39 samples tested positive for RSV-A (30.2%), two were positive for RSV B (1.6%), one was positive for PIV-3 (0.8%) and one was positive for PIV-4 (0.8%). No samples were positive for PIV-1 or PIV-2. Of the 39 RSV-A positive samples, 18 were collected from children <1 one year of age, 18 were collected from children between 1-5 years of age, and two were collected from patients >6 years of age. The date of the patient's birth was missing for one of the RSV-A positive specimens. A multivariable analysis found the odds of children <1 year of age testing positive for RSV-A were 32.7 (95% CI: 3.9, 276.2) times larger than >18 years of age, and the odds of patients hospitalized at Kapit Hospital testing positive for RSV-A were 3.2 (95% CI: 1.3, 7.8) times larger than patients hospitalized at Sibu Hospital. **Conclusions:** This study found a high prevalence of RSV-A among pneumonia patients admitted to the two hospitals. Subsequently, Sibu Hospital adapted the molecular assays with the goal of providing more directed care for such pneumonia patients.

Board 258. Increased Burden of Respiratory Syncytial Virus in Southern California, 2016-18

A. Hawksworth[1], P. Kriner[2], M. Fiero[2], E. Iniguez-Stevens[3], E. Fabian[3], Y. Medrano[3], P. Kammerer[1], M. Ricketts[1], C. Myers[4]

[1]Henry M. Jackson Foundation for the Advancement of Military Medicine, Bethesda, MD, USA, [2]Imperial County Public Health Department, El Centro, CA, USA, [3]California Department of Public Health, Sacramento, CA, USA, [4]Naval Health Research Center, San Diego, CA, USA

Background: Respiratory syncytial virus (RSV) is recognized as a significant contributor to respiratory morbidity and mortality worldwide, particularly in young children. An ongoing respiratory illness surveillance program in Southern California among civilians near the US-Mexico border and US Department of Defense beneficiaries included RSV testing since 2012. **Methods:** Upper respiratory specimens from patients presenting with respiratory illness at clinics and hospitals in Southern California were tested at a single lab using a validated real-time PCR panel that included RSV. Surveillance and testing methods remained consistent between 2012 and 2018. **Results:** Among 12,350 samples collected, 875 (7%) were RSV-positive. 58% of RSV cases were among children < 5 yrs old and 82% of RSV cases occurred in winter months (December-February). Hospitalized patients had a significantly higher proportion of RSV as compared to outpatients (11% vs. 6% overall; 17% vs. 10% in winter; $p < .0001$). A significant ($p <.0001$) increase in the proportion positive was observed during recent winters, with 16% RSV positive during winters of 2016-18 (range 14-21%) compared to 9% during winters of 2012-15 (range 6-15%). The number of samples collected was relatively consistent, with means of 930 and 1019 during winters of 2012-15 and 2016-17, respectively. **Conclusions:** The increased RSV burden in recent seasons is concerning from a public health perspective, especially in light of the association of RSV with an increased risk of hospitalization. As this surveillance was limited to the Southern California region, investigation of RSV trends in other areas is warranted.

Board 259. Respiratory Syncytial Virus among Children Hospitalized with Acute Lower Respiratory Infection in Kashmir, a Temperate Region in Northern India

S. Saha[1], P. Koul[2], K Koul[2], H. Mir[2], V. Potdar[3], M. Chadha[3], D. Iuliano[4], K. Lafond[4], A. Krishnan[5]
[1]Influenza Program, US Centers for Disease Control and Prevention, New Delhi, India, [2]Sher-i-Kashmir Institute of Medical Sciences, Srinagar, India, [3]National Institute of Virology, Pune, India, [4]US Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]All India Institute of Medical Sciences, New Delhi, India

Background: Acute lower respiratory infections (ALRI) are a leading cause of hospitalizations in children especially due to viral pathogens. We studied the prevalence of respiratory viruses among children aged <5 years hospitalized with severe acute respiratory infections (SARI) in Kashmir, India. **Methods:** A prospective observational study in two tertiary care hospitals was conducted from October 2013–September 2014 enrolling children aged <5 years with SARI, defined as history of or measured fever (≥38°C) with cough and onset in the last 7 days requiring hospitalization in children aged ≥3-59 months and for children aged < 3 months a physician-diagnosed acute lower respiratory infection. Hospitalized children were screened within 24 hours for eligibility to systematically enroll two SARI case-patients per day. Clinical data and nasopharyngeal swabs were collected from enrolled participants. Samples were tested for respiratory syncytial virus (RSV) A and B, influenza viruses, rhinoviruses (HRV), adenovirus (ADV), bocavirus (BoV), human metapneumovirus (hMPV) A and B, enteroviruses, coronaviruses (OC43, NL65,C229E), and parainfluenza viruses (PIV) 1, 2, 3 and 4 using standardized duplex real-time polymerase chain reaction. **Results:** Among 4,548 respiratory illness admissions screened, 1,026 met the SARI case definition, and 412 were enrolled (aged 15 days to 58 months, median 12 months). Of them, 257 (62%) were positive for any virus; RSV was most commonly detected (n=118; 28%) followed by HRV (n=83; 20%), PIVs (n=31; 8%), influenza viruses (n=18; 4%), BoV (n=15; 4%), coronaviruses (n=16; 4%), ADV (n=14; 3%), enteroviruses (n=11; 3%), and hMPV (n=9; 2%). Fifty-four cases had evidence of co-detection. Influenza-associated SARI were more common in children aged 1-5 years (14/18; 78%) while the majority

of RSV detections occurred in children <12 months (83/118; 70%). Of the RSV viruses typed (n=116), the majority were type B (94, 80%). Phylogenetic analysis of G gene of RSV showed circulation of the BA9 genotype with 60 base-pair nucleotide duplication. **Conclusions:** Respiratory viruses, especially RSV, contributed to a substantial proportion of SARI hospitalizations among those <5 years in north India. Such etiology data help guide clinicians for appropriate treatment strategies for hospitalized SARI case-patients.

Board 260. Respiratory Viruses Associated with Severe Acute Respiratory Infection (SARI) among Children under Five Years Old in Morocco, during Two Seasons 2014-16

A. Bimouhen[1], F. El Falaki[1], Z. Regragui[1], H. Ihzmade[1], S. Benkerroum[1], Y. Bakri[2], A. Barakat[3], H. Oumzil[1]
[1]National Influenza Center. Virology Department, National Institute of Hygiene, Rabat, Morocco, [2]Department of Biology, Mohammed V University of Rabat, Morocco, [3]World Health Organization. Regional Office for the Eastern Mediterranean (EMRO), Cairo, Egypt

Background: Severe acute respiratory infection (SARI) is one of the leading causes of morbidity and mortality in infants and children under five years, especially in resource limited settings. In Morocco, data regarding the viral etiology of SARI among child are still scarce. The present study aims to determine the respiratory virus associated with SARI among children under five years. **Methods:** A total of 467 nasopharyngeal samples were collected from children under 5 years old, subjects were recruited during hospitalization in pediatric and pediatric intensive care units of public sentinel hospitals between September 2014 and August 2016. Samples were analyzed at the National Influenza Center (NIC) by real-time PCR using a multiplex kit (Fast Track Diagnostics™®) for the detection of influenza A and B viruses, respiratory syncytial virus, adenovirus, para-influenza viruses (1-4), human coronaviruses, rhinovirus, and human metapneumovirus. All positive samples were retested by a RT-PCR monoplex assay. **Results:** One or more respiratory viruses were detected in 404 (86.5%) of the study population. The most frequently detected viruses were respiratory syncytial virus (39.8%), adenovirus (13.8%), and influenza viruses (9.8%). The rates of single, double, and triple infection were (79%), (19%), and (2%), respectively. **Conclusions:** The results of our study showed a significant prevalence of respiratory syncytial virus among the children with SARI. The viral circulation was noted during a frame time ranging from November to April with a winter peak in January; our results are in line with reported data from other parts of the world, stating that respiratory syncytial virus is the leading cause of lower respiratory tract infections in infants and young children.

Board 261. Middle East Respiratory Syndrome in Humans: Current Knowledge Gaps for Effective Public Health Response

S. Malik[1], A. El Kholy[1], M. Obtel[2], M. Van Kerkhove[3]
[1]World Health Organization Eastern Mediterranean Regional Office, Cairo, Egypt, [2]Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [3]WHO Health Emergency Programme, World Health Organization, Geneva, Switzerland

Background: The Middle East respiratory syndrome coronavirus (MERS-CoV) continues to pose threats to global health security. The majority of cases (over 85%) reported to date globally have been from the countries in the Middle East. Being a new virus, presumed to be zoonotic in origin, and given its ability to cause severe diseases in humans, MERS-CoV continues to evoke global concern about its potential to cause a global pandemic. Since the detection of this virus in 2012, several important knowledge and information gaps continue to haunt the global scientific communities. The absence of such crucial information is a limiting factor in developing effective public health control measures and intervention strategies to minimize the risk of infection. **Methods:** In order to identify current knowledge gaps associated with MERS, we conducted a systematic review of available literature published between 2012 and 2017. We used PRISMA guidelines and identified 314 relevant, peer-reviewed publications from Embase, Google Scholar, and PubMed. Of these, 208 were selected for inclusion in our review based on the considerations of available knowledge gaps that have important implications for control. **Results:** Among the knowledge gaps identified that have implications for public health control, the most important are risk factors for transmission in humans; role of laboratory-positive asymptomatic cases on onward transmission; exposure risk factors for healthcare workers that result in infection; risk factors for hospital outbreaks and role of administrative and environmental controls for stopping the hospital outbreaks; behavioral risk factors that may put certain group of people at higher risk of illness; and seasonal trend of the disease. **Conclusions:** Although there has been substantial MERS-CoV research since 2012, significant knowledge gaps persist. Uncertainties about the virus's origin, transmissibility, and period of infectiousness need to be addressed to gain better understanding for effective global response. These areas merit urgent attention using a unified One Health approach.

Board 262. Genomic Sequence and Growth Characterization of Novel MERS Coronaviruses from Saudi Arabia

A. Tamin[1], S. Sakthivel[1], C. Paden[1], K. Queen[1], Y. Tao[1], Y. Li[1], J. Zhang[1], H. Al-Abdely[2], A. Assiri[2], A. Alsharef[2], H. Jokhdar[2], C. Midgley[1], J. Watson[1], S. Gerber[1], S. Tong[1], N. Thornburg[1]
[1]CDC, Atlanta, GA, USA, [2]Saudi Arabia Ministry of Health, Riyadh, Saudi Arabia

Background: Middle East respiratory syndrome (MERS) is a viral respiratory illness first reported in Saudi Arabia in September 2012 caused by the human coronavirus (CoV), MERS-CoV. Globally, as of January 31, 2018, 27 countries have reported human MERS-CoV infections with 2,143 laboratory-confirmed cases and 750 deaths. This report describes isolation of the virus from human clinical specimens and their characterizations with genomic sequencing, electron microscopic study, and growth characteristics of these primary viral isolates from Saudi Arabia. **Methods:** Each step of virus isolation and handling was performed in a biosafety cabinet within a BSL-3 containment laboratory using approved personal protective equipment and biosafety protocols. Clinical specimens (sputum, throat, nasopharyngeal swabs in Universal Transport Media, blood, urine, and feces) were serially diluted in a 96 wells flat-bottom plates; Vero cell suspension (2 x 10^4 cells/well) in DMEM with 10% FBS and penicillin-streptomycin and fungizone were added; the plates were incubated in 37°C/5% CO_2 incubator, and checked daily for cytopathic effect (CPE). RNA was extracted from monolayers exhibiting CPE and tested by MERS-CoV specific real time-RT PCR to confirm identity of the viral isolates. Novel viruses were passaged, examined by electron microscopy (EM), sequenced by Sanger and next generation sequencing methods,

and were used for growth curve analyses. **Results:** To date, we have isolated 13 novel strains of MERS-CoV from Saudi Arabia from respiratory clinical specimens. Genomic sequencing and phylogenetic analysis of novel viral isolates suggest all 13 viruses belong to clade B, lineages 4 and 5. **Conclusions:** The majority of novel viral isolates had full-length genomes, but three strains had genomic deletions. The deletions were in the 5' untranslated region (9 nt), ORF1a (3 nt), or the 3' end of ORF3 (41 nt). All the 13 MERS-CoV strains replicated in Vero and Huh7 cells. MERS-CoV infection in both cells show fusion and syncytia formation. However, Huh7 cells showed more significant and extensive syncytia formation compared to Vero cells. Viruses with deletions in the 5' UTR and ORF1a exhibited impaired viral release in Vero cells.

Board 263. Withdrawn

Board 264. Morbidities & Mortalities of (MERS-COV) Epidemic Threatens Opportunities and Containment Strategies

H. Hussain
Dubai Health Authority, Dubai, United Arab Emirates

Background: MERS virus causing acute severe respiratory diseases has been reported in 2012 in Saudi Arabia. Confirmed cases of virus were presented with severe acute respiratory illness. **Methods:** Electronic databases were searched using a pre-defined search strategy. Additional references from the bibliographies of retrieved articles were also reviewed and experts in the area were contacted. The initial literature search identified 47 papers. **Results:** Since 2012 the cases have been reported in 21 countries, yet most of the reporting still comes from Arabian Peninsula region. Almost 1700 cases have been reported, almost more than 700 case-patients died about 35%, The main country affected by the disease is Saudi Arabia, which reported the highest incidence, followed by died and UAE as 81 cases were diagnosed among which 15 died (18.5.6%). So far, all the cases have been linked to six countries in or near the Arabian Peninsula. Sporadic cases have been identified in the United States. This virus has spread from ill people to others through close contact. The virus has not been shown to spread in a sustained way in communities. The situation is still evolving. **Conclusions:** The disease is taking propagating epidemic curve and trending towards more spreading and adding more and more cases at the beginning of the epidemic, by time increasing number of index cases led to change to new epidemiological curve pattern into explosive curve. * Approximately 35% of reported patients with MERS have died. * Although the majority of cases of MERS in humans have been attributed to human-to-human infections in health care settings, current scientific evidence suggests that dromedary camels are a major reservoir host for MERS-CoV. However, the exact role of dromedaries in transmission of the virus and the exact route(s) of transmission are unknown. *The virus does not pass easily from person to person unless there is close contact, such as occurs when providing unprotected care to a patient. Health care-associated outbreaks have occurred in several countries, with the largest outbreaks in Saudi Arabia, United Arab Emirates, and the Republic of Korea. *The case-fatality ratio was found to increase significantly with age. Containment strategies Breaking transition chain -Infection prevention and control measures are critical -Health care professionals are directly concerned -Deep Gap analysis studies to address virus circulating understanding the risks of this virus.

Board 265. MERS-CoV Outbreak at Domat Al-Jandal Hospital

A. Al-Guaimy
Field Epidemiology Training Program, Riyadh, Saudi Arabia

Background: Saudi Arabia was the first to report MERS-CoV in the Middle East region in 2012. Several outbreaks have occurred since that time. In August 2017, an outbreak of MERS-CoV at Al-Jouf province in Saudi Arabia was possibly linked to an index case-patient who was admitted to the hospital while infectious. **Methods:** List of cases were obtained from hospital administration. Information was collected by interviewing the infection control team, the outbreak team at the hospital, and the local MERS-CoV coordinator and by observing the most relevant sections at the hospital. **Results:** A total of 13 cases of MERS CoV infection were reported at Domat Al-Jandal hospital. Of these 13 cases, 8 cases were in health care workers (3 physicians and 5 nurses), 3 cases were in contacts of the index case-patient. Most case-patients acquired infection by person to person transmission at male medical ward and intensive care unit; only 3 contact cases were infected when they brought the primary case-patient to the hospital. The attack rate among physicians was 12% and among nurses was 9.8%. We found that late diagnosis, improper isolation of patients, and non-compliance on infection control protocols are the leading causes of spread of the infection. **Conclusions:** Sorting and examining patients carefully at triage and emergency before admission to hospital, adhering to infection control protocols, and applying effective isolation measures are a must to stop or prevent any MERS-CoV infection at hospitals.

Board 266. Contemporaneous Outbreaks of Middle East Respiratory Syndrome in Two Hospitals in Riyadh, Saudi Arabia, May—June 2017

H. Amer[1], K. Alanazi[2], M. Killerby[3], H. Biggs[3], G. Abedi[3], H. Jokhdar[2], A. Alsharef[2], M. Mohammed[2], O. Elneil[2], A. Alamri[2], S. Bereagesh[2], S. Tawfik[2], H. Alresheedi[2], R. Alhakeem[2], A. Hakawi[2], H. Alfalah[1], S. Tong[3], X. Lu[3], K. Queen[3], Y. Li[3], S. Sakthivel[4], Y. Tao[3], J. Zhang[3], C. Paden[3], H. Al-Abdely[2], A. Assiri[2], S. Gerber[3], J. Watson[3]
[1]King Saud Medical City, Riyadh, Saudi Arabia, [2]Ministry of Health, Riyadh, Saudi Arabia, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Battelle, contractor to Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Middle East respiratory syndrome coronavirus (MERS-CoV) is known to cause severe respiratory illness and has been associated with large, hospital-based outbreaks, sometimes involving multiple facilities. We describe the epidemiologic, molecular, and serologic investigation of two contemporaneous healthcare-associated outbreaks of MERS-CoV in Riyadh, Saudi Arabia, during May—June 2017, and explore infection control implications. **Methods:** Contact tracing and testing was performed at two hospitals (A and B), one clinic, and one outpatient dialysis unit. Laboratory confirmation was performed by real-time RT-PCR and/or genome sequencing. Available health care personnel (HCP) cases and HCP-contacts of cases were interviewed to understand exposures and submitted serum for serologic testing. **Results:** Forty-eight cases were identified, 38 linked to Hospital A and 10 to Hospital B. At each hospital, transmission links were traced to a single index case. Four cases were associated with superspreading events (epidemiologically linked to ≥5 secondary cases); all four were severely ill, initially unrecognized as MERS-CoV cases, and subsequently died. Three of the four cases had aerosol-generating procedures associated with subsequent cases among exposed HCP. Full genomic se-

quences from specimens from Hospital A clustered separately to those from Hospital B, suggesting two distinct outbreaks. The Hospital A cluster was genetically related with the camel MERS-CoV from KSA (KT368879) and the Hospital B cluster to the human MERS-CoV from KSA (KX154684). Of 17 HCP-cases available for serologic testing, 4 (24%) were seropositive. Of 114 HCP contacts of cases, 4 (4%) were seropositive. **Conclusions:** We describe two distinct healthcare-associated outbreaks, each initiated by a single index case originating from different sources and characterized by multiple superspreading events. Severe illness, delayed recognition and implementation of infection prevention and control measures likely contributed to secondary transmission. Prompt contact tracing, monitoring and testing, and implementation of recommended transmission-based precautions for suspected cases quickly halted transmission in both outbreaks. Serologic investigation revealed limited transmission beyond confirmed cases.

Board 267. Evaluating the Potential Impact of Targeted Vaccination Strategies against Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Outbreaks in the Healthcare Setting

F. Abdirizak, G. Chowell, R. Lewis
Georgia State University, Atlanta, GA, USA

Background: The severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) are two coronaviruses with demonstrated potential to generate significant nosocomial outbreaks. In particular, MERS has continued to pose a significant threat in the Middle East since 2012. Currently, no licensed vaccine or drug treatment is available to treat patients infected with either coronavirus. However, there are some MERS vaccines in the preclinical stage of development. **Methods:** We sought to evaluate the potential impact of targeted vaccination strategies for mitigating SARS and MERS outbreaks in healthcare settings by using simple statistical methods and detailed historic transmission trees describing the progression of prior nosocomial outbreaks of SARS and MERS. Our proposed vaccine strategies target two groups, which have been disproportionately affected during past outbreaks: Patients and healthcare workers. We assumed vaccination coverage levels at 50% and 75%. **Results:** Our study found that vaccine strategies targeting patients averted nearly 50% or more of MERS and SARS cases. **Conclusions:** Thus, considering that SARS and MERS are amplified in healthcare settings owing to diagnostic delays and suboptimal infection control measures our results support the vaccination strategies targeting patients to mitigate transmission in the healthcare setting.

Tropical Infections

Board 268. Epidemiology of Imported Malaria among Travelers and Expatriates in the State of Qatar, 2016

H. Al-Romaihi[1], N. Ganesan[1], E. Farag[1], S. Hamad J. Al Thani[1], S. Shawky[2]
[1]Ministry of Public Health, Doha, Qatar, [2]Social Research Centre, The American University in Cairo, Cairo, Egypt

Background: Malaria remains a major public health concern in many countries. Imported malaria is expanding in the Eastern Mediterranean Region and the state of Qatar is no exception as the country is considered an international travel hub for connecting flights from more than 150 destinations with 30 million international travelers and expatriates passing over Hamad International Airport. The aim of the study is to fill a large gap in the existing knowledge base on imported malaria in the State of Qatar in an attempt to add depth to the malaria prevention and control program. **Methods:** A descriptive epidemiological study was conducted using the available reported surveillance data from all medical facilities in the country. All reported cases who had a positive thick and thin blood smear confirmatory test for malaria during the year of 2016 were considered **Results:** During the period of 2016, 493 malaria cases were reported. Almost all except one were in non-Qataries. The majority were male expatriates in the age group 15-44 years. One-fifth of cases were in need of hospital care and 87.8% reported recent travel to malaria endemic area. The majority of cases were reported in Pakistanis (33.7%) and Indians (33.9%). However cases from Nepal (4.9%), Sudan (9.1%) and other countries (19.4%) were also reported. The most common and higher number of species was *Plasmodium vivax* (72.1 %), followed by *Plasmodium falciparum* (23.1%). Eight cases (1.6%) had mixed *Plasmodium falciparum* and *plasmodium viva*x infection. This infections were reported in all nationalities except Nepal. The mixed infections were mainly reported in Sudanese (8.9%). **Conclusions:** Our results confirm the existence of imported malaria in the State of Qatar. Malaria infection affects young male expatriates from malaria endemic areas and may constitute a health threat to nationals. Both *Plasmodium vivax* and *Plasmodium falciparum* were diagnosed in the country.

Board 269. Crimean-Congo Hemorrhagic Fever Outbreak in Central Uganda–August 2017

S. Kizito[1], P. Okello[1], L. Nyakarahuka[2], S. Balinandi[2], S. Mulei[2], J. Kyondo[2], A. Tumusiime[2], J. Ojwang[3], B. Kwesiga[1], A. Ario[4], J. Lutwama[2], B. Zhu[5]
[1]Uganda Public Health Fellowship Program, Kampala, Uganda, [2]Uganda Virus Research Institute, Entebbe, Uganda, [3]US Centers for Disease Control and Prevention, Kampala, Uganda, [4]Uganda Public Health Fellowship Program, Ministry of Health, Kampala, Uganda, [5]US Centers for Disease Control and Prevention, Uganda and Division of Global Health Protection, Center for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: On August 20, 2017, two cases of Crimean-Congo Hemorrhagic Fever (CCHF) were reported in Kyankwanzi and Nakaseke Districts, central Uganda. CCHF is the most widespread and highly fatal tick-borne viral hemorrhagic fever (VHF) which represents a global health security threat. Humans are infected through tick bites or contact with blood or body fluids of infected animals or persons. Symptoms include fevers, fatigue, and spontaneous bleeding. We investigated to determine the risk factors for the outbreak and to recommend control measures. **Methods:** A suspected case was defined as sudden onset of fever (>38°C) for ≥3 days between July 1 and September 30, 2017, plus any of the following: spontaneous bleeding or bruising, laboratory evidence of low leucocyte and platelet counts unexplained by other causes in a resident of the two affected districts. A confirmed case was a suspected case that tested positive for CCHF by both RT-PCR and IgM serology. Medical records review and active case-search was conducted in the affected community. A 1:4 case-control study was conducted to compare potential exposures of case-patients and controls (case-patients' asymptomatic neighbors, matched by sex and age). Blood samples of cattle and goats from farms where confirmed case-patients worked were tested for CCHF infection

using IgG ELISA. **Results:** In addition to the two initial confirmed case-patients (both survived), five patients met the suspected case definition among 23 medical records reviewed (two of whom died). All case-patients were men. Tick exposure (i.e., being bitten by ticks or squashing ticks bare-handed) was reported by 4/7 (57%) suspected and confirmed case-patients and 3/28 (11%) controls (mOR=11, 95%$CI_{Fisher\ exact}$=1.1-112). Sero-positivity for CCHF was found in 60% (37/62) of cattle and 24% (5/21) of goats. **Conclusions:** Tick exposure was associated with developing symptoms consistent with CCHF. We recommended sensitization, health education, isolation of case-patients, and tick control reach-outs to farmers.

Board 270. When There Is a Will, There Is a Way: Evolution of Ebola Diagnostics during the 2014-2016 West African Outbreak

G. Olinger[1], H. Wood[2], L. Presser[1], K. Yeh[1], J. Michelotti[1], D. Roberts[2], J. Coffin[1]
[1]MRIGlobal, Gaithersburg, MD, USA, [2]MRIGlobal, Palm Bay, FL, USA

Background: Ebola virus (EBOV) is a zoonotic filovirus that can produce highly lethal disease in humans. The first reported outbreak of Ebola Zaire (EBOV-Z) occurred in 1976 in Yambuku health zone in northwestern Democratic Republic of Congo (DRC). In 2014, the largest outbreak of EBOV occurred in West Africa and continued until 2016. The global response to the 2014-2016 Ebola Outbreak included many international health organizations and partners. When the outbreak began, there were a few assays, which had US FDA Emergency Use Authorization (EUA) status to diagnose the disease. As the outbreak progressed, these assays evolved to meet the demands and clinical needs. Point of Care (POC) availability, biosafety, and simplicity of use were the leading drivers during the outbreak. **Methods:** The goal is to provide an objective review of diagnostic evolution during the outbreak. In addition to a literature review, we report our collective personal experience acquired in the outbreak in 2014-2016 and now in the recovery phase. The team worked in mobile and fixed placed laboratory settings using a variety of assays developed to respond to the outbreak. The team was also involved in the assessment and EUA filings for several novel diagnostic tools. **Results:** Our team worked in all West African countries and had experience with no less than five assays used to diagnose EBOV and to release patients from (Ebola Treatment Units (ETU). Combined, the team analyzed >25,000 EBOV patient samples. The team was engaged in both CLIA and EUA processes for several assays and adaptation of the assays for various patient specimens beyond plasma. The team continues to support the training of partner country laboratory staff in West Africa. **Conclusions:** Our team's objective consideration on the deployment of pre-positioned EUA assays and the evaluation of new assays offers a unique insight. Under very difficult conditions, government, academic, non-governmental organizations (NGO), and commercial entities worked steadily to improve, reinforce safety, and simplify the diagnosis process. Early drivers for POC, biosafety, and simplicity of use resulted in decreased turnaround time, ease of sample processing, and standardization of diagnostic endpoints and controls. A variety of regulatory and operational challenges are still being garnered that will offer critical lessons learned for future outbreak responses.

Board 271. Stillbirths and Neonatal Deaths during the Ebola Outbreak, Sierra Leone, 2014–2015

Titilope Oduyebo[1], Sarah Bennett[1], Alhaji Nallo[2], Denise Jamieson[3], Sascha Ellington[1], Kerry Souza[1], Dana Meaney-Delman[1], John Redd[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Sierra Leone Ministry of Health and Sanitation, Freetown, Sierra Leone; [3]Emory Department of Obstetrics and Gynecology, Atlanta, GA, USA

Background: Limited data are available about the effect of the Ebola outbreak on stillbirth and neonatal mortality in Sierra Leone. Data collected through Sierra Leone National Ebola Laboratory Database provided a unique opportunity to examine stillbirth and neonatal deaths during the Ebola outbreak and to review the effect of the EVD outbreak on the country's MCH indicators. **Methods**: We used data from the Sierra Leone National Ebola Laboratory Database to identify all stillbirths and neonatal deaths tested for Ebola virus during the 2014–2015 outbreak in Sierra Leone. We estimated an annualized rate of stillbirths and neonatal deaths, identified the proportion of stillbirths and neonatal deaths attributable to Ebola, and estimated the proportion of all tested deaths attributable to still births and neonatal deaths. **Results**: From July 2, 2014, through October 18, 2015, 1726 stillbirths and 4708 neonatal deaths were tested for Ebola virus ribonucleic acid, representing 3% and 7% of total deaths tested, respectively. The numbers of stillbirths and neonatal deaths tested varied by district and increased over time, stabilizing around week 18 of 2015. Twenty-five stillbirths and neonatal deaths were positive for Ebola virus ribonucleic acid, accounting for 0.39% of stillbirths and neonatal deaths tested and 0.29% of total Ebola virus disease cases. The annualized total number of reported stillbirths in 2015 was higher than expected (3078 vs 1634), while the number of neonatal deaths was lower (6350 vs 7771). **Conclusions**: Stillbirth and neonatal death reporting and testing improved over time, demonstrating that it is possible to systematically capture stillbirths and neonatal mortality during a widespread and disruptive infectious disease outbreak. This systematic recording of stillbirths and neonatal deaths can be used in conjunction with future retrospective surveillance data to understand and respond to the adverse effects of the Ebola virus disease crisis on maternal and child health as well as to guide response efforts for subsequent infectious disease outbreaks.

Board 272. Comparative Survival of Two Ebola Surrogate Viruses

K. Erukunuakpor, S. Mosley, A. Aung, L. Casanova
Georgia State University, Atlanta, GA, USA

Background: The 2014 Ebola outbreak demonstrated that patients in the active phase of infection excrete bodily fluids that contain a high titre of infectious virus. Transfer of patient fluids create a risk for contamination of surfaces. Understanding the survival of the Ebola virus can help assess the potential of surfaces as sources of virus transmission, as well as control measures to prevent transmission. This study assessed the effects of temperature and relative humidity (RH) on the survival, on surfaces, of two bacteriophages (Φ6, a virus with a lipid envelope like Ebola, and MS2, a non-enveloped virus that may serve as a conservative surrogate). **Methods:** 20 µL of phosphate buffered saline (PBS) containing both viruses (approximating body fluid viral load of 10^6 viruses) was inoculated on stainless steel coupons (1cm^2). Coupons were placed in controlled environments at 22^0C and 20%, 40%, 60% and 80% RH. Coupons were sampled for virus recovery

immediately after inoculation (time 0), after drying of PBS, and then at 24-hour intervals for 14 days. Survival was expressed as $\log_{10}(N_t/N_0)$, where N_0 is the plaque forming units (PFU) of infectious virus at time 0 and N_t is the PFU of infectious virus at time t. **Results:** For Φ6, time to 6 $\log_{10}$ (99.99%) reduction was 8 days at 20%, 7 days at 40%, 2 days at 60%, and 6 days at 80%. At all RH, MS2 remained infectious up to 14 days. Reduction of MS2 at 14 days was 4.8-$\log_{10}$ at 20%, 4.1-$\log_{10}$ at 40%, 3.7$\log_{10}$ at 60%, and 1.3-$\log_{10}$ at 80%. Using linear regression, the slope of the survival curve for Φ6 was -0.72 ± 0.11 at 20%, -0.86 ± 0.29 at 40%, -5.52 ± 0.0 at 60%, and -0.85 ± 0.21 at 80%, the slopes were significantly different (p = 0.001). MS2 slopes were -0.18 ± 0.03 at 20%, -0.17 ± 0.03 at 40%, -0.26 ± 0.01 at 60% and -0.08 ± 0.01 at 80%, the slopes were significantly different (p<0.001). **Conclusions:** Transfer of viruses to environmental surfaces can occur from infected patients, and this risk may exist for Ebola. Φ6, an enveloped surrogate for Ebola, remained infectious for up to 8 days. MS2, a non-enveloped surrogate, remained infectious for 14 days. The recovery of infectious viruses for days on a non-porous surface typical of a healthcare environment reinforces the need for structured and effective disinfection of environmental surfaces in healthcare, particularly during care of patients with serious communicable diseases such as Ebola.

Board 273. Detection and Characterization of Environmental Strains of *Mycobacterium ulcerans* from the Southwest Region of Cameroon

S. Esemu[1], A. Darby[2], R. Post[3], L. Ndip[1], B. Makepeace[4]
[1]Laboratory for Emerging Infectious Diseases, University of Buea, Buea, Cameroon, [2]Institute of Integrative Biology, University of Liverpool, Liverpool, United Kingdom, [3]Department of Disease Control, Faculty of Infectious Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom, [4]Institute of Infection & Global Health, University of Liverpool, Liverpool, United Kingdom

Background: *Mycobacterium ulcerans* is an environmental bacterial pathogen that causes Buruli ulcer; an emerging, treatable, but neglected skin infection. The disease manifests as slowly-developing unspecific indolent nodules, papules, or induration by edema, which can progress to necrotizing skin ulcers. Buruli ulcer is endemic in Cameroon and 15 other African countries and from 2001 - 2014, the number of Buruli ulcer-endemic health districts in Cameroon rose from two to 64. The transmission dynamics of *M. ulcerans* are not yet understood. **Methods:** In order to identify potential reservoirs of *M. ulcerans* and to determine the genetic diversity of *M. ulcerans* strains circulating within the South West Region of Cameroon, this cross-sectional study obtained 1,102 aquatic Hemiptera from 25 freshwater bodies in both Buruli ulcer-mesoendemic and -hypoendemic sites during July 2017. **Results:** Using taxonomic keys, written descriptions, specimen comparisons, and image verification, the aquatic bugs were placed into eight families and 29 genera. Specimens in each genus were further separated into morphotypes, generating a total of 109 (of which 34 were only represented by one specimen each); subsequently, 331 individual specimens were retained for species confirmation. The most abundant families were the Gerridae (water striders) and Veliidae (riffle bugs), dominated by *Limnogonus* spp. and *Rhagovelia* spp., respectively. The remaining 771 specimens were subjected to real-time PCR targeting the bacterial RNA polymerase β-subunit (*rpoB*) gene, which was used to detect and quantify DNA from the *M. ulcerans-M. marinum* complex in 8.9% of specimens. This comprised 7.9% (21/266) from mesoendemic sites and 9.5% (48/505) from hypoendemic sites (not statistically significant, $p = 0.457$). Twenty individual bugs positive for the *M. ulcerans-M. marinum* complex are undergoing Illumina sequencing to characterize strains present in the Southwest Region of Cameroon. **Conclusions:** This is the first large scale survey of potential *M. ulcerans* reservoirs in the Southwest Region of Cameroon. The diversity of aquatic Hemiptera in this region is very high, with widespread evidence of infection with the *M. ulcerans-M. marinum* complex. Genome sequencing will allow molecular epidemiological comparisons with other regions of Cameroon.

Board 274. Spatial Distribution and Temporal Trends of Leprosy, Uganda, 2012–2016

F. Mugabe[1], A. Ario[2], M. Lamunu[1], R. Majwala[1], J. Kawuma[3], F. Aceng[2]
[1]National Tuberculosis and Leprosy Program, Kampala, Uganda, [2]Uganda Public Health Fellowship Program, Kampala, Uganda, [3]German Leprosy Relief Association, Kampala, Uganda

Background: Leprosy is one of the neglected diseases that pose a big challenge to public health in Uganda. It is currently in 40% of the districts in the country; 42 districts reported cases in 2016. We assessed spatial and temporal trends of leprosy in Uganda during 2012-2016 to provide information to inform control measures. **Methods:** We analyzed data from the leprosy surveillance system managed by the National Tuberculosis and Leprosy Program where we used quarterly reports on leprosy case finding from the districts. We identified new leprosy cases diagnosed by Uganda health services during 2012-2016. We evaluated the leprosy incidence by person and place. We used logistic regression analysis to evaluate the temporal trends. We used the 2014 census data as the population estimates. We used QGIS software to determine the spatial analysis. We drew choropleth maps showing leprosy incidence rates per 100,000 populations for Uganda districts, 2012-2016. **Results:** Overall, the incidence of leprosy decreased by 7% annually (p=0.0001) in Uganda. The decrease was statistically significant in eastern (14%/year, p=0.0008) and central (11%/year, p=0.03) regions, and not significant in western (9%/year, p=0.12) and northern (4%/year, p=0.16) regions. The combined incident rates from 2012-2016 for the ten most affected districts showed that 70% were from the northern region, 20% were from the eastern region and 10% were from the central region. Some of the reported district leprosy cases are not indigenous. **Conclusions:** Leprosy incidence decreased in Uganda during 2012-2016; however, the declining trends are not consistent in all regions. We recommend intensification of leprosy control interventions through stronger partnerships, health education, and strengthening community outreach.

Board 275. The Prevalence of *Trypanosoma cruzi* in Mexican Free-Tailed Bats (*Tadarida brasiliensis*) at Three Maternity Roosts in Oklahoma

M. Nichols, W. Lord, M. Haynie, R. Brennan, W. Monterroso
University of Central Oklahoma, Edmond, OK, USA

Background: *Trypanosoma cruzi* is a vector-borne protozoan parasite that infects 8 million individuals in Central and South America and is the etiological agent of Chagas disease. The prevalence of endemic *T. cruzi* in Oklahoma is poorly studied and historically characterized by three reported canine and raccoon zoonotic trypanosomiases. We suspect Mexican free-tailed bats (*Tadarida brasiliensis*) contribute to the enzootic emergence of *T. cruzi* in Oklahoma by their annual migration from Central and South America to North American maternity

roosts. **Methods:** 361 Mexican free-tailed bats were sampled at three maternity roosts in Oklahoma for *T. cruzi*. We collected tissues from the uropatagium and plagiopatagium and used the DNeasy Blood and Tissue Kit to extract DNA. *T. cruzi* DNA was amplified by PCR using the primers TCZ1/TCZ2 and amplicons ran through gel electrophoresis and observed under a UVP Imager. **Results:** One juvenile Mexican free-tailed bat was positive for *T. cruzi* resulting in a prevalence of 0.27% of the 361 sampled bats. The positive sample was sequenced and uploaded to GenBank (#MG869732). **Conclusions:** This is the first confirmed report of a wild bat naturally infected with *T. cruzi* in Oklahoma, and the fourth reported zoonotic isolation in the state. Our findings identify a reservoir host that migrates to endemic and non-endemic areas and a possible transmission nexus between endemic *T. cruzi* reservoirs. The epidemiologic risk to humans in Oklahoma is unknown, but can be understood through future research on identifying foci of sylvatic and peridomestic transmission; current *T. cruzi* prevalence in wild and domestic Oklahoma mammalian reservoirs; and the impending impact of climate change on the vector, host, and parasite biogeography in Oklahoma.

Board 276. Outbreak Investigation of Cutaneous Leishmaniasis in District Kilasaifullah, Pakistan, November 2017-February 2018

S. Riaz, A. Saeed
Field Epidemiology and Laboratory Training Program, Quetta, Pakistan

Background: On 10 January 2018, the MS district headquarter hospital of Kilasaifullah reported the presence of more than 100 leishmaniasis patients in different parts of district Kilasaifullah, Balochistan. Reportedly, the most affected area was Union Council Shinghora, located close to the famous Muslimbagh Camp, which was hosting thousands of Afghan refugees. Provincial Disease Surveillance and the outbreak response unit of the health department in Quetta were contacted for confirmation, quantifying of outbreak, and taking necessary actions to control them. **Methods:** Case was defined as illness in any person of any age group, gender reported to/from health facilities, community of reported UCs of district Kilasaifullah with appearance of one or more skin lesions, typically on uncovered parts of body from 1 November – 28 February 2018. Descriptive study was carried out, affected areas were visited, hospital records were checked, and active case finding was done. Surveillance data were analyzed to identify cases and affected areas, and to gather information about risk factors if any. **Results:** 196 cases were identified in 16 UCs. 31% (n= 62) belonged to Shinghora, 21% (n= 43) from Kanmitarzai, 18% (n= 37) from Mahajarada, and 16% (n= 32) from Rabri killi; were identified as the most high risk UCs. 67% (n= 133) cases belonged to age group of 25-35 years.75 % (n= 148) cases were in men. 50% (n=99) cases were reported in January while 23% (n= 47) cases were reported in February. In all patients (100%), cases were clinically diagnosed as cutaneous leishmaniasis. Frequent history of travel, low socioeconomic status of the residents, humid climate, suburban population and presence of high density of rodents in area were identified as some of the possible risk factors. **Conclusions:** Outbreak was controlled. On recommendations, existing surveillance system for leishmaniasis was strengthened, indoor residual spray and fumigation for vector control carried out, injection glucantime were arranged, bed nets and insect repellants were provided.

Board 277. Assessment of Challenges and Proposed Activities to Strengthen the Management of Patients with Cutaneous Leishmaniasis in Alta Verapaz, Guatemala, 2017

I. Pérez[1], R. Mendizábal-Cabrera[1], E. Duran[2], B. Arana[1], J. Bryan[3], N. Rizzo[1]
[1]Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Ministerio de Salud Pública y Asistencia Social, Guatemala, Guatemala, [3]Center for Disease Control and Prevention, Central American Region, Guatemala, Guatemala

Background: Cutaneous leishmaniasis (CL) is a neglected tropical disease and endemic in the northern region of Guatemala. According to previous studies, the prevalence of the disease in this region is approximately 1.1%. The management of patients with CL is based on national guidelines, which include active and passive surveillance, timely diagnosis, notification of cases, and control and prevention measures. There are factors that limit the application of the national guidelines at the health district level; we conducted an assessment to identify the needs and challenges faced by health personnel in the management of patients with CL. **Methods:** In coordination with the Ministry of Public Health and Social Assistance, we conducted a qualitative assessment in four health districts of Alta Verapaz (Chahal, Fray Bartolomé de las Casas, Chisec and Cobán). We used focus groups and in-depth interviews to collect information on challenges in and proposed solutions related to a) prevention, b) sample collection and diagnosis, c) treatment, and D) follow-up of cases and monitoring. **Results:** Thirty-four (34) health workers involved in the management of patients with LC participated, the majority male (24/34, 71%). Participants identified the geographic isolation of the affected population and the lack of resources in the health system as the main factors limiting the management of patients with CL in Alta Verapaz. There is unawareness about CL in the communities and voluntary collaborators. In addition, only the laboratory or nursing staff is authorized to collect samples. However, there is no availability of transportation or per diem for health personnel to reach communities or to acquire supplies for taking samples. The turn-over of health personnel is high, so they fail to acquire the necessary experience for the diagnosis and management of the disease. In addition, the health services do not have equipment to perform the recommended test (EKG, liver enzymes or pregnancy for women of childbearing age) prior to starting treatment. **Conclusions:** To overcome these challenges active involvement of the communities in the detection and monitoring of cases is needed, using mapping and sectorization of the districts to decide placement of resources, and strengthening of local health personnel and community members through regular training.

Board 278. Investigation of Suspected Cutaneous Leishmaniasis at Village Gulderi, District Nowshera, Pakistan, January 2016

N. Jamal, A. Ameen
FELTP, Islamabad, Pakistan

Background: On 14 January 2016, an increased number of patients with multiple skin lesions were reported by community representatives of Gulderi village, District Nowshera to Disease Surveillance & Response Unit (DSRU). To assess the possibility of cutaneous leishmaniasis (CL), DSRU launched an outbreak investigation in the affected village to identify the presence of disease and associated risk factors to

initiate control measures, and to suggest recommendations. **Methods:** A descriptive study was carried out on 15-17 January 2016. The hospital's record was reviewed and active case finding was done. A case was defined as illness in any person of any age group and gender belonging to Gulderi village, with appearance of one or more skin lesions or ulcerations, typically on uncovered parts of the body from 16 September 2015 to 15 January 2016. Data were collected on a pre-tested questionnaire. Five samples were sent to laboratory for confirmation. **Results:** A total of 61 cases were identified. Overall attack rate was 0.6%. 61% (n=37) had less than four months duration for onset of symptoms while 39% (n=24) cases had more than four months duration. 70% (n=43) cases were women while 30% (n=18) cases were men. Male to female ratio was 3:7. Mean age was 19 years (range <1 - 60). 31% (n=19) cases belonged to 0-9 years age group followed by 30% (n=18) from 10-19 years. All five samples were positive for CL parasite. Multiple sand dumps due to construction of a dam, Low socio-economic status, humid environment, and rodents were identified as possible risk factors. **Conclusions:** District authorities removed the sand dumps along with mechanical vector control activities. Existing surveillance system was strengthened with the provision of bed nets and insect repellants to the community. A health awareness campaign was initiated. Regular follow-up was carried out and no new cases were identified.

Board 279. Evaluation of the Risk of Reintroduction of Onchocerciasis to Guatemala by Military Peacekeeper Missions to Onchocerciasis—Endemic Democratic Republic of Congo

R. Mendizábal-Cabrera[1], F. Enríquez[2], V. Cama[3], O. de León[1], C. Serrano[1], J. Bryan[4], R. Turcios[3], N. Rizzo[1]
[1]Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Servicio de Sanidad Militar, Guatemala, Guatemala, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Centers for Disease Control and Prevention, Central American Region, Atlanta, GA, USA

Background: Guatemala had four of the 13 endemic foci for onchocerciasis in the Americas in 2015. After over 17 years of mass administration of ivermectin, WHO verified Guatemala as onchocerciasis-free in September 2016. Nonetheless, onchocerciasis reintroduction is still possible given the wide distribution of onchocerciasis vector *Simulium*-genus black flies and that Guatemalan military personnel regularly participate in United Nations peacekeeping missions in onchocerciasis-endemic Democratic Republic of Congo (DRC). Peacekeeping deployments began in 2005 and last from nine to 12 months. Imported malaria has been described among returning Guatemalan peacekeepers. **Methods:** We proposed to assess the risk of onchocerciasis reintroduction to Guatemala by peacekeepers returning from DRC-deployments. We evaluated IgG4-antibody response to the *Onchocerca volvulus* OV-16 antigen retrospectively among participants of missions between 2005 and 2016, and prospectively among recently returned participants of the 2017 mission. We collected from all participants' demographic and clinical information exploring onchocerciasis-compatible symptoms, and serum specimens. We conducted a cross-sectional serological survey. **Results:** Among the 196 participants (116 in 2005-2016 missions and 80 in the 2017-mission), 97% (190/196) were male, with a median age of 30 years (range 20-59). Thirty percent (58/196) participated in one mission, 49% (97/196) in two missions, 15% (29/196) in three or four missions and 6% (12/196) in five or more. Thirty-five percent (68/196) lived in regions of Guatemala with onchocerciasis-endemic foci before DRC deployment. Twenty-three percent (46/196) reported onchocerciasis-compatible symptoms including nodules, skin rash and eye discomfort. All participants evaluated to date have been negative for anti-OV-16 IgG4-antibodies. Given that antibody response to *O. volvulus* is often delayed by months after exposure, follow-up of this population is justified. We plan to follow the 2017 cohort for one year to evaluate seroconversion. **Conclusions:** Continued surveillance for reintroduction of onchocerciasis into the Americas is essential, with serology as a valuable post-elimination surveillance tool. In addition, we recommend evaluation of additional infections, especially those of epidemic potential.

Laboratory: Sequencing

Board 280. Evaluation of Illumina's MiniSeq Sequencing Platform

Angela Poates[1], Ashley Sabol[2], Eija Trees[2]
[1]IHRC, Inc., Atlanta, GA, USA; [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: PulseNet Central supports implementation of whole genome sequencing for foodborne disease surveillance and outbreak detection by providing validated and standardized protocols to a vast array of laboratories with different needs and testing throughputs. New technologies that may meet the needs of these laboratories must continuously be evaluated. Currently, the Illumina MiSeq platform is the most widely used WGS platform within the network. Recently Illumina released the MiniSeq, which utilizes two-channel sequencing by synthesis technology. It has a lower price point and boasts a shorter turnaround time from initiating sequencing to data generation than the MiSeq. Here we present the preliminary results for the validation of the MiniSeq and data comparison against the MiSeq. **Methods**: For the initial validation phase, 25 Escherichia coli isolates (6 serogroups) previously sequenced on the MiSeq, were sequenced on the MiniSeq. A second subset of 7 E. coli isolates (2 serogroups) whose genetic relationships to belong to the "gray zone" (10-20 SNPs) was also sequenced. CG-Pipeline was used for quality checks and read cleaning. High quality single nucleotide polymorphism (hqSNP) analysis was performed using the lyve-SET pipeline version 1.1.4f (github.com/lskatz/lyve-SET) with appropriate external (PacBio) reference genomes. Phylogenetic trees and hqSNP matrices were created to evaluate the correlation of the data generated by the two platforms. **Results**: Preliminary results indicate that the data generated by the MiniSeq is of comparable quality to that generated by the MiSeq. HqSNP analysis reveals no greater than a 1 SNP difference between MiSeq and MiniSeq sequences. Phylogenetic trees and matrices generated from MiniSeq data appear to be concordant with those generated using data acquired on the MiSeq. **Conclusions**: The MiniSeq would be advantageous to laboratories with a smaller budget, and ideal for laboratories with either a low or a medium throughput. However, there is some concern that shorter read length chemistry will lead to poorer assemblies and possibly missing allele calls in wgMLST analysis. Future goals include sequencing additional isolates and comparing outbreak datasets for other PulseNet organisms using both hqSNP and wgMLST analysis.

Board 281. An Evaluation and Comparison between Ion Torrent S5 and Illumina MiSeq Sequencing Platforms for Whole Genome Sequencing of *Escherichia coli*

Y. Joung[1], C. VanTubbergen[2], A. Sabol[1], H. Carleton[1], T. Griswold[1], E. Trees[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA,
[2]Colorado School of Public Health, Fort Collins, CO, USA

Background: Next Generation Sequencing technology has evolved during the past decade with sequencing platforms that have the capacity to deliver more accurate and high-resolution data. In line with the advancement in technology, PulseNet, the national network for foodborne disease surveillance, is currently implementing whole genome sequencing for early detection of outbreaks. This study evaluates the data generated by two NGS sequencing platforms, the Illumina MiSeq and the Ion Torrent S5, in an effort to offer a viable alternative for the laboratories in the network. **Methods:** Twenty-five *Escherichia coli* isolates of various serogroups were sequenced on both platforms. Libraries for the S5 were prepared with the KAPA Fragmentation and Library Preparation Kit and sequenced using Ion S5 Sequencing Reagents for 400 base pair (bp) and Ion 530 chips. MiSeq libraries were prepped with the Illumina Nextera XT kit and sequenced using 2x250 bp v2 chemistry. Both read sets were cleaned and analyzed using Kraken and MIDAS for taxonomic classification, BioNumerics v7.6 for wgMLST and VirulenceFinder, ResFinder, and SerotypeFinder (CGE) for gene comparison. **Results:** Overall, the raw read quality of S5 data was lower than the MiSeq data (Q30: 25<x<30), however, S5's greater coverage and longer read lengths sufficiently compensated for the lower quality scores. Compared to the MiSeq data, Ion Torrent assemblies showed a higher number of contigs (~100), but comparable N50 values and lower ambiguous base (N) counts which resulted in a slight increase in the average number of consensus allele calls. Kraken, MIDAS, and SerotypeFinder correctly predicted all species and serotypes in both datasets, and there were no differences in the prediction of antimicrobial resistance determinants and critical virulence genes. The wgMLST pairwise comparisons showed < 10 discrepancies in allele calls between the same isolate sequenced in both platforms. **Conclusions:** MiSeq and S5 platforms both generated quality data for the *E. coli* sample set for comprehensive analyses. However, as the current BioNumerics workflow is optimized for the MiSeq data, further examination will be needed to identify the cause of the discrepancy in the allele calls. Additional goals include expanding the validation to other foodborne organisms, such as *Listeria, Campylobacter,* and *Salmonella enterica* spp.

Board 282. Evaluation of the Oxford Nanopore MinION Sequencer for Virus Discovery, Identification, and Characterization

Y. Tao, C. Paden, J. Zhang, S. Tong
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The ability to quickly recognize and respond to wide variety of etiologies causing outbreaks is a challenge to the public health system. Common respiratory and gastrointestinal syndromes have a broad differential diagnosis and can be caused by a variety of pathogens. Furthermore, the emergence and rapid spread of novel and re-emerging pathogens highlight the need for early detection, accurate etiological identification, and rapid response at the origin of the outbreak. Next generation sequencing (NGS) has become a valuable tool in pathogen detection and characterization. However, the currently dominant NGS platforms are not suitable for field applications—they are sizable instruments, require a large capital investment. Sequencing at the site of an outbreak overcomes the quality and bureaucratic issues involved in shipping samples. The Oxford Nanopore MinION is a portable and inexpensive device that promises rapid analysis of data, ideal for use in the field. The objective of this study is to evaluate MinION in detecting and sequencing of a variety of viral pathogens compared to Illumina MiSeq. **Methods:** First, we tested 40 positive respiratory samples of known etiology using 17 pan-viral group PCR assays that target conserved sequences among the members of a virus family or genus and have the capacity to amplify known and potentially novel viruses. These amplicons were pooled and sequenced by MinION in comparison to MiSeq. Second, we used MERS-CoV isolates to determine the quality, accuracy and sensitivity of amplicon sequencing. The amplicons from random amplification or sets of tiling amplicons—either in singleplex or multiplexed—were sequenced by MinION and MiSeq. **Results:** Evaluation with 40 clinical samples multiplexed per MinION run, showed a 97% concordance (72/74 viruses) with MiSeq testing. MERS-CoV targeted sequencing showed >99.98% accuracy at the consensus level with sensitivity comparable to MiSeq, while the read-level accuracy was 88-90%. We multiplexed at least 5 genomes per run without reducing sensitivity. **Conclusions:** The short turnaround time and ability to inexpensively produce data near the site of collection using MinION will allow frontline public health laboratories to conduct initial tests, enabling a more rapid and efficient response to outbreaks of unknown etiology.

Board 283. Evaluation of the Oxford Nanopore MinION for Low-Cost Rabies Virus Sequence Typing

C. Gigante, R. Condori, K. Wilkins, H. Zhao, Y. Li
Poxvirus and Rabies Branch, Division of High Consequence Pathogens and Pathology, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Rabies is a fatal zoonotic disease with no proven cure once symptoms have developed, and there is an international effort to eliminate human rabies transmitted by dogs by 2030. Across the globe, rabies prevention and eradication efforts are hampered by a lack of information about the distribution and spread of rabies virus variants. Rapid, cost-effective variant typing using sequencing could provide critical information about viral spread, virus-host relationships and viral evolution that can inform control and vaccination strategies. **Methods:** The Oxford Nanopore MinION sequencer allows for cost-effective portable sequencing with fast, real-time data analysis. It is poised for deployment in resource-limited areas. **Results:** We evaluated the MinION for use in rabies sequence typing, and our experiments revealed successful detection and identification of divergent rabies virus isolates. Sequencing of PCR amplicons produced partial and whole genome rabies virus sequences for monitoring rabies spread in several countries. The error rate in raw sequencing reads (about 12%) includes random errors that can be easily corrected. Error-corrected consensus sequences achieved high accuracy when compared to Illumina and Sanger sequencing methods. By multiplexing samples, the projected cost of rabies virus sequencing using the MinION is much lower than current Sanger sequencing methods, and the cost can be further reduced as the MinION flow cell improves. **Conclusions:** Taken together, our evaluation suggests that MinION sequencing is capable of producing informative rabies sequences from clinical and field samples. Future work will focus implementing live sequence typing using

a real-time sequence analysis pipeline for deployment in public health labs and in the field. Disclaimer: Use of trade names and commercial sources is for identification only and does not imply endorsement by the Centers for Disease Control and Prevention, the Public Health Service, or the US Department of Health and Human Services.

Board 284. A Comparison of Next Generation Sequencing Library Preparation Using Illumina Nextera XT and New England Biolabs NEBNext Ultra II Kits

J. Truong[1], A. Sabol[2], E. Trees[2]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: As a public health surveillance network for foodborne bacteria, PulseNet is continually testing new whole genome sequencing platforms and library preparation kits for potential use within the network. PulseNet's current standard whole genome sequencing (WGS) workflow is based on reagents provided by Illumina. The objective of this study is to provide public health laboratory partners a cost-effective alternative to the Illumina library preparation by evaluating the New England Biolabs NEBNext Ultra II FS DNA Library Prep kit against the Illumina Nextera XT library preparation kit. **Methods:** Libraries for twenty-five *Salmonella enterica* isolates of eight serotypes were prepared using the NEBNext Ultra II kit at a 5-minute fragmentation time. Prepped libraries were sequenced on the Illumina MiSeq using 2x250 v2 chemistry, and the resulting data was compared to data from the same isolates processed using the Nextera XT kit. Average read lengths, coverage, and quality scores were compared between datasets from both kits. The reads were cleaned using CG-pipeline (https://github.com/lskatz/CG-Pipeline), and hqSNPs were extracted using Lyve-SET (v1.1.4f) (github.com/lskatz/lyve-SET) with the following parameters: 95% frequency, 20x minimum coverage, and phage masking on the appropriate reference genome. **Results:** The libraries from NEBNext Ultra II had average read lengths from 234 to 246bp with average Q30 of 35.6 compared to Nextera XT's average read lengths from 186 to 242bp with average Q30 of 34.3 for the same set. Adequate coverage was obtained for analysis purposes with both kits. There were 0 hqSNP differences identified in pairwise comparisons for the same isolate prepared by both kits. When comparing unrelated isolates, a similar number of hqSNP differences was observed. **Conclusions:** Our results show that the two kits exhibit comparable performance in generating libraries with acceptable read lengths, coverage and quality scores. The similarity in hqSNP counts between datasets suggests that either kit can be used to prepare libraries for sequence generation on the MiSeq, but additional validation is necessary. Future work will include testing the kit with various other organisms characterized by PulseNet.

Board 285. A Whole Genome Multi-Locus Sequence Typing Workflow for Reference Characterization, Surveillance and Outbreak Detection of Shiga Toxin-Producing *Escherichia coli* (STEC)

R. Lindsey[1], H. Pouseele[2], M. Schroeder[1], E. Trees[1], P. Gerner-Smidt[1], H. Carleton[1]
[1]CDC, Atlanta, GA, USA, [2]Biomerieux, Sint-Martens-Latem, Belgium

Background: Shiga toxin-producing *Escherichia coli* (STEC) is an important foodborne pathogen capable of causing mild to severe disease in humans. The Enteric Diseases Laboratory Branch is working to replace traditional methods with those using whole genome sequence (WGS) data by developing an allele database of individual *Escherichia* genes in BioNumerics 7.6 (Applied Maths, Austin, TX). This will allow surveillance for outbreak detection and reference characterization of STEC in a single workflow using whole genome or core genome multi-locus sequence typing (wgMLST, cgMLST), *in silico* PCR, and BLAST based gene identification. **Methods:** The *Escherichia* v4 allele database includes 2,513 core loci from the EnteroBase cgMLST scheme and accessory genome loci identified from EnteroBase and from 320 reference sequences representing the clinically relevant diversity of *Escherichia* strains for a total of 23,183 loci. In version 4 mobile and repetitive loci were removed from the scheme because they made it unstable. To validate wgMLST in Bionumerics, a comparison between the average number of wgMLST allele calls to the average number of single nucleotide polymorphism (hqSNP) (LYVE-SET pipeline: github.com/lskatz/lyve-SET) was conducted using 319 epidemiologically confirmed isolates from past outbreak investigations. **Results:** wgMLST using the Applied Maths BioNumerics 7.6 v4 allele database correctly clustered surveillance isolates by the outbreak and in concordance with hqSNP data. The *E. coli* genotyping plugin correctly detected expected serotypes, virulence genes and pathotypes. **Conclusions:** Loci from the Enterobase cgMLST allele database were included within our *Escherichia* wgMLST scheme to have concordance between the two schemes and to build a stable strain nomenclature for global use. wgMLST and the associated genotyping tools in BioNumerics offer is a promising and user-friendly high resolution tool for *Escherichia* characterization and surveillance.

Board 286. Bioinformatic Pipeline for the Analyses of Whole Genome Sequencing Data for Legionnaire's Disease Outbreak Investigations

W. Haas[1], K. Nieselt[2], K. Musser[1], P. Lapierre[1]
[1]Wadsworth Center, NYSDOH, Albany, NY, USA, [2]University of Tuebingen, Tuebingen, Germany

Background: Whole genome sequencing provides the most detailed genetic fingerprint of a bacterial isolate. However, the analysis of the data remains a bottleneck. Using a modular approach, we developed a pipeline that automates all bioinformatic processing steps. We demonstrate its usefulness for Legionnaire's Disease (LD) outbreak investigations to compare isolates down to the single base level while taking the organism's genetics into account. **Methods:** The modular pipeline consists of modules for read-preprocessing, reference genome selection, mapping, *de novo* assembly, phylogenetic analysis, and variant calling. The resulting analyses pipeline was able to process batches of multiple samples. Sequencing reads from *Legionella pneumophila* isolates associated with LD outbreaks were selected as test samples, while reference genomes were retrieved from the NCBI database. **Results:** Raw sequencing reads were processed to produce assembled genome sequences. The species' high genome plasticity necessitated two reference selection steps to identify the best matching genome for variant calling. The pipeline was able to perform all bioinformatic processing steps within 20 to 60 minutes, depending on the number of reads and the processing steps required. In one test, 25 samples were processed without any human intervention. Most importantly, the results were *on par* with previous genome analyses and epidemiological information. Small amounts of DNA contamination in the samples were filtered out by the pipeline. Samples that were too far outside the norm (e.g. insufficient reads, incorrect species) caused the pipeline to terminate early. In those cases, all temporary data were preserved for failure analysis and the next sample was processed by the pipeline. Processing data

from actual LD outbreaks correctly distinguished different clusters of isolates and corroborated the source of the outbreak. **Conclusions:** While no software can replace the experience and intuition of a human being, a well-designed pipeline can perform routine tasks in an expedient and timely manner. This gives scientists more time to focus on problematic cases and extract meaning from the results. The program presented here not only facilitates LD outbreak investigations, but can easily be adapted to other species and tasks.

Board 287. Data Management, Workflows, and Communication for Whole-Genome Sequencing-Based Surveillance of Foodborne Pathogens in a Large State Public Health Laboratory

M. Dickinson, M. Anand, D. Baker, J. Carey, A. Cukrovany, N. Dumas, J. Hayes, P. Lapierre, E. Lasek-Nesselquist, C MacGowan, A. Mehta, L. Mingle, A. Robbins, L. Thompson, A. Saylors, M. Shudt, S. Wirth, C. Walsh, D. Wroblewski, K. Musser, W. Wolfgang
Wadsworth Center, New York State Department of Health, ALBANY, NY, USA

Background: The need to develop new workflows and data management systems to accurately curate and communicate whole-genome sequencing (WGS) results is an evolving challenge. The Wadsworth Center (WC) is the public health reference laboratory for New York State (NYS) and a PulseNet Area Laboratory. In 2012 the WC implemented WGS to enhance detection of foodborne pathogen outbreaks. In 2013, 282 genomes were sequenced and analyzed. In 2017 this number increased to 1709 genomes. To accommodate increased workloads and multiple end users, customized workflows and data management systems were implemented to improve communication and assessment of data. **Methods:** IT staff, bioinformaticians, epidemiologists, supervisors, technicians and federal partners were consulted to guide decisions impacting data management and workflow. To accurately capture, track and transmit WGS data and analytical results, a new module was created in our Laboratory Information Management System (LIMS) that allows us to: link multiple identifiers to a single sample, batch samples to simplify data entry, export sample information to populate the MiSeq sample sheet, and assign samples to an NCBI Bioproject and internal studies. Python scrips were developed to accurately import WGS metadata into our LIMS. A sample log was instituted to track all samples through the sequencing process. A SharePoint site was created to securely communicate WGS results and interpretations with NYS Epidemiologists. **Results:** Managing data in our LIMS and using automated scrips that directly import data has reduced transcription errors and sample mix-ups. It has also reduced staff time spent entering and retrieving data. The SharePoint site has facilitated efficient two-way communication with our NYS epidemiologists that is more rapid and traceable. **Conclusions:** As technology and workflows change, and end user needs evolve, we have found that having a flexible and customizable data management system has been invaluable.

Board 288. Amplicon Prediction Pipeline for an Extended MLST Approach to Culture Independent Pathogen Subtyping

S. Lucking[1], S. Im[1], L. Ruthotto[2], Y. Vigfusson[2], R. Mitchell[2], E. Trees[1], J. Besser[1], H. Carleton[1], A. Williams-Newkirk[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Emory University, Atlanta, GA, USA

Background: Isolate whole genome sequencing (WGS) is a powerful tool in enteric disease surveillance. The declining availability of isolates due to the adoption of culture-independent diagnostic tests threatens culture-dependent surveillance systems making the development of direct-from-specimen subtyping methods critically important. Highly multiplexed amplicon sequencing (HMAS) is a potentially cost-effective and scalable method that may achieve a resolution similar to that of isolate WGS, but software for the selection of informative and amplifiable loci for HMAS panels is lacking. To address this gap, we developed a pipeline to design extended multilocus sequence typing (eMLST) schemes for enteric pathogen subtyping. **Methods:** Our amplicon prediction pipeline uses freely available open source software and takes as input annotated genomes in GenBank format. Core orthologous genes are identified, and primer pairs are designed to generate ~250bp amplicons at each orthologous site. Amplicon size was chosen to work with the Fluidigm Juno, but can be adjusted for compatibility with any HMAS platform. Predicted amplicons are then filtered for the inclusion of SNPs and may also be filtered for primer specificity to the target pathogen if appropriate test data are provided. The filtered set of candidate amplicons and primer pairs are returned for further use in development of and eMLST scheme. **Results:** As a proof of concept, 266 *Salmonella bongori* and *enterica* genomes consisting of 68 serotypes and representing the diversity of non-typhoidal *Salmonella* were submitted for analysis through our pipeline. 5,366 candidate amplicons containing SNPs were identified from the 1,585 core orthologous genes found in the input. Primer pair specificity was tested using 4 metagenomics data sets from 2 *Salmonella* outbreaks, yielding 4,434 candidate primer pairs specific for *Salmonella*. **Conclusions:** This proof of concept demonstrates that our pipeline successfully generates candidate amplicons for use in direct-from-specimen enteric pathogen HMAS subtyping panels. The final set of subtyping makers will be chosen for optimal identification of outbreak-associated samples using user-provided training genomes. Primer pairs for the final targets will be validated in-vitro for possible deployment to public health partners for use in outbreak surveillance.

Board 289. Development of Strain Nomenclature Based on Core Genome MLST for Surveillance of Shiga Toxin-Producing *Escherichia coli*

M. Patel[1], R. Lindsey[1], H. Pouseele[2], P. Gerner-Smidt[1], M. Schroeder[1], E. Trees[1], H. Carleton[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Applied Maths, Sint-Martens-Latem, Belgium

Background: Surveillance in the US to identify outbreak clusters caused by Shiga toxin-producing *Escherichia coli* (STEC) relies on identifying named pulsed-field gel electrophoresis (PFGE) patterns with an observed frequency above baseline over a defined time period. As surveillance transitions to whole genome sequencing (WGS) as the primary molecular tool, there is a need to develop a WGS-based nomenclature to identify closely related STEC isolates. Thus, we evaluated hierarchical nomenclature based on the core genome multi-locus

sequence typing (cgMLST) scheme developed by EnteroBase for surveillance and cluster detection. **Methods:** A copy of the EnteroBase cgMLST scheme was deployed in BioNumerics® 7.6 locally. In total, 8643 genomes from clinical, food, and environmental isolates from the United States were split into training and test sets after passing QC metrics (>40x coverage, genome size 4.4-6.1 MB, contigs <510) and a cutoff of >90% cgMLST allele calls. Alleles were called from assembled genomes at 85% homology; start and stop codons were required. The genomes were then hierarchically clustered using single-linkage at increasing similarity thresholds. Each cluster was assigned a name, i.e. 1.1.1.1.1, where each digit references a cluster at a specified similarity threshold. Thresholds were assessed for stability and optimized to reduce the amount of name changes over time as new genomes were added to the hierarchy of clusters. Sensitivity and specificity were assessed for capturing potential outbreak clusters using genomes that belonged to the same MLST Achtman sequence type and epidemiologically confirmed outbreak cluster. **Results:** Percent thresholds of 6.01%, 4.58% 3.14% 1.51% and 0.00% corresponding to approximately 151, 115, 78, 38, and 0 allele differences, respectively were found to exhibit stable behavior resulting in only 1.67% name changes over time. Sensitivity and specificity were found to be (100.00%, 89.06%), (100.00%, 90.67%), (100.00%, 92.36%), (100.00%, 95.05%) and (83.91%, 99.97%) at the 6.01%, 4.58% 3.14% 1.51% and 0.00% thresholds, respectively. **Conclusions:** Nomenclature based on cgMLST is a promising tool to use in cluster detection from WGS data. Further work is needed to improve the % cgMLST allele calls and to test the nomenclature on a more geographically diverse dataset.

Board 290. Whole Genome MLST-Based Typing and Strain Nomenclature for *Clostridium difficile* Isolates

K. De Bruyne[1], S. Kiekens[1], B. West[2]
[1]Applied Maths NV, Sint-Martens-Latem, Belgium, [2]Applied Maths, Inc., Austin, TX, USA

Background: *Clostridium difficile* is a bacterium that causes symptoms ranging from diarrhea to life-threatening inflammation of the colon, most commonly affecting older or immunocompromised adults in hospitals or long-term care facilities. In recent years, *C.difficile* infections have become more frequent, severe and difficult to treat. Rapid typing and characterization methods are essential epidemiological tools to prevent and control infection. Although bacterial WGS has become feasible in smaller clinical laboratories, non-standardized data analysis remains a bottleneck for routine surveillance. In this work, we assessed wgMLST and wgSNP for *C.difficile* typing. **Methods:** We created a core (n=1999 loci) and pangenomic (n=6713 loci) schema based on 259 reference sequences reflecting the known diversity of *C.difficile*. Also capturing the accessory loci greatly increased the discriminatory power of the schema. Adding MLST, CWP, and loci associated with antibiotic resistance and virulence maximized consistency with classical typing methods. Assembly-free and BLAST-based algorithms determined locus presence and detected allelic variants. wgSNP further characterized defined clusters by mapping the reads to a reference chosen from within the cluster and filtering the variants. High-throughput data processing pipelines in BioNumerics® implemented both methods on publicly available data. **Results:** We ran wgMLST on +1,500 samples to identify closely related clusters. We detected a wide diversity of samples and defined clusters at various allele difference cutoffs, allowing the creation of a stable strain nomenclature on the sample set. The defined thresholds determined 36 clusters for which additional resolution was obtained by running the wgSNP analysis, identifying linked clinical cases and linking additional metadata (e.g. date of isolation, geo information) to the results. **Conclusions:** WGS combined with automated analysis pipelines holds great promise for bacterial epidemiological surveillance. The pangenomic schema for *C.difficile* includes over 8000 loci and allows for the detection of subtype- or outbreak-specific markers. BioNumerics® and integrated wgMLST and wgSNP functionality allows for accessible cluster analysis and typing of *C.difficile* isolates down to strain level.

Board 291. Targeted Metagenomics through Marker Creation—T-MArC

D. Yarmosh, J. Bagnoli, J. Jacobs
MRIGlobal, Gaithersburg, MD, USA

Background: Metagenomic sample identification is increasingly being applied toward pathogen detection. Current metagenomic sequencing methods rely on shotgun sequencing. Reads are inherently ambiguous both due to loss of source organism and inter-species genetic similarity. Identification programs attempt to clarify which reads belong to which organism, but pathogens typically share the majority of their genomic sequence with nonpathogenic strains or species. Thus, unambiguous pathogen detection is difficult to produce with confidence. In conjunction with standard pathogen detection techniques, which offer good sensitivity, a more specific method can produce confidence in a pathogen ID. We have developed T-MArC, such a method that leverages characteristic regions of arbitrary genome. **Methods:** This pipeline uses the program ShortBRED to identify these unique regions. ShortBRED can be trained on genomes of every strain of a given pathogen to identify sequences that indicate a specific organism and distinguish it from related species. These sequences are developed into "core markers" and should be unique to the target. The markers generated by ShortBRED were further refined through the use of BLAST. The markers that pass this are considered highly unique and termed "true markers." These are stored as a database to be used for highly-specific pathogen identification. Fastq samples run through any metagenomics profiler generate an initial identification report. If any organism that is related to a BSAT pathogen is detected, this pipeline is initiated and the fastq files are run against the appropriate marker database resulting in rapid disambiguation of these related taxa. **Results:** We have shown modest reduction in *Bacillus anthracis, Vibrio cholerae,* Venezuelan Equine Encephalitis virus, and *Orthopox virus* detection sensitivity while also showing a complete removal of false positive detection events and total disambiguation from closely related organisms. **Conclusions:** This is a novel use of the ShortBRED algorithms as well as a significant step toward improving the specificity of metagenomic species identification. There are many attempts to leverage the differences in a genome that distinguishes any given pathogen for specific identification, but this is among the first methods to tie together the recognition of these unique regions and the analysis in comparison to these regions.

Board 292. Evaluation of Fecal Nucleic Acid Stabilization Methods for Culture-Independent Pathogen Subtyping

Y. Gao[1], K. Dillon[2], J. Hensley[2], B. Aspinwall[2], E. Trees[3], J. Besser[3], H. Carleton[3], A. Williams-Newkirk[1], A. Huang[3]
[1]IHRC, Inc., Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [3]Centers for Diseases Control and Prevention, Atlanta, GA, USA

Background: Culture-independent diagnostic tests allow for efficient diagnoses of foodborne pathogens, but they do not yield isolates critical for outbreak surveillance and investigation. The development of new culture-independent subtyping techniques will rely on well-preserved stool samples with stable microbiome profiles. Currently, clinical labs typically store stools at room temperature or 4°C in transport media such as Cary-Blair (CB). This may alter the fecal community composition and make downstream analyses unreliable. This study evaluated alternative, commercially available preservation methods for fecal nucleic acids for use in metagenomic and subtyping studies. **Methods:** OMNIgene®•GUT kit (DNA Genotek) and Stool Nucleic Acid Collection and Preservation Tubes (Norgen Biotek) were tested using 5 clinically healthy stools that were homogenized, pooled, and spiked with 10^6 CFU/mL of pathogenic *Escherichia* and *Salmonella* strains. Samples were either incubated at room temperature for the entire test, or shifted to 40°C for 72 hrs in the first week to mimic possible temperature abuse during transport. Samples were tested on days 0, 7, 14, 21, and 28 for DNA quality, pathogen recovery by qPCR, and bacterial community composition by 16S rRNA V4 sequencing. Unpreserved stools at -20°C were used as positive controls, and stools in CB were negative controls for nucleic acid stability. **Results:** By all measures, samples in both kits all had stabilized, well-preserved nucleic acids that were most similar to frozen, unpreserved positive control samples. While spiked-in pathogen levels fluctuated in CB stools, they remained unchanged in OMNIgene- and Norgen-preserved samples at all temperatures and time points, suggesting no cell growth or DNA degradation. DNA sequencing of 16S rRNA showed that samples preserved in OMNIgene or Norgen kits in all conditions tested have similar bacterial community composition and membership to the Day 0 and positive controls. **Conclusions:** Both the OMNIgene and Norgen kits are promising methods for fecal nucleic acid preservation. Future tests will include variables such as extended storage time, combination of CB with the new preservative, and complex disease state stool types. The evaluation will also take into account considerations such as cost-per-kit and ease of use.

Board 293. Sequencing *Salmonella* on an Illumina NextSeq, the New York State Experience: Impact on Cost, Quality, and Turn-Around Time

S. Wirth, D. Baker, N. Boucher, A. Cukrovany, M. Dickinson, E. Lasek-Nesselquist, P. Lapierre, C. MacGowan, M. Palumbo, M. Shudt, L. Thompson, J. Williams, D. Wroblewski, N. Dumas, K. Musser, L. Mingle, W. Wolfgang
NYSDOH Wadsworth Center, Albany, NY, USA

Background: Since 2013, the New York State Department of Health Wadsworth Center (WC) has performed whole-genome sequencing (WGS) for enteric pathogen surveillance on the Miseq platform. In 2017, the WC implemented sequencing of all *Salmonella* with a NextSeq as a way to increase capacity (80 samples per run) and decrease costs. **Methods:** All isolates are analyzed by pulsed-field gel electrophoresis (PFGE) and serotype determined by PFGE pattern or conventional serotyping. Eighty samples are batched, diluted into 96-well plates, and transferred to our core sequencing facility for library prep and sequencing on a NextSeq. Raw data files are streamed to a local server. After the run is complete, data is converted from BCL to fastq files and merged into one R1 and one R2 per sample, using bcl2fastq software. SeqSero is used to infer serotype from the fastq files. The SeqSero-inferred serotype results are imported into our Laboratory Informattion Management System (LIMS) and compared to the previously determined serotypes as a QC step. *Salmonella* Enteritidis (SE) and *Salmonella* Typhimurium (STM) samples are analyzed through in-house pipelines to detect local clusters. **Results:** WC completes 1-3 NextSeq runs per month. Sequencing on the NextSeq is projected to save $96,000 annually. However, batching has resulted in an increased median turn-around time (TAT) for the NextSeq of 14-43 days as compared to the MiSeq TAT of 9 days. To date, only 2% of samples failed sequencing quality metrics. Sequencing all *Salmonella* has resulted in an increased number of clusters reported to NYS epidemiologists with 19 SE clusters and 26 STM clusters reported in 2017. **Conclusions:** The NextSeq enables higher sequencing throughput for *Salmonella* at a 33% decreased cost without sacrificing sequence quality, but TAT is increased. TAT is expected to improve as we extend NextSeq sequencing to additional pathogens.

Board 294. Comparison of Shotgun and Amplicon Sequencing for Antimicrobial Resistance Determinant Detection in Stool and Isolate Samples

J. Rowell[1], A. Williams-Newkirk[1], A. Huang[1], J. Hensley[1], K. Dillon[1], Y. Gao[1], J. Shay[1], J. Chen[1], N. Kanwar[2], R. Selvarangan[2], K. Weltmer[2], D. Payne[1], I. Plumb[1], J. Besser[1], E. Trees[1], C. Harrison[2], M. Wikswo[1], B. Aspinwall[1], J. Rasheed[1], K. Walthall[1], C. Friedman[1], H. Carleton[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Children's Mercy Hospitals, Kansas City, MO, USA

Background: Characterization of the resistome of complex metagenomic samples has broad applications for medicine, public health, and food safety. Existing methods rely on the costly, laborious, and biased phenotypic or genotypic testing of bacterial isolates. Emerging techniques such as highly multiplexed amplicon sequencing (HMAS) panels and shotgun sequencing (SS) enable detection of multiple antimicrobial resistance determinants (ARDs) directly from complex samples such as stool. These techniques may help streamline laboratory-based public health surveillance for ARD. We compared two methods of ARD detection in pediatric stools and derived isolates: SS and an ARD HMAS panel. **Methods:** Ten stool samples were collected by the New Vaccine Surveillance Network and sent to CDC for testing. Antibiotic-resistant bacteria were isolated from 4 stools. We performed SS on isolates using Illumina MiSeq and on source stools using Illumina HiSeq sequencers. HMAS libraries were prepared for both isolates and stools using the Fluidigm Juno to amplify 749 amplicons targeting 111 different ARDs. Primers were selected from a published microarray, and amplicons were sequenced on the MiSeq. Isolate and metagenomics stool SS reads were trimmed, assembled, and screened for ARDs using ResFinder (2.1). HMAS reads were assembled, trimmed, and mapped to the ResFinder reference sequence database. Reference coverage and depth were used to determine gene presence. ARD calls from each sequencing method and sample type were compared for congruence. **Results:** We detected 5 ARDs across all isolates using SS: *bla*CTX-M, *bla*TEM-1B, *dfrA1*, *aadA1*, and *bla*CMY-2 and *bla*CMY-62. HMAS isolate results largely agreed,

detecting *bla*CTX-M, *bla*TEM-1B, and *aadA1*. HMAS stool testing detected *bla*CTX-M, *bla*TEM-1B, and *dfrA*, but not *aadA1*. Ability to detect *dfrA* and *bla*CMY was limited because the specific variants were not present on the primer panel. All ARDs found from SS of the isolates were also present in stool SS. **Conclusions:** Detection of ARDs using SS and HMAS of isolates and stool largely agreed. All ARDs present in the samples and included on the HMAS panel were detected. Future work will include adjustments to amplicon panel primer pairs to improve specificity and ARD coverage. Additional testing will be done using SS and HMAS on healthy and disease state samples with culture-confirmed ARDs.

Board 295. Optimization of Predictive Antimicrobial Resistance Analytics for State Public Health Laboratories

G. Wilson[1], E. Mircoff[2], K. Libuit[1], K. Gruszynski[3], L. Turner[1]
[1]Commonwealth of Virginia Division of Consolidated Laboratory Services, Richmond, VA, USA, [2]The Ohio State University College of Public Health, Columbus, OH, USA, [3]Lincoln Memorial University Department of Veterinary Medicine, Harrogate, TN, USA

Background: Antimicrobial-resistant (AMR) pathogens pose a significant public health threat, causing more than two million illnesses annually. Phenotypic antimicrobial susceptibility tests (ASTs) are the most definitive measure of bacterial isolate antimicrobial resistance; however, the AST scope within state public health laboratories has been historically limited. An alternative approach to antimicrobial susceptibility testing is the use of open-source annotation tools to predict AMR phenotypes from whole-genome sequence (WGS) data. **Methods:** Publicly available tools for resistome prediction were researched and incorporated into computationally efficiency workflows. ARIBA was selected for its unique approach to identifying AMR determinants through local assembles of short-read sequences. Both the CARD and Arg-ANNOT databases were selected for AMR determinant annotation due to database comprehensiveness and prevalence of use in the scientific community. A dataset of short-read sequences of 65 zoonotic *Salmonella* isolates (4 pan-susceptible [6.15%], 47 mono-resistant [72.31%], and 14 multi-drug resistant [21.54%]) was analyzed using ARIBA against CARD and/or ARG-ANNOT to identify AMR determinants and conferred phenotypes. Predicted AMR determinants were correlated with the AST phenotypic profile of each isolate to assess the accuracy of WGS-based methods for AMR prediction. **Results:** Out of 520 points of comparison, the sensitivity and specificity using CARD was 91.21% and 85.78% and the sensitivity and specificity using ARG-ANNOT was 92.31% and 97.44%, respectively, when databases were queried independently. Concatenation of the CARD and ARG-ANNOT databases yielded an improved sensitivity of 98.90% (specificity of 85.55%). **Conclusions:** Optimal phenotypic predictions from WGS data were achieved through a custom workflow deploying ARIBA with both ARG-ANNOT and CARD. Each database possessed insufficiencies, specifically in regards to Tetracycline and Fluoroquinolone resistance, resolved in part by the other database once they were collectively utilized. Applying predictive AMR analytics will allow public health labs to rapidly (6-12 min/isolate) assess the incidence of AMR pathogens within and across jurisdictions and monitor for emerging patterns of resistance.

Board 296. *De novo* Prediction of Pyrazinamide Resistance in *Mycobacterium tuberculosis* from Structural and Evolutionary Information

J. Carter[1], T. Walker[1], S. Walker[2], T. Peto[2], D. Crook[3], P. Fowler[2]
[1]University of Oxford, Oxford, United Kingdom, [2]University of Oxford, National Institute of Health Research Oxford Biomedical Research Centre, Oxford, United Kingdom, [3]University of Oxford, National Institute of Health Research Oxford Biomedical Research Centre, Public Health England, Oxford, United Kingdom

Background: In 2016, tuberculosis (TB) infected 10.4 million and killed 1.7 million people, making it the leading cause of death by infectious disease. Pyrazinamide (PZA) is a critical component of both first-line and multiple drug resistant (MDR) TB treatment regimens; it acts on non-growing "persister" bacteria, shortening treatment times and increasing their sterilizing effects. However, the evolution of PZA resistance has been implicated in poor treatment outcomes. PZA is a prodrug that is converted to its active form by an enzyme called pncA, a nonessential gene that contains mutations in the majority (72-99%) of PZA-resistant isolates. Advances in next-generation sequencing and PCR-based line probe assays have enabled the detection of emerging resistance from genotype more quickly than from standard drug susceptibility testing. However, resistance-causing mutations have been found dispersed across the promoter and open reading frame of the *pncA* gene, complicating the development of a complete catalogue of resistant mutations. A method to predict resistance for all possible nonsynonymous single nucleotide polymorphisms (SNPs) in pncA would increase our ability to detect and respond to emerging PZA resistance. **Methods:** This study exploits the availability of (i) a high-resolution crystal structure of pncA from *M. tuberculosis* and (ii) large mutation databases (289 unique nAAs) in order to estimate sequence-based structural properties that machine-learning classification models can exploit to differentiate between PZA-resistant and -sensitive SNPs. **Results:** Applying the model to the test set (86 nAAs) yields 85% sensitivity and 80% specificity in classifying pncA SNPs associated with phenotypic resistance/sensitivity. The model was also validated using sequence and phenotype data from clinical isolates. **Conclusions:** Alongside recent advances in genetics-based diagnostic technologies, this technique provides proof-of-concept for allowing *de novo* identification of emerging PZA resistance, enabling more rapid clinical responses. Importantly, this model is able to make a prediction for every possible SNP in pncA, enabling its extension to novel SNPs detected in emerging outbreaks. Future work could extend this analysis to predict resistance in other prodrug antibiotics such as ethionamide and delamanid.

Late Breakers

Board LB-28. Level of Awareness of Disease Transmission between Humans and Wild Animals at the Interface of Queen Elizabeth National Park, Uganda

S. Nabambejja, J. Nizeyi
Makerere University, College of Veterinary Medicine, Animal Resources and Bio Security, Kampala, Uganda

Background: Zoonotic transmission along the human-wildlife interface has of recent become an important aspect in the prevention and surveillance of diseases, with increased interaction among humans,

livestock, and wild animals with about 70% of zoonotic diseases originating from the wild. We assessed the level of local knowledge about disease transmission between people living in close proximity with wild animals in the southern sector of Queen Elizabeth National Park. **Methods:** A total of 60 households in Ishasha were surveyed using a questionnaire to obtain information on common diseases and transmission mechanisms. Interviews were conducted in three villages bordering the protected area and random sampling was used. Secondary data were collected from the annual reports of the Health Centers II and III that are frequented by the people in the study area. **Results:** The study showed that many wild animals come to the communities for drinking water at the river (61.1%, N=60). Most of the study participants, 96.7 % (N=60), indicated that they have gardens near or at the border line with the national park and 95 % (N=60) carried their lunch to the gardens since they spend many hours tilling land. After eating, they disposed of the waste or food remains in the gardens in which wild animals come to raid. We found that 55% (N=60) believed that wild animals can transmit diseases to people while 93% (N=60) were not aware that people carry pathogens that can be transmitted to wildlife; 94.8% (N=60) confessed that they defecate in bushes or makeshift latrines. **Conclusions:** People living adjacent to protected areas are unaware of disease transmission between humans, livestock, and wild animals. The open water sources are shared with wildlife and domestic animals and there are no extension services of sensitizing people on the primary health care.

Board LB-29. Implementation of Q Fever Diagnostics in Georgia

M. Zakareishvili
Laboratory of the Ministry of Agriculture, Tbilisi, Georgia

Background: Q fever is caused by infection with *Coxiella burnetii*, a bacterium that affects humans and animals. The common method of infection is contact with contaminated milk, meat, or wool and particularly birthing products. During 2013-2016, the laboratory of the Ministry of Agriculture (LMA) was involved in GG20 with the aim of *Coxiella burnetii* lab diagnostics implementation in Georgia. Q fever diagnostics were not conducted until 2013, and there was no information about the prevalence of the disease. **Methods:** Bacterial growth of *Coxiella* requires BSL-3 laboratory facilities. Bacteriology testing included the use of solid and liquid second-generation acidified citrate cysteine media, which was prepared using the SOP. The NMII strain was cultured as a positive control in liquid ACCM-2 and validated with the *Coxiella* PCR assay with positive results. The bacterial samples were divided into aliquots and stored at -80°C. Suspect-positive samples were cultured at the Lugar Center. A total of 89 IFA-positives and 14 weak PCR-positives from the Shedding study were cultured, and tested by molecular biology. **Results:** A total of 103 samples were cultured and found negative. Thirteen PCR-positive samples collected under the Shedding Study were cultured by the bacteriology laboratory and were tested by PCR on day 14 and day 30 of culture; of these samples, a single day-14 milk sample culture was positive by PCR, but negative when tested on day 30. PCR was performed on day 14 of culture. A total of 568 IFA-positive samples, including shedding study (156 swabs, 119 milk, and 293 blood/serum), were cultured and appeared negative by PCR, except one milk sample which was cultured and positive by PCR. **Conclusions:** The GG-20 project was the first investigation of *C. burnetii* in animals. As a result we are able to see what animals have the potential to spread the disease in local, stationary, and nomadic livestock. This project provided a foundation for future research, and studies for *C. burnetii* will be included in the existing public control program in Georgia.

Board LB-30. Improvement of Brucellosis Laboratory Diagnostics in Animals in Georgia

I. Beradze
Laboratory of the Ministry of Agriculture, Tbilisi, Georgia

Background: Brucellosis is a bacterial zoonosis resulting in significant economic losses due to reduction in animal populations and human death and suffering. The Laboratory of the Ministry of Agriculture (LMA) actively works to improve brucellosis diagnostics. **Methods:** During 2008-2011, LMA collected 7763 blood/serum and 2040 milk samples. The main goal was to improve brucellosis diagnostics and implement new tests in Georgia, and enhance the capacity to identify and conduct surveillance for brucellosis in animals in Imereti, Kvemo Kartli, and Kakheti. The samples were tested by bacteriology (Gram stain test; biochemical tests for oxidase, catalase, and urease, hydrogen sulfide and triple sugar iron (TSI) metabolism, serum agglutination and acriflavin, dye sensitive, *Brucella* dye with basic fuchsin, *Brucella* dye with thionin), serology (Rose Bengal, ELISA) and molecular biology (PCR and AMOS PCR) tests. Later, fluorescence polarization antibody assay (FPA) was implemented as confirmatory serology test. **Results:** A total of 33 strains have been isolated during 2008-2011. Within the brucellosis state program, 35527 different clinical samples (blood, serum, etc.) were collected from all regions of Georgia during 2014-2017. Sixty-six strains (53 *B. abortus* and 13 strains *B. melitensis*) have been isolated from cattle and small ruminants. FPA was implemented as a confirmatory serology test. **Conclusions:** Isolated cultures through bacteriology tests were retested by PCR and AMOS PCR assay differentiated specific *Brucella* species. *B. abortus* and *B. melitensis* strains are circulating in Georgia and the majority of positive results are from the Kvemo Kartli region. FPA as confirmatory serology test has been implemented. Bacteriology is able to identify *Brucella* spp. based on morphology, staining and biochemical tests and to compare with Bruc.Ladder test results. Better laboratory diagnostics help to the accurate and efficient surveillance system and brucellosis comprehensive control program in Georgia.

Board LB-31. Characterizing Human Target Cell Infection by Three Geographically Distinct Isolates of Mayaro Virus

A. Patel, J. Dailey, M. Dulcey, R. Pu, A. Vittor
University of Florida, Gainesville, FL, USA

Background: Mayaro virus (genus Alphavirus, family Togaviridae) is an emerging arthropod-borne virus transmitted by *Haemagogus* mosquitoes in sylvatic regions of Central and South America. Like chikungunya virus, Mayaro virus (MAYV) infection leads to fever, maculopapular rash, and arthralgia. Much is unknown pertaining to regional differences in MAYV in vitro infectivity in human cells. Here we describe viral kinetics, cytopathic effects, and human target cell susceptibility to three geographically distinct MAYV isolates represented genotypes D and L (Uruma, Peru, and Brazil). **Methods:** MAYV susceptibility of key human target cells (human dermal fibroblasts, human embryo kidney [HEK293], and skeletal muscle satellite cells) and Vero E6 cells was visualized using immunofluorescence microscopy, and quantified by flow cytometry at 0, 24, 48, and 72h post infection (p.i.). Viral kinetics were determined for each cell line from 0-72h p.i. at MOI=1, followed by plaque assays on Vero E6 cells to

determine viral titers. Cytopathic effect was observed and compared across viral isolates and cell lines with crystal violet staining. **Results:** Immunofluorescence and flow cytometry revealed that human dermal fibroblasts, skeletal muscle satellite cells, and Vero E6 cells were susceptible to each MAYV isolate, though to differing degrees, and HEK293 became infected at much lower rates (MAYV-Uruma > MAYV-Peru > MAYV-Brazil). Viral replication kinetics assays showed that peak viral titers occurred for all three viral isolates around 24h p.i, reaching $1x10^8$ pfu/ml. MAYV-Uruma reached this peak the fastest, followed by MAYV-Peru and then MAYV-Brazil. Crystal violet staining also demonstrated lower viral pathogenesis with greater cell survival and decreased cell apoptosis for MAYV-Uruma, Peru, and Brazil, respectively. **Conclusions:** These results indicate that MAYV can infect human dermal fibroblasts, which are abundant at the initial site of exposure. Further, skeletal muscle satellite cells are very susceptible to MAYV, in line with clinical symptoms. Some differences in infectivity are apparent across different MAYV isolates, and may contribute to variable virulence and pathogenicity. These findings advance our understanding of MAYV infection of human target cells, and provide some initial data with regards to MAYV phenotypic variation based on geography.

Board LB-32. First Serologic Evidence of Emerging Zoonotic Alphaviruses in Humans from a Remote Indigenous Community in the Peruvian Amazon

J. Pérez Lazo[1], J. Carrera[2], E. Serrano[3], J. Maguiña[4], G. Mentaberre[3], A. Lescano[4], A. Valderrama[2], P. Mayor[3]
[1]University of Liverpool, Liverpool, United Kingdom, [2]Gorgas Memorial Institute of Health Studies, Panama City, Panama, [3]Universitat Autònoma de Barcelona, Barcelona, Spain, [4]Universidad Peruana Cayetano Heredia, Lima, Peru

Background: Mayaro virus (MAYV), Venezuelan equine encephalitis virus (VEEV), and Madariaga virus (MADV) are alphaviruses that co-circulate in South America. However, the acute febrile illness caused by these viruses resembles other arbovirus infections leading to misdiagnosis. Moreover, most surveillance studies in Peru have been carried out in urban cities but not in indigenous communities in the Peruvian Amazon. **Methods:** The study was conducted in Nueva Esperanza, a remote indigenous community in the northeast Peruvian Amazon where the main occupations are small-scale agriculture, fishing, logging, and subsistence hunting. Serum samples from 70 volunteers from Nueva Esperanza were tested for MAYV, MADV, and VEEV antigen using capture enzyme-linked immunosorbent assays (ELISA) and confirmed using a plaque reduction neutralization test (PRNT). Additionally, blood samples from 90 wild animals harvested by hunters were tested for MAYV by PRNT. **Results:** The seroprevalence for MAY in humans was 24% (17/70), 16% for VEEV (11/70), and 1.5% (1/70) for MADV. Hunting activity and cohabiting with hunters were the main risk factors for Mayaro seroconversion. The highest MAYV seroprevalence in wild animals was observed in armadillos, followed by monkeys, peccaries, agoutis, and pacas. However, reservoir hosts for MADV and VEEV were not studied and remain unknown. **Conclusions:** These findings show a greater geographic range of MAYV in the Peruvian Amazon, not only restricted to main cities in the Peruvian Amazon where most MAYV isolates were reported but also in remote indigenous communities. Moreover, the chronic debilitating joint pain associated with Mayaro fever may severely impair the livelihoods of MAYV-infected people. Further studies are also needed to assess the epidemiological role of the studied animals in MAYV, MADV, and VEEV circulation.

Board LB-33. Novel G4P[49] Rotavirus Strains Identified in a Diarrheal Outbreak in Piglets in Bangladesh, February, 2014

S. Sarkar[1], M. Esona[2], R. Gautam[2], C. Castro[3], S. Khan[4], E. Gurley[1], U. Parashar[2], E. Kennedy[2], M. Bowen[2], M. Rahman[1]
[1]icddr,b, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [4]University of Guelph, Guelph, ON, Canada

Background: Group A rotavirus (RVA) associated diarrhea in piglets represents one of the major causes of morbidity and mortality in pig farms worldwide. A diarrhea outbreak occurred among nomadic piglets in north-western district of Bangladesh in February 2014. Outbreak investigation was performed to identify the cause and epidemiological and clinical features of the outbreak. **Methods:** Rectal swabs and clinical information were collected from diarrheic piglets (n=36). Rectal swabs were tested for group A rotavirus RNA by real-time reverse transcription polymerase chain reaction (rRT-PCR) using rotavirus NSP3-specific primers. Genotyping was performed for G (VP7) and P (VP4) genotypes using next generation sequencing. **Results:** We found that the morbidity rate was 61% (50/82) among piglets in the nomadic pig herd and the case-fatality rate was 20% (10/50) among piglets with diarrhea. The clinical signs were watery diarrhea, lack of appetite, or reluctance to move in the studied piglets. All diarrheal piglets were positive for a novel rotavirus strain, G4P[49], similar with Indian and Chinese strains; it predominantly consists of porcine or porcine-like G4 human strains and is genetically distant from Bangladeshi human G4 strains. The genome constellation of the novel rotavirus strains was classified as G4-P [49]-I1-R1-C1-M1-A8-N1-T7-E1-H1. **Conclusions:** Our study results indicate that the diarrhea outbreak occurred among nomadic piglets due to the novel rotavirus strain G4P[49]. Identification of this novel strain warrants further exploration for disease severity and zoonotic potential.

Board LB-34. Risk Assessment of Human Behaviors that May Impact the Health of the Mountain Gorillas around Bwindi Impenetrable National Park, Western Uganda

J. Nizeyi, L. Mugisha, S. Nabambejja
Makerere University, College of Veterinary Medicine, Animal Resources and Bio Security, Kampala, Uganda

Background: Human behaviors have been found to play a role in transmission of disease-causing agents among humans, their domestic animals, and wild animals, especially where the levels of human-animal interactions are very high, as in the case of mountain gorillas. There is increased traffic of pedestrians in Bwindi's southern sector and shared use of fallow gardens by gorillas, domestic animals, and humans due to wild animal habituation and highly promoted eco-tourism, which is increasing the chances of exchanging disease agents. **Methods:** Using self-administered questionnaires and interviews, a cross-sectional study was carried out to assess the human-risk behaviors that could be contributing to environmental loading with materials that are potential vehicles of pathogens in the southern sector of BINP. **Results:** The study indicated that the average age of the park staff

was 32.7 ±7.57 years. Overall, 68.6% of the park staff indicated that they relieve themselves in shallow dug cat holes while in the field in the park, while 31.4% relieve themselves in the bushes. The common methods of solid waste disposal documented during the study were by use of the provided trash cans (69.4%) and returning the waste back to the camp area (69.4%), as per instructions given to tourists. About 40 local people were transiting through the forest; 72.5% were men and 27.5% were women. Most of them (82.5%) confessed to using forest bushes to relieve themselves when they are on their journey. The solid wastes were not buried and it is no surprise that they do not dig cat holes since they don't carry tools with them. **Conclusions:** The registered human behaviors are a source of environmental contamination and potential routes for pathogen transmission to the endangered mountain gorillas. Hence, public health education and sensitization, intensification in law enforcement, and active epidemiological surveillance are recommended in an effort to ensure the long-term survival and conservation of mountain gorillas.

Board LB-35. Investigation of Three Geographically-Distinct Anthrax Outbreaks in Uganda, 2018

C. Cossaboom[1], D. Lowe[1], L. Nyakarahuka[2], H. Mwebesa[3], P. Tusiime[3], I. Makumbi[3], D. Ndumu[4], W. Nguma[4], P. Drileba[3], M. Neckyon[4], C. Godfrey[3], G. Asiimwe[4], R. Downing[2], J. Buule[2], M. Sekamatte[5], J. Homsy[6], V. Brown[6], B. Zhu[6], L. Nelson[6], J. Salzer[1], A. Vieira[1], L. Campbell[1], W. Bower[1], C. Kolton[1], R. Stoddard[1], C. Marston[1], A. Hoffmaster[1], H. Walke[1], J. Aceng[3], J. Sentumbwe[4]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uganda Virus Research Institute, Entebbe, Uganda, [3]Republic of Uganda Ministry of Health, Kampala, Uganda, [4]Republic of Uganda Ministry of Agriculture, Animal Industry, and Fisheries, Entebbe, Uganda, [5]Republic of Uganda Ministry of Health, Zoonotic Disease Coordination Office, National One Health Platform, Kampala, Uganda, [6]US Centers for Disease Control and Prevention, Kampala, Uganda

Background: Anthrax, caused by *Bacillus anthracis*, is a naturally-occurring zoonotic bacterial disease. Since early 2018, anthrax cases in humans and livestock have been reported from three geographically distinct districts in Uganda: Arua, Kween, and Kiruhura, for which a multi-sectoral One Health investigation was launched. **Methods:** Response teams performed human and animal case investigations and community and clinician sensitization. Teams provided anthrax control recommendations on human exposure and case identification, post-exposure prophylaxis and treatment, safe sample collection, livestock vaccination, and livestock carcass disposal. Teams collected specimens from livestock carcasses and swabs from cutaneous cases in humans. The InBios Active Anthrax Detect (AAD), a lateral flow assay to detect capsular polypeptide of *B. anthracis*, was deployed along with Gram staining for presumptive diagnosis of anthrax in livestock carcasses at the local level. **Results:** In Arua, 55 probable cases in humans and 666 livestock deaths were reported since February 2018; four of five livestock carcasses tested were AAD-positive and gram-positive rods were identified by microscopy, consistent with *B. anthracis*. In Kween, 76 probable cases in humans and 14 livestock deaths have been reported since April 2018; three cases in humans were PCR-confirmed, and two of three livestock carcasses were AAD-positive. In Kiruhura, 26 probable cases in humans and 35 livestock deaths have been reported since May 2018 and eight of nine livestock carcasses were AAD-positive. All cases in humans are associated with direct contact or consumption of meat from anthrax-suspect livestock carcasses. Confirmatory testing on both human and livestock specimens is underway in Uganda and at CDC Atlanta. **Conclusions:** Continued multi-sectoral support and One Health response are critical to continue identifying cases in humans and livestock, determine the extent of the outbreaks, and implement proper prevention and control methods. AAD is a valuable tool to improve low-resource countries' abilities to rapidly presumptively diagnose and manage epizootics, reducing human transmission risk and further environmental contamination.

Board LB-36. Anthrax Laboratory Studies and GIS Analyses in Georgia, 2015-2017

L. Kerdzevadze
Laboratory of the Ministry of Agriculture, Tbilisi, Georgia

Background: Anthrax is a bacterial zoonosis caused by *Bacillus anthracis*, a spore-forming, soil-borne bacterium with a remarkable ability to persist in the environment. Found on nearly every continent, the disease is considered a re-emerging zoonotic disease, and despite the development of anthrax vaccines for animals and humans, the disease continues to be endemic in many countries, including Georgia. During 2015-2017, Laboratory of the Ministry of Agriculture (LMA) conducted anthrax laboratory studies (bacteriology and molecular biology) using geographic information system (GIS) and spatial analyses. The purpose of this study was to describe and mapping anthrax foci in the eastern part of Georgia: Kvemo Kartli and Kakheti regions. **Methods:** Samples were collected from Kvemo Kartli (312) and Kakheti (688) and tested by LMA using standard bacteriological (Gram stain; gamma phage lysis; motility test; DFA) and molecular biology (PCR) methods. In order to identify and map anthrax-positive sites, for better visualization and interpretation, GIS was developed. **Results:** Based on laboratory diagnostics, 26 (3%) out of 1000 samples were positive. These positives were dispersed in different rayons of the targeted regions, Kvemo Kartli and Kakheti. Cultures isolated through bacteriology tests were confirmed by PCR assay. Spatial analysis and risk factor mapping were conducted using geographic information systems (GIS). **Conclusions:** Despite the endemic nature of the disease in Georgia, few studies have been conducted on the distribution of *B. anthracis* using GIS analyses as additional tool to the laboratory tests. Identifying the potential geographic distribution of *B. anthracis* in Georgia represents an important step in controlling and preventing anthrax and to improve understanding of anthrax ecology and ecological risk factors. Laboratory results and accurate maps should be useful in identifying areas of risk for humans and determining surveillance vaccination priorities for livestock.

Board LB-37. Clinical and Epidemiological Features of Human Rabies Cases in Bangladesh, 2011-2015

U. Siddiqui[1], S. Ghosh[1], M. Rana[1], S. Chowdhury[2], R. Bhowmik[3], M. Kafi[4], S. Mahmudullah[1], M. Islam[1], B. Ahmed[5], S. Tahmina[1]
[1]Communicable Disease Control, Directorate General of Health Services, Ministry of Health and Family Welfare, Dhaka, Bangladesh, [2]Chittagong Veterinary and Animal Sciences University, Chittagong, Bangladesh, [3]John Jay College of the City University of New York, New York, NY, USA, [4]University of Dhaka, Dhaka, Bangladesh, [5]The United Nations Children's Fund (UNICEF), Dhaka, Bangladesh

Background: Bangladesh has reduced the death of rabies case-patients by 50% over the last few years. Clinical and epidemiological knowledge of human rabies is crucial to direct further research investigation and to implement disease control measures. **Methods:** We re-

viewed the patient records of 422 people reported from the Infectious Disease Hospital (IDH) in Dhaka, Bangladesh from 2011 to 2015 who had a clinical diagnosis of rabies. We used the WHO case definition for clinical rabies. **Results:** Male patients outnumbered female patients by 2.3 to 1 and 48% were under the age of 15 years. Eighty-two percent (n=346) of the case-patients came from rural areas. Dogs with unknown vaccination status (n=412, 98%), comprised the majority of exposures (n=380, 90%). The exposures mostly involved the lower limbs (n=320, 76%), with the majority categorized as WHO Category III (n=399, 95%). Seventy-eight percent (n=327) of the victims did seek treatment from traditional healers and 12% (n=51) received post-exposure prophylaxis (PEP). No history of receiving pre-exposure rabies vaccination was found. The incubation period varied, with the highest number of cases occurring in 0-90 days post-exposure categories. The shortest and longest reported incubation periods were 5 days and 370 days, respectively. Infections resulting from bites on the head and neck appeared to have a shorter incubation period, compared with infections resulting from bites to the lower extremity. Clinical symptoms included hydrophobia (97%), aerophobia (84%), photophobia (10%), and hypersalivation (7%). The case-fatality rate was 100%. **Conclusions:** Better comprehension of clinical disease indications may help efforts to save patients with rabies. Knowledge of epidemiological factors can improve preventative efforts to ease rabies suffering. Improving treatment-seeking behavior of the bite victims through awareness education, ensuring better accessibility and availability for the provision of rabies PEP, and implementing a countrywide dog vaccination campaign will help prevent human deaths from rabies.

Board LB-38. Development of a Glycoprotein-Based ELISA for Diagnosis of Rabies Virus-Neutralizing Antibody

D. Han, S. Park, Y. Lee, H. Lee
National Institute of Health, Korea Centers for Disease Control & Prevention, Cheongju, Republic of Korea

Background: Rabies is a fatal zoonotic disease in both humans and animals. Although rabies is 100% lethal, it is 100% preventable through proper vaccination. Therefore, measuring the neutralizing antibody after vaccination is important for preventing human rabies. However the current widely used method, rapid fluorescent focus inhibition test (RFFIT), is a time-consuming and complex process and should use live rabies virus. **Methods:** In the present study, we developed a new diagnosis method using glycoprotein-based indirect enzyme-linked immunosorbent assay (ELISA) for measuring the neutralizing antibody titer in human serum. **Results:** We prepared recombinant glycoprotein of the rabies virus which was isolated from a Korean rabies patient, and the protein was used as an antigen to measure the neutralizing antibody titer in ELISA. Of 350 sera, 270 were vaccinated with pre or post exposure prophylaxis using rabies vaccine and 130 of the 270 were positive sera that showed more than 0.5 IU/ml by RFFIT. The 50 sera were from patients with other diseases such as encephalitis and meningitis, which have symptoms similar to rabies. Thirty healthy sera were used as a negative control. The results showed that neutralizing antibody titer by two methods, the glycoprotein-based ELISA and RFFIT, had a significant correlation. **Conclusions:** Our new diagnosis method is more objective, easier, and faster than RFFIT. It is also safe for the experiments because it does not use live virus. Therefore, our method showed the possibility of substitution for RFFIT as it was highly likely to be developed as on-site application or rapid kit. ※ This study was supported by a research grant (2016-NG52001-00) from the Korea Centers for Disease Control and Prevention. Some of the biospecimens were provided by the Gyeongsang National University Hospital and Ajou University Hospital, which are members of Korea Biobank Network. (1910/2000 words)

Board LB-39. Combining Culture with Real-Time PCR for Improved Detection of Spotted Fever Group *Rickettsia*

M. Condit, C. Kato
Rickettsial Zoonoses Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Spotted fever group rickettsiosis (SFGR) is caused by obligate intracellular bacteria from the genus *Rickettsia*. SFGR patients have low bacteremia at the early acute stage of illness (< 100 bacteria/mL) in circulating whole blood. Acute phase SFGR may be diagnosed by molecular methods in tissue biopsies and less frequently in blood and serum, due to this low bacteremia. The PanR8 real-time PCR assay has a LOD of ~9 copies/rxn (with 95% efficiency), reflecting a sample containing ~1,800 copies/mL of blood. This may result in false negatives for cases with strong clinical descriptions of SFGR. In this study, *Rickettsia conorii* (Rco), *Rickettsia parkeri* (Rpa), and *Rickettsia rickettsii* (Rri) were used to understand growth dynamics of SFGR to define a method for the cell culture enrichment for an application in acute patient samples. **Methods:** Forty copies of cultured Rco were spiked into 6 mL of media and inoculated into confluent 25 cm^2 tissue flasks (TF) of uninfected Vero E6 cells. Supernatant (sup) and cells were sampled on days 1-5, followed by DNA extraction and quantitation using the PanR8 assay. Flasks were either continually sampled or only sampled once at each time point (endpoint, EP) to see if decreasing culture volume affected Rco growth. Decreasing total culture volume from a 25 cm^2 TF to a 10 cm^2 TF was evaluated to determine effects on detection time. Rri and Rpa were evaluated on days 3-7 in the 10 cm^2 TF. **Results:** Results indicate no difference in doubling time (DT) during the log phase of growth. More copies of Rco were detected in cells at 1.27×10^7 copies/flask compared to EP cells at 6.09×10^6 copies/flask by day 5 ($p < 0.0001$). Cells and sup associated Rco were detected consistently by days 2 and 3. Decreased DT was seen in the sup from the 10 cm^2 TF from 5.4 hr to 3.6 hr, and no change was observed in cells. By day 5 more Rco copies were detected in 10 cm^2 TF cells, increasing from 6.09×10^6 copies/flask to 1.08×10^7 copies/flask ($p = 0.03$). Day 3 sampling of both Rpa and Rri supernatant showed detection at 242.5 copies/flask and 2320.1 copies/flask respectively. **Conclusions:** Results indicate that all 3 strains can be detected in sup and cells by day 3. These data show that consecutive sup sampling beginning day 3 in a 10 cm^2 TF is recommended for repeatable detection of low copy number samples.

Board LB-40. Risk of Yellow Fever Virus Introduction in the United States from Brazil during 2016-2018

I. Dorigatti[1], S. Morrison[2], C. Donnelly[1], T. Garske[1], S. Bowden[2], A. Grills[3]
[1]Imperial College London, London, United Kingdom, [2]Centers for Disease Control and Prevention, Eagle Medical Services, LLC, Atlanta, GA, USA, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Southeast Brazil has experienced two large yellow fever (YF) outbreaks since 2016. While the 2016-17 outbreak mainly affected the states of Espírito Santo and Minas Gerais, the 2017-18 YF out-

break has primarily involved the states of Minas Gerais, São Paulo, and Rio de Janeiro, the latter two of which are highly populated and popular destinations for international travelers. **Methods:** We modified a previously established modeling framework to quantify the risk of YF virus (YFV) introduction into United States (US) cities via air travel from Brazil, including both incoming Brazilian travelers and returning US travelers. Additionally, we assessed the impact that vaccination of US travelers and the population of southeast Brazil has on the risk of YFV introduction. **Results:** During both the 2016-17 and 2017-18 YF outbreaks in southeast Brazil, three international airports (Miami, New York-John F. Kennedy (JFK), and Orlando) were predicted to be at risk of receiving at least one person with YF infection potentially capable of seeding local transmission. Additionally, incubating or active YFV infections among residents of Brazil traveling to the US drove the risk of YFV introduction into these locations. Lastly, further analyses showed that Orlando and New York–JFK would not have been at risk during the 2016-2017 outbreak if Brazil's southeast states increased vaccination coverage. **Conclusions:** Understanding the risk of importation can aid public health decisions related to vaccination strategies and help target interventions. Improved vaccination coverage in YF outbreak areas reduced the risk of importation to the United States; the risk can be further reduced by encouraging vaccination of US travelers to outbreak areas. CDC's Division of Global Migration and Quarantine strives to prevent the introduction, transmission, and spread of communicable diseases using the most effective, innovative, efficient, and least restrictive actions. Supporting outbreak control efforts at the source is an effective preventive measure. Additionally, decision-makers can employ more focused courses of action such as information gathering and assessments; expanded communication mechanisms to provide specific recommendations for travelers; enhanced partner engagement; and targeted interventions at ports of entry.

Board LB-41. Identification of Yellow Fever Vaccine Deserts in the United States, 2017

S. Bowden[1], S. Morrison[1], E. McIntyre[2], A. Grills[3]
[1]Centers for Disease Control and Prevention, Eagle Medical Services, LLC, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, Booz Allen Hamilton, Atlanta, GA, USA, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Before the onset of the temporary complete depletion of the only licensed yellow fever vaccine (YF-Vax) in the United States in July 2017, approximately 4,500 travel clinics administered yellow fever vaccine to travelers. Until the expected return of YF-Vax availability at the end of 2018, its manufacturer has made an alternative yellow fever (YF) vaccine, Stamaril, available at 269 locations across the United States, under an expanded access investigational new drug protocol. Because of this decrease in the number of clinics administering vaccines, we sought to identify YF vaccine deserts to inform the placement of potential future Stamaril clinic locations. **Methods:** We first identified high-need states, meaning those where the median household drive-time to a Stamaril clinic was at least double the median household drive-time to a YF-Vax clinic. We then identified airports in high-need states with a drive-time >90 minutes to a Stamaril clinic. Next, we performed a spatial hot-spot analysis (Getis-Ord G_i^*) to identify airports in high-need states with high travel volume to countries with a YF vaccine requirement or recommendation. We also performed this analysis on airports with a >90-minute drive-time to a Stamaril clinic in all 50 states. **Results:** We identified 13 high-need states based on our drive-time criteria. Within these states, 71% (72/102) of airports had a drive-time longer than 90 minutes to a Stamaril clinic; of those, 81% (58/72) had travel volume to countries with a YF vaccine requirement or recommendation. Within all 50 states, 49% (200/408) of airports had a drive-time of more than 90 minutes to a Stamaril clinic; of those, 89% (177/200) had travel volume to countries with a YF vaccine requirement or recommendation. Among all subsets, Wichita, Kansas, was consistently identified as a hot-spot for high travel volume. **Conclusions:** Access to YF vaccine is limited, YF outbreaks have recently occurred in areas with high connectedness with the United States, and travel volume to these regions from the United States does not appear to be decreasing. Therefore, we sought to identify YF vaccine deserts to identify potential locations of future Stamaril clinics. Hot-spot analyses showed that, based on both state-level need and long drive-time from an airport to a Stamaril clinic, an optimal location for an additional Stamaril clinic may be Wichita, Kansas.

Board LB-42. Wild Yellow Fever: Public Health Emergency: Study of Cases in Emílio Ribas Institute of Infectology - IIER, Sao Paulo, Brazil, January to March 2018

A. Ribeiro, R. Cavalin, J. Suleiman, J. Costa, M. Vasconcelos, C. Málaque, J. Sztajnbok
Instituto de Infectologia Emílio Ribas, São Paulo, Brazil

Background: Yellow fever is an infectious disease caused by an arbovirus that is endemic in the tropical forests of America and Africa. In Brazil, from 1980 to 2016, 797 confirmed cases of wild yellow fever-WYF were reported, with expansion of viral circulation. In 2018, 1127 cases of WYF and 328 deaths were confirmed, 455 cases (40.3%) in the state of São Paulo, data until April 3. **Methods:** A descriptive study of patients with suspected yellow fever, notified by the Epidemiology Service-IIER, from the epidemiological investigation forms of notifiable diseases. Statistical analyses, as square chi or non-parametric test were performed. The logistic regression model was used to evaluate factors associated with death, $p < 0.05$ was significant in SPSS program. **Results:** The IIER is a referral hospital for infectious diseases in São Paulo. There were 99 suspected cases of yellow fever-YF, with 72 confirmations (72.7%) and 21 deaths, lethality (27.8%). All cases were laboratory-confirmed by RT-PCR or serology-IgM and classified as WYF. The metropolitan region of São Paulo was the main region of infection. The case-patients were predominantly male (80.6%), 30 to 59 years old (56.9%), and white (65.3%). History of vaccination against YF was reported in 9 cases (12.5%). The most important symptoms were: fever (98.6%), nausea (76.4%), and myalgia (79.2%). When comparing the deaths and the cures, we found a statistical difference between the median age-year (55x37) and the following laboratory tests: leukocytes-cel/mm^3 (6000x3050), platelets/mm^3 (110,000x75,000), glutamic oxaloacetic transaminase-U/L-GOT (8966x1357), glutamic pyruvic transaminase-U/L (3320x1420), total bilirubin-mg/dL (6.2x1.1), urea-mg/dl (46x28), creatinine-mg/dl-CR (5.8x0.9), and International Normalized Ratio-*INR* (2.4x1.2). From the regression model, the GOT->1841 ORadj 12.92 (1.50-111.37) and CR->1.2 ORadj 81.47 (11.33-585.71) variables were independent factors associated with death, $p < 0.05$. **Conclusions:** Yellow fever is an emergency, requiring alert for case detection and implementation of control measures such as vector actions to prevent re-urbanization and maintenance of high vaccine coverage.

Board LB-43. Chikungunya: Strategic Plans for Public Health in a Local Community in Honduras

Z. Reyes[1], V. Gonzales[1], A. Araque[2]
[1]Universidad Tecnológica Centroamericana, Tegucigalpa, Honduras, [2]Secretaria de Salud de Honduras, Comayagua, Honduras

Background: Chikungunya virus (CHIKV) is a mosquito-borne arbovirus that causes chikungunya fever, a severe, debilitating disease that often produces chronic arthralgia. In 2015, there was a worldwide spread in which the disease came to Latin America. Honduras presents climatic, geographic, and epidemiological conditions suitable for transmission of vector-borne diseases. Few data and reports are available in Central America countries, especially Honduras. Proper community participation on vector control was necessary to control and mitigate the effects of *Aedes* transmission. **Methods:** A cross-sectional descriptive study of the statistical bases of the regional health office of Comayagua department were patients diagnosed with chikungunya virus infection during the period between January 2016 to December 2017. **Results:** A total of 395 cases were confirmed in the city of Comayagua. A total of 92.2% of these cases were reported in 2016, in 13 municipalities. A dramatic decrease of cases was found in 2017, where only 22 cases were reported in 3 municipalities. **Conclusions:** Chikungunya is an emergent infectious disease that cannot be underestimated. Most cases were reported during weeks 26-32 in the year 2016; this is consistent with the season of rain in the country. A lower rate of cases was found in the year 2017 in comparison with 2016. In 2017, only 3 municipalities in the city of Comayagua reported cases. The burden of the virus is found in 3 municipalities that have the highest concentration of people and inadequate waste management.

Board LB-44. Spatio-Temporal and Socio-Demographic Patterns of Chikungunya, Dengue, and Zika Infections in Mexico in 2016-2017

T. Kobayashi[1], K. Mizumoto[1], M. Jiménez-Corona[2], C. Ruiz-Matus[2], P. Kuri-Morales[3], G. Chowell[1]
[1]Georgia State University, Atlanta, GA, USA, [2]Dirección General de Epidemiología, Mexico Ministry of Health, Mexico City, Mexico, [3]División de Estudios de Postgrado Facultad de Medicina, UNAM, Mexico City, Mexico

Background: Chikungunya, dengue, and Zika viral infections are vector-borne diseases that are endemic in Mexico. Here we analyze the relationship between onset timing and climate data and socio-economic variables across the country. **Methods:** We collected weekly incidence data, daily climate data, and socio-economic status on each state of Mexico during 2016-2017. The data sources are the Mexican surveillance system, the Weather Underground, OECD.org, and INEGI Mexico. We measured the direct distances from six southernmost states of Mexico (i.e., Campeche, Chiapas, Oaxaca, Quintanaroo, Tabasco, and Yucatan) to all other states and compared them with the timing of the state-level curves. Then we performed step-wise multivariate analysis on weather and socio-economic variables to find the ones that best predicted the onset timing of the three infections. **Results:** Chikungunya and dengue both show "south-to-north" spreading patterns, especially in the states that are located along the coastlines of Mexico. Onset timings of chikungunya, dengue, and Zika epi-curves can be predicted by some socio-economic variables with the coefficients of determination of 0.7540, 0.8472, and 0.8949, respectively. **Conclusions:** The coastline and south-to-north patterns of spreading, as well as socio-economic factors, may be good predictors of epidemic onset for these vector-borne infectious diseases.

Board LB-45. TEPHINET's Management Response to the Zika Emergency in the Americas (2016-2018)

M. Mansur[1], A. Hilmers[1], L. Alonso[2], J. Arrasco[3], L. Boodram[4], A. Cabello[5], P. Dely[6], M. Garcia[7], J. Ojeda[8], R. Pimentel[9], F. Prieto[10], D. Herrera-Guibert[1]
[1]TEPHINET-Task Force for Global Health, Atlanta, GA, USA, [2]Ministry of Health, Montevideo, Uruguay, [3]CDC-Peru, Lima, Peru, [4]Caribbean Public Health Agency-CARPHA, Port-of-Spain, Trinidad and Tobago, [5]Ministry of Health, Asuncion, Paraguay, [6]Ministry of Health, Port-au-Prince, Haiti, [7]Ministry of Health, Brasilia, Brazil, [8]Ministry of Health, Quito, Ecuador, [9]Ministry of Health, Santo Domingo, Dominican Republic, [10]National Institute of Health, Bogota, Colombia

Background: In September 2016, TEPHINET Secretariat led the response to Zika in the Americas by launching interventions in the areas of Field Epidemiology Training Programs (FETPs), vector control (VC), and neurological disorders studies (ND). We explain the strategy and mechanisms implemented by TEPHINET to respond to this emergency. **Methods:** TEPHINET set up a coordination team, conducted regular visits and communications with health ministries in 13 affected countries (Brazil, Colombia, Dominican Republic, Ecuador, Grenada, Guatemala, Haiti, Jamaica, Paraguay, Peru, St. Vincent and Grenadines, Trinidad and Tobago, and Uruguay), and developed an action plan as part of a comprehensive regional project management (PM) system, identifying critical drivers. The PM system consisted of a) short and medium term planning (Phase 1: 09/ 2016–09/ 2017; Phase 2: 10/2017–05/ 2018), with an emphasis on sustainability; b) finance, procurement, logistics support, technical assistance, technology transfer; c) implementation of Zika Response Country Action Plans, and d) M&E framework. **Results:** TEPHINET allocated 8.5 million USD in 18 months to conduct Zika laboratory and surveillance activities in 13 countries and develop local health workforce capacities (1,100 trainees). Fifty Zika-related applied epidemiology studies were conducted. Twelve new laboratories and research facilities for VC interventions were developed. A GIS system for *Aedes aegypti* surveillance in Colombia, Peru, and DR was strengthened. NDs such as Guillain-Barre syndrome associated with Zika were studied in Colombia, Guatemala, and Peru. Over 60 visits were conducted from 03/2017-05/2018 with interactions among over 120 project staff and public health officers across the 13 countries. **Conclusions:** TEPHINET demonstrated the capacity to implement a rapid response to address Zika emergency based on its strategic vision, flexibility, organization, and interaction with the programs in the adoption of an Agile PM system and the existence of an active network of FETPs in the Americas. The information collected through this experience will inform future field interventions.

Board LB-46. Obstetric Ultrasound Service Delivery: Assessment Tools Used in the Context of the Zika Virus Epidemic in Five USAID Priority Countries

L. Noguchi[1], J. Hermida[2], B. Kallam[1], A. Abuhamad[3]
[1]MCSP/Jhpiego, Washington, DC, USA, [2]USAID ASSIST/URC, Quito, Ecuador, [3]EVMS, Norfolk, VA, USA

Background: Zika virus infection in pregnancy has been shown to cause severe adverse effects on fetal development, some of which may be detected during obstetric ultrasound. However, in some set-

tings, it may be unclear whether obstetric ultrasound services and health system referral networks have adequate capacity to detect and appropriately refer patients with suspected cases of congenital Zika syndrome (CZS). As part of ongoing quality improvement (QI) activities undertaken by USAID ASSIST (in Guatemala, El Salvador, Dominican Republic, and Honduras) and USAID Maternal and Child Survival Program (MCSP) (Haiti), we aimed to develop tools to assess the capacity of obstetric ultrasound service delivery settings to detect features of CZS, with the ultimate goal of improving care and referral pathways in these countries. **Methods:** A multi-disciplinary group of maternal-fetal medicine specialists, ultrasonographers, and global health technical and program advisors from the Maternal and Child Survival Program, USAID ASSIST, Society for Maternal Fetal Medicine, and American Institute of Ultrasound in Medicine collaborated to design these assessment tools. Tools were translated into Spanish and French and adapted to a mobile tablet system using SurveyCTO. **Results:** Four surveys were developed: (1) ultrasound provider capacity; (2) structured service delivery observation; (3) ultrasound practice capacity and referral patterns; and (4) ultrasound equipment and environment of care. Assessment tool content covers many relevant areas, including capacity for fetal biometry and anatomic survey (including key features associated with CZS), provider training and certification, ultrasound-related infection prevention and control practices, service delivery infrastructure, health system referral pathways, and other assessments to better understand care and referral of pregnant women with suspected and confirmed ZIKV infection. **Conclusions:** Obstetric ultrasound assessment tools were used in five countries in Latin America and the Caribbean to inform recommended referral pathways for pregnant women with suspected and confirmed ZIKV infection. Assessment tools, which will become available in three languages for public use and adaptation in June 2018, will be shared during the presentation.

Board LB-47. Zika Virus Testing of Amniotic Fluid in Colombia

M. Mercado[1], E. Ailes[2], M. Daza[3], V. Tong[2], J. Osorio[3], D. Valencia[2], A. Rico[1], R. Galang[2], M. González[1], J. Ricaldi[4], K. Anderson[2], N. Kamal[5], J. Thomas[5], J. Villanueva[5], J. Moore[6], D. Meaney-Delman[7], S. Gilboa[2], M. Honein[2], D. Jamieson[8], M. Ospina Martínez[1]
[1]Instituto Nacional de Salud, Bogotá, Colombia, [2]Division of Congenital and Developmental Disorders, National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Research Division, Vysnova Partners, Bethesda, MD, USA, [4]Division of Bacterial Diseases, National Center for Immunization and Respiratory Diseases, Atlanta, GA, USA, [5]Division of Preparedness and Emerging Infections, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]Eagle Medical Services, LLC, Atlanta, GA, USA, [7]Office of the Director, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]Emory University, Atlanta, GA, USA

Background: Zika virus (ZIKV) infection during pregnancy can cause serious birth defects, including brain abnormalities. Prenatal maternal serum and urine should be tested for ZIKV when maternal infection is suspected. Amniotic fluid has also been tested for ZIKV; however, data are limited on the relationship between the detection of ZIKV ribonucleic acid (RNA) in amniotic fluid and ZIKV-associated birth defects. We describe the results of ZIKV testing in amniotic fluid in the context of ZIKV testing of other clinical specimens and the frequency of ZIKV-associated birth defects. **Methods:** As part of national surveillance for ZIKV, amniotic fluid and other clinical specimens collected from January 2016 to January 2017 were sent to the Colombia National Institute of Health (INS). Amniotic fluid, serum, urine, cord blood, umbilical cord, placental tissue, and cerebrospinal fluid were tested for the presence of ZIKV RNA using a singleplex real-time reverse transcriptase-polymerase chain reaction assay. ZIKV-associated birth defect information was abstracted from medical records, which included results from prenatal and postnatal imaging and physical exams at birth. A chi-square test was used to compare the frequency of ZIKV-associated birth defects by detection of ZIKV RNA in amniotic fluid. **Results:** Among 128 women with amniotic fluid specimens sent to INS for testing, 47% (n=60) had a ZIKV RNA positive amniotic fluid sample and 54% (n=69) had a pregnancy with evidence of a ZIKV-associated birth defect. No statistically significant difference ($p>0.05$) was observed between the presence or absence of ZIKV RNA in amniotic fluid and the presence or absence of ZIKV-associated birth defects. Among 94 women with amniotic fluid and at least one other specimen tested, 76% (n=71) had at least one ZIKV RNA positive specimen, with 19% (n=18) ZIKV RNA positive in amniotic fluid only, 31% (n=29) ZIKV RNA positive in other specimens only, and 26% (n=24) ZIKV RNA positive in both amniotic fluid and other specimens. **Conclusions:** Testing of amniotic fluid provided additional cases of maternal ZIKV infection; however, the presence of ZIKV-associated birth defects was not predicted by the presence of ZIKV in amniotic fluid. These data suggest that ZIKV-associated birth defects cannot be reliably diagnosed with amniotic fluid sampling.

Board LB-48. Confirmed Urological Sequela in the Settings of Congenital Zika Syndrome

L. Costa Monteiro, J. Fontes, G. Cruz, M. Moreira
IFF/FIOCRUZ, Rio de Janeiro, Brazil

Background: Congenital Zika syndrome (CZS) is an emerging infectious disease that affects the central nervous system. The CNS structures that control the lower urinary tract are among the damaged areas. A urological sequela, neurogenic bladder (NB), was confirmed in the first 22 patients (https://doi.org/10.1371/journal.pone.0193514). Goal: To investigate NB in the settings of CZS and to identify urological risk indicators to mitigate the impact of the disease. **Methods:** Extensive bladder function testing (dx.doi.org/10.17504/protocols.io.k5vcy66) was performed in all 67 CZS patients who were referred to our urology clinic. These patients were drawn from the Institutional CZS cohort. ZIKA virus infection was previously confirmed by maternal history/positive PCR. Microcephaly and other central nervous system abnormalities were established based on neurological assessment and associated imaging of the central nervous system (CT head and/or brain MRI). **Results:** NB was confirmed in 65 patients (97%). In 62 the bladder was overactive, the vesical pressure was higher, and the bladder capacity reduced. These are all high-risk urological indicators that can lead to renal impairment if left untreated. **Conclusions:** Neurogenic bladder, a known treatable health condition, was confirmed and needs to be tested in the settings of congenital Zika syndrome.

Board LB-49. Performance Evaluation of InBios ZIKV Detect 2.0 IgM Capture ELISA for Detection of Zika Virus Exposure

J. Sarwar, N. Parameswaran, K. Venkateswaran
Omni Array Biotechnology, Rockville, MD, USA

Background: InBios ZIKV Detect™ IgM Capture ELISA was the first commercial immunoassay, intended for the presumptive detection of Zika virus IgM antibodies in human sera in specific populations, that received an Emergency Use Authorization (EUA) from the FDA on August 17, 2016. This public health laboratory assay showed excellent positive and negative percent agreements for the detection of IgM antibodies to Zika virus (ZIKV) when tested with a set of positive and negative samples tested by CDC MAC-ELISA/PRNT/PCR tests. A recent modification to this method has been authorized by FDA on May 18, 2018 by allowing a name change to ZIKV Detect 2.0 IgM Capture ELISA. In this study, we evaluated the performance of this recent IgM Capture ELISA using well characterized human serum/plasma samples. **Methods:** ZIKV Detect 2.0 kit was evaluated by performing 126 samples that were Zika virus-positive (tested by PCR or PRNT or MAC-ELISA), dengue virus-positive, West Nile virus-positive, chikungunya virus-positive, and normal human serum or plasma samples. ZIKV Detect IgM Capture ELISA kit (RUO) was also used for comparison for testing 115 of these samples. ZIKV Detect 2.0 ELISA assay performance was assessed by calculation of sensitivity, specificity, and area under the curve (AUC). Inter-rater agreement of both versions of the ELISA tests was assessed by calculating the kappa coefficient. **Results:** ZIKV Detect 2.0 IgM Capture ELISA was found to be a convenient test that can be done in half a day for the detection of Zika virus infection. ZIKV Detect 2.0 data analysis algorithm is easier than the previous version and gave clear differentiation of ZIKA reactive and non-ZIKA reactive antibody in the sample. ZIKV Detect 2.0 ELISA showed a sensitivity of 88.37%, a specificity of 97.50%, and an AUC of 0.929 in this evaluation. ZIKV Detect 2.0 showed better sensitivity and specificity than the ZIKV Detect ELISA. The inter-rater agreement indicates a moderate strength of agreement between the two tests, with kappa coefficient being 0.59 (95% confidence interval: from 0.438 to 0.741). **Conclusions:** InBios ZIKV Detect 2.0 IgM Capture ELISA is a valuable, convenient, and reliable laboratory test for the presumptive detection of ZIKV infection.

Board LB-50. Barriers to Zika Virus-Related Counseling and Use of Public Health Alerts among NYC Healthcare Providers

A. Viswanath[1], C. Quinn[2], E. Poirot[2], S. Patel[1], R. Piltch-Loeb[3], D. Abramson[3]
[1]NYC Department of Health and Mental Hygiene, New York, NY, USA, [2]NYC Department of Health and Mental Hygiene & Centers for Disease Control and Prevention, New York, NY, USA, [3]New York University, New York, NY, USA

Background: During emerging outbreaks, public health agencies must rapidly communicate clinical guidance to healthcare providers. The New York City Department of Health and Mental Hygiene (DOHMH) sent 16 email health alerts during the 2016 Zika outbreak, encouraging providers to screen pregnant women for Zika exposure and to counsel women trying to conceive against travel to areas with Zika transmission. To evaluate the impact of our emergency health alerts, we studied associations between use of information sources and knowledge-related barriers to counseling. **Methods:** We sent surveys to 44,455 unique NYC provider email addresses using multiple health department data sources. We assessed Zika-related clinical behaviors and the use of information sources to stay updated about Zika. We restricted analyses to prenatal care providers. Based on significant chi square associations and Fisher's exact test results, we ran unadjusted bivariate logistic regressions to examine associations between DOHMH information source use and knowledge-related counseling barriers. **Results:** Of 1,447 complete responses, 251 (17.3%) providers delivered prenatal care in 2016; of these, 208 (82.9%) were physicians. Among prenatal care providers, the most commonly cited counseling barriers were competing priorities for clinical counseling (47.8%) and limited time with patients (42.2%). Other reported barriers were lack of knowledge about risk factors, prognosis, and treatment options (16.7%); lack of testing knowledge (14.7%); lack of treatment options (12.7%); and language barriers (6.4%). Reported use of any DOHMH information sources to stay informed about Zika resulted in lower odds of knowledge-related barriers (OR: 0.21, 95% CI 0.08 – 0.55) compared with no use of DOHMH sources. **Conclusions:** Among responding NYC prenatal care providers, use of DOHMH information sources lowered the odds of knowledge-related Zika counseling barriers. Local health departments should seek to increase the reach of their emergency messaging to clinicians. Providers should consult these sources during outbreaks to stay up-to-date on emergent clinical guidance.

Board LB-51. Zika Virus Knowledge, Attitudes, and Practices among Medical Students in North Carolina, United States

M. Stafford[1], S. Prabhu[2], A. Shetty[1]
[1]Wake Forest School of Medicine, Winston-Salem, NC, USA, [2]Manipal University, Udupi, India

Background: Infections with Zika virus (ZIKV) have a clinical spectrum ranging from a flu-like illness in adults to congenital Zika syndrome in newborns. No vaccine is currently available, but candidate vaccines are being tested. This study assessed ZIKV knowledge, attitudes, and practices (KAP) among students at Wake Forest School of Medicine (WFSM) in North Carolina, an area where ZIKV has not yet made widespread impact, and explored factors which influence acceptability of a potential ZIKV vaccine. **Methods:** A semi-structured, anonymous questionnaire was administered to 211 students at WFSM. The questionnaire assessed demographics, KAP, vaccine acceptability, and sources of ZIKV information. Knowledge and attitude scores were calculated and factors associated with acceptability of a vaccine were determined using univariate and multivariate analysis. **Results:** Survey responses yielded a mean knowledge score of 11.77 (SD 3.60) out of 20. A total of 59.9% of students reported moderate knowledge scores (7-13). Female students earned higher average knowledge scores than their male peers. The mean attitude score was 34.73 on a scale of 13-65. A majority of students (85.71%) indicated a positive attitude (13-39) toward ZIKV importance and severity. Most (98.6%) students had not received ZIKV training and 75.9% were unsure if government action toward ZIKV had occurred. The internet was the most common source of ZIKV information and scientific articles were the most common trusted source of public health information. A majority of students agreed they would receive a potential vaccine (73.4%) and recommend one to their patients (76%). Male students and students with low knowledge scores or negative attitude scores were less willing to receive a vaccine. **Conclusions:** A majority of students demonstrated a positive attitude toward ZIKV and willingness to accept and recommend a vaccine. However, this study revealed a need

for improvement of ZIKV knowledge among medical students. Use of the internet and scientific articles should be considered in future efforts to improve education and increase vaccine acceptability.

Board LB-52. Community Support for Novel *Aedes aegypti* Control Methods after the Zika Outbreak in Puerto Rico

C. Pérez-Guerra[1], S. Ramos-Díaz[1], C. Rosado-Santiago[1], K. Marrero-Santos[1], A. Harris[2], L. Sánchez-González[1], A. Romero[1], M. Hayden[3], G. Paz-Bailey[1]
[1]Dengue Branch, Centers for Disease Control and Prevention, San Juan, Puerto Rico, [2]Puerto Rico Vector Control Unit, San Juan, Puerto Rico, [3]Trauma, Health, and Hazards Center, University of Colorado, Colorado Springs, CO, USA

Background: The introduction of Zika virus in 2016 in Puerto Rico resulted in 40,576 cases, 4,047 pregnant women infected, and 47 cases of congenital Zika syndrome. During the Zika outbreak, there were no effective vector control interventions available to slow transmission. The public health response focused on promotion of individual approaches, which traditionally have low success. CDC is currently establishing a community platform in Puerto Rico to evaluate the epidemiologic impact of a novel mosquito control strategy. The purpose of this study was to determine community support for *Aedes aegypti* control methods. **Methods:** We conducted four group discussions from April to May 2018 with leaders and residents selected through a snowball technique in 14 clusters. Discussions were led using a semi-structured guide and a slide set with descriptions and illustrations of the control methods. We conducted a content analysis of written notes and session recordings based on six categories using MAXQDA 12 software. **Results:** Thirty-two people from eight clusters participated. Support for all interventions was moderate to high. Methods familiar to participants received more support. Benefits for the Autocidal Gravid Ovitraps included no use of chemicals; disadvantages were high-cost, and lack of commitment from residents to maintain them. For *Wolbachia* replacement, benefits included lack of adverse effects to the environment and disadvantages included no reduction in mosquito bites, lack of evidence of efficacy, and concerns about the bacteria effects. Advantages for *Wolbachia* suppression and/or genetically modified mosquitoes (GMO) included the reduction in the number of mosquitoes. Disadvantages included mistrust of mosquito laboratory procedures, cost, and lack of sustainability. Participants wanted more information about impact, risks, and experiences in other countries in order to support implementation in their communities. **Conclusions:** Implementation of these methods is feasible if comprehensive education is provided to community members and government funding is allocated to ensure sustainability.

Board LB-53. Persistent Zika Virus Infection of HUVECs Regulates Endothelial Permeability, Matrix Metalloproteases, and Cytokines Activation

T. Uppal[1], S. Khaiboullina[1], S. Jeor[1], A. Rizvanov[2], S. Verma[1]
[1]University of Nevada, School of Medicine, Reno, NV, USA, [2]Kazan Federal University, Kazan, Russian Federation

Background: The brain deformities in newborns infected with Zika virus (ZIKV) present a new potential public health threat to the worldwide community. The detailed mechanism of ZIKV-associated fetal brain damage is still largely unknown; however, it is apparent that the virus crosses the placental barrier to infect the fetal brain. Endothelial cells are the key structural components of tissue barriers, including the placental barrier. Damaged endothelium or disruption of adherens junctions could compromise endothelial barrier integrity causing leakage and inflammation, hence facilitating leukocytes migration. Endothelial cells are often targeted by viruses, including the members of the *Flaviviridae* family such as DENV and WNV; however, little is known about the effects of ZIKV infection of endothelial cell functions. **Methods:** Human umbilical cord endothelial cells (HUVECs) were infected with PRVABC59 (Human/2015, Puerto Rico, South America) and IBH30656 (Human/1968, Nigeria) ZIKV strains (MOI ~0.1). Total RNA, proteins, and supernatants were collected and used for analysis of the transcriptional activation, protein expression, and cytokine and matrix metalloprotease (MMPs) release. **Results:** Our data, for the first time, demonstrate that cytokine profile of ZIKV-infected endothelial cells gets affected and identified a significant change in the levels of 13 and 11 cytokines by PRVABC59 and IBH30656 ZIKV strains, respectively. Importantly, these cytokines activated by ZIKV infection of HUVECs include chemokines attracting mononuclear leukocytes (monocytes and lymphocytes) as well as neutrophils. Furthermore, we, for the first time, show that ZIKV infection of HUVECs increases endothelial permeability. **Conclusions:** We reason that increased endothelial permeability could be due to apoptosis of endothelial cells caused by caspase-8 activation and degradation of extracellular matrix by MMPs in ZIKV-infected cells.

Board LB-54. Stability of Ebola and Rift Valley Fever Viruses in Semen and Blood Matrices during Typical Field Laboratory Storage Conditions

B. Erickson, K. Patel, C. Chiang, W. Davis, S. Nichol, J. Klena
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Current recommendations are that viruses in clinical material should be stored at -170°C to maintain stability. However, access to cold units may not be immediately available such as sampling at field sites or small treatment centers. Variable storage conditions creates challenges for interpreting future infectivity studies. This study aims to determine the effect that field laboratory storage conditions have on virus stability in blood and semen matrices during typical times between collection and transport to cold storage. **Methods:** Pooled plasma or semen specimens were spiked with either Rift Valley fever virus lacking the NSs and NSm genes (ΔΔRVFV) or Ebola virus (EBOV) and aliquoted for storage at 37°C, 4°C, -20°C, or -170°C. Both viruses contained green fluorescent protein (GFP). $TCID_{50}$ and real-time RT-PCR (qRT-PCR) for virus targets and internal controls were completed at day 0, 1 day (ΔΔRVFV only), 3 days (EBOV only), 1 week, 1 month, 2 months, 3 months, 4 months (EBOV only), and 6 months (ΔΔRVFV only). **Results:** For -170°C and -20°C storage temperatures, no significant changes in the $TCID_{50}$ or qRT-PCR cycle threshold (Ct) values for either ΔΔRVFV over three months or EBOV over four months were observed. At six months, ΔΔRVFV in semen at -20°C showed a 2-log decrease in $TCID_{50}$; no other changes were noted. For 4°C storage, the $TCID_{50}$ dropped below the limit of detection (LoD) for ΔΔRVFV semen between 3-6 months and EBOV semen between 1-2 months; a change in Ct values was not observed with either virus. ΔΔRVFV plasma stored at 4°C dropped less than 2 logs by 6 months while EBOV did not change over 4 months and neither virus showed a Ct change. For semen specimens stored at 37°C, the $TCID_{50}$ was below the LoD by day 7 for ΔΔRVFV and day 3 for EBOV. The Ct values declined as well and were >35 by 2 months for ΔΔRVFV and EBOV. At 37°C, the plasma $TCID_{50}$ was below the LoD by 1 month

for both viruses; however, Ct values remain unchanged. **Conclusions:** When it is not possible to quickly store specimens at -170°C, short-term storage at 4°C and even longer at -20°C should be sufficient to preserve ΔΔRVFV and EBOV. Storage for even a short amount of time at 37°C would be expected to have a negative impact on the virus. Small fragments of RNA, detectable by qRT-PCR, were shown to be more tolerant of temperature in both matrices tested.

Board LB-55. Prevalence *Y. enterocolitica* among People for 2012-2017 in Azerbaijan

S. Ibrahimova, R. Ismayilova, S. Shikhaliyeva, R. Abdullayev
Republican Anti-Plague Station, Baku, Azerbaijan

Background: Azerbaijan is a country at the crossroads of Eastern Europe and Western Asia that has a history of environmental *Yersinia* species foci. The Republican Anti-Plague Station (RAPS) in Baku is responsible for surveillance, identification, documentation, and preventive measures against very dangerous infections including yersiniosis and brucellosis. Yersiniosis, caused by *Yersinia enterocolitica* (YE), is characterized by a lesion of the gastrointestinal track and general intoxication that can cause the degeneration of the musculoskeletal system, liver, and other organs. Over the past years in Azerbaijan, two serotypes have been generally considered to be the causative agents of yersiniosis, strain O: 3 (biogroup 4) and O: 9 (biogroup 2) (YE). A strong serological cross-reaction appears between different species of *Brucella* and YE serotype O:9, which seriously complicate the diagnostic works of brucellosis and yersiniosis in humans. This cross-reaction often makes it impossible to perform a differential serological diagnosis between *Brucella* and YE. Brucellosis is a highly contagious zoonosis disease with great significance in medicine. The ability to differentially diagnose YE and *Brucella* spp is critical for defining appropriate therapeutic regimes. **Methods:** Clinical serum samples were investigated by indirect hemagglutination reaction (IHAR) for the detection of antibodies for YE. Data suggest that IHAR was the most promising method and deserved efforts for its further development. The work is conducted in a biological safety cabinet (BSCs class AII), using all required personal protective equipment (PPE). **Results:** During the period 2012-2017, 4,265 samples suspected of yersiniosis were received by RAPS. As part of our diagnostic algorithm, samples were tested for YE by IHAR. Out of these samples, 299 (6.28%) were positive by IHAR for serogroup O:3 and 369 (8.7%) for serogroup O:9. **Conclusions:** We recommend diagnostic methods by using ELISA. By using this method, a differentiation between antibodies against YE 0:9 and brucellosis can be done with high sensitivity and accuracy.

Board LB-56. Evaluating Fluticasone Propionate as a Treatment for Late Stage Pneumonic Plague

S. Huckuntod, S. Banerjee, R. Pechous
University of Arkansas for Medical Sciences, Little Rock, AR, USA

Background: Plague, caused by inhalation of *Yersinia pestis,* is a fatal disease that causes death within six days without antibiotic intervention in humans. *Y. pestis* is able to be transmitted directly from infected individuals via respiratory droplets, which enhances its ability to be spread in epidemics and pandemics. Late-stage pneumonic plague is very difficult to treat, as antibiotics must be delivered within 24 hours after the onset of symptoms to be effective. Previous work showed that inflammation-mediated pulmonary damage contributes to the difficulty of treating late-stage disease. Here, we utilize a murine model of infection to determine the effectiveness of global immune suppression using corticosteroids to enhance survival of late-stage pneumonic plague. **Methods:** Female C57BL/6 mice received 200 µg fluticasone propionate or DMSO (vehicle) daily via the intranasal route beginning 3 days prior to intranasal infection with fully virulent *Y. pestis* CO92. Mice were then infected with lethal doses (10^4 CFU) of *Y. pestis* and were left untreated or treated every 8 hours with streptomycin beginning 24 hours (early detection) or 48 hours (late-stage) post-infection (hpi). Additionally, 10 mice received co-treatment with both fluticasone propionate and streptomycin beginning at 48 hpi. Survival throughout the course of the experiment was recorded over time for one week. **Results:** Administering antibiotic treatment within 24 hpi resulted in 100% survival. However, similar to what is seen during human infection, when streptomycin was delivered at 48 hpi during late-stage disease, survival decreased significantly. Mice pretreated with fluticasone propionate and administered streptomycin beginning at 48 hpi exhibited increased survival compared to mice receiving only streptomycin treatment beginning at 48 hours, indicating that suppression of host inflammatory responses may aid in treating patients with pneumonic plague. **Conclusions:** These results suggest that delivery of corticosteroids may enhance antibiotic efficacy to treat late-stage pneumonic plague. Further, the ability to introduce a scenario where a substantial number of mice survive infection allows for characterization of host pulmonary conditions that define survival and lethality in pneumonic plague.

Board LB-57. An Ex Vivo Human Tissue Platform Reveals the Role of Pla in Initial Interactions of *Yersinia pestis* with the Human Lung Environment

S. Banerjee[1], S. Huckuntod[1], R. Kurten[2], R. Pechous[1]
[1]University of Arkansas for Medical Sciences, Little Rock, AR, USA, [2]Arkansas Children's Hospital Research Institute, Little Rock, AR, USA

Background: *Yersinia pestis* causes primary pneumonic plague, a fast and deadly form of pneumonia. The time from inhalation of the pathogen to death in humans is typically between 4 and 7 days unless antibiotics are administered within 24 hours after the onset of symptoms. A hallmark of the disease is a biphasic progression marked by an early pre-inflammatory phase followed by a pro-inflammatory phase. The virulence of *Y. pestis* is largely attributed to the delivery of *Yersinia* effector proteins into the cytosol of target cells via the Ysc type 3 secretion system and a handful of virulence factors including the plasminogen-activating protease *pla*. During pneumonic plague, *pla* is important for bacterial survival and proliferation in the lung. The role of *pla* in shaping the early events that define the pre-inflammatory disease phase is unknown and is difficult to characterize in the standard infection platforms (cell culture and mouse model of infection). **Methods:** We have developed an *ex vivo* human tissue infection platform for the analysis of early events in the alveolar space during pulmonary infection with *Y. pestis* using human precision-cut lung slices (HPCLSs) from human donor lungs. HPCLSs are viable in culture, maintain ciliary motility for ~3 months, and are responsive to infection and treatment with chemical agents. We have infected HPCLSs and C57BL/6 mice with *Y. pestis* CO92 and CO92 lacking *pla* to study early events dictating the progression of pneumonic plague, and to better define the role of *pla*. **Results:** Our results indicate that HPCLSs infected with a CO92 *pla* strain show decreased levels of Yop injected cells compared to CO92 WT infection, and the absence of *pla* induces increased IL-8 (neutrophil chemo-attractant) production. Infection of mice with CO92 *pla* resulted in increased early innate immune influx compared

to wild-type infection, resulting in decreased bacterial burdens in the lung and indicating an early anti-inflammatory role for *pla*. **Conclusions:** Our findings suggest that the fate of *Y. pestis* infection of the lung is decided extremely early during infection, and presence of *pla* tilts the balance in favor of the pathogen. Further, these studies establish a highly relevant and viable platform that complements existing animal models to evaluate early host/pathogen interactions in human lungs that may be applicable to other important pathogens.

Board LB-58. Investigation of Falciparum Malaria Outbreak in Laghman Province, September 2017-January 2018: Descriptive Epidemiology

M. Sahak[1], F. Arifi[2]
[1]World Health Organization, Kabul, Afghanistan, [2]Ministry of Public Health, Kabul, Afghanistan

Background: Cases of malaria dropped from 205.2 to 11.4 per 1000 between 1990 and 2016, while the SDG goal is 0.005 cases per 1000. **Methods:** The surveillance focal point at Ghazi-Abad Health Center reported increased cases of PF malaria during September-November 2017 based on weekly data analysis. The Rapid Response Team (RRT), mainly composed of Surveillance and Communicable Disease Control Program staff, visited the field to actively find malaria cases, identify risk factors, and to timely control the outbreak. The cases were tested with RDT (95% sensitivity), and the RDT result was verified by microscopy (99% accuracy). **Results:** From September 2017 through January 2018, 1626 clinical malaria cases were actively detected in Alishang district of Laghman province, among which 51% were confirmed positive with RDT (64 *P. falciparum*, 32% *P. vivax*, and 4% mixed). The cases were reported in different months starting from September 2017 (2%), October (28%), November (37%), December (26%) and ending in January 2018 (7%). Most of the cases were reported from Watan-Gatoo (14.3%), Haji-Abad (13%), Shamsa-Khail (11.9%), Jamshed-Abad (11.5%), and Ghazi-Abad (8.7%) villages. Additionally, 36.5% of cases were confirmed among females and 63.5% among males. The average age of detected case-patients was 19 years; the youngest was 2 and the oldest was 60 years old. Common symptoms were headache and fever (both 100%), and 94% had nausea. Due to timely interventions and proper treatment, none of the patients had complications or died. For treatment, 71% received artemisinin combination therapy and 29% chloroquine. A majority (70%) of the confirmed case-patients didn't use a bed net, and 58% slept outdoors. RRT provided health education, distributed bed nets to community members, and treated the diagnosed case-patients. By January, the confirmed cases reached zero. **Conclusions:** During the largest *P. falciparum* outbreak in Afghanistan, improved surveillance and a capable and equipped RRT made a huge contribution to controlling the outbreak.

Board LB-59. *Plasmodium falciparum* Reduction in Transfusable Whole Blood Products Treated with Riboflavin and Ultraviolet Light

E. Gosney[1], S. Keil[1], C. Olver[2], D. Donaghy[2], S. Marschner[1]
[1]Terumo BCT, Lakewood, CO, USA, [2]Colorado State University, Fort Collins, CO, USA

Background: Asymptomatic blood donors still present a risk to transfusion recipients; however, a riboflavin and ultraviolet light (Rb + UV) based pathogen reduction technology (PRT) has been developed to reduce transfusion-transmitted (TT) infections, as well as to prevent transfusion-associated-graft-versus-host disease. Riboflavin binds nucleic acids present in both leukocytes and pathogens and when exposed to UV light irreparably modifies these nucleic acids, thereby rendering them unable to replicate. A clinical trial, African Investigation of Mirasol System for Whole Blood (AIMS), demonstrated that the Rb + UV PRT system could reduce in vivo TT-malaria when whole blood (WB) was collected in citrate-phosphate-dextrose (CPD) anticoagulant (AC). However, outside of the United States citrate-phosphate-dextrose-adenine (CPDA-1) AC is more common. The purpose of this study was to evaluate the effectiveness of the Rb + UV PRT system against *P. falciparum* using WB collected in CPDA-. **Methods:** Five WB units collected in CPDA-1 were inoculated with red blood cells parasitized with *P. falciparum* (3D7 strain). Following inoculation, a pretreatment sample was collected. The WB unit was then treated with the Rb + UV PRT system and a post-treatment sample was collected. The pre- and post-treatment samples were adjusted to a 2% hematocrit and serially diluted. Multiple replicates were cultured at each dilution for up to 21 days. These replicates were scored for the presence of infectious *P. falciparum*. Infectious dose (ID_{50}) titers were calculated using the Spearman-Karber method. **Results:** The average pre-treatment and post-treatment titers were 7.4 ± 0.4 log ID_{50}/mL and $\leq 1.1 \pm 0.1$ ID_{50}/mL log, respectively. The infectious load was reduced to the limit of detection in all five treated units, resulting in an average log reduction of $\geq 6.3 \pm 0.4$. **Conclusions:** The Rb + UV PRT system reduced *P. falciparum* by $\geq 6.3 \pm 0.4$ log in CPDA-1 compared to $\geq 6.4 \pm 0.8$ log in previous in vitro studies using CPD. This reduction in CPD effectively reduced TT-malaria in vivo. It can be expected that Rb + UV treatment will be equally effective in reducing TT-malaria for WB collected in CPDA-1.

Oral Presentation Abstracts

J1. Molecular Epidemiology

3:30-5:00 pm International Ballroom D

Distributed Cloud-Based Bioinformatics for Microbial Characterization and Outbreak Surveillance

J. Sevinsky, L. Fink
Colorado Department of Public Health and Environment, Denver, CO, USA

Background: Whole genome sequencing (WGS) has revolutionized microbial characterization and outbreak detection. Outbreaks can be detected sooner and with greater sensitivity, leading to earlier public health interventions. Unfortunately, the ability to analyze the results of WGS experiments is still beyond the reach of most state public health labs. **Methods:** The Google Cloud Platform (GCP) was used to develop linux-based bioinformatics pipelines for WGS quality control (QC), microbial characterization, and outbreak detection. WGS QC pipelines clean and trim reads, and calculate genome coverage (CG Pipeline). Microbial characterization pipelines detect contamination (Kraken), predict species (Mash) and serotype (SeqSero and Serotypefinder), and identify antimicrobial resistance and virulence factors (Abricate). Outbreak detection pipelines use a combination of reference-free and reference-based (Lyve-SET) algorithms for hqSNP analysis. Pipelines are maintained, versioned, and stored as custom virtual machine (VM) images for distribution. **Results:** VM instances created from custom images hosted by the GCP can efficiently and inexpensively analyze WGS data for microbial characterization and outbreak detection. QC of a 32 isolate MiSeq run can be performed in less than 2 hours for about $0.50. And for less than $5.00 (24 hours of compute time), a full QC, characterization, and outbreak detection analysis can be performed. This bioinformatics platform is in full production use at CDPHE and supports many PHLs throughout the mountain region. **Conclusions:** Powerful bioinformatics pipelines are now available to every state PHL, provided they can access the GCP. The pipelines hosted on these VMs are fully automated using custom scripts, requiring little to no previous experience with the linux operating system. Furthermore, given the stable nature of stored images, results between different PHLs will be consistent in both results and format, allowing effective outbreak surveillance between PHLs.

Norovirus Outbreaks in China during 2014-2017

Lu Ran[1], Shuyu Wu[2], Yiyao Lian[1], Li Luo[1], Qiaohong Liao[1], Miao Jin[3], Zhaojun Duan[3], Jeanette Rainey[2], Zhongjie Li[1]
[1]Division of Infectious Disease, Chinese Center for Disease Control and Prevention, Beijing, China; [2]Division of Global Health Protection, Center for Global Health, US Centers for Disease Control and Prevention, Beijing, China; [3]National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China

Background: China established a National Emergency Public Health Event Information Management System (Event System) in 2004, requiring local public health agencies to report norovirus outbreaks >20 cases within 7 days. CaliciNet China was developed to identify norovirus strains associated with outbreaks. **Methods**: We captured norovirus outbreak data from the Event System and linked these data to laboratory based strain information from CaliciNet for outbreaks occurring from January 1, 2014 to December 31, 2017. We analyzed the combined dataset to describe the number and location of outbreaks as well as the most likely mode of transmission and strain distribution. **Results**: During the project period, 30,842 cases were reported from 616 outbreaks; the majority (n=325, 53%) occurring in 2017. The median outbreak size and duration time was 34 cases (range: 5 to 753) and 5 days (range: 7 hours to 32 days), respectively. No deaths have been identified. Of all reported outbreaks, 542 (88%) occurred in school settings, including 246 (40% of total) in primary schools, and 80 (13%) in other settings including community, hospital, nursing home and cruise ships. The majority of outbreaks (n=388, 63%) were due to human-to-human transmission, followed by multiple modes (n=43, 7%), and contaminated water (n=37, 6%) and food (n=31, 5%); the remaining had unknown modes of transmission (n= 111, 18%). Transmission was most frequently associated with improper handling of infectious human material, causing environmental contamination. The predominant strain during 2014 and 2015 was GII.P17/GII.17 and during late 2015 and 2016 was GII.P17/GII.17. A new recombinant of GII.P16/GII.2 became dominant in September 2016 and continued through August 2017, representing 92% of all outbreak-related noroviruses detected during that period. Since September 2017, GII.P16/GII.2 has decreased to 49% of all specimens tested while GII.P12/GII.3 and GII.Pe/GII.4_Sydney 2012 have increased to 16% each. **Conclusions**: Norovirus outbreaks are common and can cause large sized outbreaks in China, particularly in school settings due to human-to-human transmission. The dominant virus strain shifted over time, and new recombinant viruses associated the increased numbers of outbreaks in 2017. Proper handling of infectious material, environmental disinfection, and hand hygiene could decrease norovirus outbreaks when new noroviruses emerge.

Large-Scale Surveillance of Wild Bird Populations for Emergent Influenza Viruses

S. Bevins, J. Baroch, B. Schmit, T. Gidlewski, T. Deliberto
National Wildlife Research Center, Fort Collins, CO, USA

Background: Avian influenza viruses have a worldwide distribution and wild birds are the primary wild reservoir. High pathogenic avian influenza viruses cause concern because of potential economic consequences associated with outbreaks in domestic poultry and because of the possibility of zoonotic transmission. We describe a surveillance framework designed to monitor avian influenza viruses in wild birds throughout the United States and summarize our findings from the previous three years. **Methods:** Targeted surveillance was implemented throughout the US in 2015 and has continued through 2018. Surveillance focused on ducks in the order Anseriformes in order to maximize influenza virus detection. Oropharyngeal and cloacal swabs were collected and tested within three days using rRT-PCR for influenza A viruses. Any positive samples underwent additional screening to identify, isolate, and sequence H5 and H7 viruses. **Results:** From 2015 through 2018, 110,000 wild bird samples were collected. Influenza A prevalence ranged from 6.3% to 31.0%, depending on time of year. Up to 3.5% tested positive for H5 viruses each month and up to 4.3% tested positive for H7 viruses. Surveillance identified several high pathogenic viruses that were believed to no longer be circulating widely and identified a low pathogenic H7 virus that had >99% sequence identity to a domestic poultry outbreak. **Conclusions:** Wild bird data are an essential component of any influenza research or management effort that uses a One Health approach. The novel surveillance framework and resulting data have informed poultry producers, researchers, and gov-

ernment agencies on avian influenza virus occurrence on the landscape and associated infection risk. These data have provided real-time information on avian influenza virus emergence, have revealed dramatic shifts in virus prevalence in a relatively short time frame, have shed light on spatial spread over time, and have served as an early warning system for novel high pathogenic viruses.

Linked Whole Genome Sequencing and Epidemiological Analysis Reveals Nationally Distributed Clusters of *M. abscessus* that Cross Disease Boundaries and Are Unlikely to Be Spread Through Person-to-Person Transmission

S. Lipworth[1], N. Haugh[1], M. Minaji[2], B. Muller-Pebody[2], N. Phin[2], E. Smith[3], E. Robinson[3], T. Walker[1], T. Peto[1], D. Crook[1]
[1]Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom, [2]Public Health England, London, United Kingdom, [3]Regional Mycobacterial Reference Laboratory, Public Health England, Birmingham, United Kingdom

Background: *Mycobacterium abscessus* is an emerging pathogen in chronic respiratory diseases such as cystic fibrosis (CF) that is associated with accelerated lung function decline and resistance to multiple antibiotics. Recent concern regarding the potential for person-to-person transmission in CF units has been fueled by a large genomic study which demonstrated globally distributed clusters of *M. abscessus* clones. Two small single CF center studies linking genomic and epidemiological data have come to opposing conclusions regarding whether person-to-person transmission occurs. **Methods:** Sequencing was performed as part of the routine Public Health England clinical diagnostic service on 573 isolates of *M. abscessus* from 314 patients under the care of 44 centers across England between 2014-2017. Phylogenetic trees were constructed using IQ-TREE and adjusted for recombination with ClonalframeML. 95% of within patient diversity fell within 20.5 SNPs; we therefore adopted the previously reported cut-off of 19 SNPs to infer genetic relatedness which may be compatible with recent transmission. Patient demographics, GP practice, dates of hospital admissions and outpatient appointments were used to inform epidemiological analysis utilizing data from the Hospital Episode Statistics database which was linked to genomic data using NHS numbers. **Results:** There were 37 genomic clusters (median size 2, range 2-22); 186 patients had non-clustered isolates. Genomic clusters spanned geographical centers and disease strata, containing closely related isolates from patients at different centers with CF, COPD, non-CF bronchiectasis and 'other' diagnoses. Contrary to recent reports, CF patients were significantly more likely to have an unclustered vs clustered isolate (p=0.007). There was no significant difference between the proportions of epidemiological links between patients with a clustered vs unclustered isolate. There was no relationship between the Haversine distance between the patient's postcodes and the genetic distance of their isolates (p=0.9). **Conclusions:** We have shown that genomic clusters of *M. abscessus* are not specific to CF patients. This study suggests that person-to-person transmission is unlikely and that alternative reservoirs and transmission modalities for infection require investigation.

Antibiotic Resistance among Group B Streptococcal Isolates From Invasive Early- and Late-Onset Disease in the United States, 2006-2015

S. Nanduri[1], C. Smelser[2], N. Alden[3], L. Harrison[4], P. Vagnone[5], R. Lynfield[5], N. Spina[6], L. Dufort[6], A. Thomas[7], M. Farley[8], J. Jain[1], T. Pondo[1], L. McGee[1], B. Beall[1], S. Schrag[1]
[1]Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]New Mexico Depatment of Public Health, Santa Fe, NM, USA, [3]Colorado Department of Public Health and Environment, Denver, CO, USA, [4]University of Pittsburgh, Pittsburgh, PA, USA, [5]Minnesota Department of Health, St. Paul, MN, USA, [6]New York State Department of Health, Albany, NY, USA, [7]Oregon Department of Human Services, Portland, OR, USA, [8]Emory University School of Medicine and Atlanta VA Medical Center, Atlanta, GA, USA

Background: Early-onset disease (EOD; infants aged 0-6 days) and late-onset disease (LOD; age 7-89 days) due to group B *Streptococcus* (GBS) are leading causes of infant morbidity. Antibiotics are used to prevent and treat GBS disease. While GBS non-susceptibility to beta-lactams is rare, resistance to macrolides has increased. In the United States, population-based surveillance for invasive GBS disease is carried out through Active Bacterial Core surveillance (ABCs). We describe antibiotic resistance among isolates from EOD and LOD cases recovered during 2006-2015. **Methods:** We identified GBS isolates from blood or CSF of infants residing in 7 ABCs sites. Antimicrobial susceptibility testing was done using broth microdilution and interpreted using Clinical & Laboratory Standards Institute guidelines. The Cochrane-Armitage test was used to evaluate resistance trends. Whole-genome sequencing was performed on year 2015 isolates to characterize resistance determinants. **Results:** Susceptibility data was available from 1727 (91%) of 1898 cases identified. All were susceptible to penicillin, ampicillin, cefazolin and vancomycin. Forty-five percent (774/1727) of isolates were resistant to erythromycin and 21% (359/1727) showed constitutive resistance to clindamycin. Proportion of isolates resistant to erythromycin increased significantly (2006: 35%; 2015: 49%, $P<0.05$). The proportion showing constitutive resistance to clindamycin did not increase significantly (2006: 15%; 2015: 26%, $P=0.32$). The proportion of isolates with macrolide resistance was highest for serotype II (erythromycin-resistance=66%; constitutive clindamycin-resistance=54%) and serotype V (erythromycin-resistance=61%; constitutive clindamycin-resistance=48%). The most common resistance determinants in 86 isolates resistant to erythromycin from 2015 were *ermB* (33%), *mef* (30%), *ermTR* (27%), and *ermT* (10%). Sixty-three (73%) erythromycin-resistant isolates were also clindamycin-resistant; constitutive resistance was primarily associated with *ermB* and inducible resistance with *ermT* or *ermTR*. **Conclusions:** GBS isolates from EOD and LOD remain susceptible to beta-lactams. Clindamycin resistance is common and highlights the importance of susceptibility testing before use of clindamycin for intrapartum antibiotic prophylaxis.

Can Social Media Advance Science? A Case Study from the 2016 *Elizabethkingia anophelis* Outbreak

A. Guinn[1], K. Holt[2]
[1]US Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]University of Melbourne, Melbourne, Australia

Background: Social media provides a platform for sharing information, entertainment, and news. Some estimates predict that 2.9 billion

people collectively will be on social media platforms by 2020. With popular memes and themes circulating through various channels, one might wonder whether these tools can garner attention for more than photographs of kittens and kids. Public health agencies have discovered the utility and power of social media for promoting behavior change and communicating during emergencies. However, can social media be useful for communicating with scientific audiences on complex topics? **Methods:** The Office of Advanced Molecular Detection (OAMD) in the National Center for Emerging and Zoonotic Infectious Diseases (NCEZID) of the US Centers for Disease Control and Prevention (CDC) opened a Twitter account and sent its first tweet on May 5, 2015. The purpose of @CDC_AMD is to provide updates on the AMD program, share scientific insights from AMD activities, and provide information on training and fellowship opportunities. OAMD also promotes open sharing of scientific data, when available, including links to sequence data made available through open source databases. **Results:** During an outbreak of an unusual bacterium, *Elizabethkingia,* in the United States, Wisconsin state public health officials reached out to CDC scientists for assistance in identifying and characterizing the pathogen. After sequencing *Elizabethkingia anophelis* bacterial isolates using available next generation methods, NCEZID scientists uploaded the raw genomic data to a public database and asked OAMD to broadcast its availability through Twitter. On March 18, 2016, OAMD posted a tweet that simply stated the availability of *Elizabethkingia anophelis* genome data with a link to NCBI. Within 48 hours, scientists from around the globe were accessing and analyzing the data and discussing their findings in real time through Twitter and online blogs. **Conclusions:** In the case presented, we will demonstrate how key social media players spurred an international collaboration following a single tweet. Through examination of this example, this presentation will explore possibilities for social media to act as a platform for open data sharing and advancing science.

J2. Preparedness and Response

3:30-5:00 pm International Ballroom E

Early Warning Alert and Response Network in Emergencies: An Evaluation Protocol to Guide Better Emergency Response to Outbreaks

A. Lubna[1], M. Obtel[2], P. Mala[1], F. Husain[3], K. Cordes[4], S. Malik[1]
[1]World Health Organization Eastern Mediterranean Regional Office, Cairo, Egypt, [2]Faculty of Medicine and Pharmacy, University of Mohammed V, Rabat, Morocco, [3]United States Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]University of Nevada, Nevada, NV, USA

Background: Humanitarian emergencies disrupt functioning health systems enhancing the risk of health threats and its spread to vulnerable populations. The World Health Organization (WHO) established early warning alert and response network (EWARN) in 1999 which uses syndromic surveillance and relies on simple case definitions of epidemic-prone diseases of a country to early detect outbreaks and mount rapid response. The other aim of EWARN is to monitor the weekly trend of other diseases of public health importance. EWARN In 2012, WHO published standard guidelines for EWARN implementation without any standardized guidelines for evaluation of the system. This necessitated the need for a uniform and consistent method for evaluation of EWARN system that would allow standardized and comparable evaluations across countries. **Methods:** The US Centers for Disease Control and Prevention (CDC) and the WHO Regional Office for the Eastern Mediterranean (EMRO) collaborated to develop a guidance that would allow a standardized method and process for EWARN Evaluation. The contents of the protocol was guided by the review of public health surveillance system evaluation guidelines and by methods, approach and tools used in previous EWARN evaluations conducted by WHO and CDC in Sudan, South Sudan, Pakistan over the past 8 years. The draft protocol was pilot tested in Iraq and Sudan in February 2016 before finalized through a consultative workshop held in Cairo in 2016 taking into consideration the findings and result from the pilot evaluation. **Results:** The evaluation protocol has sections on pre-evaluation, system evaluation, and conclusions and recommendations in addition to a section on remote evaluation which will allow organizations to use remote methods when security situations may compromise accessibility **Conclusions:** Standardized evaluation of EAWRN systems using the newly developed guidance will improve better understanding of the surveillance quality and performance of the system in detecting and responding to outbreaks.

Establishing and Sustaining National Multisectoral One Health Coordination Mechanisms to Prevent, Prepare for, Detect, and Respond to Public Health Threats

S. Duale[1], S. Scribner[1], A. Kitua[2], D. Mutonga[3], S. Benigno[4], L. Gbaguidi[5], S. Agbo[5], M. Rasmuson[1], R. Salerno[1], K. Zimmerman[1], K. Taratus[1], H. Petrozzola[6]
[1]USAID P&R Project / DAI Global Health, Bethesda, MD, USA, [2]USAID P&R Project / DAI Global Health, Kampala, Uganda, [3]USAID P&R Project / Palladium, Kampala, Uganda, [4]USAID P&R Project / DAI Global Health, Bangkok, Thailand, [5]USAID P&R

Project / DAI Global Health, Abidjan, Côte d'Ivoire, [6]USAID P&R Project / TRG, Bethesda, MD, USA

Background: The One Health approach calls for interdisciplinary engagement and collaboration across the human, animal (including wildlife), and environmental health sectors. It is emerging as a promising strategy to better prevent, detect, and respond to emerging pandemic threats. An effective One Health (multisectoral) coordination mechanism is among the core capacities to meet the requirements of the 2005 International Health Regulations (IHR). **Methods:** The Preparedness and Response (P&R) project, funded by the United States Agency for International Development (USAID), has been playing a catalytic role over the past three years in the establishment or strengthening of multisectoral coordination mechanisms called National One Health Platforms (NOHPs) in 16 countries in Africa and Asia. NOHPs are typically comprised of representatives from the Ministry of Health, Ministry of Agriculture, and Ministry of Environment, and frequently also include actors from other government offices as well as some donors and NGOs. **Results:** NOHPs in Cameroon, Cote d'Ivoire, Mali, Rwanda, Sierra Leone, Tanzania and Uganda have conducted successful multisectoral prioritization of zoonotic diseases to guide their implementation of the GHSA zoonotic disease action package. NOHPs have contributed to effective multisectoral responses to disease threats including outbreaks of Anthrax (Tanzania), Congo-Crimea Hemorrhagic Fever and Marburg virus disease (Uganda), and Avian Influenza (Bangladesh and Cameroon). NOHPs are also contributing to address the threat of anti-microbial resistance in countries such as Bangladesh and Kenya. **Conclusions:** This presentation will elaborate on the achievements of NOHPs in selected African and Asian countries and discuss lessons learned, challenges, and recommendations for using multisectoral coordination mechanisms for strategic, effective, and sustainable actions to improve global health security. The P&R Project experience shows the uniqueness of each country situation and identifies facilitating factors and challenges to sustaining multisectoral coordination to prevent, detect and respond to emerging and re-emerging diseases of pandemic threat.

"Connecting Organizations for Regional Disease Surveillance" (CORDS): Building a Safer World for Communities in Underserved Regions

E. Orefuwa[1], S. Bino[2], M. Rweyemamu[3], J. Lutwama[4], A. Soebandrio[5], M. Abdallat[6], S. Ly[7], M. Libel[8], C. Longuet[1]
[1]Connecting Organisations for Regional Disease Surveillance, Lyon, France, [2]Southeast European Center for Surveillance and Control of Infectious Diseases, Tirana, Albania, [3]Southern African Centre for Infectious Disease Surveillance, Morogoro, United Republic of Tanzania, [4]East Africa Integrated Disease Surveillance Network, Entebbe, Uganda, [5]Asia Partnership on Emerging Infectious Diseases Research, Jakarta, Indonesia, [6]Middle East Consortium on Infectious Disease Surveillance, Amman, Jordan, [7]Mekong Basin Disease Surveillance Consortium, Phnom Penh, Cambodia, [8]Ending Pandemics, San Francisco, CA, USA

Background: Infectious diseases leading to epidemics often emerge among communities in underserved regions. They may travel swiftly across borders, with no boundaries between animals and humans. Efforts to stop their spread must do the same. This principle is behind CORDS (www.cordsnetwork.org), an NGO comprised of six networks covering 28 countries: the Asia Partnership on Emerging Infectious Diseases Research (APEIR), the East African Integrated Disease Surveillance Network (EAIDSNet), the Middle East Consortium on Infectious Disease Surveillance (MECIDS), the Mekong Basin Disease Surveillance network (MBDS), the Southern African Centre for Infectious Disease Surveillance (SACIDS) and the Southeast European Center for Surveillance and Control of Infectious Diseases (SECID). The objectives of CORDS are Improving Capacity, Advancing One Health, Promoting Innovation, and Building Sustainable Networks. **Methods:** In pursuit of these objectives, CORDS member networks promote or undertake community-level disease surveillance, especially in cross-border areas. They have also carried out international tabletop exercises to inform policy development; convened experts from four continents to share best practices during Ebola and Zika outbreaks; developed a virtual One Health group to improve surveillance and response, conducted a vector-borne disease gap analysis in three regions and other activities related to timeliness of disease detection and response. CORDS promotes information exchange and collaboration between disease surveillance networks across geopolitical and sectoral boundaries. **Results:** CORDS has strengthened regional network capacity and catalyzed innovation for One Health community participatory surveillance, linking disease hotspots with other regional networks, utilizing a nimble approach based on trust and friendship across borders, regions and continents. It has also contributed to shaping a nascent infectious disease surveillance network in West Africa. CORDS has concluded that small data from the field is important for global health security. **Conclusions:** CORDS offers a global platform to test and scale up surveillance innovations in human and animal health to better prevent, detect and respond to emerging infectious diseases and empower local communities.

OIE Laboratory Twinning Projects: A Global Tool to Strengthen Laboratory Capacity for Control of Terrestrial and Aquatic Animal Diseases

G. Pavade, K. Hamilton, T. Brand
World Organisation for Animal Health (OIE), Paris, France

Background: Laboratory twinning is a popular and comprehensive laboratory capacity building program applied by the World Organisation for Animal Health (OIE) since 2008 to expand global geographical coverage of expertise and capacity for animal diseases and zoonoses in priority countries. **Methods:** Each twinning project links an existing OIE reference laboratory or collaborating center with a selected national laboratory that aims to improve capacity for a specific disease. A twinning proposal is filled on a template and jointly submitted by the partner laboratories to OIE. The proposal passes through an evaluation process and then depending upon availability of funds the projects are approved to start. Knowledge and skills are exchanged through this project by training, technical support, and guidance over a determined period. **Results:** Currently 43 projects have been completed and 34 projects are ongoing covering various animal diseases. Some of the diseases for which laboratory capacity improved were avian influenza, Newcastle disease, infectious bursal disease (avian), FMD, contagious bovine pleuro pneumonia, brucellosis (bovine), PPR (sheep and goat), African and classical swine fever (swine), rabies (canine), equine influenza, African horse sickness, glanders (equine), infectious salmon anemia, and shrimp diseases (aquatic diseases). Through these twinning projects, several national laboratories in Asia, Africa, Europe, the Middle East, and the Americas developed technical capacity and expertise in a whole range of skills including epidemiology, food safety, serology, virology, molecular diagnostics, and compliance with OIE standards. In addition to technical expertise in the disease or topic itself, each project addressed quality assurance, biosafety and

biosecurity, animal welfare, responsible science, and ethics. **Conclusions:** The national laboratories continued their developments in collaboration with the OIE reference laboratory or collaborating centre in the post-twinning phase and eight laboratories have successfully applied to become an OIE reference centre so far and three laboratories are waiting for recognition. The twinning collaboration resulted in long-lasting links and mutual benefits for partner institutes, strengthened global disease surveillance and scientific networks, and advanced collaborative research for better science and scientific publications.

Building a Foundation in Surveillance and Laboratory Capacity to Rapidly Detect Public Health Threats—Uganda, 2016-2017

K. Kugeler[1], M. Lamorde[2], A. Mpimbaza[3], J. Borchert[1], R. Walwema[2], J. Kapisi[3], G. Appiah[4], F. Kizito[2], A. Sserwanga[3], A. Kusemererwa[3], H. Kajumbula[5], R. Ransom[4], V. Brown[6], J. Namuganga[3], H. Tasimwa[5], E. Mintz[4], J. Homsy[6], G. Odongo[4], M. Workneh[7], Y. Manabe[7], A. Tagoola[8], J. Nanteza[9], G. Aniku[10], M. Kamya[3], R. Stoddard[4], R. Galloway[4], J. Kayiwa[11], E. Mossel[1], R. Rosenbery[1], P. Mead[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Infectious Diseases Institute, Kampala, Uganda, [3]Infectious Diseases Research Collaboration, Kampala, Uganda, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Makerere University, Kampala, Uganda, [6]Centers for Disease Control and Prevention, Kampala, Uganda, [7]Johns Hopkins University, Baltimore, MD, USA, [8]Uganda Ministry of Health, Jinja, Uganda, [9]Uganda Ministry of Health, Mubende, Uganda, [10]Uganda Ministry of Health, Arua, Uganda, [11]Uganda Virus Research Institute, Entebbe, Uganda

Background: Surveillance for infectious diseases requires both timely reporting networks and laboratory capacity. In Uganda and many other countries, resources are inadequate to support this essential public health function, thereby limiting early detection of outbreaks and monitoring of important disease trends. **Methods:** Through Global Health Security Agenda partnerships, we modified an existing malaria surveillance system to allow identification and tracking of other causes of febrile illness among children admitted at six government hospitals. Capacity for blood culture was established at each hospital, along with options for serologic testing for select vector-borne and zoonotic conditions. Detailed demographic, clinical and laboratory data for all admissions are captured through a web-based system built on the DHIS-2 platform and hosted at Uganda's Public Health Emergency Operations Center. **Results:** Between July 2016-December 2017, patient data were collected from 30,605 admissions; the majority were associated with documented fever (26,642 [87%]) and tested for malaria (26,616 [87%]). Overall prevalence of malaria was 53% (range: 4%-79% across hospitals). Antimalarial and antibiotic use before admission was common (20% and 15%, respectively). Overall mortality was 3.5% (range: 1%-9%). Of >4,800 blood cultures performed, 3% yielded pathogens, including several WHO antimicrobial resistance priority pathogens, some with multidrug resistant phenotypes (e.g., *Acinetobacter* spp., *Pseudomonas* spp., ESBL-producing *Enterobacteriaceae*, *Staphylococcus aureus*, and typhoidal and non-typhoidal *Salmonella* spp.). Baseline low-level circulation of leptospirosis and flaviviruses was documented. In 2017, a single case of *Neisseria meningiditis* infection was rapidly detected, allowing for timely response to avert a potential outbreak. **Conclusions:** This project leverages prior surveillance investments to better track causes of illness, generate antimicrobial susceptibility results, improve clinical care, inform policy planning, and allow for monitoring of public health interventions. The synergistic surveillance and laboratory improvements build a foundation to enhance capacity to detect, report, and rapidly respond to public health concerns in Uganda.

Assessing Capacities for Pandemic Influenza Preparedness and Response through IHR Joint External Evaluation in Low and Middle-Income Countries

W. Zhou[1], N. Kandel[2], J. Lamichhane[1], R. Sreedharan[2], W. Zhang[1]
[1]Global Influenza Programme of Infectious Hazard Management Department, World Health Organization, Geneva, Switzerland, [2]Core Capacity Assessment, Monitoring and Evaluation of Country Health Emergency Preparedness & IHR (2005) Department, World Health Organization, Geneva, Switzerland

Background: WHO recently published a pandemic preparedness checklist for supporting countries to develop or update pandemic preparedness plans for sustainable and resilient pandemic response. It mapped pandemic response capacities with the indicators of IHR (2005) core capacities and Joint External Evaluation (JEE) to draw direct link of the essential capacities needed to manage the risk and impact of pandemic influenza with the core capacities required to manage broader health security threats. **Methods:** This analysis uses 29 JEE indicators of 14 technical areas mapped with the pandemic preparedness capacities outlined in the checklist to assess 5 key areas of the checklist in 41 low and middle-income countries (LMICs) that have published their JEE reports. The 5 key areas are preparing for an emergency; surveillance, investigation and assessment; health services and clinical management; preventing illness in community; and evaluation, testing, and revising plans. The scores of indicators are converted to percentages. The averages are presented using the means of the corresponding indicators or technical areas from the 41 LMICs. **Results:** The averages for the five key areas are 46%, 53%, 42%, 47%, and 37%, respectively. In preparing for an emergency, the highest is risk communication (53%) and lowest is Points of Entry (38%). In surveillance, investigation, and assessment, the highest is seasonal influenza surveillance (61%) and lowest is laboratory (47%). In health services and clinical management, the highest is treatment and patient management (48%) and lowest is personnel (34%). In preventing illness in the community, non-pharmaceutical interventions is highest (49%), while antiviral preparedness is lowest (29%). **Conclusions:** More efforts are needed in supporting LMICs to build essential capacities for pandemic response. The WHO pandemic preparedness checklist is an effective tool for assessing capacities and identifying priorities for pandemic preparedness in the context of strengthening IHR core capacity and health security.

J3. Viral Zoonoses

3:30-5:00 pm International Ballroom A/B/C

Marburg Virus Disease Outbreak: Kween District: Uganda, September–November, 2017

B. Zhu[1], L. Nyakarahuka[2], I. Komakech[3], A. Muruta[4], A. Nakinsige[4], A. Ario[5], L. Bulage[6], B. Kwesiga[5], D. Opio[5], L. Nakiire[5], P. Eyu[5], I. Nkonwa[5]
[1]CDC, Kampala, Uganda, [2]Uganda Virus Reseach Institute, Kampala, Uganda, [3]WHO, Kamapala, Uganda, [4]Ministry of Health Uganda, Kampala, Uganda, [5]FETP - Uganda, Kampala, Uganda, [6]AFENET, Kampala, Uganda

Background: Marburg virus (MARV) infection leads to severe hemorrhagic disease in humans and non-human primates. Exposure to Egyptian fruit bats through visiting bat-infested caves or consuming contaminated bushmeat can cause human infections. On 17th October 2017, a deceased individual in Kween District, Uganda tested positive for MARV. On 18th October, the national rapid response team (NRRT) responded to this outbreak and institute control measures. **Methods:** A suspected case in a person was defined as sudden onset of fever ≥37.5°C with ≥3 of: anorexia, headache, vomiting, abdominal pain, diarrhea, intense fatigue, myalgia or joint pain, history of contact with a patient with similar symptoms; OR sudden-onset unexplained bleeding; OR unexplained sudden death. Confirmed cases were suspected cases with positive MARV RT-PCR and ELISA tests. Probable cases were suspected cases epidemiologically-linked to confirmed cases. Suspected or probable cases were ruled out as cases if they tested negative for MARV. Active case search and medical-record reviews were conducted for case finding. Contacts of case-patients were identified and followed up for 21 days. **Results:** Two confirmed and one probable cases were identified. The primary case-patient, a 30-year-old male hunter who reportedly visited bat-infested caves and ate bushmeat, fell ill on 16th and died on 24th September. The second case-patient (confirmed), his 50-year-old sister, cared for him in the hospital; she developed symptoms on 4th and died on 13th October. The 42-year-old third case-patient (confirmed), a brother to the other two, cared for the second case-patient, developed symptoms on 18th and died on 26th October. The NRRT identified and followed up 339 other contacts of the three case-patients; none have tested MARV-positive as of 22nd November. **Conclusions:** Close, direct contact led to MARV transmission among family members during this outbreak. Enhanced surveillance and contact-tracing are the key for early identification and effective control of future Marburg virus disease outbreaks.

Trends and Epidemiology of Crimean-Congo Hemorrhagic Fever (CCHF) in Afghanistan (2011-2017)

M. Rasooly
Ministry of Public Health, Kabul, Afghanistan

Background: Crimean-Congo hemorrhagic fever (CCHF) is caused by infection with a tick-borne virus *Nairovirus*. Animal herders, livestock workers, and slaughterhouse workers in endemic areas are at high risk of CCHF. Healthcare workers in endemic areas are at risk of infection through unprotected contact with infectious blood and body fluids. There is scarcity of information about CCHF in Afghanistan. The aim of this study is to describe the trend and epidemiology of CCHF in Afghanistan between 2011-2017. **Methods:** This was a retrospective study of the data collected by a disease surveillance system in Afghanistan. We reviewed and analyzed the data from the current disease surveillance system used by the Ministry of Public Health Afghanistan called National Disease Surveillance and Response. A descriptive analysis of the CCHF data performed by place, person, and time of occurrence of the disease covered 2011-2017. **Results:** The median age of the CCHF case-patients was 30 years. The number of CCHF cases have dramatically increased from 10 in 2011 to 259 cases in 2017. The case-fatality rate of disease was reported at 19.6 % in 2017. The majority of the CCHF outbreaks occurred during the summers. The outbreaks were reported from 27 out of 34 provinces of the country, predominantly in Herat and Kabul provinces. About 65% of the cases were reported among men. The cases mostly occurred among housewife own animals (23%), followed by shepherds (19.8%) and butchers (13.2%). **Conclusions:** CCHF outbreaks have increased tremendously in Afghanistan since 2011. Better coordination with the animal sector, enhanced effective surveillance focus on the high risk and endemic areas, and the general public and health care providers need to become aware on the prevention and control of CCHF. Further research is needed to determine the burden of the disease among animals.

The Rabies Puzzle in India: A One Health Approach to Understanding a Multi-faceted Problem

A. Vanak[1], D. Rao[2], A. Kulkarni[2], I. Banerjee[3], N. Panchamiya[3], A. Belsare[4], A. Kumar[2]
[1]ATREE Wellcome Trust/DBT India Alliance, Bangalore, India, [2]ATREE, Bangalore, India, [3]ResQ CT, Pune, India, [4]University of Idaho, Moscow, ID, USA

Background: Rabies is a wholly preventable zoonotic disease that kills ~20,000 people/annum in India. The failure to control rabies in India is a multi-faceted problem: a lack of systematic surveillance, limited knowledge on rabies dynamics in multi-host systems and poor implementation of mitigation measures. **Methods:** We used a triangulation approach involving field research, laboratory analyses, and model simulations to understand rabies transmission dynamics. We particularly focus on multiple hosts where they naturally occur, along the urban-rural landscape. In Phase 1 of the project, we sampled 990 dogs, 20 Indian foxes, 7 jackals, and 8 jungle cats to quantify the prevalence of rabies antibodies in unvaccinated populations. To test efficacy of field vaccinations, we initiated longitudinal trials of 254 dogs in rural and urban areas, and tested all suspected rabid animals for antigens. Finally, we fitted Indian foxes, golden jackals, and free-ranging dogs with GPS tracking devices to determine the potential for contact and transmission. **Results:** Despite no history of vaccination, 51% of rural dogs and 22% of wild carnivores showed detectable neutralising antibody titres to rabies, suggesting non-lethal natural exposure to RABV. In urban areas, most dogs had no detectable rabies antibodies. Among vaccinated dogs, 84% had protective antibody titres at six months post-vaccination. In four months of field testing (N = 118 tested), 55% of suspected rabid dogs in Pune city tested positive for rabies. The tracking of wild and domestic carnivores indicate that dogs overlap heavily with wild canids, thus allowing for the strong potential of spillover/spillback of rabies. **Conclusions:** Current methods of rabies control in India have been poorly implemented and therefore, insufficient to achieve herd immunity in the large free-ranging dog population. Using a One Health approach for better understanding rabies dynamics in India will allow for the development of targeted intervention techniques for the control of rabies.

The Cost of Rabies Post-Exposure Prophylaxis in Minnesota, 2017-2018

S. Johnson[1], C. Klumb[2], S. Holzbauer[3], J. Scheftel[2]
[1]CSTE/Minnesota Department of Health, Saint Paul, MN, USA, [2]Minnesota Department of Health, Saint Paul, MN, USA, [3]CDC/Minnesota Department of Health, Saint Paul, MN, USA

Background: Rabies is a viral neurologic disease transmitted through the bite of a rabid animal. Rabies post-exposure prophylaxis (PEP) consists of a single weight-based dose of human rabies immune globin (HRIG) and a series of four rabies vaccinations administered over 2 weeks. The Minnesota Department of Health (MDH), Minnesota Board of Animal Health, and University of Minnesota conduct rabies surveillance where MDH provides rabies risk analysis through 24/7 telephone consultation. This service receives 2,500 calls annually and provides advice on rabies PEP and animal testing. The cost of submitting an animal for rabies testing is $30; however, the rabies PEP cost and financial burden to patients is unknown. We sought to determine the cost of PEP in Minnesota (MN). **Methods:** A convenience sample of MN urgent care clinics (UCs), clinics, and hospitals with emergency departments (EDs) was contacted about cost of rabies PEP for a hypothetical 165 lb person with a non-bite bat exposure. Facilities were identified through a MDH-maintained list of health care facilities and divided by their location either in or outside the Minneapolis/St. Paul metropolitan area. Contact with each facility was attempted at least 3 times, and health care personnel were asked to share billing fees for rabies vaccine, HRIG, vaccine and HRIG administration, and ED and office-level visits and indicate if any financial discounts were provided. **Results:** A total of 51 EDs, 48 UCs, and 207 clinics provided billing information. The median total cost of all four visits for PEP was $7,195 (range, $3,764-21,754) and the median cost for HRIG alone was $4,210 (range, $934-15,279). The median cost of PEP obtained during an ED visit was $11,083 (range, $5,060-21,754), vs. $6,701 (range, $5,030-17,619) for an UC visit, and $7,195 (range, $3,764-16,285) for a clinic visit. Among metro and non-metro facilities, UCs had the largest total median price difference from $6,701 for metro UCs to $13,121 for non-metro UCs. **Conclusions:** When the animal is available, confinement and observation, or testing, is preferable for most potential rabies exposures. When rabies PEP is necessary, there can be great variability in the cost to patients, primarily driven by the cost of HRIG. Creative approaches involving input from patients, healthcare facilities, and insurance companies are needed to achieve consistent pricing.

Fifteen Years of Enhanced Rabies Related Lyssavirus Surveillance in South Africa

W. Markotter[1], J. Coertse[1], L. Nel[2]
[1]Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences, University of Pretoria, Pretoria, South Africa, [2]Centre for Viral Zoonoses, Department of Microbiology and Plant Pathology, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa

Background: The genus *Lyssavirus* consists of 14 officially recognised viral species, several of which are associated with bats and all capable of causing rabies. Several of these viruses have been detected on the African continent, with Lagos bat (LBV), Duvenhage (DUVV), and Mokola (MOKV) virus sporadically detected in South Africa; little is known about the epidemiology and reservoir species involved. **Methods:** In 2003 we initiated surveillance and tested bat brain (n=1190) and serum samples (n=1000) for the presence of lyssavirus RNA and antibodies using a pan lyssavirus qRT-PCR and rapid fluorescent focus inhibition test (RFFIT). Basic host ecology data was also collected. We retrospectively investigated spill-over animal cases previously reported to be rabies virus infections and characterized the etiological agent involved using conventional RT-PCR and DNA sequencing. **Results:** Eighteen new cases of rabies related lyssavirus infections have been identified in the past fifteen years; 12 LBV infections (9 in *Epomophorus wahlbergi* bats, 1 domestic cat, 1 dog, 1 water mongoose); 1 DUVV infection in a *Nycteris thebaica* bat and 5 MOKV infections (4 in cats and 1 in a dog). Human exposures were reported in several of these cases and post exposure prophylaxis was initiated. Serological analyses in bat populations indicated high LBV seropositivity (40-60%) in frugivorous bats (*Epomophorus wahlbergi* and *Rousettus aegyptiacus)* linked to the age and reproductive season of bats, 17.6% against DUVV in the insectivorous bat, *Nycteris thebaica,* and very low (2%) DUVV seropositivity in *Miniopterus natalensis*. **Conclusions:** LBV and DUVV are present in South African bat populations; however, only 0.8% of bat brain samples were positive, representing a total of 44 investigated bat species. Two frugivorous bat species are implicated as hosts for LBV and a single insectivorous bat species for DUVV. In addition to identifying high risk reservoir species, we could also identify high risk periods for infection linked to host ecology. Spill over infections are not always fully characterized and often assumed to be rabies virus infections. We identified rabies related lyssavirus infections retrospectively in vaccinated cats and dogs suggesting that rabies virus-based commercial vaccines do not provide protection against the more diverse lyssaviruses.

Exposures among Middle East Respiratory Syndrome Coronavirus Patients—Saudi Arabia, July–October 2017

A. Hakawi[1], E. Rose[2], M. Mohammad[1], O. Abdalla[1], G. Abedi[2], A. Alamri[1], S. Bereagesh[1], A. Asiri[1], H. Jokhdar[1], J. Watson[2], H. Biggs[2]
[1]Ministry of Health of Saudi Arabia, Riyadh, Saudi Arabia, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Middle East respiratory syndrome coronavirus (MERS-CoV) is an emerging infectious disease known to cause severe respiratory illness in humans. Since its identification in 2012, more than 2,100 confirmed cases have been reported, with death occurring in 35–40% of case-patients. Identified risk factors for infection include camel contact and healthcare exposure. We investigated MERS-CoV cases reported to the Saudi Arabia Ministry of Health (MoH) during July 1–October 31, 2017 to assess patient exposures. **Methods:** Confirmed case-patients without a link to a known hospital or household outbreak were classified as sporadic, and their exposures were further investigated. Sporadic case-patients were interviewed by telephone using a standardized questionnaire about demographics and activities during the 14 days before symptom onset (exposure period). For deceased or unavailable case-patients, relatives were interviewed. When otherwise unavailable, patient information was obtained from local public health officials. **Results:** Among 61 MERS-CoV cases reported to the MoH during the study period, 42 (69%) were classified as sporadic. Of these, 35 (83%) case-patients were interviewed, and 7 (17%) were followed up with through local public health officials. The mean age of sporadic patients was 57 years (range: 25–90) and 35 (83%) were men. Thirty-two (76%) had co-morbidities and 23 (55%) died. During the exposure period, 21 (50%) patients reported camel contact, of whom 13 (62%) had frequent camel contacts, such as owning, shepherding, or

butchering camels. Of those without reported camel contact, 8 (19%) visited a healthcare facility, and 5 (12%) denied high–risk (i.e., camel or healthcare–related) exposures. Exposure data were insufficient to characterize 7 (17%) cases. **Conclusions:** Frequent camel contact was common among sporadic case-patients of MERS-CoV in Saudi Arabia, indicating continued zoonotic transmission to humans. In addition to possible unrecognized healthcare–associated transmission, MERS-CoV infection occurs in a small proportion of persons without known high–risk exposures.

J4. Late Breakers I

3:30-5:00 pm Grand Ballroom A/B

Outbreak of Nipah Virus in Kerala, India, 2018

G. Arunkumar[1], J. Abdulmajeed[1], S. Aswathyraj[1], D. Santhosha[1], M. Shakir[1], J. Anup[1], N. Sudheesh[1], J. Anitha[1], S Robin[1], S. Sabeena[1], G. Nivedita[1], A. Anoop Kumar[2], S. Chandni[3], D. Asha[4], A. Sukumaran[4], F. Amar[5], K. Sajeeth Kumar[3], K Sakeena[6], V. Jayasree[4], V. Rajendran[3], K. Reena[5], R. Sarita[5]
[1]Manipal Centre for Virus Research, Manipal Academy of Higher Education, Manipal, India, [2]Baby Memorial Hospital, Kozhikode, India, [3]Government Medical College, Kozhikode, India, [4]Directorate of Health Services, Government of Kerala, Kozhikode, India, [5]Directorate of Health Services, Government of Kerala, Trivandrum, India, [6]Directorate of Health Services, Government of Kerala, Malappuram, India,

Background: Nipah virus (NiV) is a highly fatal emerging zoonotic virus with potential threat to global health security. India had earlier reported two NiV outbeaks. On 17 May 2018, a 26-year-old male presented to a hospital in Kozhikode district of Kerala, with symptoms suggestive of encephalitis. His brother had died due to similar illness on 5 May. The etiology was identified as NiV on 18 May by Manipal Center for Virus Research (MCVR). Here, we describe the epidemiological and laboratory investigation of this outbreak. **Methods:** We confirmed NiV by detecting viral RNA via real-time PCR of specimens from throat swabs, blood, urine and CSF. The virus was sequenced using Next Generation Sequencing and subjected to phylogenetic analysis. We conducted an epidemiological investigation to describe the outbreak and to elucidate the transmission dynamics during the outbreak. **Results:** During the period 2 to 29 May 2018, 19 cases were identified including the index case and 18 laboratory confirmed cases. The NiV of the current outbreak was 98% similar to Bangladesh lineage of NiV (NiV-BD). Median age of cases was 38.5; 12 (63.2%) cases were males. The median incubation period was 11 days (6 – 14 days); of the 19 cases, 17 (89.5%) cases had respiratory symptoms and 15 (79%) had encephalitis. The case fatality rate was 89.5% with 17 deaths and two survivors. The index case acquired disease in the community (zoonotic transmission); all others acquired it in three healthcare settings where index case or a confirmed case was treated. The cases include three family members and 16 close contacts in hospital settings. The major risk factors were close proximity (nursing, feeding or carrying a NiV infected person) enabling droplet infection and inadequate barrier infection control practices. Public health response by Kerala Health Services was launched on 18 May with isolation of cases, contact tracing, enforcing hospital infection control practices, etc. Since 30 May, no new cases have been reported. **Conclusions:** This is the first recorded NiV outbreak in South India and the third in India. Early laboratory confirmation and immediate public health response contained the outbreak. To institutionalize this success, we should promote early reporting of outbreaks and the culture of laboratory confirmation including access to apex laboratories and improvement of infection control practices.

Multi-Sectoral Emergency Response to the Nipah Outbreak, Kerala India, May 2018

S. Singh[1], M. Dhuria[1], S. Jain[1], P. Ravindran[2], A. Bahl[1], P. Khasnobis[1], S. Kulkarni[1], T. Dikid[1], S. Venkatesh[3]
[1]National Centre for Disease Control, Delhi, India, [2]Emergency Medical Relief, DGHS, Delhi, India, [3]Directorate General of Health Services, Delhi, India

Background: Nipah virus (NiV) infection is an emerging zoonosis (natural reservoir bats) with a high case fatality rate (CFR). In India, outbreaks have only been reported from West Bengal but never southern India. On May 19, 2018, Kerala state reported an outbreak of NiV to the National Centre for Disease Control (NCDC) soon after receiving confirmation of tested samples from GHSA-supported Manipal Centre for Virus Research (MCVR). Ministry of Health and Family Welfare (MoHFW) initiated a multi-sectoral public health response in coordination with the Kerala government, to contain the outbreak. **Methods:** MoHFW conducted rapid risk assessment and set up a response system. Incident Command System under NCDC was activated. The government of India deployed a multidisciplinary team led by NCDC, including National Institute of Virology (NIV), All India Institute of Medical Sciences, Department of Animal Husbandry, Dairying and Fisheries, Division of Emergency Medical Relief, and Safdarjung Hospital to assist the Kerala state government in epidemiological investigation, active case detection, contact tracing, clinical management, and implementation of infection prevention and control (IPC) practices. MCVR and NIV provided laboratory support. **Results:** We identified 19 cases with 18 (95%) laboratory confirmed; 17 died (CFR=89%). Multi-disciplinary central team began the response on May 20. The outbreak was notified to World Health Organization under International Health Regulations. NCDC led daily situation monitoring with states and investigation team and developed risk communication materials. From 19 cases, we identified 2,649 contacts and observed for 21 days. Serum samples were collected from 312 symptomatic contacts; only 18 were positive. All fifteen suspect cases from six other states tested negative. IPC measures including patient isolation and use of personal protection equipment were implemented. Among 52 bat samples, 10(19%) tested positive. **Conclusions:** This was first reported outbreak of NiV in south India. Multisectoral coordination, real-time data sharing, rapid contact tracing, timely diagnosis, and effective IPC led to successful outbreak containment.

Pteropus Bats Positivity for Nipah Virus from Kozhikode, Kerala, India: Possible Link of Infection to Human

D. Mourya[1], P. Yadav[1], A Sudeep[1], M. Gokhale[1], R. Gangakhedkar[2], B. Bhargava[2]
[1]ICMR-National Institute of Virology, Pune, India, [2]Indian Council of Medical Research, New Delhi, India

Background: Outbreaks of human Nipah virus (NiV) infections occurred in five Asian countries, viz., Malaysia, Singapore, Bangladesh, Philippines, and India. Due to the widespread distribution and vast flight range of primary reservoir pteropid bats, it has been estimated that approximately 250 million susceptible individuals reside in the outbreak-prone areas of Bangladesh and India. On 20 May 2018, State Ministry of Health and Family Welfare, Kerala state had declared outbreak of NiV in Kozhikode district of Kerala. Prior to this outbreak, India had seen two outbreaks in the past; Siliguri, West Bengal (2001) and Nadia, West Bengal in (2007). During previous outbreaks, no study was conducted to determine presence of NiV virus in the primary reservoir *Pteropus* species of bats. **Methods:** Study was conducted to understand the presence of NiV in bats in the affected area, Kozhikode district of Kerala State. Two locations were selected near the affected area. A total 52 *Pteropus giganteus* bats were collected. Keeping in the view of the prevailing panic situation, the health authority did not permit drawing blood samples or performing the necropsy of the bats in that area. Thus, after anesthesia, throat swab and cloacal swab samples from each captured bat were collected on site. **Results:** A total of 19 percent [10/52] of the bats were found positive for NiV of these 15% swab samples (Ct values ranged 29 to 36) and 8% cloacal swab (Ct values ranged 31 to 37). **Conclusions:** Earlier studies conducted in 2015 in the northeast region had shown the circulation of NiV in *Pteropus* bats with overall 8% positivity. Comparatively, positivity of bats in Kerala was higher than detected in North East region. At present, it is attributed that the bats may be the probable link of infection to initiate index case. It is worth noting that high quantum of virus detected in the throat swabs and known persistence of virus for a couple of hours on the contaminated fruits is important for public health. This suggests that there is a need to enhance the awareness in the community that fruits eaten by bats/birds should not be consumed and should be destroyed, so that other animals also do not contract this infection. Data on the bat positivity with Bangladesh strain of NiV in Northeast India to other end of the country, i.e., Kerala state, suggest the possibility of a wider circulation of NiV in India.

Near Real-Time Risk Assessment of Ebola Spillover: An Open-Source, Publicly Available Platform for Satellite-Based Change Detection

S. Malloy[1], K. McAfee[1], D. Abernathy[1], J. Horack[2], E. Newton[3], E. Root[1], A. Sauer[3], A. Steen[3]
[1]The Ohio State University, Columbus, OH, USA, [2]The Ohio State University College of Engineering, Columbus, OH, USA, [3]Battelle Center for Science, Engineering and Public Policy, Columbus, OH, USA

Background: Zoonotic spillover of emerging infectious diseases continues to threaten global health security, as demonstrated by the ongoing Ebola Virus Disease (EVD) outbreak in Équateur province, Democratic Republic of the Congo. Drivers of this complex phenomenon have been identified, including ecosystem fragmentation, population growth, and human activity in close proximity to wildlife, but few tools have been developed to understand how these dynamics precipitate the risk of spillover in real time. We describe an approach to improve spatial and temporal forecasting of zoonotic spillover in general, and EVD in particular, through the utilization of near real-time satellite imagery. **Methods:** We utilize a spatial reduction approach to identify areas at high risk of zoonotic spillover, with a prototype design calibrated to EVD in the Democratic Republic of Congo. Beginning with an estimation of the ecological niche of Ebola virus, we utilize change detection algorithms to characterize intact ecosystems using medium-resolution satellite imagery. These algorithms generate automated alerts of rapid change, which are then target areas for further classification using high spatial resolution and hyperspectral imagery. This method of tip and cue not only identifies habitat disruptions within the suspected spatial bounds of EVD, but also delineates the type of human activity responsible. Types of activity able to be classified include migration, agriculture, infrastructure development and conflict. **Results:** We demonstrate an integrated, user-friendly and open source application that generates near real-time risk assessments

of EVD spillover in the Democratic Republic of the Congo. Alerts of rapid change are generated at a spatial resolution of 30 meters and a temporal resolution of 1 week; further analysis with high spatial and hyperspectral imagery can improve spatial resolution by one order of magnitude and characterize disturbance type with high confidence. We report a statistically significant number of alerts in the suitable intact forest bordering the suspected index case in the current Équateur province outbreak. **Conclusions:** Near real-time assessment of the primary known drivers of zoonotic spillover can improve the spatial and temporal resolution of EVD surveillance, and should contribute to a proactive risk reduction strategy.

Habitat Fragmentation and Land-Use Change as Drivers of Yellow Fever Outbreaks in South America

A. Hamlet, N. Ferguson, T. Garske
Imperial College London, London, United Kingdom

Background: Yellow fever (YF) is an arbovirus of the family flaviviridae found in Africa and South America. In South America YF is transmitted in two cycles: the jungle cycle between non-human primates and sylvatic *Haemogogus* and *Sabethes* mosquitoes, and an urban cycle propagated by *Aedes aegypti*. Here we investigate the role of land-use change and habitat fragmentation on the inter-annual occurrence of YF in South America. **Methods:** We fit a series of random forest and poisson regression models to the number of months YF occurred in a 1st administrative division, for the period 2002-2016 using several covariates measuring land-use, habitat fragmentation, and climate. This was done using averaged covariates in a static model, and by considering time using a time-series model. The best performing models were combined using their akaike information criterion to produce weighted models. These were evaluated using a spatial block bootstrapping method. **Results:** Both time-series and static weighted models accurately captured the trends observed in the data, and with the inter-annual model capturing the relative level of transmission in a year with respect to others over the time-period. The most influential covariates were habitat fragmentation, cropland, and changes in land-cover over time. The magnitude, or even direction, of covariates in the short term do not always reflect long-term changes to suitability. In some cases this may highlight transition periods where the risk of slyvatic spillover is greatest, or represent long-term changes in the transmission. **Conclusions:** These findings may help to explain Brazil's ongoing YF outbreak (the largest since records began), which has occurred outside the traditional endemic zone, but in areas with increasing cropland and habitat fragmentation. Applications of these findings may guide proactive vaccination or surveillance in areas where the risk of YF may increase with land conversion. This could reduce the risk of future large-scale outbreaks.

A Scoping Review of Chikungunya Virus and Its Vectors from Global Evidence

M. Mascarenhas[1], S. Garasia[1], P. Berthiaume[2], T. Corrin[1], J. Greig[1], V. Ng[1], I. Young[3], L. Waddell[1]
[1]National Microbiology Laboratory, Public Health Agency of Canada, Guelph, ON, Canada, [2]National Microbiology Laboratory, Public Health Agency of Canada, St. Hyacinthe, QC, Canada, [3]Ryerson University, Toronto, ON, Canada

Background: Chikungunya virus (CHIKV) has caused major epidemics globally over the last two decades and is quickly expanding into new areas. Although this mosquito-borne disease is self-limiting and not associated with high mortality, it can lead to severe, chronic, and disabling arthritis, thereby posing a heavy burden to healthcare systems. The two main vectors for CHIKV are *Aedes aegypti* and *Aedes albopictus* (Asian tiger mosquito); however, many other mosquito species have been described as competent CHIKV vectors in scientific literature. With climate change, globalization, and unfettered urban planning, CHIKV poses a significant public health risk to many countries. A scoping review (ScR) was conducted to collate and categorize all pertinent information from published scientific literature on a priori defined aspects of CHIKV and its competent vectors. **Methods:** Our protocol ensured transparency, reproducibility, and consistency. It included 1) establishing a research question, 2) conducting a comprehensive, stringent literature search in seven databases, 3) relevance screening of captured articles according to inclusion/exclusion criteria, 4) characterizing all relevant articles, and 5) collating and summarizing results from extracted data. Screening and data characterization tools were uniformly implemented on all articles by two independent reviewers. **Results:** Results from 1,920 relevant articles show that CHIKV research is reported predominantly in areas after major outbreaks have occurred. There has been an upsurge in CHIKV publications since 2011, especially after first reports of CHIKV emergence in the Americas. A list of hosts and vectors that could potentially be involved in the sylvatic and urban transmission cycles of CHIKV has been compiled in this scoping review. In addition, a repository of CHIKV mutations associated with evolutionary fitness and adaptation has been created by compiling and characterizing these genetic variants as reported in scientific literature. **Conclusions:** Results from this scoping review provide researchers and policymakers with information that could be used to prevent and mitigate public health risks and severe outcomes arising from CHIKV, in addition to highlighting research gaps and areas with abundant research on chikungunya that could be used to prioritize future research.

Wednesday, August 29

Poster Abstracts

Poster / Exhibit Hall

Infections in Infants and Pregnant Women

Board 297. Seroprevalence of Selected Congenital Infections among Pregnant Women in Coatepeque, Guatemala

M. Lopez[1], A. Espinoza-Bode[2], L. Grajeda[1], N. Nuñez[3], B. Lopez[2], A. Balish[4], T. Lo[4], J. Bryan[4], J. Juarez[3], A. Gomez[3], A. Perez[3], C. Cordon-Rosales[1], O. Henao[4], J. McCracken[1]
[1]Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Centers for Disease Control and Prevention, Central American Regional Office, Guatemala, Guatemala, [3]Ministry of Public Health and Social Assistance of Guatemala, Guatemala, Guatemala, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Worldwide, congenital infections of concern include toxoplasma (toxo), other infections (syphilis and HIV), rubella, cytomegalovirus (CMV)—or collectively TORC, and Zika virus (ZIKV). In Guatemala, there are little data available on the seroprevalence of these organisms in pregnant women because of limited routine testing. In response to the 2015-2016 ZIKV outbreak, we conducted a prospective cohort study to identify maternal-infant infections in Coatepeque, Guatemala. **Methods:** Between May and November 2017, women aged 16-40 years with singleton pregnancies of <20 weeks gestation were enrolled with 429 tested for TORC and 434 for ZIKV infections. Serum samples were processed using Chemiluminescent Microparticule Immunoassay to detect IgG and IgM antibodies to toxo, CMV and rubella infections. An IgG avidity test for IgM positive samples was done to determine timing of toxo infections. Rapid tests were used for HIV and syphilis. IgM ELISA assays and rRT-PCR were used to identify ZIKV and DENV infections. **Results:** Seroprevalence of TORC infections were: toxo 69.9% IgG, 1.4% IgM; rubella 80.0% IgG, 0% IgM; and CMV 99.8% IgG, 0.7% IgM. Of 5 women with IgM to toxo, 3 were identified as acute infections via IgG avidity testing. One participant had HIV antibodies (0.2%), and none tested positive for syphilis. ZIKV IgM antibodies were found in 38 participants (9.1%), and among these, 27 were negative for DENV IgM (73.0%). None were ZIKV or DENV rRT-PCR positive. **Conclusions:** Serology shows nearly all of this population had previous exposure to CMV when entering the study and very low seroprevalence for HIV. Approximately one-third and one-fifth of participants are susceptible to toxo and rubella, respectively. The IgM results for ZIKV and DENV suggest recent flavivirus infection, and we cannot rule out infections during early pregnancy. Incorporation of infection prevention recommendations, vaccine use and routine testing into the national guidelines for antenatal care will reduce the risk of infections and improve early detection of congenital infections in Guatemala.

Board 298. Early-Onset Neonatal Sepsis by Group B *Streptococcus agalactiae* and *Escherichia coli*

M. Taminato[1], A. Pignatari[2], D. Fram[2], F. Balbino[2], S. Nascimento[2], D. Brabosa[2]
[1]School of Nursing - Federal University of São Paulo, São Paulo, Brazil, [2]UNIFESP, Sao Paulo, Brazil

Background: Sepsis is a major challenge to the reduction of infant mortality rates, despite recommendations for screening and prophylaxis during pregnancy for invasive diseases, and it is an important risk for mortality in this population. In Brazil it is estimated that about 60% of neonatal deaths occur from preventable causes. High rates of fetal, early-onset neonatal sepsis (EOS) and early neonatal mortality are related to the poor quality of pre-natal attention, bad diagnosis of changes in pregnancy and deficit in professional training on the care of the mother and the newborn. Group B *Streptococcus agalactiae (GBS)* was the most common pathogen in term newborns and *Escherichia coli* (*E. coli*) most common in preterm infants. **Methods:** A case-control study, which was carried out from 2008 to 2018 on newborns at São Paulo Hospital, matching 1: 2. Univariate analyses were carried out to compare variables between groups (case and control). **Results:** The overall incidence of GBS was 0.24 per 1000 live births and *E. coli* infection was 0.40 per 1000 live births. Mortality associated with sepsis was 12.5%. The incidence density of sepsis by selected clinical characteristics and invasive procedures, extreme prematurity (<28 weeks gestational age), 5-minute Apgar score ≤3, assisted ventilation, the presence of a central venous catheter, and surgical intervention were all significantly associated with a higher incidence of sepsis. **Conclusions:** Invasive procedures in association with prematurity are risk factors for acquiring sepsis, especially in settings with a high intensity of colonization pressure, which is characteristic for developing countries. Early-onset GBS incidence declined in Brazil, which is currently adopting GBS screening.

Board 299. Invasive Group A Streptococcal Postpartum Infections in Minnesota, 2000–2016

A. Bell[1], S. Milder[1], R. Danila[1], R. Lynfield[1], C. Van Beneden[2], B. Jewell[1], K. Como-Sabetti[1]
[1]Minnesota Department of Health, Saint Paul, MN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Recent childbirth is a risk factor for invasive group A *Streptococcus* (iGAS) infection. We compared postpartum (PP) iGAS infections with iGAS infections in non-postpartum (nPP) women. **Methods:** Minnesota Department of Health conducts statewide active surveillance for iGAS infections (infection in which GAS is isolated from a normally sterile site) as part of CDC's Active Bacterial Core surveillance. PP cases were iGAS infections among women who delivered an infant or miscarried ≤ 30 days before illness. We reviewed medical records and compared PP cases to nPP iGAS cases among women of child-bearing years. All available isolates were *emm* typed at CDC. **Results:** Among 347 women aged 17-43 years with iGAS infection during 2000-2016, 70 (20%) had PP infections. These GAS PP infections included endometritis (57%), bacteremia (21%), and puerperal sepsis (21%); 1 patient died. Nearly all (91%) women with PP iGAS infection received prenatal care; 93% underwent vaginal delivery; and 1 had prolonged rupture of membranes. Among women with PP infection, 14% of delivered infants were preterm. Most (87%) infants survived without illness, 9% survived but had a clinical infection (bacteremia, meningitis, or otitis media; infection type unknown for

2 infants), and 4% died (stillbirth or neonatal death). Overall, women with PP iGAS infections were younger than women with nPP iGAS infections (median age 30 vs. 34 years, p=0.002) and less likely to have a comorbidity (44% vs 64%, OR= 0.44, p=0.004). There were no injecting drug users (IDU) or solid organ malignancies among PP cases compared to 7% IDU (p<0.001) and 5% (p<0.001) solid organ malignancies among women with nPP infections. Inpatient length of stay was shorter for women with PP iGAS infections compared to women with nPP infections (median 4 days vs. 6 days, p=0.009). GAS isolates from women with PP infection were more likely to be *emm* 28 than nPP isolates (23% vs 12%, OR = 2.25, p=0.030). **Conclusions:** Although uncommon, PP GAS infections occurred in generally healthy, young women who received adequate prenatal care; 13% of infections were associated with neonatal morbidity and mortality. Additional investigation into modifiable risk factors for PP iGAS infection would be useful in determining potential measures to prevent these GAS infections.

Board 300. Trends in Incidence of Invasive Early- and Late-Onset Group B Streptococcal Disease, United States, 2006-2015

S. Nanduri[1], S. Petit[2], C. Smelser[3], M. Apostol[4], N. Alden[5], L. Harrison[6], R. Lynfield[7], K. Burzlaff[8], L. Dufort[8], W. Schaffner[9], A. Thomas[10], M. Farley[11], J. Jain[1], T. Pondo[1], L. McGee[1], S. Schrag[1]
[1]Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Connecticut Department of Public Health, Hartford, CT, USA, [3]New Mexico Department of Public Health, Santa Fe, NM, USA, [4]California Emerging Infections Program, Oakland, CA, USA, [5]Colorado Department of Public Health and Environment, Denver, CO, USA, [6]University of Pittsburgh, Pittsburgh, PA, USA, [7]Minnesota Department of Health, St. Paul, MN, USA, [8]New York State Department of Health, Albany, NY, USA, [9]Vanderbilt University School of Medicine, Nashville, TN, USA, [10]Oregon Department of Human Services, Portland, OR, USA, [11]Emory University School of Medicine and Atlanta VA Medical Center, Atlanta, GA, USA

Background: Despite declines following recommendations for intrapartum antibiotic prophylaxis, group B *Streptococcus* (GBS) remains a leading cause of neonatal sepsis and meningitis in the United States. We describe trends in incidence and serotype distribution of invasive GBS disease among young infants in the United States from 2006-2015 as identified through Active Bacterial Core surveillance (ABCs), a multi-site population-based surveillance system covering nearly 10% of US births. **Methods:** An invasive case was defined as illness in an ABCs-area resident with isolation of GBS from a normally sterile site. We defined cases occurring from 0-6 days of life as early-onset disease (EOD) and from 7-89 days as late-onset disease (LOD). To estimate incidence rates (cases per 1000 live births), we used live births from state vital records for denominators. We used the Cochrane-Armitage test to evaluate significance of trends. We analyzed serotype data from 7 of 10 ABCs sites that collect GBS isolates. **Results:** During 2006-2015, ABCs identified 1,277 EOD and 1,388 LOD cases. From 2006-2015, while EOD incidence declined significantly from 0.37 to 0.23 (P<.0001), LOD rates varied between 0.29 and 0.34. Of 1898 cases identified from 7 sites that collect GBS isolates, serotype data were available for 1741 (91.4%). Among EOD cases, serotypes Ia (27.3%) and III (27.3%) were most common. Among LOD cases, serotype III was most common and increased (2006: 51.2%; 2015: 69.9%, P<0.0001). Among EOD and LOD cases, 6.2% were due to serotype IV. The five most common serotypes (Ia, Ib, II, III and V) caused 93% of EOD and 94% of LOD. **Conclusions:** While EOD rates continued to decline between 2006-2015, LOD rates were stable. A vaccine covering the most common serotypes might further reduce EOD and prevent LOD, for which there is no public health intervention.

Board 301. Group B *Streptococcal* Bacteremia Burden and Trends over Time, 2007-15, Thailand

W. Paveenkittiporn[1], C. Bunthi[2], A. Kerdsin[3], S. Thamthitiwat[2], S. Bhengsri[2], T. Akarachotpong[2], P. Srisaengchai[2], J. Rhodes[4], C. Gregory[2], H. Baggett[2], S. Schrag[4]
[1]Thailand National Institute of Health, Nonthaburi, Thailand, [2]Global Disease Detection Center, Thailand MOPH-US CDC Collaboration, Nonthaburi, Thailand, [3]Kasetsart University Chalermphrakiat, Sakon Nakhon, Thailand, [4]Division of Bacterial Diseases, National Center for Immunization and Respiratory Diseases, US CDC, Atlanta, GA, USA

Background: Infection with group B *Streptococcus* (GBS) is a leading cause of young infant sepsis and an emerging cause of adult invasive disease. However, data on incidence among adults in middle and low income countries are lacking, and the young infant burden in Southeast Asia has not been characterized. We analyzed population-based bloodstream infection data from two provinces in Thailand and sterile site infection data from sentinel hospitals with national representation. **Methods:** Cases were defined as isolation of GBS from blood (population-based surveillance among hospitalized residents of two provinces, 2007-15) or from any sterile site (patients cared for at 25 provincial, regional, or private hospitals, 2014-15). Incidence rates in the 2 provinces were calculated using live births (per 1000) for young infants (<3 months of age) or population denominators (per 100,000) for adults (>=18 years). Temporal trends were assessed by linear regression. **Results:** In the 2 provinces, 10,208 young infants had at least one blood culture (89/1000 live births, median blood volume: 1 ml, interquartile range: 0.5-3.0), yielding 15 GBS cases (80% age 0-6 days). Overall young infant disease incidence was 0.13/1000 live births and by year ranged from 0.0 (2009, 2011, 2013) to 0.36 (2015). Among adults, 373 cases were identified. Adult disease incidence was 5.1/100,000 and increased with age (18-49 years: 2.3, 50-64: 7.4, 65+: 14.3) and over time (2007: 2.6; 2015: 7.8; p= 0.03). In the sentinel hospital system there were 16 cases in young infants (88% from blood; 19% age 0-6 days) and 655 cases in adults (84% from blood; 38% > 64 years). Among adult case-patients, 19% had diabetes, 6% renal disease, 6% liver disease, 3% cancer, 3% heart disease; 19% died in hospital and 7% were referred for additional treatment. Predominant serotypes from the sentinel system were III (47%), V (21%) and II (15%). **Conclusions:** Invasive GBS disease incidence among Thai adults is substantial and comparable to US estimates from 1990-2007: 7.3 per 100,000. Underlying illnesses were less common than in the United States (e.g., 19% vs. 44% for diabetes), but clearly play a major role in increasing incidence among adults. The low incidence in young infants may reflect incomplete ascertainment, but is consistent with previous findings from Asia. Further strain characterization is needed to help guide vaccine development.

Board 302. Respiratory Illness and Birth Weight in Infants with Prenatal Exposure to Maternal Influenza Infection during 2013-2017 in Bangladesh

Z. Akhtar[1], P. Ghosh[1], F. Chowdhury[1], M. Rahman[1], K Zaman[1], D. Iuliano[2]
[1]icddr,b, Dhaka, Bangladesh, [2]CDC, Atlanta, GA, USA

BBackground: Pregnant women and infants are at high risk of complications from influenza virus infection. There is limited information in Bangladesh on how influenza effects these populations to guide future public health measures. We followed pregnant women and their infants aged <6 months to measure the frequency of influenza and assess the effect of prenatal exposure to maternal influenza virus infection among infants. **Methods:** We enrolled pregnant women from 8 sub-districts in Bangladesh in four influenza seasons (2013-2016); infants were enrolled at birth. Pregnant women were followed weekly through delivery by phone or home visit to identify onset of influenza-like-illness (ILI) defined as subjective fever and cough in the last 7 days. Infants were monitored weekly after birth through 6 months for onset of acute respiratory infection (ARI), defined as >2 respiratory symptoms (cough, rhinorrhea, or difficulty breathing reported as tachypnea) in the previous 7 days. Staff collected nasopharyngeal swabs for ILI and ARI episodes and tested for influenza viruses by real-time RT-PCR. Low birth weight was defined as <2500 grams. **Results:** We followed 6850 pregnant women and 6841 infants. Among 737 women with ILI and 2566 infants with ARI, 26% (193) and 2% (56) were positive for influenza, respectively. Among 193 women with influenza, 182 (94%) had infection during the third trimester, none were hospitalized, and all recovered. ARI among infants occurred within 1-25 weeks of age, with the highest number of infections occurring at three weeks of age. The mean gestational age at birth for influenza positive mothers, influenza negative mothers with ILI, and mothers without ILI was 37.0 weeks. Among 6252 infants with birth weight available, 880 (14%) had low birth weight. Low birth weight occurred in 13% (24/186) of infants of influenza-positive mothers, 15% (73/497) of influenza negative mothers with ILI, and 14% (783/5569) of mothers without ILI. **Conclusions:** During 2013-2016, influenza infection was not commonly identified among pregnant women and their infants. Additional years are needed to better understand the effect of influenza infection on pregnant women and infants. Low birth weight was similar in infants born to all mothers, suggesting that influenza infection did not impact birth weight.

Board 303. Changing Estimates of Incidence of Congenital Zika Syndrome with Changing Case Definitions

H. Mocelin[1], T. Prado[1], P. Freitas[1], G. Rodrigues[2], E. Caetano[3], A. Bertolde[4], F. Perez[5], L. Riley[6], E. Maciel[1]

[1]Lab-Epi UFES – Laboratory of Epidemiology, Federal University of Espírito Santo. Program of Post-graduation in Public Health of the Federal University of Espírito Santo, Vitoria, Brazil, [2]Secretaria Estadual de Saúde do Espírito Santo, Vitoria, Brazil, [3]Neurologist at a referral hospital for Zika Virus Congenital Syndrome, Vitoria, Brazil, [4]Statistical Department, Federal University of Espírito Santo, Vitoria, Brazil, [5]Departments of Communicable Diseases and Environmental Determinants of Health, 15 Pan American Health Organization, Washington, DC, USA, [6]University of California, School of Public Health, Division of Infectious Disease and Vaccinology,., Berkeley, CA, USA

Background: In 2015, the world paid attention to an explosive pandemic of Zika virus (ZIKV) infection associated with microcephaly in Brazil. The frequent changes in recommendations for notification and case definition of ZIKV infection or congenital Zika syndrome (CZS) may have contributed to varying estimates of incidence of this syndrome in different regions of Brazil. The aim of this study was to describe how changes in case notification based on different CZS case definitions may have affected disease estimates. **Methods:** We conducted a retrospective cohort study of reported cases of children with microcephaly and CZS in the state of Espírito Santo (ES), Brazil from January 1, 2015 to December 31, 2016 notified by the State Department of Health (SESA). We analyzed cases that were reported under the first (November 2015) and last protocol in 2017 (with no specification of month). **Results:** In the state of ES, from January 2015 to December 2016, 264 pregnant women suspected of having been exposed to ZIKV were notified and 49 newborns were confirmed to have CZS according to the 2015 protocol in force on the date of classification. Of these newborns with confirmed CZS, 17 (35%) did not have microcephaly according to the 2017 protocol. Based on the protocol of 2015, 26 (53%) children would have been confirmed to have ZIKV infection, through microcephaly finding. Based on the 2017 protocol, 8 (16%) children would have been diagnosed with infection of Zika virus, already framed in the new terminology CZS and no more microcephaly by ZIKV. The serologic tests used to confirm CZS in the most recent protocol were not routine at the beginning of the epidemic. **Conclusions:** The first protocol was more comprehensive, the last more specific, expressing the risks of early undetected Zika congenital syndrome. Surveillance for the disease and clinical protocols need to be scaled up.

Board 304. Overview of Zika en Embarazadas y Niños en Colombia (ZEN): A Prospective Cohort Study Examining Zika Virus Infection during Pregnancy and Risk of Adverse Pregnancy, Birth, and Infant Outcomes

M. Mercado[1], H. Rodriguez P.[1], D. Valencia[2], V. Tong[2], M. Gonzalez[1], M. Osorio Merchan[1], S. Gilboa[2], C. Johnson[3], Y. Ortiz Gómez[1], J. Martín Rodriguez[1], S. Kim[4], C. Renquist[2], H. Baquero Latorre[5], E. Ailes[2], M. Honein[2], D. Jamieson[6], M. Ospina Martínez[1]
[1]Instituto Nacional de Salud, Bogotá, Colombia, [2]Division of Congenital and Developmental Disorders, National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]National Institute for Occupational Safety and Health (NIOSH), Centers for Disease Control and Prevention, Cincinnati, OH, USA, [4]Division of Reproductive Health, Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Universidad del Norte, Barranquilla, Colombia, [6]Emory University, Atlanta, GA, USA

Background: Since its first identified case of Zika virus (ZIKV) infection in October 2015, Colombia has reported over 106,000 suspected ZIKV infection cases, including those in almost 20,000 pregnant women. ZIKV infection during pregnancy can cause serious fetal harm, including microcephaly and related brain anomalies. Knowledge gaps remain about the extent of risk associated with ZIKV infection for a range of adverse pregnancy, birth, and infant outcomes. To help address these questions, the Colombian INS and US CDC are implementing *Zika en Embarazadas y Niños en Colombia* (ZEN), a prospec-

tive cohort study of 1,500 pregnant women, male partners, and their infants in multiple sites throughout Colombia. **Methods:** Pregnant women were enrolled in their first trimester of pregnancy and will be followed until their infants are 6 months old, while male partners will be followed through the end of their partner's second trimester. ZEN objectives are to (1) describe sociodemographic and clinical characteristics of the population, (2) identify risk factors for ZIKV infection in pregnant women and their infants, (3) assess the risk for adverse maternal, fetal, and infant outcomes associated with ZIKV infection, and (4) assess modifiers of the risk for adverse outcomes among pregnant women and their infants following ZIKV infection. To identify critical windows of infection for adverse outcomes and monitor persistence of ZIKV, sequential ZIKV testing of serum or urine using reverse transcription-polymerase chain reaction (rRT-PCR) will be performed for pregnant women (biweekly until 34 weeks gestation, and monthly until pregnancy end), male partners (monthly until their partner's 27th week of gestation) and infants (biweekly until 6 months of age). Female and male participants are interviewed using structured questionnaires about risk factors for ZIKV infection, symptoms of ZIKV infection, and risk factors for adverse outcomes. Clinical information will be abstracted from medical records of pregnant women and their infants. **Results:** ZEN enrollment occurred between February 9, 2017 and January 31, 2018. **Conclusions:** ZEN results will help guide recommendations for preventing ZIKV infection, improve counselling of patients about the risks of ZIKV to themselves and their families, and help agencies prepare to provide services to affected children and their families.

Board 305. Surveillance of Microcephaly and Other Congenital Central Nervous System Malformations: The Colombian Experience during the 2015-2016 Zika Virus Epidemic

M. Ospina Martínez[1], M. Mercado[1], R. Galang[2], C. Moore[2], M. Gonzalez[1], D. Valencia[2], E. Cuevas[1], O. Pacheco Garcia[1], A. Bermudez[1], V. Tong[2], C. Renquist[2], M. Dominguez[2], S. Gilboa[2], N. Rozo Gutierrez[3], M. Honein[2], F. Prieto Alvarado[1]
[1]Instituto Nacional de Salud, Bogotá, Colombia, [2]Division of Congenital and Developmental Disorders, National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Since 2008, the Colombian Instituto Nacional de Salud (INS) has conducted national surveillance of birth defects as part of its SIVIGILA surveillance system. During the 2015-2016 Zika virus (ZIKV) outbreak in the Americas, INS established an enhanced surveillance protocol to monitor potential increases in microcephaly and other congenital central nervous system (CNS) malformations, to investigate possible causes, and to direct appropriate follow-up care. **Methods:** SIVIGILA received notification from physicians if microcephaly (head circumference below the 3rd percentile expected for sex and gestational age) or other CNS malformations were diagnosed prenatally. The surveillance protocol required an inpatient neonatal evaluation soon after delivery, including a complete physical and neurological exam, and a head ultrasound. If microcephaly or other CNS malformations were noted, further evaluation was recommended by the protocol. Cases were classified into etiological categories: congenital ZIKV infection, other infectious agents, genetic, multifactorial, additive, and unknown; this classification was based on laboratory evidence and extensive review of the clinical findings from medical records by qualified clinicians. Data reported here are from the implementation of the enhanced protocol to births in 2016. **Results:** During 2016, SIVIGILA was notified of over 900 cases of microcephaly and other CNS malformations. Based on preliminary analysis, these numbers represent about a 40% increase compared to 2015. Case classification is ongoing. Furthermore, work is ongoing to review all cases of microcephaly and other congenital CNS malformations reported for 2017. **Conclusions:** This Colombian enhanced surveillance protocol, built on an already existing surveillance platform, serves as a model of a comprehensive approach to investigating complex congenital conditions of unknown etiology and building capacity to detect emerging health public health threats. Adequate identification, notification and classification is essential in order to quantify the number of Zika-associated birth defects, and follow-up care is essential to fully characterize the impact of congenital ZIKV infection during pregnancy.

Board 306. The Zika Virus Infection in Pregnant Women in Honduras (ZIPH) Cohort Study

P. Buekens[1], J. Alger[2], M. Cafferata[3], A. Berrueta[3], H. Bock[4], C. Bustillo[5], A. Calderón[6], A. Callejas[7], M. Castillo[7], A. Ciganda[3], I. Fuentes[5], J. Funes[7], J. Garcia[2], S. Gilboa[8], E. Harville[1], W. López[2], I. Lorenzana[9], M. Tulio Luque[9], C. Maldonado[10], R. Oberhelman[1], C. Ochoa[11], K. Pastrana[5], L. Parham[9], H. Rodríguez[11], V. Tong[8], D. Valencia[8], D. Varela[12], M. Ward[1], D. Wesson[1], C. Zúniga[13]

[1]Tulane University School of Public Health and Tropical Medicine, New Orleans, LA, USA, [2]Departamento de Laboratorio Clínico, Hospital Escuela Universitario, Tegucigalpa, Honduras, [3]Instituto de Efectividad Clínica y Sanitaria, Buenos Aires, Argentina, [4]Región Sanitaria Metropolitana del Distrito Central, Secretaría de Salud de Honduras, Tegucigalpa, Honduras, [5]Departamento de Ginecología y Obstetricia, Hospital Escuela Universitario, Tegucigalpa, Honduras, [6]Centro de Salud Alonso Suazo, RSMDC, Secretaría de Salud de Honduras, Tegucigalpa, Honduras, [7]Neonatología, Departamento de Pediatría, Hospital Escuela Universitario, Tegucigalpa, Honduras, [8]Division of Congenital and Developmental Disorders, National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA, [9]Centro de Investigaciones Genéticas (CIG), Escuela de Microbiología, UNAH, Tegucigalpa, Honduras, [10]Oftalmología, Departamento de Pediatría, Hospital Escuela Universitario, Tegucigalpa, Honduras, [11]Hospital General San Felipe, Tegucigalpa, Honduras, [12]Neurología, Departamento de Pediatría, Hospital Escuela Universitario, Tegucigalpa, Honduras, [13]Departamento de Vigilancia de la Salud, Hospital Escuela Universitario, Tegucigalpa, Honduras

Background: The full spectrum of long-term complications of Zika virus (ZIKV) infection has not been thoroughly described, especially among children without clinical evidence of congenital Zika syndrome at birth, and among children born to ZIKV infected but asymptomatic mothers. We are currently conducting a prospective pregnancy cohort study in Honduras that will allow us to study ZIKV infection in a different context than South American countries. **Methods:** Enrollment in the cohort is ongoing in one health center. Women are enrolled at their first prenatal visit. Data on socio-demographics, ZIKV symptoms during pregnancy, and information to locate women for additional follow-up are collected through interview at enrollment. Maternal blood is collected immediately after enrollment and tested for ZIKV immunoglobulin M (IgM) by enzyme-linked immunosorbent assay (InBios, Seattle, WA). We plan to conduct ZIKV and dengue virus polymerase chain reaction testing. We expect more than 90% of the women to de-

liver in one of two public hospitals in Tegucigalpa. Longitudinal follow-up will be conducted for children of women with positive ZIKV IgM and a comparison group of children born to women with no evidence of ZIKV infection at enrollment. Neurodevelopment will be assessed with Bayley Scales of Infant and Toddler Development, 3rd edition. **Results:** From July 2016 to February 2018, we have enrolled 2,143 women at their first prenatal visit. Gestational age at enrollment was <14 weeks for 56.9% of the cohort, 14-28 weeks for 25.2%, and > 28 weeks for 17.9%. Thirty-seven women (1.7%) were symptomatic at enrollment. About half of the enrolled participants have already delivered. Analyses of birth outcome data are ongoing. **Conclusions:** We have been enrolling pregnant women at the first prenatal visit since the peak of the ZIKV epidemic in Honduras. This study will allow us to better understand the longer-term outcomes of children exposed to ZIKV during pregnancy.

Board 307. Prevalence of Small for Gestational Age among Live Births with Confirmed and Possible Prenatal Exposure to Zika Virus Infection, United States Zika Pregnancy and Infant Registry, 2015-2017

R. Simeone[1], A. Jones[1], S. Ellington[1], M. Reynolds[1], C. Shapiro-Mendoza[1], E. Lee[2], H. Cooper[2], K. Aviles[3], J. Prieto[3], E. Ellis[4], J. Dunn[5], A. Griffin[6], A. Mafotsing Fopoussi[7], N. Ahmad[8], V. Glaze[8], L. D'Amico[9], C. Suarez[9], S. Browne[10], J. Popovitch[11], D. Perella[12], M. Honein[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]New York City Department of Health and Mental Hygiene, New York City, NY, USA, [3]Florida Department of Health, Tallahassee, FL, USA, [4]US Virgin Islands Department of Health, Christiansted, Virgin Islands, USA, [5]Massachusetts Department of Public Health, Boston, MA, USA, [6]California Department of Public Health, Oakland, CA, USA, [7]Maryland Department of Health , Baltimore, MD, USA, [8]New York State Department of Health, Albany, NY, USA, [9]New Jersey Department of Health, Trenton, NJ, USA, [10]Virginia Department of Health, Newport News, VA, USA, [11]Illinois Department of Public Health, Springfield, IL, USA, [12]Philadelphia Department of Public Health, Philadelphia, PA, USA

Background: The United States Zika Pregnancy and Infant Registry (USZPIR) monitors infant outcomes from pregnancies with confirmed and possible Zika virus (ZIKV) infection. A higher prevalence of ZIKV-associated birth defects (birth defects) among nucleic acid test (NAT) confirmed ZIKV infection compared to possible ZIKV infection has been reported. **Methods:** We examined associations between NAT confirmed ZIKV infection during pregnancy and small for gestational age (SGA; birthweight <10th percentile for gestational age and sex) among live births stratified by birth defects. NAT-confirmed ZIKV infection was defined as a positive nucleic acid test in maternal, infant, or placental specimens; possible ZIKV infections were those with serologic evidence and were the comparison group. **Results:** From December 2015-December 2017, 5579 singletons were reported to the USZPIR; 36% from the US States and 64% from US Territories. Among 1567 State and 3170 Territory live births with gestational age and weight at delivery, 12% and 10% were SGA and 6% and 4% had birth defects, respectively. In the States, among live births with birth defects, the prevalence of SGA was higher among pregnancies with NAT-confirmed ZIKV (68%) compared to possible infection (34%) (prevalence ratio (PR): 2.0 (95% confidence interval: 1.1, 3.6)). The association between NAT-confirmed infection and SGA among those without birth defects was not significant (PR: 1.3 (0.8, 1.9)). In the Territories, among those with birth defects, the prevalence of SGA was similar for NAT-confirmed (45%) and possible ZIKV infection (43%) (PR: 1.0 (0.6, 1.8)); a similar association was observed among those without birth defects (PR: 0.8 (0.6, 1.0)). **Conclusions:** The prevalence of SGA might be higher among pregnancies with NAT-confirmed ZIKV infection compared to possible infection. This finding was observed only in pregnancies with birth defects in the States. Results are limited by differences in completeness of data collection, testing, and reporting within USZPIR.

Board 308. Stopping the Next Zika: Lessons Learned to Help Protect Mothers and Babies from Emerging and Existing Threats

K. Polen, S. Ellington, S. Gilboa, J. Moore, C. Green, S. Fehrenbach, A. Colson, M. Honein

Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: From H1N1 to Ebola to Zika, the public health community has recently faced a series of complex and unpredictable outbreaks. The Zika virus outbreak served as a reminder of the vulnerability of pregnant women and babies to emerging infectious diseases and of the destructive consequences that can result from infections during pregnancy. Zika virus, like rubella decades before, demonstrated how an infection can lead to devastating birth defects and lifelong challenges. The outbreak revealed gaps in public health and healthcare readiness, and in particular, readiness to address how emerging diseases impact pregnant women, babies, and families. **Methods:** CDC, along with state, local, and territorial public health partners rapidly created an integrated surveillance system, the US Zika Pregnancy and Infant Registry, to monitor pregnant women and infants with Zika virus infection. We also mobilized to engage and communicate with healthcare professionals on guidance for patients, support local health departments with the greatest needs, and connect families affected by Zika virus with specialized care. These critical resources can be mobilized again to support maternal and child health after the recent hurricanes, during the current opioid and neonatal abstinence syndrome epidemics, and for future threats. **Results:** The US Zika Pregnancy and Infant Registry has monitored over 7,200 pregnant women in the US states and territories. Follow-up of their infants will be critical to understand the impact of Zika virus infection during pregnancy. Data collected through the registry were critical to answer key questions about risk from infection, improve counseling of patients, inform clinical guidance for care of pregnant women and infants, identify and refer children for medical services, help agencies prepare to provide services to affected families, and improve Zika virus prevention efforts. **Conclusions:** The creation and implementation of the US Zika Pregnancy and Infant Registry represents a major paradigm shift towards ensuring that pregnant women and babies are monitored and the public health and medical community is quickly informed about the risks of emerging threats to this population. This enhanced surveillance system can be leveraged in future emergencies to inform public health action to help mothers and babies.

Board 309. Health System Preparedness and Response to the Emergence of Zika in Iquitos and Piura, Peru: A Qualitative Comparative Case Study

R. Iguiñiz -Romero[1], L. Guerra-Reyes[2]
[1]Universidad Peruana Cayetano Heredia, Lima, Peru, [2]Indiana University Bloomington, Bloomington, IN, USA

Background: Since 2016 Zika has emerged as a new public health threat in Latin America. The multiple virus transmission pathways, and the effects of congenital syndrome present a new and increasing burden to the public health services. During the 2016 emergency, Peruvian health authorities issued alerts and guidelines for emergency surveillance and response. Zika prevention has been included into existing vector-control activities and pre-natal counseling but little is known about how existing guidelines and monitoring have worked in practice. **Methods:** We provide a comparative case study of Zika preparedness and response in practice. Using a Rapid Ethnographic Assessment methodology, we collected data from health networks in Iquitos and Piura, two Peruvian cities with high prevalence of *Aedes aegypti*. Data were collected through semi-structured interviews and focus groups with health professionals, women and men from the community. The sample included 22 men, 28 women from 18 to 50 years old in each location, 6 health professionals in Iquitos and 18 in Piura. All study protocols were approved by accredited institutional review boards internationally and in Peru. **Results:** Extensive local knowledge of *Aedes aegypti* as carrier of dengue led health providers to overlook Zika virus infection risks. No active Zika virus monitoring is being conducted, leading to a misleading perception of safety. Policy guidelines and emergency response protocols have not been adjusted to monitor long-term scenarios, and those available have not been incorporated at the local level within Peruvian Health System. Health personnel responsible for infant care have not received any information about Zika, or how to identify potential signs of Zika syndrome, evidencing a lack of long-term planning related to possible Zika congenital syndrome cases. **Conclusions:** It is crucial to develop policies and protocols that incorporate surveillance protocols within regular health visits, not only for women, but for men and specially for children. Health personnel, such as nurses and pediatricians, need to know about Zika congenital Zika syndrome and what surveillance actions to deploy. Health systems' policies and protocols need to move from emergency response interventions to developing health prevention and monitoring guidelines at local and intermediate levels of care.

Board 310. Local Response to an Emerging Infectious Disease: Results and Lessons from a Urosurvey to Investigate Local Zika Virus Transmission

S. Lutchman, B. O'Sullivan, R. Parkes
Florida Department of Health in Palm Beach County, West Palm beach, FL, USA

Background: Zika virus (ZIKV) is a mosquito borne disease that may result in congenital abnormalities like microcephaly when contracted during pregnancy. On August 22, 2016, the Florida Department of Health (DOH) in Palm Beach County confirmed a case of local, non-travel related ZIKV. DOH Bureau of Epidemiology (BOE) requested a urosurvey to assess for evidence of ongoing local transmission of ZIKV. This deployment was also used as an opportunity to assess county readiness to respond to an emerging infectious disease in a vulnerable population. **Methods:** An incident command structure (ICS) was implemented for this investigation to organize survey teams and coordinate with outside groups. Teams from the environmental health (EH) section of DOH-Palm Beach and local mosquito control assessed the survey area for mosquito breeding sites. A respondent was eligible for the urosurvey if they resided in the survey area, and had no history of travel in the preceding two weeks or sexual contact with a person with travel history to an area of ongoing ZIKV transmission. For the urosruvey, residents were asked to give urine for Real-time Polymerase Chain Reaction (RT-PCR) testing. Pregnant women in the survey area were advised to go to a DOH clinic for serum testing. DOH-Palm Beach carried out a reconnaissance of homes in a 150-meter radius around the local ZIKV case. **Results:** On September 1 and 2, 2016, a total of 182 homes in the survey area were visited. Survey teams were multilingual, and able to conduct interviews in English, Spanish and Haitian Creole. 18 mosquito breeding sites were identified and mitigation done. 72 urine samples were collected from residents for testing. Women who self-identified as being pregnant were offered ZIKV prevention kits consisting of bed netting, non-spermicidal condoms and insect repellants. All urine samples were negative for ZIKV by RT-PCR. **Conclusions:** There was no evidence of ongoing local ZIKV transmission. DOH-Palm Beach was able to implement the ICS and deploy teams within 72 hours of the urosurvey being requested by BOE. Teams completed the urosurvey over two days, and lab results were available the day after sample collection. This prompt and timely action indicates Palm Beach County's readiness for response to emerging infectious diseases

Influenza Vaccines, Preparedness, and Response

Board 311. Dose Effect of Influenza Vaccine on Protection against Laboratory-Confirmed Influenza Illness among Children 6 Months to 8 Years of Age in Southern China, 2013-2016 Seasons: A Matched Case-Control Study

C. Fu[1], C. Greene[2], Q. He[3], Y. Liao[4], Y. Wan[5], J. Shen[3], C. Rong[1], S. Zhou[6]
[1]Zhejiang Chinese Medical University, Zhejiang, China, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Guangzhou Center for Disease Control and Prevention, Guangzhou, China, [4]Southern Medical University, Guangzhou, China, [5]University of Nebraska-Lincoln, Lincoln, IL, USA, [6]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: We conducted a matched case control study in China during 2013-16 influenza seasons to estimate influenza vaccine effectiveness (VE) by dose among children aged 6 months to 8 years. **Methods:** Cases were laboratory-confirmed influenza infections identified through the influenza-like illness sentinel surveillance network in Guangzhou. Age and sex matched community controls were randomly selected through the expanded immunization program database. We defined priming as receipt of ≥1 dose of influenza vaccine during the immediate prior season. **Results:** In total, 4,185 case-control pairs were analyzed. Among children 6-35 months, VE for current season dose(s) across the three seasons were 58%(95%CI:40-71), 13%(95%CI:-11,32), 62%(95%CI:39-76); among unprimed children, VE for 1 vs 2 current season doses were 44%(95%CI:4-68) vs 70% (95%CI:50-82), -4%(95%CI:-58,31) vs 20%(95%CI:-11,43), and 48%(95%CI:-8,75) vs 67%(95%CI:39-82). Among all children aged

3-8 years, VE for current season dose(s) across study seasons were 61%(95%CI:31-78), 45%(95%CI:23-60), 35%(95%CI:3-57). VE for unprimed children receiving 1 dose only in current season was insignificant and lower than among all children. **Conclusions:** Findings support utility of providing second dose ("booster dose") of seasonal influenza vaccine to unprimed children aged 6-35 months, and the need to study further dose effect of a booster dose among unprimed children aged 3-8 years in China.

Board 312. Demographic Differences in Flu Vaccination among Florida's High School Students: Evidence from 2017 Florida Youth Risk Behavior Survey

W. Al Khoury, C. Bhatt
Florida International University, Miami, FL, USA

Background: CDC declared an influenza (flu) epidemic in the United States. Children, older adults, and high school students are among the most vulnerable groups. CDC indicates Florida as one of the states with high influenza-like illness and recommends periodic flu vaccination in preventing transmission. This study examines prevalence of flu vaccination in Florida high school students and presents analysis for students not receiving flu vaccination. **Methods:** Data from the 2017 Florida Youth Risk Behavior Survey were analyzed for data on students not receiving flu vaccine; and if received, where. Bivariate analyses were conducted to identify characteristics associated with students who did not receive flu vaccination. **Results:** In 2017, of the 6171 Florida high school students responding to the survey, 44.5% did not receive flu vaccination in the prior 12 months. Girls (53.3%), whites (46.8%), and heterosexuals reported higher rates for flu vaccination than Blacks (26.8%), Hispanics (20.8%), and students who identified as gay, lesbian, or bisexual (54%). Students 16 years and older (45.5%) reported lower rates than younger students. Predictors of students reporting no flu vaccination were female (OR: 1.321 p=0.001), Black (OR: 0.686 p=0.001), Hispanic (OR: 0.689 p=0.001) and gay, lesbian & bisexual (OR: 1.528 p=0.12). The largest number of students indicated receiving their flu vaccination at doctor's offices (30.6%) with lower numbers indicating health department (2.4%), pharmacy (2.6%), and school (2.6%). **Conclusions:** Flu vaccination coverage was less than forty-five percent in Florida in 2017. Female, white, and sexual minority students were less likely to receive flu vaccination. Given that the Healthy People 2020 set a vaccination benchmark of 70%, the flu vaccination coverage in Florida's high school students raises a red flag that needs to be addressed based on the results hereby identified.

Board 313. Do Thai Physicians Recommend Seasonal Influenza Vaccines to Pregnant Women? A Cross-Sectional Survey of Physicians' Perspectives and Practices in Thailand

P. Praphasiri[1], D. Ditsungneon[1], A. Greenbaum[3], F. Dawood[3], P. Yoocharoen[4], D. Stone[5], S. Olsen[3], K. Lindblade[3], C. Muangchana[6]
[1]Influenza Program, Thailand Ministry of Public Health—US Centers for Disease Control and Prevention Collaboration, Nonthaburi, Thailand, [3]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Department of Disease Control, Ministry of Public Health, Nonthaburi, GA, USA, [5]Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]National Vaccine Institute (public organization), Nonthaburi, Thailand

Background: Physicians play a major role in influencing acceptance and uptake of vaccines. However, little is known about physicians' perspectives on influenza vaccination of pregnant women in Thailand, for whom vaccine coverage is estimated at <1%. **Methods:** In 2013, a self-administered questionnaire on physicians' perceptions, attitudes and practices related to influenza vaccination for pregnant women was distributed to 1,134 hospitals with an antenatal care clinic (ANC) in Thailand. At each hospital, one physician working at the ANC completed the survey. Predictors of routine recommendation of influenza vaccine were analyzed utilizing log-binomial regression. **Results:** Results A total of 580 (51%) complete responses were received from physicians practicing at ANCs. A favorable attitude towards vaccination was expressed by 436 (75%) physicians, however only 142 (25%) reported routinely recommending influenza vaccine to pregnant women in their current practice. Physicians were more likely to recommend influenza vaccine routinely when they had more than three years of practice (prevalence ratio [PR] 1.9, 95% CI 1.2±2.3), had treated pregnant women for influenza (PR 1.8, 95% CI 1.3±2.7), perceived the influenza vaccine to be effective (moderate level: PR 1.6, 95% CI 1.1±2.4; high level: PR 1.9, 95% CI 1.3±2.9) and were aware of the Ministry of Public Health's (MOPH) recommendation of influenza vaccination in pregnancy (PR 1.3, 95% CI 1.1±1.7). Vaccine not being available, perception that policy was ambiguous and lack of awareness of MOPH recommendations were the most commonly cited barriers to routine recommendation of influenza vaccine. **Conclusions:** Despite a national policy to vaccinate pregnant women for influenza, only 25% of Thai physicians working in ANCs routinely recommend vaccination. Strategies are needed to increase vaccine availability and free vaccine services, address clinician concerns over vaccine effectiveness and expand healthcare provider awareness of MOPH recommendations.

Board 314. Predictors of Seasonal Influenza Vaccination among Older Adults in Thailand

P. Praphasiri[1], D. Ditsungnoen[1], S. Sirilak[2], J. Rattanayot[3], P. Areerat[4], F. Dawood[5], K. Lindblade[5]
[1]Influenza program, Thailand MOPH-US CDC Collaboration, Nonthaburi, Thailand, [2]Technical Health Office, Thailand Ministry of Public Healt, Nonthaburi, Thailand, [3]National Health Security Office, Bangkok, Thailand, [4]Nakhon Phanom Provincial Health Office, Nakhon Phanom, Thailand, [5]Influenza Division, United States Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Observational studies of influenza vaccine effectiveness (VE) are vulnerable to confounding by factors that are associated with both influenza vaccination and effectiveness. To identify potential confounders for a cohort study to assess influenza VE, we conducted a population-based, cross-sectional survey to measure vaccine coverage and identify factors associated with influenza vaccination among older Thai adults. **Methods:** We selected adults aged ≥65 years using a two-stage, stratified, cluster sampling design. Functional status was assessed using the 10-point Vulnerable Elders Survey; scores ≥3 indicated vulnerability (i.e. at greater risk of mortality). Extra vaccine was brought to increase coverage and provided for free. Questions about attitudes and cues to action towards vaccination were based on the Health Belief Model. Distances between participants' households and the nearest vaccination clinic were calculated. Vaccination status was determined using the national influenza vaccination registry. Preva-

lence ratios (PR) and 95% confidence intervals (CIs) were calculated using log-binomial multivariable models accounting for the sampling design. **Results:** We enrolled 581 participants, of whom 60% were female. The median age was 72 years; 41% (N=236) had at least one chronic underlying illness, 24% (N=138) met the criteria for vulnerable functional status, and 23% (N=135) did not leave the house on a daily basis. Thirty-four percent of participants were vaccinated (95% CI 2.1-4.3). In multivariable models, no variable related to functional status was associated with vaccination status. The strongest predictors of vaccination were distance to the nearest vaccination center (PR 3.0, 95% CI 1.7±5.1 for participants in the closest quartile compared to the furthest), high levels of perceived benefit of influenza vaccination (PR 2.8, 95% CI 1.4±5.6), physician's attitudes toward vaccination (PR 2.7, 95% CI 1.5±5.1). **Conclusions:** Strategies that emphasize benefits of vaccination and encourage physicians to recommend annual influenza vaccination could improve influenza vaccine uptake among older Thai adults. Outreach to more distant and less mobile older adults may require mobile clinics to improve influenza vaccination coverage.

Board 315. Immunogenicity Following Influenza Vaccination among Thai Older Adults with and without Prior Vaccination

J. Mott[1], P. Prabda Praphasiri[1], P. Puthavathana[2], D. Ditsungnoen[1], M. Chittaganpich[3], J. Patumanond[4], F. Dawood[6], K. Lindblade[5], K. Prasert[4]
[1]CDC-Thailand MOPH Collaboration, Bangkok, Thailand, [2]Mahidol University, Bangkok, Thailand, [3]Thailand National Influenza Center, Bangkok, Thailand, [4]Nakhon Phanom Provincial Hospital, Nakhon Phanom, Thailand, [5]World Health Organization, Geneva, Switzerland, [6]Influenza Division, US CDC, Atlanta, GA, USA

Background: We measured duration of influenza vaccine immunogenicity among Thai adults > 65 years and its association with previous vaccination status. **Methods:** Adults ≥65 years (n=370) were vaccinated with two trivalent inactivated Southern Hemisphere vaccines 12 months apart in 2015 and 2016 as part of a prospective study. Hemagglutination inhibition (HI) assays were performed using goose RBC on sera collected at five time points: baseline (before first vaccination), 1, 6 and 12 months after 1st vaccination, and 1 month after 2nd vaccination. Vaccination status in 2014 was collected from medical records. We assessed geometric mean titers (GMT), and seroprotection (HI titer >40) by 2014 vaccination status, adjusting for age and gender using generalized linear regression and logistic regression as appropriate. **Results:** Baseline GMTs of those vaccinated in 2014 (n=203) were significantly higher than those not vaccinated (n=167) for A(H1N1) pdm09 (15 vs 3) A(H3N2) (32 vs 8) and B (14 vs 4) (all p<0.01). Adjusted baseline seroprotection was also greater in those vaccinated in 2014: A(H1N1)pdm09 (40% vs 12%), A(H3N2) (54% vs 26%) and B (37% vs 16%) (all p<0.01). At 1 month post 2015 vaccination, GMTs in those vaccinated and not vaccinated in 2014, respectively, were 68 and 60 for A(H1N1)pdm09, 368 and 289 for A(H3N2), and 83 and 60 for B (p<0.01 for B only). One month, adjusted 2015 seroprotection rates increased and were not significantly different by 2014 vaccination status for A(H1N1)pdm09 (78% vs 70%), but were significantly higher in those vaccinated in 2014 for A(H3N2) (97% vs 90%, p=0.01) and B (87% vs 74%, p<0.01). The 6 and 12 months seroprotection rates, regardless of 2014 vaccination status, were 57% and 47% against A(H1N1)pdm09; 85% and 80% for A(H3N2) and 59% and 49% for B. Following the 2016 vaccination, seroprotection increased to 89%, 99% and 86% for A(H1N1)pdm09, A(H3N2), and B, respectively. Seroprotection in 2016 was significantly lower for A(H1N1)pdm09 among those vaccinated in 2014 compared to those not vaccinated in 2014 (84% vs. 94%; p<0.01), although high in both groups. **Conclusions:** Regardless of 2014 vaccination status influenza vaccination elicited good humoral response and seroprotection in Thai older adults for all vaccine types and subtypes.

Board 316. Effectiveness of Trivalent Inactivated Influenza Vaccine among Community-Dwelling Older Adults in Thailand: A Two-year Prospective Cohort Study

K. Prasert[1], J. Patumanond[2], P. Praphasiri[3], D. Ditsungnoen[3], S. Siriluk[4], M. Chittaganpich[5], F. Dawood[6], J. Mott[6], K. Lindblade[6]
[1]Nakhon Phanom Provincial Hospital, Nakhon Phanom, Thailand, [2]Thammasat University, Pathum Thani, Thailand, [3]Influenza program, Thailand MOPH-US CDC Collaboration, Nonthaburi, Thailand, [4]Health Technical Office, Thai Ministry of Public Health, Nonthaburi, Thailand, [5]National Institute of Health, Thai Ministry of Public Health, Nonthaburi, Thailand, [6]Influenza Division, United States Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Older adults are at increased risk for severe influenza, but robust prospective studies of influenza vaccine effectiveness in this population are limited, particularly in middle-income countries. During the 2015 and 2016 influenza seasons, we conducted a two-year prospective longitudinal cohort study to measure the effectiveness of Southern Hemisphere trivalent inactivated influenza vaccine (IIV3) to prevent laboratory-confirmed influenza among community-dwelling older Thai adults aged ≥ 65 years. **Methods:** After an enhanced vaccination campaign to encourage vaccine coverage among high-risk groups, we enrolled a cohort of 3,320 older adults in 2015. Trained health volunteers collected data on baseline characteristics including functional status at enrollment and followed participants for two years with weekly surveillance for new or worsened cough with nasal swab collection for influenza virus testing by rRT-PCR during illness episodes. VE was estimated as 100% × (1- Relative Risk) of laboratory-confirmed influenza among vaccinated versus unvaccinated participants. Propensity score stratification was used to adjust for age, sex, functional status, co-morbidity, educational level and smoking status. **Results:** Among the cohort, 1,666 (52%) received influenza vaccine in 2015 and 1,498 (48%) in 2016. The incidence of influenza during the two seasons was 14.3/1000 person-years among vaccinated participants and 20.2/1000 person-year among unvaccinated participants. The adjusted VE was -4% (95% CI, -83%–40%) during 2015, when there was poor antigenic match between the dominant circulating A/H3N2 viruses and the vaccine strain, and 50% (95% CI, 12%–71%) during 2016 when dominant circulating A/H3N2 and vaccine strains were well-matched. Of all three influenza virus types/subtypes in both years, significant protection was observed only against influenza A/H3N2 virus in 2016 (adjusted VE, 49%; 95% CI, 3%–73%). **Conclusions:** During a season with a good match between circulating and vaccine strains, IIV3 was moderately effective against laboratory-confirmed influenza among older adults in Thailand.

Board 317. Seasonal Influenza Vaccine Effectiveness among Persons with Chronic Obstructive Pulmonary Disease in Thailand, 2011-2013: A Retrospective Cohort Analysis

P. Praphasiri[1], K. Prasert[2], J. Patumanond[3], D. Ditsungnoen[1], J. Rattanayot[4], J. Thungthong[4], K. Lindblade[5], F. Dawood[5], J. Mott[5]
[1]Influenza program, Thailand MOPH-US CDC Collaboration, Nonthaburi, Thailand, [2]Nakhon Phanom Provincial Hospital, Nakhon Phanom, Thailand, [3]Thammasat University, Pathum Thani, Thailand, [4]National Health Security Office, Nonthaburi, Thailand, [5]Influenza Division, United States Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: We estimated influenza VE against respiratory illness hospitalizations and all-cause mortality among patients with COPD in Thailand during 2011-2013 influenza seasons. **Methods:** We assembled a retrospective cohort of Thai adults aged ≥18 years with COPD prior to each season using ICD-10 codes (J40, J41 and J44.1) to identify participants from a public COPD clinic. Data on COPD history, hospitalizations and influenza vaccination status were abstracted from the National Health Security Office. Mortality data were obtained from the National Vital Statistics Office. Influenza VE was estimated by comparing numbers of ICD-10 coded discharge diagnoses for influenza and pneumonia (J9-J18), and COPD exacerbations (J44.1) and all-cause deaths in each season between vaccinated and unvaccinated COPD patients using Poisson regression analysis. Propensity scores were used to match for age, sex, smoking status, severity of COPD, and numbers of COPD exacerbations and hospitalizations in the previous year. **Results:** Overall, 117,894 COPD patients were included in the cohort; median age was 70 years (IQR 61-77) and 90,161 (77%) were male; influenza vaccination coverage was 35% in 2011 and 41% in both 2012 and 2013. The predominant circulating strain in 2011 was A (H3N2), well-matched by the vaccine strain. In 2012 and 2013, predominant circulating strains were B and A (H3N2) respectively, but vaccine strains had a poor antigenic match. VE against influenza hospitalizations was significant in 2011 (54%; 95% CI, 26%-72%), but non-significant in 2012 (22%; 95% CI, -12%-46%) and 2013 (9%; 95% CI, -14%-27%). VE against pneumonia, COPD exacerbation and death ranged from 51%-57% in 2011, 32%-35% in 2012 and 29%-43% in 2013 (all p<0.001). **Conclusions:** Influenza vaccination provided protection against ICD-10 coded influenza when there was a good match between circulating and vaccine strains. Significant VE against pneumonia, COPD exacerbations and deaths may suggest possible extended benefits of influenza vaccination among persons with COPD.

Board 318. Blunting of Serum Hemagglutinin Inhibition Antibody Response to 2010-11 Trivalent Influenza Vaccines Is Associated with Receipt of Specific Prior Inactivated Influenza Vaccines and Mediated by Antibodies to These Vaccine Strains

J. Reich[1], A. Naleway[2], S. Ball[3], V. Veguilla[1], M. Gaglani[4], M. Thompson[1]
[1]US Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [2]Kaiser Permanente, Center for Health Research, Portland, OR, USA, [3]Abt Associates, Atlanta, GA, USA, [4]Baylor Scott and White Healthcare, Garland, TX, USA

Background: Despite growing consensus that repeated vaccinations with inactivated influenza vaccines (IIVs) can blunt serum hemagglutinin inhibition (HI) antibody response to vaccination, the underlying immune mechanisms remain unclear. We examined whether antibodies to historic vaccine strains prior to vaccination mediate the inverse association between receipt of specific prior trivalent IIVs (IIV3s) and HI response post-vaccination. **Methods:** A study sample of 577 healthcare personnel (HCP) with at least four years of vaccination records from a 2010-11 prospective cohort study in Oregon and Texas contributed pre-season and ~30 days post-IIV3 sera. HI assays were performed against the A(H3N2) and B influenza components of the 2010-11 trivalent (IIV3) vaccine and the 4 prior IIV3s. Estimates of mean fold change (MFC) in HI after vaccination and of mediation effects (using the product of coefficient strategy) were adjusted for age, sex, race, education, household size, care setting, and study site. **Results:** Adjusted MFC to 2010-11 IIV3's A(H3N2), A/Perth/2009 was inversely associated with the number of 2006-07 and 2007-08 IIV3s received ($F[2,567] = 13.99$, $p < .0005$, partial $\eta 2 = .047$) but not associated with the receipt of 2008-09 and 2009-10 IIV3s ($p = .36$). This inverse association was significantly mediated by pre-vaccination antibodies to the A(H3N2), A/Wisconsin/2005 strain in these earlier vaccines (-.15; 95% CI = -.30, -.02). Adjusted MFC to 2010-11 IIV3's B/Brisbane/2008 (B/Victoria lineage) was inversely associated with receipt of the 2009-10 IIV3 (with homologous B/Victoria) ($F[1,565] = 31.93$, $p < .0005$, partial $\eta 2 = .053$) and 2008-09 IIV3 ($p = .07$) and the sum of 2006-07 and 2008-09 IIV3s received ($p = .03$). These inverse associations were significantly mediated by pre-vaccination antibodies to B/Florida/2006 (B/Yamagata) (-.28; 95% CI = -.81, -.06) and B/Malaysia/2004 (B/Victoria) (-.28; 95% CI = -.93, -.01). **Conclusions:** Blunted HI antibody responses to the A(H3N2) and B/Victoria components of the 2010-11 IIV3 were associated with receipt of specific IIV3s during the prior 4 years and mediated by pre-vaccination antibodies to these specific IIV3s. Understanding underlying mechanisms may have implications for influenza vaccine strain selection and the evaluation of alternative vaccines.

Board 319. Analysis of Impact of Flu Vaccination on Acute Respiratory Viral Infections (ARVI) Morbidity among Population in South Kazakhstan Region, 2010-2015

K. Tulendieva
Epidemiological Surveillance Department of Consumers' Rights Protection, Shymkent, Kazakhstan

Background: Presently vaccination is the most effective method of prevention of flu and its complications. The purpose of this study was to analyze the impact of increase of coverage of the population of South Kazakhstan region with flu vaccination and decrease of the ARVI morbidity. **Methods:** Analysis was performed of the data of flu vaccination of risk groups, including children under one year and pregnant women. Data on ARVI morbidity during 2010-2015 and data on vaccination were taken from the reports of the Epidemiological Surveillance Department of South Kazakhstan region. **Results:** Coverage with flu vaccination of the risk groups was annually increasing and in 2015 it reached 16% (450,000/2,800,682) from the total population. The ARVI morbidity rate in the entire population in 2010 was 2,010.4 per 100,000 of population and decreased 3.2 times to 609.9 per 100,000 of population in 2015. Annual growth was observed from 2010 to 2015 of specific weight of the vaccinated main risk groups: healthcare workers by 51%, children with chronic pulmonary and cardiovascular diseases, immune deficiency by 39%, adults with chronic co-morbidities by 27%, persons above 65 by 17%, and annual cov-

erage of pregnant women on second or third trimester from 34,443 in 2010 to 37,969 in 2015. Starting from 2013 and until 2015 vaccination was performed in the region with coverage of at least 90% of children from 6 months to one year. The ARVI morbidity in this age group decreased 3.3 times. Annual increase of vaccination coverage of pregnant women from 86.1% in 2012 to 95% in 2015 decreased the morbidity 1.5 times from 4,828.8 per 100,000 of population in 2012 to 3,022.7 per 100,000 of population in 2015. **Conclusions:** Following the increase of vaccination coverage of the population in South Kazakhstan region the trend was observed of decrease of ARVI morbidity rates among population and main risk groups, among pregnant women and children under one year.

Board 320. Post-Licensure Surveillance of Trivalent Adjuvanted Influenza Vaccine (Fluad®) in Adults Aged >65 years, United States, Vaccine Adverse Event Reporting System (VAERS), July 2016-June 2018

M. Cano, P. Lewis, C. Ng, P. Moro, P. Haber
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Trivalent adjuvanted influenza vaccine (aIIV3; Fluad®) was approved in 2015 for adults aged >65 years. Data on aIIV3 safety in a US population are limited. **Methods:** We analyzed aIIV3 Adverse Event Reports (AEs) from 07/1/2016-03/31/2018 in the Vaccine Adverse Event Reporting System (VAERS), a national spontaneous reporting system. Medical records were reviewed for serious reports (i.e., death, hospitalization, prolonged hospitalization, life-threatening illness, permanent disability). The most frequently reported MedDRA Preferred Terms (PTs) were compared with high-dose trivalent inactivated influenza vaccine (TIV-HD). We also compared proportions of Guillain Barré Syndrome (GBS), anaphylaxis and injection site reactions. **Results:** During 2016-18, VAERS received 512 reports following aIIV3; 18 (3.5%) were serious, including two deaths (0.4%), both due to chronic cardiac conditions. During the same period, VAERS received 4344 TIV-HD reports; 170 (4%) were serious and included 10 (0.2%) deaths. Mean age of 73 years was similar in both groups. The safety profile was similar in both groups; the most frequent PTs were pain in extremity (21% vs. 17%), injection site erythema (18% vs. 19%) and injection site pain (14% vs. 16%). We observed higher proportions of vaccination errors with aIIV3 vs. TIV-HD, 4.5% and 1.7%, respectively. Most frequently reported vaccination error was incorrect dose (44%) for aIIV3 and administration contraindication (42%) for TIV-HD. The proportions of GBS after aIIV3 and TIV-HD were similar (0.6% vs. 0.7%, respectively), likewise for injection site reactions (35 % vs. 37%), and for anaphylaxis (0% vs. 0.2%). **Conclusions:** Our analysis of VAERS reports of aIIV3 did not identify any new or unexpected pattern of AEs.

Board 321. Public Awareness Status against Influenza A H1N1: A Comparative Case Study at District Lahore and Multan, Punjab, Pakistan

M. Mahmood[1], F. Munir[2], A. Rehman[3], S. Khan[4], F. Ali[5], U. Ghani[6]
[1]District Health Authority, Lahore, Pakistan, [2]Institue of Education and Research, University of the Punjab, Lahore, Pakistan, [3]Government Degree College for Boys, Jaranwala, Jaranwala, Pakistan, [4]University of Sargodha, Sargodha, Pakistan, [5]Office of the CEO Health Multan, Multan, Pakistan, [6]Directorate General Health Punjab, Lahore, Pakistan

Background: Influenza, frequently called as "flu," has become a serious issue of public health concern since last few years. The average number of cases per year due to severe influenza like infections (ILIs) ranges from 3 to 5 million with approximate 500,000 deaths worldwide. In Pakistan high incidence of ILIs are reported during winter season. Since 2009, out breaks of the novel virus influenza AH1N1 have been reported from different areas of the country with many morbidities and mortalities. Recent outbreak has been reported from southern districts of the Punjab in last months of 2017 where more than 106 cases were confirmed along with 35 deaths. Government authorities have taken immediate measures thereby vaccinating all contacts of the patients, awareness of the masses and free treatment facilities at all hospitals. Aside from in-time reporting at hospital for treatment, it is much more important to be aware of personal protection measures at household level to minimize the spread influenza virus. **Methods:** In the above context this comparative study was planned to know the level of public awareness about preventive practices against ILIs in district Lahore (low infected) and district Multan (highly infected). Instrument of the study was structured questionnaire about the preventive practices against ILIs. Data was collected from 200 subjects (100 from each district) by using random sampling technique and analyzed. **Results:** Findings of the study revealed that over 55 percent people of the district Lahore and 70% people of the district Multan are not aware of preventive measures against ILIs particularly influenza AH1N1. **Conclusions:** It was concluded that the status of public awareness about preventive measures of ILIs (particularly influenza AH1N1) amongst the people of the Punjab province is much low and is one of the major factor of frequent outbreaks being reported from different parts of the Province.

Board 322. Molecular Characterization of Influenza Viruses Circulating in Casablanca, Morocco from 2013 to 2018

L. Anga[1], A. Faouzi[1], A. Idrissi[2], N. Elmdaghri[1], J. Nourlil[1]
[1]Institut Pasteur, Casablanca, Morocco, [2]Regional Observatory of Health - Ministry of Health., Casablanca, Morocco

Background: Influenza viruses are a major cause of acute respiratory infections and causes high morbidity and mortality associated with substantial health and economic burdens. Therefore, surveillance and molecular characterization of influenza viruses remains a crucial tool of both preventive and curative control. The objectives of this study are the identification and molecular characterization of human influenza viruses circulating in Casablanca from season 2013-2014 to 2017-2018. Influenza viruses are a major cause of acute respiratory infections and a public health problem that causes high morbidity and mortality associated with substantial health and economic burdens. Therefore, surveillance and molecular characterization of influenza viruses remains a crucial tool of both preventive and curative control. The objectives of this study are the identification and molecular characterization of human influenza viruses circulating in Casablanca from season 2013-2014 to 2017-2018. **Methods:** A total of 984 Nasopharyngeal samples from outpatients with clinical influenza-like illness (ILI) were collected from week 45/2013 to week 08/2018 and analyzed by RT-real time PCR targeting the hemagglutinin and neuraminidase genes, positive samples for influenza viruses were inoculated on Madin-Darby canine kidney cell line for virus isolation followed by nucleotide sequencing. **Results:** Two hundred fifty-one (36.79%) sam-

ples were positive for influenza. Influenza A viruses were detected in 260 (71.62%) specimens, of which 83 (31.92%) were A /H1N1 pdm09 and 170 (65.38%) were A/H3 subtype. Influenza B virus was detected in 92 (36.65%). Furthermore, the findings in the present study confirm the variability of influenza circulating strains from one season to another. During 2015-2016 and 2017-2018, influenza B lineage detected were not included in the trivalent influenza vaccines. **Conclusions:** The continuous monitoring and molecular characterization of influenza viruses is an essential tool for understanding their epidemiological and virological characteristics and their matching with seasonal vaccine strains. The results presented during this study period suggest that a quadrivalent vaccine, including both Yamagata and Victoria lineages, should be considered for future influenza vaccination to ensure higher levels of protection.

Board 323. Pandemic Influenza Surveillance: Learning From the Past to Improve Future Responses

B. Paterson[1], W. Zhou[2], C. Blackmore[3]
[1]University of Newcastle, Newcastle, Australia, [2]WHO, Geneva, Switzerland, [3]WHO Europe, Copenhagen, Denmark

Background: Evaluations conducted after the 2009 A(H1N1)pdm09 influenza pandemic provided an opportunity to review the effectiveness of influenza surveillance systems and consider requirements for future pandemics. **Methods:** Desk-top review of published English language articles on pandemic influenza surveillance. Referenced documents were primarily sourced through a Medline search using the terms "pandemic AND surveillance" AND published after the start of the 2009 influenza pandemic (April 2009). Reference lists of relevant articles were hand searched to obtain additional relevant articles. **Results:** Key evaluation findings were: During the pandemic, epidemiology and laboratory personnel were quickly overwhelmed. Triggers are needed for when to cease surveillance activities. Case-based reporting should cease once there is broad community transmission. A surveillance model relying on syndromic data and selective, systematic virologic testing may be more revealing than focusing on laboratory-confirmed cases. The heterogeneous nature of the pandemic demonstrated the need for flexibility of case definitions and transition between pandemic phases. There needs to be an agreed standardised minimum dataset at national and international levels to enable decision making, utilising electronic reporting and databases, with epidemiologists to analyse and interpret the data. Estimation of deaths was problematic and yet was the most commonly requested data by decision makers. Hospital data were key to understanding severity and progression of the pandemic but collection was a burden on clinicians. Need to distinguish between laboratory testing for diagnostic purposes versus testing for surveillance purposes. Systematic laboratory testing is only justifiable for the first few hundred domestic cases. Modeling was less useful than expected, particularly in the early stages of the pandemic but contributed to decision making, especially vaccination production and distribution. Research processes need to be streamlined during a pandemic, and protocols for sharing surveillance data agreed upon prior to a pandemic **Conclusions:** Pandemic influenza surveillance evaluations highlighted key surveillance issues that should be considered when planning and implementing pandemic surveillance.

Board 324. Tool for Influenza Pandemic Risk Assessment (TIPRA)

A. Hammond, K. Vandemaele, G. Samaan, M. Samaan, W. Zhang
World Health Organization, Geneva, Switzerland

Background: TIPRA is a globally-applicable hazard-assessment tool for influenza viruses with pandemic potential designed by WHO, based on the US CDC's Influenza Risk Assessment Tool (IRAT). It supports timely and updatable risk assessments, identifies knowledge gaps, facilitates prioritisation of viruses for further action, and complements existing influenza risk analysis platforms. TIPRA does not predict which virus will cause the next pandemic, quantify the exact risk statistically, or eliminate the need for technical experts. **Methods:** TIPRA asks the risk question: "What is the risk of sustained human-to-human transmission of the virus?" and examines likelihood and impact. Information about the virus is gathered systematically and presented in a virus profile document. Global technical experts are then invited to score the various risk elements based on the document, characterise the risk and indicate their confidence in the breadth and quality of available data used for risk assessment. The overall virus risk score is then computed using an additive model. The technical experts discuss their findings and provide an overall level of confidence in the risk assessed. **Results:** TIPRA has been utilised on four influenza viruses - A(H5N6), A(H7N9), A(H9N2) and A(H1N1) TRIG. These risk assessments document the current knowledge base of these viruses that might pose threats to a human population, identify knowledge gaps and prompt further investigations including research and surveillance, and facilitate information sharing between scientists, policy-makers and other stakeholders. Relative scoring of these viruses assessed to date will be presented graphically, as will examples of the aggregated risk element scores and the key recommendations derived from the risk assessments. **Conclusions:** Continued use of the tool to validate and refine it are priority activities. Alignment of TIPRA with other tools in the influenza risk assessment landscape also establishes a pipeline for consistent and comprehensive influenza risk assessment along the animal-human interface and maximises the utility of TIPRA outputs for influenza pandemic planning and preparedness. TIPRA's contributions toward broader preparedness and response measures like the IHR be clarified to beneficiaries so that countries can appreciate its unique role in the assessment of the pandemic potential of influenza viruses.

Board 325. Pandemic Influenza Risk and Impact Management: Building Sustainable and Resilient Capacities for Pandemic Response–the WHO's Approaches

W. Zhou, J. Lamichhane, W. Zhang
Global Influenza Programme, World Health Organization, Geneva, Switzerland

Background: Pandemic influenza is unpredictable but recurring events that can have serious consequences on human health and economic well-being worldwide. Advance planning and preparedness to ensure the capacities for pandemic response is critical for countries to mitigate the risk and impact of a pandemic. **Methods:** Following the 2009 influenza pandemic, WHO updated its pandemic influenza preparedness guidance and finalized it in 2017 - the "Pandemic Influenza Risk Management" framework. To facilitate applying the strategies and approaches outlined in the guidance into practice, WHO reviewed best practices and lessons learned from the 2009 pandemic and organized consultations and public comments for developing a package

of practical tools including a checklist, an essential steps guide, and a simulation exercise guide. **Results:** The checklist ensures that all the essential response capacities are taken into consideration in pandemic preparedness planning. It innovatively mapped pandemic preparedness activities with the indicators of IHR (2005) core capacity monitoring framework and Joint External Evaluation (JEE) tool to draw direct link of the essential capacities needed to manage the risk and impact of pandemic influenza with the core capacities required to manage broader health security threats. The essential steps guide focuses on the processes of pandemic preparedness planning to ensure that the objectives are clear and the essential steps and actions are taken in developing or updating a pandemic preparedness plan, which is imperative for the pandemic influenza preparedness plan to be instrumental in guiding pandemic preparedness and response practices. The simulation exercise guide provides countries an easy to use practical tools for designing and carrying out the type of simulation exercises that best fit their needs in evaluating and validating their pandemic influenza preparedness plans. **Conclusions:** This package of practical tools support countries' efforts in pandemic influenza preparedness in the context of strengthening IHR core capacity and health security.

Board 326. WHO Guidance for Surveillance during an Influenza Pandemic: 2017 Update

W. Zhou, B. Paterson, J. Lamichhane, K. Vandemaele, J. Fitzner, A. Hammond, W. Zhang
Global Influenza Programme, World Health Organization, Geneva, Switzerland

Background: Surveillance during an influenza pandemic provides essential information on which pandemic response decisions are based. In early 2009, WHO published a guidance on surveillance during an influenza pandemic. Since then, WHO has made significant progresses in further developing standards and guidance relating to influenza surveillance and pandemic preparedness. Additionally, key surveillance issues that should be considered when planning and implementing pandemic surveillance were highlighted by the IHR (2005) review in relation to the 2009 influenza pandemic. These developments prompted WHO to update the surveillance guidance. **Methods:** The updating process started with a review of lessons learned from the surveillance experiences during the 2009 pandemic as well as best practices, followed by an WHO internal consultation during which the lessons learned and best practices were presented and discussed. An updated guidance was then drafted and presented to a consultation meeting for review and discussion. The comments and suggestions received from the consultation were analyzed and properly addressed in finalizing the document. **Results:** The updated guidance focuses on the key surveillance components during an influenza pandemic: verification and detection, risk and severity assessment, and monitoring the pandemic. Major updates include: reference to the global pandemic phases described in the updated WHO pandemic preparedness guidance "Pandemic Influenza Risk Management"; outlines of roles and responsibilities of Member States and WHO; information on risk and severity assessments to be conducted by Member States; links of surveillance objectives and public health actions; emphasis of the importance of the detailed information of early cases; resources of protocols for special studies; and references of up-to-date guidelines and best practices. **Conclusions:** This guidance outlines the surveillance strategies and essential data requirements that Member States can use throughout the course of an influenza pandemic to enable timely risk and severity assessments and inform evidence-based decisions for pandemic response.

Board 327. Reinforcing Response to an Influenza Pandemic under the Pandemic Influenza Preparedness Program--Experience from a Country in the Eastern Mediterranean Region of WHO

S. Triki[1], M. Obtel[2], G. El Falah[1], M. Elhakim[3], A. Elkholy[3], A. Abubakar[3], S. Malik[3], M. Bigdeli[1]
[1]World Health Organization, Country Office, Rabat, Morocco, [2]Laboratory of Community Health, Preventive Medicine and Hygiene, Laboratory of Epidemiology, Clinical Research and Biostatistics, Department of Public Health, Faculty of Medicine and Pharmacy, University Mohammed V, Rabat, Morocco, [3]Infectious Hazard Management, Health Emergencies department, EMRO/WHO, Cairo, Egypt

Background: Pandemic Influenza Preparedness Framework Partnership Contribution (PIP-PC) started to support Morocco as other countries in the Eastern Mediterranean Region since 2013 to develop their national surveillance systems. The Ministry of Health of Morocco has implemented, under PIP support agreement, the activities of annual multi-sectorial capacity building plans to strengthen the National capabilities of the surveillance and response system to better monitor trends of the circulating influenza viruses. This research aimed to present the progress made in the influenza surveillance and response areas in Morocco from 2013-2017. **Methods:** A review of the activities implemented, under the PIP plan, was realized to identify the main areas of reinforcement. Annual PIP monitoring indicators were explored. In addition, standardized questionnaires were administered to responsible and main actors in the influenza surveillance system. **Results:** This review showed that most of the PIP indicators were performed as : sharing data with GISRS and EMFLU platforms in a weekly basis since 2014; Influenza Like-Illness (ILI) and Sever Acute Respiratory Infection (SARI) surveillance system involving all Moroccan sentinel sites is functional during the influenza season; a weekly epidemiological influenza bulletin is regularly developed and shared with the main actors in the surveillance system since 2015 and an interactive interface and real-time sharing of animals and human health data (one health data) is established. In addition, since 2016, around 31 Rapid Response Teams (RRTs) were trained on the response to an epidemic risk of an novel influenza virus. **Conclusions:** Under the support of PIP program since 2013, Morocco has a functional and performant influenza surveillance system. The early warning capabilities to detection of a new respiratory virus are continually improving

Board 328. One Hundred Years of Influenza Since the 1918 Pandemic--Is China Prepared Today?

R. Zhang[1], X. Dong[2], D. Wang[3], L. Feng[2], L. Zhou[2], R. Ren[2], C. Greene[1], Y. Song[1], E. Azziz-Baumgartner[4], S. Zhou[1], Z. Feng[2]
[1]US CDC, Beijing, China, [2]China CDC, Beijing, China, [3]Chinese National Influenza Center, China CDC, Beijing, China, [4]US CDC, Atlanta, GA, USA

Background: Almost 100 years after the 1918 influenza pandemic, China experienced its largest, most widespread epidemic of human infections with avian influenza A(H7N9), the influenza virus with greatest pandemic potential of all viruses assessed by US Centers for Disease Control and Prevention's Influenza Risk Assessment Tool. We describe China's developments in influenza over the past centu-

ry and ask, what are China's strengths and challenges in pandemic preparedness today? **Methods:** We conducted a historical review of influenza pandemics in China over the past 100 years and milestones in China's capacity to detect and respond to influenza using PubMed, China Knowledge Resource Integrated Database and archived WHO Bulletins, and interviewed China CDC influenza experts to identify current challenges to pandemic preparedness. **Results:** The 1918 influenza pandemic, per local media reports, caused illness and mortality throughout China. The 1957, 1968 and 1977 influenza pandemics likely originated in China, prompting national influenza detection and response capacity building. The Chinese National Influenza Center (CNIC) was established in 1957. In 1977, CNIC developed research infrastructure around the country. Both the 2003 Severe Acute Respiratory Syndrome (SARS) epidemic and the 2009 influenza pandemic triggered additional investment in influenza; CNIC established an extensive influenza surveillance network and in 2010 it became the world's 5th WHO Collaborating Centre for Influenza. Since 2013, China has responded to six epidemics of avian influenza A(H7N9) virus. Although 90% H7N9 cases had live poultry exposure, live poultry trade continues to flourish with inconsistent implementation of system reforms. Seasonal influenza vaccination in China is low (coverage <2%) and infrastructure to vaccinate high risk populations rapidly is limited. The 2017-2018 winter influenza season unveiled insufficient healthcare surge capacity. **Conclusions:** Over the past century, China has become a global leader in influenza detection and response. Remaining challenges include healthcare surge capacity, multi-sectoral systematic planning during inter-pandemic periods, and infrastructure to support rapid vaccination during pandemics. Overcoming these challenges requires greater investment in China's public health and healthcare systems.

Board 329. WHO Public Health Research Agenda for Influenza–2017 Update: Advance Science to Address Unmet Public Health Needs

W. Zhou, J. Lamichhane, W. Zhang
Global Influenza Programme, World Health Organization, Geneva, Switzerland

Background: Since the publication of the 2009 Research Agenda, followed by the publication of the progress review in 2013, much has been learned about influenza. Some knowledge gaps have been filled, but others remain challenging to the scientific community. To identify the remaining and emerging knowledge gaps and stimulate research to address unmet public health needs, WHO initiated the process of updating the WHO Public Health Research Agenda for Influenza. **Methods:** To ensure the technical expertise for updating the research agenda, technical working groups were established. The subject matters experts of each working group exchanged ideas through a web-based platform and via teleconferences to identify key accomplishments, unmet public health needs and major knowledge gaps and corresponding priority areas for influenza research. A Consultation meeting was held for more in depth discussions followed by a public comment period of two month. The inputs received from the public comment were analyzed and properly addressed in finalizing the updated research agenda. **Results:** Results:The updated research agenda focuses on 1) reducing risk; 2) limiting spread; 3) minimizing impact; 4) optimizing treatment; and 5) promoting new tools. Supported by the background documents that summarize the key accomplishments, unmet public health needs, and remaining and emerging knowledge gaps, the high priority areas were identified and research recommendations to address the unmet public health needs were developed. Potential indicators for monitoring and evaluation of the public health impacts of the research recommendations were also discussed and identified in the updating process. **Conclusions:** The updated research agenda emphasizes the high priorities influenza research in addressing unmet public health needs. The outcomes of such researches are expected to benefit the global public health communities by reducing the burden of seasonal epidemic influenza, the risk of emergence and the impact of pandemic influenza over the next 5–10 years.

Board 330. A Data-Driven Tool for Local Influenza Response Policy

R. Payne[1], G. Nowak[2], R. Uniszkiewicz[3], R. Comeau[3], T. Fahey[3], R. Tubbs[3], L. Hall[3], D. Sanders[3], J. Johnson[3]
[1]Battelle Memorial Institute, Hampton, VA, USA, [2]Navy and Marine Corps Public Health Center, Portsmouth, VA, USA, [3]Naval Medical Center Portsmouth, Portsmouth, VA, USA

Background: Naval Medical Center Portsmouth (NMCP) modified an existing policy for the 2017-2018 influenza season from requiring unvaccinated staff to wear facial masks during the entire influenza season to a targeted masking approach. The goal of the policy is to reduce the spread of influenza, however, by modifying the policy NMCP sought to improve compliance by timing the policy with the first signs of local elevated influenza activity. NMCP partnered with the Navy and Marine Corps Public Health Center's EpiData Center (EDC), which conducts routine influenza surveillance for the Department of the Navy, to develop a data driven tool that tracks local influenza activity. **Methods:** The team considered several Military Health System data sources and methodologies to develop the tool, including laboratory-positive cases, dispensed influenza-specific antivirals, and medical encounters for influenza-like illness, which tend to be closely aligned despite having different clinical implications. The team also considered Virginia Department of Health surveillance data and Navy-wide data sources, but ultimately the focus was not narrow enough. The team chose laboratory-positive cases for the tool and a regional area of stand-alone military treatment facilities was identified for inclusion. The EDC established a surveillance alert threshold for when masking should be initiated/ended. The threshold was calculated by establishing an off-season baseline and adding two-standard deviations. Weekly laboratory-positive cases would be identified using an existing algorithm and displayed along with the threshold. The EDC tested the model using data from the past three seasons, which showed a reduction in masking weeks. **Results:** The EDC delivered the tool to NMCP on a weekly basis beginning in October 2017. The NMCP team began requiring masking during week 51, reducing masking time by nearly two months. The policy implementation preceded a consistent increase in influenza activity, demonstrating appropriate timing. **Conclusions:** The regionally based, data-driven tool was valuable for NMCP leaders in the timing of the masking policy and provided an ongoing situational awareness of local influenza activity. In the future, NMCP will continue to use the tool to guide the timing of prevention/mitigation strategies and hopes to use the tool to assess the impact of targeted masking on local influenza activity.

Board 331. Workplace Attendance with Acute Respiratory Illness or Influenza: Effect of Access to Telework

F. Ahmed[1], J. VanWormer[2], J. King[2], M. Gaglani[3], M. Nowalk[4], R. Zimmerman[4], M. Jackson[5], L. Jackson[5], E. Martin[6], C. Cheng[6], B. Flannery[1], J. Chung[1], A. Uzicanin[1]
[1]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [2]Marshfield Clinic Research Foundation, Marshfield, WI, USA, [3]Baylor Scott and White Health, Texas A&M College of Medicine, Temple, TX, USA, [4]University of Pittsburgh, Pittsburgh, PA, USA, [5]Kaiser Permanente Washington Health Research Institute, Seattle, WA, USA, [6]University of Michigan, Ann Arbor, MI, USA

Background: CDC's Community Mitigation Guidelines include recommendations on nonpharmaceutical interventions to mitigate influenza spread during a pandemic. Measures that may be recommended include increasing physical distance between persons and options for teleworking. We assessed the association between access to telework and workplace attendance among adults aged 19-64 years with medically attended acute respiratory illness (ARI) or seasonal influenza. **Methods:** Study enrollees included persons seeking care for ARI at ambulatory care facilities affiliated with five centers participating in the US Influenza Vaccine Effectiveness Network during the 2017-18 influenza season. A follow-up survey administered approximately 7-14 days after enrollment was used to collect information on access to telework and work attendance during the first 3 days of illness. Preliminary data were analyzed for three of the five collaborating centers for the period December 2017 to January 2018. **Results:** Data on 424 adults aged 19-64 years with ARI or influenza who were expected to work ≥35 hours in a typical week were available for preliminary analyses. Among adults with ARI or influenza and access to telework, 26% (22/84) went to work for ≥1 day during illness [the remainder did not work (27%), worked solely from home (20%), or worked both from home and from their workplace (26%)], compared to 56% (189/340) among those with no access to telework [39% did not work, 2% worked solely from home, and 3% worked both from home and from their workplace] ($P < 0.001$). Similar results were obtained among the subset of 181 adults with laboratory-confirmed influenza (24% vs. 46%, $P < 0.05$). **Conclusions:** Among adults with medically attended ARI or influenza, access to telework was associated with a decreased likelihood of going to work, which can reduce transmission to coworkers. Further analyses are pending for the complete data set from all five centers and the entire influenza season.

Board 332. Pandemic Influenza Severity Assessment (PISA)

A. Hammond, K. Vandemaele, J. Fitzner, B. Maharjan, W. Zhang
World Health Organization, Geneva, Switzerland

Background: The 2009 A(H1N1) pandemic revealed that WHO and national organizations did not have a robust and standardized method for timely assessment of the severity of pandemic influenza. In 2011, the World Health Assembly adopted a report by the *Review Committee on the Functioning of the International Health Regulations (2005) and on Pandemic Influenza (H1N1) 2009*. The committee recommended that WHO should develop and apply measures that can be used to assess the severity of every influenza epidemic (whether seasonal or pandemic) as part of pandemic preparedness. A severity assessment provides the scientific evidence needed to determine the timing, scale, emphasis, intensity and urgency of response actions.The Global Influenza Programme developed, with a group of experts, the Pandemic Influenza Severity Assessment (PISA) framework. PISA is intended for use by public health professionals at the national level, who plan to perform national influenza severity assessments, and who can contribute to global influenza severity assessments. **Methods:** The process of assessing severity at the national level is detailed in the PISA guidance. Influenza severity is defined in terms of three indicators: transmissibility, seriousness of disease and impact. Each indicator is derived from parameters collected by routine surveillance systems (e.g. weekly ILI rate can be used for the transmissibility indicator). Once a country selects appropriate parameters for each indicator, thresholds of activity (low, moderate, etc.) for each are developed using historical data. Current activity is compared to these thresholds to arrive at a qualitative assessment for each indicator. The use of qualitative severity assessments using a country's own historical data allows for comparisons of severity between countries, given differences in surveillance systems. **Results:** Anonymized country severity assessments for seasonal influenza epidemics will be graphically presented in several formats, including a heatchart and a map. **Conclusions:** During a meeting in March 2017, there was consensus that the tool should be put into use and the group identified key priorities: developing a communications strategy to address the need for messages tailored to specific audiences, and developing and disseminating training materials to increase country engagement, and refining threshold setting methods for non-temperate countries.

Societal Challenges and Solutions

Board 333. Evaluation of the Surveillance System in Adjumani District Refugee Settlements, Uganda, April 2017

D. Kadobera[1], D. Nakiganda[2], B. Kwesiga[1], E. Atuheire[1], I. Nkonwa[1], I. Nkonwa[1], A. Ario[1]
[1]FETP, Kampala, Uganda, [2]Ministry of Health, Kampala, Uganda

Background: Adjumani District has resettled refugees since onset of the South Sudan conflict in December 2013 and is currently hosting 201,400 refugees. Refugees are vulnerable to disease outbreaks and seasonal peaks in malnutrition. Since the emergency, the camp has experienced measles, cholera and hepatitis E outbreaks. Objectives: We conducted evaluation of the surveillance system in Adjumani Refugee Settlements to identify the system strengths and weaknesses and recommend improvement measures. **Methods:** We determined attributes of the surveillance system using (CDC) guidelines for public health surveillance as a reference. We interviewed the District Health Team and health facility staff using a standard questionnaire to determine their readiness to conduct Integrated Disease Surveillance and Response (IDSR) and used a checklist to ascertain availability of surveillance tools. **Results:** The surveillance system was adequate in terms of stability, acceptability and representativeness. Non-Government Organizations (NGO) facilities used separate, vertical health information system (HIS) as opposed to the standard Ministry of Health, Health Management Information System (HMIS) tools. We found poor timeliness (56%) and reporting rate (63%). There was lack of tools: there were no case investigation forms and registers were available in only 50% of facilities. The system was able to detect some outbreaks–measles in 2014 and cholera in 2015. The District Rapid Response Team (DRRT) and Epidemic Preparedness and Response Committee (DEPRC) are functional but at low grade and thus the capacity to detect

and respond to epidemics were inadequate. **Conclusions:** The surveillance system was simple, stable and able to detect alerts but acceptability by all players and timeliness were poor. We found inadequate implementation of epidemic prevention and preparedness measures by the DRRT. We recommended harmonization of NGOHIS with MoH HMIS to streamline reporting; availing of case investigation forms, case definitions booklets and charts to all health facilities; and more support supervision by the District Health Team.

Board 334. A Comparative Cost Analysis of the Vaccination Program for US-Bound Refugees

H. Joo[1], B. Maskery[1], T. Mitchell[1], A. Leidner[2], A. Klosovsky[3], M. Weinberg[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Berry Technology Solutions, Atlanta, GA, USA, [3]International Organization for Migration, Washington, DC, USA

Background: The Vaccination Program for US-bound Refugees (VPR) provides one or two doses of certain age-specific vaccines recommended by the Advisory Committee on Immunization Practices (ACIP) to US-bound refugees before departure. **Methods:** We quantified and compared vaccination costs for refugees using two scenarios: (1) the baseline of no VPR, and (2) the current situation with the VPR. Under the first scenario, refugees would be fully vaccinated after arrival in the United States. For the second scenario, refugees would receive one or two doses of selected vaccines before departure and complete the recommended vaccination schedule after arrival in the United States. The analyses were conducted for four age groups: (1) infant to 4.9 years old, (2) 5–10.9 years old, (3) 11–18.9 years old, and (4) ≥19 years old. We evaluated costs to complete the recommended vaccination schedule and for the subset of vaccines provided by the VPR. All costs were reported in 2015 US dollars. In sensitivity analyses, we performed one-way, probabilistic, and break-even analyses to evaluate the robustness of results. **Results:** For refugees in all examined age groups, costs with the VPR scenario were lower than in the scenario without the VPR. Net cost savings with the VPR ranged from $225.93 per person for the scenario with estimated Refugee Medical Assistance (RMA) or Medicaid payments for domestic costs to $498.42 for the scenario with estimated private sector payments. Limiting the analyses to only the vaccines provided by the VPR (hepatitis B; diphtheria, tetanus, and pertussis; tetanus, diphtheria; *Haemophilus influenzae* type b; poliovirus; and measles, mumps, and rubella), the average costs per person were 56% less for the VPR scenario than for the scenario without the VPR using RMA/Medicaid payments. Net cost savings with the VPR scenario were sensitive to inputs for vaccination costs, domestic vaccine coverage rates, and revaccination rates. The VPR scenario remained cost-saving across a range of plausible parameter estimates. **Conclusions:** Pre-departure VPR is cost-saving relative to post-arrival domestic vaccination of US-bound refugees.

Board 335. Etiology of Upper Respiratory Tract Infections among Displaced Rohingya Population in Bangladesh

K. Islam[1], A. Muraduzzaman[2], H. Shahalam[2], A. Maruf[2], T. Shirin[2], A. Alamgir[2], M. Flora[2]
[1]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh

Background: Recent influx of displaced Rohingya people causing huge burden of refugee population southern part of Bangladesh. They are poorly vaccinated, living in an overcrowded area with limited sanitation, hygiene and scarcity of safe water. So, when the local health authority informed about increase number of acute respiratory infection cases in refugee camps, an urgent investigation was summoned. **Methods:** On 12 December 2017 five-member IEDCR team went to a health care center in a refugee camp and approached the attending doctors and asked them to refer cases of respiratory tract infection for enrollment. After verbal consent, the team randomly collected 20 naso and oro pharyngeal swabs from the cases with proper biosafety protection. At that time the Diphtheria outbreak is ongoing in the camps and people are scared about the respiratory tract infections. The samples were transported with appropriate measures to a reference laboratory and tested for respiratory pathogens by a commercially available multiplex real-time PCR kit (FTD Respiratory pathogens 33). **Results:** Among the 20 cases 12 (60%) were female and half of them (50%) were under 10 years of age. The age range was 18 months to 70 years. The onset varied from 1 to 9 days. Majority presented with cough (90%), nasal discharge (85%), fever (75%) and sore throat (10%). Each of the two cases had symptoms of chest tightness (10%) and history of asthma (10%). Only 2 (10%) had history of exposure to poultry or animal. Laboratory results showed all the cases were infected with common respiratory viruses and 8 patients (40%) were co-infected two or more viruses. 12 (60%) were positive for R*hino* virus and 12 (60%) for *Human Corona* virus. Two cases (10%) were positive for *Influenza A* H1N1 pdm09. The other viruses are *human meta-pneumo* and *para-influenza* virus. 75% (9) cases of *Rhino* viral infection cases are under 12 years of age. **Conclusions:** During winter season, the rapid drop in temperature causes an increased number of common cold cases (by respiratory viruses, commonly rhinovirus and human coronavirus) in Bangladesh. The same viral infection trend was seen in this displaced refugee population.

Board 336. CDC Migration Health Data Management and Notification of Newly Arrived Persons with Overseas Tuberculosis Classification: eMedical to EDN

D. Lee, Y. Haber, A. Grills, N. Marano
US Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: For over 10 years, the Electronic Disease Notification (EDN) system has been employed by the Centers for Disease Control and Prevention's (CDC) Division of Global Migration and Quarantine (DGMQ) to notify US health departments of newly arrived immigrants with a medical condition of public health significance, such as tuberculosis (TB), and all newly arrived refugees. While EDN is electronic, data collection for the required overseas medical examination for US immigrant visa applicants is paper-based, leading to quality challenges such as illegible forms and late notifications. In 2018, DGMQ will implement an electronic collection of overseas medical examinations of immigrants, eliminating most paper records from the

system. **Methods:** US panel physicians certified to provide the required overseas medical examinations for US immigration will begin using a web-based system called eMedical. eMedical was developed by the Australian government for secure global submission, recording, storage, and processing of Australia's overseas medical examination data. eMedical will transmit US immigrant visa applicants' completed overseas medical examination records to CDC. CDC will store the records and transmit them to health departments via EDN within 2 days after the immigrants arrive. **Results:** This presentation will provide updates to US health departments on DGMQ's overseas migration health data and notification of newly arrived persons with overseas TB classification. We will detail the unique collaboration between federal and international partners in developing eMedical, features of eMedical, and the information flow from eMedical to the EDN system. We will also provide preliminary best practices for health departments receiving data, based on experience gained during the first phase of US eMedical implementation. **Conclusions:** This programmatic presentation will provide an understanding of improvements to the system used to collect overseas medical examination data and rapidly notify health departments of newly arrived persons with a TB classification. eMedical will improve the quality of records of the required overseas medical examination for US-bound immigrants and reduce the number of missed opportunities to identify suspected cases of TB.

Board 337. Cholera Outbreaks within Humanitarian Context: A Challenge between Disaster Management, Health Systems, and Environmental Conditions

O. Ali Maher
World Health Organization, Cairo, Egypt

Background: The Eastern Mediterranean region of the WHO, hereafter referred to as EMRO, used and still accommodates many of the world's biggest Humanitarian crises. Many of the countries in the region are either, recovering or still going through armored conflicts. Management of health systems within Humanitarian context and due to the extremely rough conditions due to constrained resources, compromised infrastructure, lack of access, and many other factors is quite different from normal context. During the past decade EMRO had witnessed many diseases outbreak within humanitarian context. In 2017 Yemen had witnessed one of the worst Cholera outbreaks in modern history with more than one million suspected cases. Cholera being a diseases with relatively easy clinical management control, is emerging as a really public health threat in countries with Humanitarian crises due to the many reasons mentioned earlier. The global humanitarian management system and the cluster approach is characterized by quite weak inter-cluster cooperation mechanisms to deal with emergency situations within an already ongoing humanitarian situations mainly due to the competition for funds. **Methods:** We tried to have a closer look at the past cholera outbreaks in some countries in the region (particularly Yemen, Somalia and Sudan) and to give an overview of the outbreak itself, analysis of the humanitarian context specially the inter-cluster cooperation mechanisms and the health system response in general. **Results:** While presenting the outbreaks we presented an overview of some of the main features of outbreak management and control from medical and public health side such as diseases surveillance system, case definitions and management and environmental conditions, mainly water and sanitation. **Conclusions:** Many outbreaks witnessed within this context showed that there is an obvious lack of concrete cooperation mechanisms between humanitarian clusters and and cluster lead agencies in activities related to outbreak control. National health systems with often compromised administrative structure and poor funding needed as well to be added as an obstacle for effective cooperation.

Board 338. Oral Cholera Vaccination Coverage in a Complex Humanitarian Setting: Lessons from Somalia, 2017

M. Lubogo[1], A. Abdinasir[2], K. David[3]
[1]World Health Organisation, Mogadishu, Somalia, [2]World Health Organisation, Cairo, Egypt, [3]Independent consultant, Nairobi, Kenya

Background: The first ever oral cholera vaccination (OCV) campaign in Somalia was implemented between March and October 2017 as part of the national cholera preparedness and response plan. The Somali Ministry of Health aimed to cover 1.1 million people aged 1 year and above in 11 high risk districts in five regions of south and central Somalia each with two doses of vaccine. It was the first time the Ministry of Health of Somalia has agreed to use OCV as part of the cholera prevention and control strategies. While OCV use has increased in recent years, more evidence is needed to understand the feasibility of attaining high vaccine coverage in complex humanitarian settings. **Methods:** A multi-stage cluster survey was conducted in each of the targeted during the campaign. The data collection for the survey was conducted by independent monitors using kob-collect data collecting system from all sites **Results:** The OCV coverage survey was conducted only 9 of the 11 target districts. Of the 3,715 eligible individuals from the first 7 high-risk districts, 92.5%, (95% CI: 91.4- 93.6) received two doses of OCV and one dose coverage of 7.0%, (95%CI: 6.0-8.2). In 2 other high-risk districts (Baidao and Jowhar), 94.1% CI: (92.9- 95.1) received 2 doses of OCV and 2.6%, CI: (2.0- 3.4) received one dose of OCV. The highest OCV coverage was recorded in Xawo Tako and Koshin districts of Hiiran region. Radio and community mobilisers were the main sources of information during the OCV campaign and contributed to the higher vaccine acceptance among the target population and the coverage. **Conclusions:** Despite many challenges, the experience in Somalia shows that OCV campaigns can be implemented in acute and protracted complex humanitarian settings as part of cholera response and preparedness plan in order to prevent or control potential cholera outbreaks.

Board 339. *Shigella* Infections in the United States Are Associated with Poverty and Crowding, FoodNet, USA, 2004–2014

T. Libby[1], P. Clogher[2], E. Wilson[3], N. Oosmanally[4], M. Boyle[5], D. Eikmeier[6], C. Nicholson[7], A. Muse[8], B. Shiferaw[9], N. David[10], A. Geissler[11], D. Vugia[12]
[1]California Emerging Infections Program, Oakland, CA, USA, [2]Connecticut Emerging Infections Program, New Haven, CT, USA, [3]Colorado Department of Public Health and Environment, Denver, CO, USA, [4]Georgia Department of Public Health, Atlanta, GA, USA, [5]Maryland Department of Health, Baltimore, MD, USA, [6]Minnesota Department of Health, St Paul, MN, USA, [7]University of New Mexico Emerging Infections Program, Albuquerque, NM, USA, [8]New York State Department of Health, Albany, NY, USA, [9]Oregon Public Health Division, Portland, OR, USA, [10]Centers for Disease Control and Prevention, Nashville, TN, USA, [11]Centers for Disease

Control and Prevention, Atlanta, GA, USA, [12]California Department of Public Health, Richmond, CA, USA

Background: *Shigella* causes an estimated 500,000 enteric illnesses in the United States annually. Two limited studies found the incidence of shigellosis increases with increasing census tract (CT) poverty, but the association with socioeconomic factors is unclear. We analyzed geocoded surveillance data from the 10 US Foodborne Diseases Active Surveillance Network (FoodNet) sites to better understand the association between poverty, crowding, and *Shigella* infections. **Methods:** We geocoded the 23,255 laboratory-confirmed *Shigella* cases reported to FoodNet during 2004–2014 and linked to CT poverty and crowding data from the 2006–2010 and 2010–2014 American Community Survey. Cases were categorized into 4 strata based on CT poverty (percentage of persons in the CT living below the federal poverty line [<5%, 5–<10%, 10–<20%, ≥20%]) and crowding (percentage of households in the CT with >1 person per room [<1%, 1–<3%, 3–<4%, ≥4%]). For each stratum, we calculated age-adjusted incidence rates (IR) and excluded persons reporting international travel in the 7 days before illness onset. Incidence rate ratios (IRR) and 95% confidence intervals (CIs) were used to compare the highest with the lowest stratum of each measure. **Results:** During 2004–2014, on average, annual FoodNet *Shigella* incidence was 4.5 per 100,000 and was highest among children aged <5 years (19.8) and among Blacks (7.3) and Hispanics (6.3) compared with Whites (2.8). The IR was significantly higher in the highest compared with the lowest poverty CTs (IRR=3.6; 95% CI 3.5–3.8). This association persisted in all sites, for both *S. sonnei* and *S. flexneri,* regardless of sex, age group, or race/ethnicity. The association with crowding was stronger for *S. flexneri* (IRR=2.7; 95% CI 2.4–2.9) than *S. sonnei* (IRR=1.7; 95% CI 1.7–1.8) and was found among all age and race/ethnicity groups and in all sites except among men in California. **Conclusions:** In the United States, *Shigella* infections are associated with poverty and crowding. Increased efforts to decrease poverty and crowding may help to reduce racial and ethnic differences in the incidence of *Shigella* infections.

Board 340. Addressing a Culture of Health Inequity in Ohio's Appalachian Region during Outbreak Investigations

M. Davis[1], M. Strite[2]
[1]Portsmouth City Health Department, Portsmouth, OH, USA, [2]Jackson County Health Department, Jackson, OH, USA

Background: Southeast Ohio is settled among the foothills of the Appalachian Mountain Range. The counties within this region are among the lowest ranking in Ohio for health outcomes. Appalachian culture is unique in the United States. In this culture it is not uncommon to ignore health problems until they become an emergency. Access to care makes a difference in health outcomes but that is only one part of the problem. Access to care has improved in our region but attitudes toward early interventions have not yet caught up. In an outbreak situation the culture of Appalachia affects every aspect of the investigation process. Understanding cultural norms within the area and adapting the investigation to match these norms is vital. During a widespread outbreak of shigellosis in Pike County, Ohio in July 2016, epidemiologists applied certain interviewing methods to reach out to potential case-patients and worked with the community to achieve the best possible investigation and outcome. **Methods:** The mirroring method was used consistently throughout the outbreak investigation in the interview process. All interviews were conducted via phone. The outbreak was investigated using the case-control method. Individuals who attended the family resort where the outbreak occurred for a set period of time were asked to call the health department to answer questions. The use of standardized questionnaires served as the basis for the interview to keep patients on track. **Results:** Using mirroring throughout the interview process helped us to identify case-patients and lead us to the discovery of more case-patients. Patients were also more willing to submit samples when mirroring was used and to lead us to new case-patients and give contact information for new patients. Utilizing social media to reach out to the community enabled a higher volume of calls to the health department regarding the outbreak. **Conclusions:** The methods used during the outbreak investigation and success in obtaining client feedback can be extrapolated to include routine disease investigation, direct patient care, and community outreach. By using mirroring in every day patient interactions, we can help to bridge the gap of cultural health inequity seen in rural Appalachia. Using cultural cues during an outbreak investigation will allow investigators to gain insights into the underlying cause of the outbreak and prevent future outbreaks.

Board 341. A Survey of Open Defecation Sites in Atlanta

D. Capone[1], A. Ferguson[2], M. Gribble[3], J. Brown[1]
[1]Georgia Institute of Technology, Atlanta, GA, USA, [2]Remerge, Inc., Atlanta, GA, USA, [3]Emory University, Atlanta, GA, USA

Background: Homeless persons (HPs) in the United States (US) who sleep in unsheltered locations experience limited access to sanitation facilities which can force some HPs to resort to open defecation. The association between open defecation (OD) and a wide range of health problems is well documented in the developing world. Despite recent disease outbreaks – notably, infections with hepatitis A virus – associated with poor sanitation in HP communities in the USA, microbial risks of OD have not been characterized in this context. **Methods:** In response to anecdotal reports of OD by homeless persons in Atlanta, we conducted a systematic block-by-block search over a predefined area (2.4 km^2) to measure the spatial distribution and enteric pathogen profile of discarded human feces in the city. **Results:** We identified and mapped 39 OD sites containing 118 stools. Of these, we analyzed 26 stool samples via multiplex RT-PCR (Luminex Gastrointestinal Pathogen Panel), a stool-based diagnostic assay identifying presence of 15 common parasitic, bacterial, and viral enteric pathogens. 23% of the 26 collected OD stools tested positive for one or more pathogen. An estimated 12% of stools were positive for enterotoxigenic *E. coli* (ETEC), 7.7% for *Giardia*, 3.6% for norovirus, and 3.6% for *Salmonella*. Ninety-two percent of documented OD sites exist within 400 meters of a HP service center. **Conclusions:** The proximity of OD sites to service centers suggests that existing facilities are not meeting the sanitary needs of the HP population. Though preliminary, these results suggest that OD in Atlanta is common and may pose risks to public health. Further work is needed to characterize risks and identify appropriate hygiene and sanitation interventions for HP populations.

Board 342. Invasive Pneumococcal Disease among Adults Living with HIV/AIDS in NYC, 2008-2016

C. Samurkas[1], D. Bloch[1], S. Braunstein[2], D. Weiss[1]
[1]NYC Department of Health and Mental Hygiene, Bureau of Communicable Disease, New York City, NY, USA, [2]NYC

Department of Health and Mental Hygiene, Bureau of HIV/AIDS Prevention and Control, New York City, NY, USA

Background: Invasive pneumococcal disease (IPD) is a common infection in people living with HIV and AIDS (PLWHA). Since the introduction of highly active antiretroviral therapy (HAART) in 1995, HIV/AIDS-related morbidity and mortality have decreased, including incidence of IPD. Recent studies suggest that despite HAART, IPD incidence is disproportionately higher among PLWHA. This study aims to quantify IPD and related death odds among PLWHA in New York City (NYC) compared to HIV-negative people. **Methods:** IPD cases among NYC residents 20 years and older reported to the NYC Department of Health and Mental Hygiene (DOHMH) from 2008–2016 were matched to the DOHMH HIV/AIDS Surveillance Registry. US Census Bureau intercensal estimates were used to compute IPD incidence rates stratified by HIV status, borough, age, and gender. Estimates of HIV prevalence were obtained from the HIV/AIDS Surveillance Data. Bivariate and multivariate logistic regression with aggregate data were used to compute odds of IPD in NYC. Cox regression was used to find IPD-related death hazard ratios. **Results:** From 2008–2016, 6084 IPD cases were reported with 1482 (24%) in PLWHA. The average annual incidence of IPD among PLWHA was 144.9 per 100,000 (95% CI 106.6, 183.2) and among HIV-negative people was 9.16 per 100,000 (95% CI 8.44, 9.88). IPD incidence decreased across the interval in PLWHA, from 225 per 100,000 in 2008 to 83 per 100,000 in 2016; incidence in HIV-negative people remained largely unchanged (11.4 per 100,000 in 2008 vs. 8.6 in 2016). In an aggregate regression model, IPD odds among PLWHA, adjusting for borough, gender, age group, and diagnosis year, was 18.8 times that of HIV-negative people (95% CI 17.6, 20.1). Cox regression showed a significantly lower hazard ratio of IPD-related death among PLWHA than HIV-negative cases adjusting for gender, age group, borough, diagnosis year, and neighborhood poverty level (HR=0.74, 95% CI 0.57, 0.96). **Conclusions:** Conclusion: HIV infection remains a serious risk factor for IPD, but does not increase risk of death among IPD cases. Analysis of CD4 count, viral load, and viral suppression status as predictors of IPD among PLWHA is pending. Given changes in HIV incidence, IPD vaccination recommendations, and HAART prevalence, it is important to continue monitoring IPD incidence among PLWHA to monitor New York State efforts to end the epidemic.

Board 343. Health Disparity and Invasive Group A Streptococcal Infections: A Multilevel Analysis Using Census-Derived Area-Based Socioeconomic Measures

I. Kamal-Ahmed[1], J. Hodges[1], R. Danila[2], M. Osterholm[1]
[1]University of Minnesota, Minneapolis, MN, USA, [2]Minnesota Department of Health, St. Paul, MN, USA

Background: Invasive Group A Streptococal (iGAS) infection disproportionately affects marginalized populations, likely due to factors associated with poverty and/or overcrowded living conditions. We examined the association of disparity measures with iGAS incidence. **Methods:** The Minnesota Department of Health Emerging Infections Program conducts active laboratory-based surveillance for iGAS; 3,600 cases were reported between 1/1/96 and 12/31/16. The residence of each case was geocoded to its corresponding census tract allowing area-based measures of poverty, racial diversity, and overcrowding living condition from the US Census and American Community Survey to be appended to each case. We divided the data into four groups of years (1996-2000), (2001-2005), (2006-2010) and (2011-2016) to observe any temporal pattern. A multilevel Poisson regression model was used to account for spatial similarity. Results: While individual predictors -- poverty, racial diversity, and overcrowded living conditions -- were strongly associated with iGAS cases, multiple regression produced an inconsistent result due to moderate to high multicollinearity between these three measures. A principal component analysis found that 73% of variance in these three measures could be attributed to a single latent variable (the first principal component). We created an index value by combining all three predictor variables (the first principal component of the correlation matrix). **Results:** Every 10% increase in this combination of predictors is associated with an increase of the case count in the first block (1996-2000) of 40% (p<.0001, 95% CI [31%-48%]), in the second block (2001-20015) of 21% (p<.0001, 95% CI [12%-29%]), in the third block (2006-2010) of 25% (p<.0001, 95% CI [17%-33%]), and in the fourth block (2011-2016) of (40% (p<.0001, 95% CI [28%-52%]). **Conclusions:** These results may explain incidence differences by race/ethnicity or other socio-economic measure and may help target interventions including use of an eventual vaccine.

Board 344. Awareness and Knowledge of Coccidioidomycosis in Arizona: Findings from the 2016 Behavioral Risk Factor Surveillance System

M. Khan[1], S. Brady, G. Adame, K. Komatsu
[1]Emory University, Atlanta, GA, USA, Arizona Department of Health Services, Phoenix, AZ, USA

Background: Coccidioidomycosis (valley fever), an infection caused by soil-dwelling fungi, is highly endemic in Arizona. Disease awareness and knowledge may be associated with early care seeking and testing. In the 2008 Behavioral Risk Factor Surveillance System (BRFSS), the Arizona Department of Health Services (ADHS) found that 20% of Arizona residents had never heard of valley fever and 36% could not correctly state how it is transmitted. We surveyed Arizona residents about valley fever in 2016 and examined associations between demographic characteristics and symptom recognition. **Methods:** Respondents to the 2016 Arizona BRFSS, an annual population-based telephone survey of the noninstitutionalized adults about health behavior and opinions, were asked to list symptoms (fever, cough, tiredness) of valley fever and state whether they knew someone who has had valley fever. Weighted estimates and inferential statistics were calculated using survey analysis procedures in SAS v9.4. **Results:** 5,328 respondents were interviewed, and 4,730 (88.8%) had complete responses available for analysis. Three percent (95% CI: 1.9%, 4.1%) of respondents did not know about valley fever. Of respondents who knew about valley fever, 30.2% (95% CI: 28.0%, 32.5%) knew someone who had valley fever. At least one symptom was identified by 39% of respondents. Fatigue was the most commonly identified symptom (22%). Only 4.8% (95% CI: 3.6%, 5.9%) correctly identified fever, cough, and fatigue as symptoms of the disease. Respondents who knew someone who had the disease were more likely to identify at least one (OR: 5.8, 95% CI: 4.6, 7.2) and all three symptoms (OR: 4.1, 95% CI: 2.6, 6.6). Recognition of at least one symptom increased with educational attainment and ranged from 16% among those without a high school diploma to 56% among those with a college degree or higher. Symptom recognition was highest among Whites (57%) and lowest among Hispanics (23%). **Conclusions:** While most Arizona residents knew about valley fever, symptom recognition was limited. Educational campaigns to increase symptom recognition for valley fever should target specific demographic groups.

Board 345. Communicating Clinical Guidance during an Emergency Response: Zika Virus Clinical Tools

J. Moore, K. Polen, C. Kilgo, K. Slaughter, J. Abercrombie, E. Johnston
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The sudden, widespread transmission of Zika virus in the Americas has led to unprecedented challenges for healthcare providers. Little was known about Zika virus before the outbreak began in 2015; since then, knowledge has increased exponentially and continues to grow. The Centers for Disease Control and Prevention (CDC) developed clinical guidance for the care of pregnant women and infants with possible Zika virus infection. CDC continues to update clinical guidance as more is learned about the virus. We describe the development, dissemination, and uptake of clinical tools to support the implementation of CDC clinical guidance. **Methods:** In collaboration with subject matter experts, health communications specialists created over 40 tools to facilitate implementation of clinical guidance and equip healthcare providers with the information needed to report cases of Zika virus infection. Examples of tools include a screening tool to identify pregnant patients for whom testing is indicated, an interactive web tool for interpreting Zika testing guidance (Pregnancy and Zika Testing Widget), sample patient counseling scripts, and a video demonstrating how to measure infant head circumference at birth. These materials, many of which are available in multiple languages, were widely disseminated through key partnership channels. CDC also conducted outreach to clinicians through webinars, presentations, partner calls, and email alerts. **Results:** Since CDC's Zika Virus Response began in 2016, these materials have been downloaded from the CDC website over 300,000 times. The videos have been viewed over 40,000 times. The Pregnancy and Zika Testing Widget has been used over 17,000 times with over 75% of the users self-identifying as clinicians. In addition to high levels of uptake, these tools were informally tested among healthcare providers and received positive feedback regarding usefulness in clinical settings. **Conclusions:** Clinical tools can assist healthcare providers in implementing clinical guidance into practice and should be considered in future emergency responses, particularly when knowledge is rapidly evolving. Carefully planned dissemination is critically important for maximizing access to and uptake of clinical tools.

Board 346. Risk Communication in Health Emergencies: The Experience of Local Journalists during the 2014-15 Ebola Outbreak in Sierra Leone

M. Winters, H. Mölsted Alvesson, H. Nordenstedt
Karolinska Insitutet, Stockholm, Sweden

Background: Risk communication in a disease outbreak has the potential to save lives and prevent further infections. However, if messages are inaccurate or can be interpreted incorrectly, risk communication can further fuel an outbreak. During the Ebola outbreak in Sierra Leone, local media (especially radio) were among the key sources of information of the public. Local media are thought to have played a role in disseminating incorrect information, especially at the start of the outbreak. Little is known about the media's side of the story. The study aims to analyse the perceived roles of Sierra Leonean journalists and their shifts in framing messages about Ebola during the outbreak. **Methods:** Semi-structured interviews were conducted with 13 journalists based in urban Freetown and rural Waterloo in February and March 2016. The majority of the journalists worked for radio stations. The mostly male journalists represented national as well as regional and local radio stations. Transcripts of the semi-structured interviews were analysed using framework analysis. The analysis was inspired by "framing theory", which poses that the media not only influences what their audience should think about, but also how they should think about it. **Results:** Preliminary analysis of the data indicates that local journalists embraced different roles during the course of the Ebola outbreak, from journalists actively seeking information from multiple formal and informal sources, to communicators with aligned messages about Ebola. All journalists reported a difficulty in dealing with conflicting messages and the lack of information in the first months of the outbreak. **Conclusions:** This qualitative study showed that local journalists in Sierra Leone are important stakeholders in risk communication and can adopt different roles during the course of an outbreak. Efforts should be made so that local journalists are well-informed and trained, to ensure their audiences receive accurate information.

Board 347. Emerging Infectious Diseases and Risk Communication: Lessons from the GCC's Experience during MERS Epidemic

M. Nour, E. Farag, M. Alhajri, H. Al-Romaihi, M. Al-Thani, S. Al-Marri
Ministry of Public Health, Doha, Qatar

Background: In the era of emerging infectious diseases, public health authorities are challenged with overwhelming uncertainty, public and media pressure, and the need to take serious decisions based on inaccurate, sometime conflicting, information particularly during the early days of an unfolding EID outbreak. In similar urgent situations, only few prioritized actions could be performed to mount a coherent response. Erupting in 2012 in KSA and Qatar then to the remaining GCCs, MERS infected 2,143 and killed 750 persons (CFR 35%). This study sought to retrospectively review the influence of the early adopted risk communication and coordination strategies during the initial response to MERS Epidemic in Qatar as a model for the GCCs. **Methods:** Based on the WHO guidelines on risk Communication and the CDC Crisis Emergency Risk Communication guidelines, we reviewed the actions prioritized for execution by the Qatari public health authorities and assessed its potential influence on the overall course of outbreak response. **Results:** The early involvement of the WHO and CDC besides other international agencies, was critical to the national response as it yielded a technical framework to guide investigation. Despite the prevailing uncertainty, the WHO and CDC support was purposefully communicated to the public to demonstrate the national efforts undertaken to find answers. Unfortunately, the failure of the Animal Health to consider the potential role of animals in the disease transmission, coupled with aggressive denial displayed from the camel owners through the social media, substantially deferred the implementation of the framework at the animal sector and further provoked the poor risk perception among the public. **Conclusions:** The adoption of transparency policy coupled with the early consultation with the international agencies helped create and prioritize the One Health approach to drive epidemiological investigation based on which risk communication strategies were implemented. The technical competencies seemed to have positively contributed to communicating the epidemic risk.

Board 348. Examining the *Emerging Infectious Diseases* Journal's Reach and Influence through Metrics

B. Breedlove[1], D. Drotman[1], S. Gregory[1], R. Tucker[1], B. Segal[1], T. Pearson-Clarke[2], S. O'Connor[1], W. Hale[1], S. Richardson[1], T. Eheman[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]CDC, EID Journal, Atlanta, GA, USA

Background: *Emerging Infectious Diseases,* an open access journal published monthly by the Centers for Disease Control and Prevention, had a 2017 impact factor of 8.22, first among open-access infectious disease journals and third among 84 infectious disease journals. The impact factor is important but does not provide a complete representation of EID's reach and influence. **Methods:** *To better understand EID's reach and influence, we examined a range of metrics:* 2016 Scopus CiteScore = *4.92*. 2017 Google Scholar h-Index 81; h5-median 114. 2017 website page views tracked by Adobe Analytics = 7,216,240 PubMed Central usage on 2017 = 3,006,586. Aggregate view on PubMed in 2017 = 78,022. More than 165,000 unique subscribers to EID's online email notifications via GovDelivery (e.g., publication of new issue, expedited content, CME articles). Received more than 2,150 articles but published 537 in 2017. Attention scores measured by Altmetric. Most frequently cited articles from Scopus. Social media metrics (e.g. Twitter, Instagram). Internal search engine feedback data. **Results:** EID's impact factor, CiteScore Metrics, and Google Scholar h-index—which track citations—showed EID's highest ever numbers during 2017. Aggregate views of EID content via PubMed declined, but PubMed Central usage was at an all-time high. Page views tracked by Adobe Analytics have increased each year. Subscribers to email notifications, sharing and reporting EID content as tracked by Altmetric, and uptake of content via social media increased in 2017. **Conclusions:** CDC does not does not record, require, collect or track any Internet users' personal information, so EID relies on these aggregated metrics to evaluate EID's reach and influence. Those data help us understand how well EID promotes the recognition of new and reemerging infectious diseases around the world and improves the understanding of factors involved in disease emergence, prevention, and elimination.

Vector-Borne Infections II

Board 349. Sylvatic Yellow Fever: Public Health Emergence

A. Ribeiro, R. Cavalin, J. Suleiman, J. Costa, M. Vasconcelos, L. Borges, R. Teixeira, C. Málaque, J. Sztajnbok
Instituto de Infectologia Emílio Ribas, Sao Paulo, Brazil

Background: Yellow fever is an infectious disease caused by arbovirus, endemic in the tropical forests of America and Africa. From 1980 to 2016, 797 cases were confirmed as sylvatic yellow fever - SYF, with expressive expansion of areas with viral circulation in Brazil. **Methods:** A cross-sectional study of patients with suspected yellow fever attended in Emílio Ribas Institute of Infectious Diseases, a reference center in the city of Sao Paulo. The suspected cases were reported by the Epidemiological Surveillance Service to the Information System for Notifiable Diseases. Appropriate statistical analyses were performed in the SPSS program. **Results:** From January to February 2018, 74 suspected cases of yellow fever were reported, 44 were confirmed (59.5%) with 12 deaths, and lethality was 27.2%. The cases were laboratory confirmed by RT-PCR and/or positive IgM serology. The majority had severe manifestations (59.1%), and all patients were infected in sylvatic areas, mostly in Mairiporã (59.1%) municipality of Sao Paulo metropolitan region. Among confirmed case-patients, 72.7% were men and 71.9% were 20 to 59 years old. History of yellow fever vaccination was reported by 17 atients (39.5%), 8 were vaccinated before symptoms, one vaccinated 30 days before, and 9 received the vaccine after disease onset. All patients reported fever, 85.7% nausea, and 79.5% myalgia. Twenty-six patients (59.1%) met the case definition at hospital admission (fever and jaundice and/or hemorrhage). Comparing deaths and cures, there was a statistical difference between the median (IQR) of age (56x36) and the following laboratory tests: Leukocytes-cel/mm^3(4900x2900), Glutamic oxaloacetic transaminase-GOT-U/L(8071x1545), Glutamic pyruvic transaminase-GPT-U/L(3266x1477), total bilirubin-TB-mg/dL(5,0x1,3), direct bilirubin-DB-md/dL(4,5x0,6), urea-mg/dl(127m5x27), Creatinine-mg/dl(4,4x0,9), INR(2,54-1,23) e Creatine phosphokinase-CPK-U/L(754,5x255,5). There was no statistical difference in platelets-u/L count. **Conclusions:** Yellow fever is currently an emergency in Brazil, and alerts for case detection and implementation of preventive measures are needed, such as vector control actions to prevent re-urbanization and improvement of vaccine coverage.

Board 350. Descriptive Epidemiology of CCHF in Afghanistan: Reported Cases to National Surveillance System, 2007-2017

H. Bakhshi[1], F. Arifi[1], N. Sahak[2]
[1]Ministry of Public Health, Kabul, Afghanistan, [2]World Health Organization, Kabul, Afghanistan

Background: Crimean Congo hemorrhagic fever (CCHF) is the most common zoonotic disease in Afghanistan, and a major public health problem. In 1998, the first CCHF outbreak with 19 cases and 12 deaths (case fatality ratio (CFR) = 63.2%) was reported in Takhar province. In recent years, several CCHF cases were reported throughout the country. The Ministry of Public Health established a surveillance system in 2006 to detect public health events, including cases of zoonotic disease, to inform policy decisions. **Methods:** This study is based on the national surveillance system's collected data from 2007 to 2017. The provincial surveillance officers conducted an investigation, provided the initial response, and collected specimens. The collected samples were tested at the Central Public Health Laboratory using ELISA. This study aimed to describe cases of CCHF in people by patients' demographic, geographical, and occupational characteristics and identify the CFR. **Results:** The surveillance system detected 801 CCHF clinical cases from 2007 to 2017 of which 35% of patients were women and 65% men. Of the 593 total collected samples, 260 were confirmed by laboratory with positive Elisa IgM /IgG. The laboratory confirmed CFR was 13.6% at national level. The leading symptoms were fever (21.1%), body pain (19.5%), headache (18.7%), dizziness (9.2%), epistaxis (8.8%), fatigue (6%), ecchymosis (5.2%), and hemoptysis (4.4%); other symptoms made up the remaining 7.2%. Most of the patients (28.6%) were 20-29 years old. Shepherds and housewives were most affected (19.8% and 23% respectively); other affected groups were butchers (13.2%), farmers (9.3%), students (7.4%), health staff (0.8%) and unspecified group (18.2%). Kabul and Hirat provinces were affected the most. The majority of cases occurred from May to September and increased annually from four cases in 2007 to 245 cases in 2017. **Conclusions:** An improved and expanded surveillance system detected more CCHF cases, and cases have increased annually. Despite this increase, laboratory capacity remains limited in Afghanistan.

Board 351. Spatial Distribution and Temporal Variation of the Risk by Zika Virus Disease in the Colombian Regions during the 2015-2016 Epidemic: A Bayesian Approach

K. Flórez[1], E. Navarro[1], H. Llinás[1], J. Acosta[1], R. Tuesca[1], A. Sisa[1], F. Pérez[2], M. Mercado[3]
[1]Universidad del Norte, Barranquilla, Colombia, [2]Panamerican Health Organization, Washington D.C, WA, USA, [3]Instituto Nacional de Salud, Bogotá, Colombia

Background: In October 2015, the first cases of Zika virus disease (ZVD) in Colombia were reported in the Caribbean region. During the next 14 months, the disease spread national-wide in different localities where *Aedes aegypti* is established. Colombia had reported over 105,000 cases of ZVD by December 2016. Regional estimated of the risk of ZVD has been calculated by measuring absolute risk. This study analyzed the risk of ZVD based on an autoregressive approach through spatio-temporal disease mapping. This approach results in estimations that are less affected by the size of small areas providing guidance for the implementation of public health interventions. **Methods:** We analyzed ZVD cases in Colombia (reported by the National Institute of Health from epi-week 32 of 2015, until epi-week 52 of 2016). Risks estimates of each region of Colombia, considering: first-order neighbors, covariates effects and three adjacent periods of time (beginning, development and end) in order to analyze the spatio-temporal progress of the disease based on extension of the Besag, York and Mollié model was undertaken. The relationship between risk and covariates was calculated. The model used the R.3.3.1 and WinBUGS 14 programs as well as QGIS 2.18.11 for mapping. **Results:** The spatial distribution of the risks and observed higher values in the Eastern (North Santander: 3.53, Santander: 2.28, Casanare: 5.01, Arauca: 3.25) and Western region of the country (Huila: 2.77, Valle del Cauca: 2.68) were obtained. These results were in agreement with the Panamerican Health Organization report 2016. An analysis considering the three adjacent periods of the epidemic phase showed higher risks values in the Central and Southern zone of the country. These are the areas of Arauca and Santander where a four-time increase in risk was reported with respect to the initial phase of the outbreak. **Conclusions:** The risk estimates and categorization by conglomerates allowed the identification of hazardous areas beyond geo-political limits in the Western and Eastern region of the country. This information can guide decision-makers in the implementation of control and prevention strategies for both Zika and other arboviruses.

Board 352. Exposure and Effects of Four Zika Prevention Interventions during the Zika Epidemic in Puerto Rico, 2016-2017

G. Earle-Richardson[1], C. Prue[1], K. Turay[1], G. Medina-Martinez[2], D. Thomas[3]
[1]National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Puerto Rico Department of Health, San Juan, Puerto Rico, [3]Field Services Branch, Division of State and Local Readiness, Centers for Disease Control and Prevention, and Commissioned Corps, United States Public Health Service, Trenton, NJ, USA

Background: As part of the Zika epidemic response in Puerto Rico during 2016-2017, CDC, CDC Foundation, and the Puerto Rico Department of Health (PRDH) supported four interventions to promote Zika prevention among pregnant women and their families. PRDH's Women, Infants, and Children (WIC) program implemented the first two, WIC Zika orientation and Zika Prevention Kit (ZPK) distribution. A third was a paid mass media campaign ("Deten el Zika"), and the fourth was an offer of free residential mosquito spraying to pregnant women. We assessed the interventions' reach and effects on ten recommended Zika prevention behaviors. **Methods:** Between July 2016 and June 2017, Puerto Rican staff interviewed a random sample of 1,329 pregnant WIC participants by telephone about their exposure to Zika prevention interventions, and their Zika prevention behaviors. **Results:** Women's exposure to a Zika prevention intervention was greatest for the WIC Zika orientation (93%), ZPK distribution (75%) and Deten el Zika (51%). The offer of free residential mosquito spraying (discontinued after September 2016) achieved a more limited reach (34%). While WIC Zika orientation consistently reached a high percentage of women, ZPK distribution did so less consistently. Women's Zika prevention behavior ranged from 4% (wearing long-sleeved shirts) to 90% (removing standing water). Insect repellent use (28%) and condom use (44%) were also common. Larvicide application increased the most over time (13% to 40%). In logistic regression models, the largest risk ratios were found for ZPK distribution and larvicide application (RR: 6.3), offer of free residential mosquito spraying and sprayed home for mosquitoes (RR: 3.6), and ZPK distribution and bed net use (RR: 3.1). **Conclusions:** ZPK distribution was associated with increased use of larvicide and bed nets. Distribution of less familiar Zika prevention items (larvicide, bed nets) with educational support appear to increase usage among pregnant women.

Board 353. Increased Incidence of Guillain-Barré Syndrome following the Zika Virus Epidemic in Rio de Janeiro, 2015-2016

J. Rafael Angelo[1], T. Fuller[2], B. Borges da Silva Leandro[3], I. Domingos[3], H. Levy[3], F. Perez[4], O. Perez[5], O. Nascimento[6], J. Campos Ferreira[6], P. Passos dos Santos[6], P. Sabroza[1]
[1]National School of Public Health, Oswaldo Cruz Foundation, Rio de Janeiro, Brazil, [2]Institute of the Environment & Sustainability, University of California Los Angeles, Los Angeles, CA, USA, [3]Oswaldo Cruz Foundation, Rio de Janeiro, Brazil, [4]Communicable Diseases and Environmental Determinants of Health Department – Pan American Health Organization, Washington, DC, DC, USA, [5]Federal University of Piaui, Teresina, Brazil, [6]Federal Fluminense University, Antônio Pedro University Hospital, Niteroi, Brazil

Background: During the Zika epidemic in Brazil in 2015-16, incidence was highest in Bahia and Rio de Janeiro. Case-control studies in Bahia have shown that Zika infection was a risk factor for Guillain-Barré Syndrome (GBS), a form of paralysis often requiring ventilator support. However, in Rio de Janeiro population-based studies of the association between Zika and GBS have not been conducted. **Methods:** The objective of this study was to assess rates of neuropathies requiring hospitalization in Rio de Janeiro following arbovirus outbreaks. We analyzed hospitalizations with GBS from 2001-2016 relative to epidemics of dengue and Zika. We utilized control charts, which are a statistical method for quality control, to identify months in which the number of GBS cases increased over the previous year(s). Finally, we carried out a retrospective chart review at Antonio Pedro University Hospital to confirm that patients hospitalized with GBS during the Zika epidemic were infected with Zika. We selected this hospital because it had the largest number of GBS patients in the state and hence offered the largest sample size for the chart review study.

Results: In 2012, hospitalizations with GBS grew 15% (n=115) compared to the previous year, and this increase coincided with the first introduction of dengue IV to Rio de Janeiro. During the Zika epidemic, there were more cases of GBS than in the previous three years (Chi2 = 195.32, $p < 0.0001$). The region of the state with the highest incidence of GBS was the eastern Rio de Janeiro metropolitan area (1.2 GBS cases per 100,000 people). Of 61 reported GBS cases in this region, 24 (39.3%) were hospitalized at Antonio Pedro University Hospital. Of these 24, our chart review indicated that infection with Zika was confirmed in 1 patient (4.2%) based on RT-PCR. Zika infection was probable for 7 other patients (29.2%) based on clinical symptoms (maculopapular rash, petechiae, and conjunctivitis). **Conclusions:** Although surveillance data indicates GBS increased during the Zika epidemic, according to chart review, Zika infection was rarely confirmed by PCR in GBS patients. Multiple arboviruses that cause neuromuscular complications are endemic in Brazil including Chikungunya, dengue, Yellow Fever, and Zika. Greater access to laboratory confirmation would improve differential diagnosis of neurological sequelae of Zika.

Board 354. Understanding Zika Knowledge and Risk Perception at the Community Level: The Role of Gender Hierarchy and Reproductive Decision-Making in Piura, Peru

L. Guerra-Reyes[1], R. Iguiñiz-Romero[2]
[1]Indiana University, Bloomington, IN, USA, [2]Universidad Peruana Cayetano Heredia, Lima, Peru

Background: Zika virus' unique characteristics: mosquito-borne, sexually-transmitted, and largely asymptomatic, but with dire consequences; severely challenge existing mechanisms for preventive care. Little is known about the social and cultural aspects which affect Zika transmission. This study addresses one such issue: reproductive decision making. A central aspect in designing and delivering effective preventive community-level messages. We explore how women and men of Piura-Peru negotiate conception and contraception; and discuss the implications of these gendered cultural patterns on Zika risk perception and prevention. **Methods:** We used a rapid ethnographic assessment methodology, including intensive fieldwork and triangulation of multiple forms of data collection: 3 focus groups (1 w/women, 1 w/men and 1 w/health providers); semi-structured in-depth interviews (28 women and 22 men); key informant interviews with reproductive health providers (16); participant observation; and secondary data collection. Interviews and focus groups were conducted by gender concordant researchers trained in qualitative interviewing. This paper reports primarily on in-depth interviews with men and women over 18 years of age, living in Catacaos, a small city in Piura. Analysis of interviews consisted in assignation of predetermined and emerging codes on verbatim transcriptions of interviews. We conducted a thematic analysis of resulting codes identifying recurrent and divergent themes in participant narratives. **Results:** Community men and women had scant knowledge of sexual or vertical transmission of Zika virus. Unequal gender hierarchies meant that male preferences guided reproductive decision-making, including type of contraception. Condoms were deemed unnecessary in committed relationships. Zika virus was conflated with Dengue, and expected to have the same symptoms and results. Women had more information about sexual health issues including detrimental effects of Zika but were not able to leverage knowledge into action due to gender inequality. **Conclusions:** Results indicate the need to incorporate clear messaging on Zika transmission which reaches both men and women as a central component of long-term prevention. Overall interventions directed at reducing gender inequality will be crucial to address female limitations to access and use contraception.

Board 355. Development of a Novel Inactivated, Vero-Cell Culture-Derived Zika Virus Vaccine Candidate

K. Dubischar[1], A. Pilz[1], R. Schlegl[1], S. Dewasthaly[1], U. Lundberg[1], A. Sampath[2], L. Lemiale-Biérinx[2], M. Duchars[2]
[1]Valneva Austria GmbH, Vienna, Austria, [2]Emergent BioSolutions, Gaithersburg, MD, USA

Background: The Zika virus (ZIKV) public health emergency once more confirmed the importance of rapid response options for development of vaccines. We report on rapid development of a ZIKV vaccine using the platform manufacturing process of licensed Japanese Encephalitis Vaccine IXIARO® as a blueprint. **Methods:** A fully characterized cGMP ZIKV seedbank (based on strain H/PF/2013) was propagated on Vero cells and conditions were optimized to obtain high viral harvest yield. Purification is performed by a sequence of effective and scaleable steps to remove host cell DNA and proteins yielding highly purified virus. Inactivation is done with formaldehyde followed by dilution to a target antigen content of 12 Antigen units (AU)/mL as determined by specific ZIKV ELISA. The final vaccine is then formulated with 0.1% Aluminium hydroxide in PBS, filled in 2R glass vials and stored at 2-8°C without additional stabilizers, preservatives or antibiotics. Preclinical testing was conducted in CD-1 mice and a repeat dose toxicology study was performed in Sprague-Dawley rats. The vaccine is currently undergoing Phase 1 clinical testing in a randomized, placebo-controlled, observer-blind study in 67 healthy volunteers. Two dose levels, 6AU/0.5mL and 3AU/0.25mL, are being evaluated in two two-dose regimens (Day 0, 7 and Day 0, 28). Safety data will be collected up to 6 months after the last vaccination and neutralizing antibody titers will be assessed 7 and 28 days after the last active dose. **Results:** Application of the IXIARO®-based process resulted in a high purity candidate vaccine. High virus neutralizing antibody titers against the homologous strain and against the heterologous African strain MR766 were observed in a dose-dependent manner in mice after one injection. A second dose 3 weeks later increased titers by approximately 100-fold. Three intramuscular injections of 4 AU (0.5 mL) in Sprague Dawley rats (Days 1, 15, 29) were generally well tolerated both locally and systemically and also induced high neutralizing antibody titers. Phase 1 clinical testing commenced in February 2018. **Conclusions:** The manufacturing process of a commercialized Japanese Encephalitis vaccine can successfully be applied to rapidly generate a high-purity, inactivated Zika Virus vaccine candidate that is now in clinical testing.

Board 356. Climate Conditions Prior to 2013 Chikungunya Outbreaks in the Americas

R. Soebiyanto[1], A. Anyamba[1], K. Linthicum[2]
[1]Universities Space Research Association / NASA Goddard Space Flight Center, Greenbelt, MD, USA, [2]US Department of Agriculture (USDA) - Center for Medical, Agricultural & Veterinary Entomology (CMAVE), Gainesville, FL, USA

ackground: In 2013, chikungunya emerged in the Americas, spreading rapidly to 33 countries in 8 months with 1.7 million suspected cases. Studies have demonstrated that variations in climate regulate populations and distribution of disease vectors that lead to the emergence and re-emergence of vector-borne diseases. This study aims to

assess climate conditions prior to and during chikungunya outbreaks in the Americas. **Methods:** We compiled and georeference chikungunya outbreak information from ProMED mail and PAHO. We use satellite-based climate data – monthly land surface temperature (LST) and rainfall – and calculate the associated anomalies. Climate anomalies were extracted for each initial autochthonous chikungunya outbreak location in the Caribbean, Central America and the northern part of south America (above equator). These values are then compared to those at the same month but from previous years to assess whether climate conditions preceding the outbreaks are different from any other years. **Results:** We found that most of the locations with initial autochthonous chikungunya cases in the Caribbean (~70% of the locations), Central America (~ 75% of the locations) and northern part of South America (~ 60% of the locations) were preceded by higher than normal LST. The anomalously high LST were observed up to 3 months preceding the outbreaks. Rainfall conditions varied across regions; anomalously low rainfall in the Caribbean and northern part of South America, anomalously high rainfall in Central America locations. Based on the anomalously high LST conditions, we use 3-monthly LST anomaly map in combination with population map to derive monthly Chikungunya risk map for part of Americas (16S – 33N, 119W – 50W). **Conclusions:** Our findings indicate that initial autochthonous chikungunya cases in the Caribbean, Central America and northern part of South America in 2013-2014 were preceded by higher than normal LST. This observation is consistent with previous chikungunya studies in East Africa (in 2004) and in South Asia (in 2005/06) which indicate that positive extremes in temperature associated with drought were a leading indicator of chikungunya activity. Our study further demonstrated how climate conditions can be used to derive risk maps that can aid public health agencies in monitoring areas at risk for chikungunya.

Board 357. Epidemiological and Entomological Investigation of Chikungunya and Dengue Fever-like Suspected Cases in Burao District, Somaliland, 2017

S. Ali[1], H. Haad[2]
[1]Ministry of Health, Hargeisa, Somalia, [2]University of Hargeisa, Hargeisa, Somalia

BBackground: Chikungunya and Dengue are mosquito-borne viral diseases transmitted by female mosquitoes mainly of the species Aedes *aegypti* and to a lesser extent Aedes *Albopictus*. Dengue has rapidly spread in all regions of WHO in recent years and has become widespread throughout the tropics, with local variations in risk influenced by rainfall, temperature and unplanned rapid urbanization. They are characterized by an abrupt onset of fever, frequently accompanied by joint pain which is often very debilitating which usually lasts for few days or may be prolonged to weeks, other symptoms such as muscle pain, headache, nausea, fatigue and rash might be also associated. The aim of this study was to conduct field investigation to identify Chikungunya and Dengue suspected outbreak in Burao district and its associated risk factors. A small scale cross-sectional study was carried out in Burao district of Somaliland where Chikungunya and Dengue like fever were reported late in 2016 and first quarter of 2017. **Methods:** Validated questionnaire was administered to 57 passive cases to capture data on demographic factors and disease histories as well as taking blood tests to detect IgM /IgG antibodies using RDTs, followed by conducting ELISA and PCR for confirmation and viral load testing besides to collect the entomological data to assess the vectors and to calculated the larva indices. **Results:** Results of the RDT showed that 15% of the suspected cases were Dengue IgG positive and same figure for Chikungunya IgG antibody. PCR findings were consistent with the results from RDTs and no viral load detected. However, for ELISA, only dengue IgM was done to detect active or recent infection and 6 cases were found to be IgM positive. On the other hand a total of 30 adult mosquito of Ae.*aegypti* and 2880 larva were collected during the study with the Breteau index of 86%. **Conclusions:** With the current weak health system in the country and huge numbers of displaced people caused by the civil wars in the Region, increases the possibilities of CHIKV/DEN outbreaks in the future. Integrated Vector Management (IVM) and strong surveillance program is recommended to be introduced in the area as well as the other prone areas of Somalia including coastal districts such as Bosaso and Mogadishu cities.

Board 358. Chikungunya: Recent Outbreak in Dhaka City, 2017

M. Flora[1], K. Islam[2], A. Muraduzzaman[1], S. Hazari[1], P. Charaborty[1], P. Ahmed[1], M. Hossain[1], A. Sharif[1], T. Shirin[1], M Salimuzzaman[1], M. Samad[1], A. Alamgir[1]
[1]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh, [2]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh

Background: Chikungunya is an arboviral vectorborne disease, transmitted to humans through the bite of infected mosquitoes. From its discovery in Africa, it gradually spread to Southeast Asia. Now the disease has spread in many parts of the world where *Aedes* mosquitoes are present. Autochthonous transmission was first reported in Bangladesh in 2008 at Poba, Rajshahi. Since then, small pockets of outbreaks were seen in different parts of Bangladesh. From late April to September 2017 a large outbreak of chikungunya fever occurred in Dhaka, the capital of and largest city in Bangladesh. It created a huge outcry and media coverage due to its emergence as a relatively less-known debilitating disease, and it caused an increased influx of patients in the hospitals. **Methods:** IEDCR is the reference government institution to perform arboviral infection tests; it had the capacity to perform multiplex real-time PCR tests to confirm infections. People from different parts of the city and hospitals came for testing. For a more sensitive case definition, we collected 3ml of blood from patients who had fever associated with joint pain and or other symptoms within 5 days of onset of symptoms. A total of 1466 samples were collected from the patients along with basic clinical and demographic data. Serums were separated and tested by RT-PCR in the reference virology laboratory. **Results:** Among the collected samples, 1043 (71%) were found positive for chikungunya viral infection. Two-thirds of the case-patients were men (65%), and the mean age of the case-patients was 34 years. Most of those infected were adults, and 9 out of 10 case-patients (90.5%) were older than 12 years. The highest chikungunya positivity showed in May, June, and July (84%, 84%, and 74% respectively) of 2017. Clinically, 92% experienced severe joint pain, while only 32% had rash within 5 days of onset of symptoms. Forty-two percent of patients complained of headache; 36% had severe weakness, and 22% vomited during episodes. **Conclusions:** The outbreak findings indicate that 71% symptomatic cases were infected with CHIKV. Further investigation will be needed for why and how this massive transmission of the organism occurred and mosquito control is needed to control of future outbreaks.

Board 359. Local Transmission of Chikungunya in Rome and the Lazio Region, Italy: The First Outbreak in a Metropolitan Area in a Western Country

F. Vairo[1], A. Mammone[1], S. Lanini[1], E. Nicastri[2], C. Castilletti[2], F. Carletti[2], V. Puro[1], D. Di Lallo[3], V. Panella[3], D. Varrenti[4], P. Scaramozzino[5], A. Di Caro[1], P. Scognamiglio[1], M. Capobianchi[1], G. Ippolito[1]
[1]Regional Service for Surveillance and Control of Infectious Diseases (SERESMI), National Institute for Infectious Diseases "Lazzaro Spallanzani" IRCCS, Rome, Italy, [2]National Institute for Infectious Diseases "Lazzaro Spallanzani" IRCCS, Rome, Italy, [3]Direzione Regionale Salute e Politiche Sociali, Regione Lazio, Rome, Italy, [4]Local Health Authority Roma 6, Albano Laziale, Italy, [5]Istituto Zooprofilattico Sperimentale del Lazio e della Toscana "M. Aleandri", Rome, Italy

Background: CHIKV has spread beyond its original tropical locations; recently, it has become an emerging issue in the temperate regions of the Northern Hemisphere. On September 7, 2017, the Lazio Regional Service for Surveillance and Control of Infectious Diseases was notified of three potentially autochthonous cases of chikungunya virus (CHIKV) infection in Anzio, a coastal town devoted to internal tourism 1 hour by car from Rome. **Methods:** An outbreak investigation based on an established surveillance system data and molecular analysis of viral variant(s) were conducted. **Results:** Between January 1 and October 30, 2017, 391 chikungunya cases were reported. Epidemiological analysis suggested the occurrence of 3 main events of local transmission. The major event involved 309 person who had a direct link with the town of Anzio and its surrounding area. The other two events occurred in people who lived in Rome (68 cases) and Latina (8 cases). Attack rate was highest in Anzio (320.4/100,000 residents); the city of Rome showed attack rates ranging from 1.30 to 13.1/100,000 residents in the different districts and Latina reported an attack rate of 7.13/100,000 residents. The cumulative incidence in the whole region was 6.61 cases/100,000 residents. Of the case-patients, 97.2% reported fever, 95.4% reported joint pain, 63.4% developed a skin rash, and 38.9% developed arthritis. On the phylogenetic tree the virus is located on a branch of the IOL sublineage that is distinct from the 2007 Italian autochthonous sequences, and doesn't show the A226V mutation. **Conclusions:** This is the first report of a chikungunya outbreak involving a highly populated urban area in a western country. The outbreak probably started in the area of Anzio and spread by continuity to neighboring villages and then to the metropolitan area of Rome and to the Latina area favored by tourists. The low incidence in a metropolitan area is likely to be related to the low *Aedes albopictus* vectorial competence for the involved CHIKV strain, to the very dry 2017 summer and to the prompt implementation of vector control measures. The introduction of CHIKV in Italy after ten years highlights the importance of an integrated multidisciplinary surveillance system and the need to increase awareness and knowledge in health care workers.

Board 360. Differences in Transmission and Disease Severity between Two Successive Waves of Chikungunya

A. Gordon[1], L. Gresh[2], S. Ojeda[2], G. Chowell-Puente[3], K. Gonzalez[4], N. Sanchez[2], S. Saborio[4], J. Mercado[4], G. Kuan[4], A. Balmaseda[4], E. Harris[5]
[1]University of Michigan, Ann Arbor, MI, USA, [2]Sustainable Sciences Institute, Managua, Nicaragua, [3]Georgia State University, Atlanta, GA, USA, [4]Ministry of Health, Managua, Nicaragua, [5]University of California, Berkeley, Berkeley, CA, USA

Background: Chikungunya, a mosquito-borne illness, was introduced into the Caribbean in 2014 and caused massive epidemics in Central and South America in 2014-2016. **Methods:** We performed a prospective pediatric cohort study of ~3,800 children in Managua Nicaragua. Children presenting with the testing definition of chikungunya-like illness or undifferentiated fever were tested for chikungunya virus (CHIKV) infection by real-time RT-PCR and serological assays. Each year, a blood sample was collected to evaluate CHIKV infection. **Results:** Between March 2014 and February 2016, while Nicaragua experienced two successive waves of chikungunya, 4,353 children participated in the cohort study. We detected 539 clinical cases of chikungunya, yielding an incidence rate of 80.2 cases per 1000 person-years (95%CI: 73.7, 87.2), and 893 CHIKV infections, yielding an incidence rate of 137.1 infections per 1000 person-years (95%CI: 128.4, 146.4). The incidence rate and overall case number were much higher in the second epidemic than the first. Interestingly, even though all children were at risk over the same time interval, the seroprevalence of anti-CHIKV antibodies increased linearly with age. The second epidemic was more severe clinically than the first, with both a higher symptomatic to inapparent ratio (1:1.20 in Epidemic 1 vs. 1:0.65 in Epidemic 2) and more severe clinical presentation among cases. Transmission intensity was also greater in the second epidemic, with a higher reproductive number. During each epidemic period, there was a sufficient number of mosquitoes in the study area to propagate an epidemic, with a higher Breteau index in year 1 than year 2. In year 2, temperature was higher overall than in year 1. **Conclusions:** During these two successive epidemics of chikungunya, the intensity of transmission and severity of clinical presentation varied, with higher intensity associated with greater severity. We hypothesize that in Epidemic 2, mosquitoes may have delivered a higher exposure dose, leading to both increased transmission intensity and increased severity.

Board 361. Chikungunya–A Reemerged Tropical Disease: Development of a Live-Attenuated Vaccine

N. Wressnigg, A. Pilz, U. Lundberg, A. Fritzer, R. Hochreiter, A. Meinke
Valneva Austria GmbH, Vienna, Austria

Background: Chikungunya virus (CHIKV) is a mosquito-borne virus resulting in many patients in chronic and incapacitating arthralgia affecting all gender and age groups. Coinciding with an adaptation enabling unusually efficient transmission by *Aedes albopictus* mosquitoes, the virus re-emerged in 2004 and rapidly spread over Africa, Asia, the Americas and locally also in Europe since then. Hence, CHIKV is regarded as one of the most-likely re-emerged viruses to spread globally and morbidity due to this virus is considered a serious threat to global public health raising an urgent demand for efficient prophylaxis. However, at present there is no treatment or vaccine available. Facing the unmet medical need for a prophylactic intervention we initiated a program to develop a vaccine candidate (VLA1553) against CHIKV infections. **Methods:** Valneva's live-attenuated CHIKV vaccine candidate is based on the La Reunion strain of the East Central South African genotype, is produced in Vero cells and purified by centrifugation, ultrafiltration, batch-chromatography and sucrose gradient centrifugation. VLA1553 is characterized by a 60 amino acid deletion in its nsP3 viral replicase complex gene leading to attenuation of the virus *in vivo.* **Results:** The safety, immunogenicity as well as protective efficacy of the vaccine candidate was evaluated in mice and non-human primates.

We demonstrate that our vaccine candidate is highly attenuated in animal models and causes no clinical manifestations typically associated with wild-type CHIKV infections in addition to strongly reduced viremia and cytokine levels. Moreover, VLA1553 is highly immunogenic, induces a strong and long-lasting neutralizing antibody response in animal models. Also cross-neutralizing antibodies against a Caribbean CHIKV strain are induced. VLA1553 protects against a high dose wild-type CHIKV challenge after a single immunization and no anamnestic response was observed after challenge. **Conclusions:** Due to its safe and immunogenic potential we will enter into a blinded, randomized phase 1 first-in-human clinical study investigating the safety and immunogenicity of three dose levels administered intramuscularly in a CHIKV-naïve population as a single-shot immunization designed to elicited long-term immunological memory (NCT: NCT03382964).

Board 362. Field Epidemiological Investigation Report of Chikungunya Outbreak in Gwadar District of Pakistan in the Month of July 2017

D. Baloch
World Health Organization (WHO), Quetta, Pakistan

Background: An outbreak of fever with severe joint pain started in the Gwadar district, of Pakistan in January 2017. An entomological and epidemiological investigation of this outbreak was conducted to ascertain the nature and cause of the outbreak. Aim: Aim of the study was to investigate the nature and cause of the outbreak and to contain its further spread. Settings and Design: It was a cross-sectional study conducted in the Gwader district, situated at a distance of about 700 km from Major city Karachi and 900 Km from provincial capital Quetta, Balochistan **Methods:** All patients attending OPD of District Health Quarter hospital and Rural health centers of district Gwadar, complaining of ever with incapacitating joint pain, were screened for chikungunya fever. House to house survey also conducted for active case search. Out of the 2617 suspected chikungunya patients, 29 blood samples were randomly drawn amongst these patients. Out of the 29 tested, 21 (72%) were positive against chikungunya virus to used real time RT PCR from NIH. House-to-house survey was conducted in the affected area for more cases and to find out the vector-breeding sites **Results:** The main breeding sites of the mosquitoes were the desert coolers of houses, water stored in metal and plastic containers, and water collections at construction sites. *Aedes* mosquitoes were present in almost the majority of houses surveyed in the area. **Conclusions:** It was concluded that the routine campaigns need to be organized regularly within the community highlighting the potential breeding grounds of mosquitoes and the possible control methods. Source reduction strategies like cleaning of desert coolers on weekly basis, emptying of water containers, and close monitoring of construction sites for potential breeding of the vector needs to be done on a regular basis to avoid future outbreaks. Establishment surveillance, particularly for dengue and chikungunya, along with appropriate response is important. Surveillance should also be strengthened in other unaffected areas to ensure appropriate and timely response.

Board 363. From Data to Decisions: Utilizing Machine Learning and Monte Carlo Simulations to Map Epidemic Potential

J. Parker, S. Griffin, M. Campbell, N. Wayant
Geospatial Research Lab, Alexandria, VA, USA

Background: Recent work in epidemic disease modeling has focused on the physical and social environment of a region and its relationship to health outcomes. This is especially true when discussing vector-borne diseases, where human-vector interaction is key to the disease's spread. However, there's not currently a clear way to include all regional variables in analysis or simulation. **Methods:** Our project focused on developing a quantitative workflow for deriving disease hazard maps of vector-borne diseases, using Dengue fever infections in Cambodia as a test area. We incorporated regional variables into a Random Forest machine-learning algorithm, which processed the province level incidence reports to the spatial distribution of both the human population and land cover variables (precipitation, NDVI, etc) down to a tactical level. We then used these calculated incidence rates in a stochastic disease progression model in both the humans and the mosquito population over time and space, including the full mosquito life cycle. **Results:** Using this process, we were able to fully simulate the spatio-temporal progression of Dengue fever in Cambodia. We were able to identify transition points in the model, representing low-medium-high levels of risk based on the incidence rates, as well as potential interventions to protect populations from disease. Further, for high incident rates scenarios, we observed traveling wave phenomena in the infected populations, and used measures of these wave fronts to connect our simulation to other types of dynamical systems. **Conclusions:** The combination of machine learning methods and Monte Carlos simulations provided a clear work flow for creating disease hazard maps of a region. Both methods provide for a rigorous treatment of error and model-free inclusion of regional variables into disease simulations. Further work will focus on simulating social events, such as mass immigration or a disaster, as well as adapting the model to other types of diseases and disease vectors.

Board 364. High Prevalence of Dengue among Pregnant Women in India

M. Alexander[1], S. Naik[2], M. Robinson[3], G. Sapkal[4], P. Awate[5], P. Deshpande[1], V. Kulkarni[1], S. Nimkar[1], P. Sambarey[2], A. Kinikar[2], V. Mave[1], N. Suryavanshi[1], R. Bollinger[3], A. Gupta[3], R. Bharadwaj[2], J. Mathad[6]
[1]Byramjee Jeejeebhoy Government Medical College-Johns Hopkins Clinical Trials Unit, Pune, India, [2]Byramjee Jeejeebhoy Government Medical College/Sassoon General Hospital, Pune, India, [3]Division of Infectious Diseases, Johns Hopkins University School of Medicine, Baltimore, MD, USA, [4]National Institute of Virology, Pune, India, [5]Integrated Diseases Surveillance Program, Dept of Health, Pune, India, [6]Weill Cornell Medical College, New York, NY, USA

Background: Mosquito-borne diseases (MBD) are endemic to India. The incidence of MBD during pregnancy and its impact on maternno-infant outcomes has not been systematically investigated in India. **Methods:** Following reports of zika detection in India, we conducted a surveillance of antenatal (AN) patients attending a tertiary care public hospital in Pune, India, from Oct 2017 to Jan 2018. During this period all AN clinic attendees were screened for symptoms of MBD (fever, conjunctivitis and rash) in the previous 15 days. Patients with any one of the symptoms underwent a symptom confirmation and were

enrolled if they had 1. Fever only, 2. Fever with conjunctivitis, 3. Fever with rash or 4. All 3 symptoms. We recorded detailed symptoms, clinical and travel history from consenting women. Blood samples were tested for Dengue, Chikungunya and Zika with Trioplex Real-time RT-PCR Assay at the National Institute of Virology (Pune). **Results:** We screened 5843 pregnant women. 106 women reported at least one positive symptom and 52 were enrolled. Enrolled women were symptomatic at a median gestational age of 28 weeks (IQR: 12-38). Of the 52 tested, 48 reports are available for dengue, chikungunya and zika. Seven (14%) tested positive for dengue; none were positive for chikangunya or zika. One patient who tested positive for dengue but negative by PCR for chikungunya had a positive chikungunya IgM ELISA result. Symptoms reported by dengue patients were fever (n = 7, 100%), conjunctivitis (n = 7, 100%), headache (n = 6, 86%), retro-orbital pain (n = 4, 57%), and myalgia or arthralgia (n = 4, 57%). Compared to pregnant women without dengue, women with dengue were significantly more likely to report conjunctivitis (100% vs 46% p=0.01, PPV = 24%) and retro-orbital pain (57% vs 14% p=0.02, PPV = 40%). Of the 17 women who have delivered (4 dengue positive, 13 dengue negative) there were no significant differences in birth outcomes (e.g. low birthweight, prematurity). **Conclusions:** Dengue infection is common in pregnant women in India. Our results suggest that conjunctivitis and retro-orbital pain are important pointers towards dengue infections. Quick survey with focused symptoms screening in AN clinics can identify women at high risk of dangerous infections and plan appropriate care.

Board 365. Prolonged Detection of Dengue Virus in the Semen of a Man Returning from Thailand to Italy, January 2018

E. Lalle, F. Colavita, A. D'Abramo, C. Castilletti, F. Carletti, S. Gebremeskel Teklè, M. Iannetta, D. Vincenti, L. Bordi, L. Scorzolini, G. Ippolito, M. Capobianchi, E. Nicastri
National Institute for Infectious Diseases Lazzaro Spallanzani IRCCS, Rome, Italy

Background: Dengue virus (DENV) is an arthropod-borne member of the Flaviviridae family. Differently from other flaviviruses such as Zika virus, sexual transmission has never been reported during DENV infection and Dengue was never detected in semen. A case of primary Dengue fever (DF) in a Caucasian man returning from Thailand to Italy on January 2018 is reported. **Methods:** The presence of DENV-RNA collected at different days from symptom onset (DSO) was studied in different biological compartments. Particularly, semen and urine specimens were assessed to study the DENV-RNA content in unfractionated samples, cellular fraction (CF) and supernatant (SP). In positive samples, negative-strand DENV-RNA was assessed. **Results:** At patient's admission (DSO 9) at the National Institute of Infectious Disease Lazzaro Spallanzani in Rome, DENV-RNA was detected in unfractionated samples of serum (38 cycle threshold, Ct, value), urine (Ct value 37) and semen (Ct value 26). During follow-up visits, DENV-RNA was undetectable in all biological samples apart from semen collected on DSO 24 (Ct value 24) and on DSO 37 (Ct value 30). Negative-strand DENV-RNA was detected in semen CF (Ct value 28 on DSO 9; Ct value 28 on DSO 24, and Ct value 29 on DSO 37) but not in semen plasma. DENV-RNA was not detected in urine CF and SP on both DSO 24 and 37. Further virological analyses including virus isolation from different biological compartments are ongoing. **Conclusions:** Dengue virus in semen has been reported in presence of undetectable DENV-RNA in urine and blood. The detection of negative-strand DENV-RNA in semen CF can be considered as a surrogate marker of ongoing viral replication. These results raise relevant concern on the epidemiologic and pathogenetic implications related to the possible risk of dengue sexual transmission in endemic and not-endemic settings.

Board 366. Evolving Spectrum of Dengue in India

K. Baruah, P. Sen
National Vector Borne Disease Control Programme, Directorate General of Health Services, Ministry of Health & Family Welfare, Government of India, Delhi, India

Background: Dengue fever is caused by a positive stranded encapsulated RNA virus belonging to the *Flaviviridae* family. In India the virus was first isolated in 1945, and the first dengue outbreak was reported in 1956. The World Health Organization (WHO) reported a 30-fold increase in global incidence of dengue over the last five decades. India contributed 6% of the dengue burden to WHO's South East Asian (SEA) Region during 2009, which increased to 26% in 2016. **Methods:** During the last two decades, the disease is spreading to new geographical areas with recurring outbreaks. Manmade ecological and lifestyle change*s* allow the vector to propagate into rural areas resulting in a rural shift of dengue. Perennial transmission was established in the southern and western parts of the country with expansion of the transmission window. All 36 states report dengue incidence. The National Vector Disease Control Programme under Ministry of Health and Family Welfare, Government of India manages dengue along with five other vectorborne diseases in the country. A network of 618 sentinel surveillance hospitals diagnose dengue free of cost to the community and 16 apex laboratories carry out serosurveillance. Entomological monitoring at the state level through 78 entomological zones, municipalities and central cross-checking organization. **Results:** During 2014, a total of 40571 cases were reported, which increased to 129166 in 2016 and 157996 in 2017. All 4 dengue virus serotypes circulate in the country. All age groups and both genders are affected, but people 15 to 45 years of age are most affected, contrary to the other SEA countries, where children are more affected. The case-fatality rate has declined from 3.3% in 1996 to 0.2% in 2015. The majority of deaths from dengue are associated with some co-morbid illness. Both *Aedes aegypti* and *Ae. albopictus* are involved in transmission. **Conclusions:** Rapid urbanization, unplanned construction, industrialization, concurrent population growth, deficient potable water, improper solid waste management, the ever-increasing automobile industry, increased population movement, and the absence of effective inter-departmental convergence are a few of the underlying causes for the geographical expansion and increasing outbreaks of dengue. In the absence of any effective drug, limited vector control options coupled with global climate change and increasing morbidity with a varying clinical spectrum, dengue has emerged as a serious public health challenge in India.

Vaccine-Preventable Diseases

Board 367. Imported *Corynebacterium diphtheriae* in Minnesota, 2014-2017

J. Griffith[1], A. Acosta[2], C. Bozio[2], H. Omar[1], P. Cassiday[2], K. Pung[1], P. Snippes[1], T. Tiwari[2]
[1]Minnesota Department of Health, St. Paul, MN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Infections caused by toxigenic *Corynebacterium diphtheriae* are rare in the United States due to widespread vaccination

but remain endemic in countries with suboptimal vaccine coverage. Diphtheria is a threat to unvaccinated persons traveling to diphtheria-endemic countries or those who may have contact with people from these areas. **Methods:** We summarized investigations of patients with *C. diphtheriae*-infected cutaneous ulcers reported to the Minnesota Department of Health (MDH) from 2014-2017. MDH confirmed *C. diphtheriae* status by culture, and isolates were sent to CDC for biotyping and confirmation of toxigenicity. **Results:** Among 5 patients with cutaneous lesions, *C. diphtheriae* initially was identified by clinical laboratories using matrix-assisted laser desorption ionization-time of flight spectrometry (MALDI-TOF). Diphtheria was not suspected in any patient and was identified solely by laboratory diagnosis. All patients were foreign born; 4 had leg lesions and 1 had an abdominal wound. Based on testing at CDC, isolates from 2 patients (leg, abdomen lesions) were confirmed as toxigenic *C. diphtheriae* biotype mitis; 3 were confirmed as non-toxigenic *C. diphtheriae*. Both patients with toxigenic *C. diphtheriae* had recent travel to East Africa, where their infections started. The 2 patients were not epidemiologically linked; neither had history of diphtheria vaccination. Contact tracing was conducted for both patients. All household contacts (4, all unvaccinated) were tested for *C. diphtheriae* and started on a prophylactic course of penicillin. Nasal and throat swabs obtained prior to antibiotic onset and 24 hours after the last dose were negative for *C. diphtheriae* by culture in all contacts. Wounds healed in both patients after appropriate antibiotic therapy. **Conclusions:** Through initial MALDI-TOF testing, *C. diphtheriae* infection was identified in patients in whom it was not suspected. Subsequent confirmation for toxigenicity allowed for prompt case investigation, preventing disease spread. This highlights the importance of referring *C. diphtheriae* isolates to state health departments for confirmatory testing. Additionally, it underscores the need to consider *C. diphtheriae* as a possible cause of cutaneous lesions in individuals with recent travel to countries with endemic diphtheria.

Board 368. Invasive *Haemophilus influenzae* and *Haemophilus influenzae* Serotype A Cases in Minnesota, 2006-2017

K. Schleiss, L. Triden, K. Como-Sabetti, R. Danila, K. Connors, P. Snippes Vagnone, R. Lynfield
Minnesota Department of Health, Saint Paul, MN, USA

Background: Invasive *Haemophilus influenzae* (HI) and HI serotype A (HIA) can cause severe disease and disproportionately affect American Indians. An increase in invasive HI cases and serotype trends was examined. **Methods:** Minnesota Department of Health (MDH) conducts active, statewide surveillance for invasive HI infections as part of CDC Active Bacterial Core Surveillance. Isolates are submitted to MDH for serotyping. Trends in HI and HIA incidence from 2006-2017 were calculated using Kendall Tau-b correlation. HIA cases were compared to non-serotype A HI (non-HIA) cases. **Results:** Results: 1,139 HI cases were reported from 2006-2017; 93% had isolates submitted. The HI incidence rate increased from 1.9/100,000 population in 2006 to 2.3/100,000 in 2017 (r_τ=0.485, p<0.05). The proportion of HIA cases increased from 3.5% in 2006 to 11% in 2017 (X^2 for trend=3.60, p<0.01). The largest increase in the proportion of HIA isolates was 9.1% in 2013 to 13.7% in 2014. No changes in the proportion of other HI serotypes (n>2) or non-typeables were observed over time. HIA cases were more likely to be American Indian (14% vs 2.2%, OR=7.42, p<0.01), <2 years old (36% vs 11%, OR=4.55, p<0.01), 2 to 5 years of age (6.5% vs 1.7%, OR=4.15, p<0.01), or reside in greater Minnesota (outside 7-county Minneapolis-St. Paul area) (66% vs 54%, OR=1.68, p<0.05) compared to non-HIA cases. HIA cases were also more likely to have meningitis (21% vs 6.7%, OR=3.62, p<0.01) and lack underlying medical conditions (29% vs 15%, OR=2.27, p<0.01). Among children ≤5 years, HIA cases were less likely to develop pneumonia than non-HIA cases (13% vs 56%, OR=0.111, p<0.01). HIA cases ≤5 years were more likely to develop meningitis than HIA cases of other ages (84% vs 32%, OR=11.6, p<0.01). HIA cases were less likely to die than non-HIA cases (3.3% vs 12%, OR=0.243, p=0.01) and be aged ≥75 years (9.8% vs 35%, OR=0.198, p<0.01). There were no differences in other case or clinical characteristics. **Conclusions:** We observed an increase in HI incidence and proportion of serotype A among HI cases in Minnesota from 2006-2017. HIA cases were more likely to be American Indian, young children (≤5 years), residents of greater Minnesota, and present with meningitis. Continued surveillance is necessary to monitor HIA trends and inform future prevention strategies including vaccine development.

Board 369. Epidemiology of *Haemophilus influenzae S*erotype A in Alaska, 2000-2017

M. Bruce, T. Zulz, D. Hurlburt, K. Rudolph, D. Bruden, R. Singleton, C. Debyle, J. Klejka, T. Hennessy
CDC, Anchorage, AK, USA

Background: Prior to introduction of the *Haemophilus influenzae* type b (Hib) conjugate vaccines in 1991, rates of Hib disease among Alaska Native (AN) people were among the highest reported in the world. Routine vaccination has reduced these rates to very low levels; however, serotype replacement with non-type b strains is of concern. **Methods:** We identified cases of invasive Hi disease in Alaska (AK) from 2000–2017 through statewide invasive bacterial disease surveillance. Medical charts were reviewed on laboratory-confirmed cases using standard forms to verify clinical presentation. Estimated population in AK as of 2016 was 739,709; AN people comprised 19% of the population. **Results:** During the study period, a total of 306 cases of invasive Hi disease were reported; 155 (51%) were typeable Hi. Of those, 61 (39%) were serotype a, 41 (26%) were serotype b, 37 (24%) were serotype f. Among 61 Hia isolates, 56 (92%) occurred in AN people; median age was 0.8 year (range 0.1-77 years); 64% were male; 12% of Hia cases (6 children, 1 adult) were fatal. Common clinical presentations included: meningitis (36%), pneumonia (28%), and septic arthritis (16%). There were no cases of epiglotittis. Overall annual Hia incidence was 0.6 cases/100,000 population. Annual incidence rates among children < 2 were 14.8 cases/100,000 persons; annual incidence rates for AN children < 2 were 50.2 cases/100,000 persons. **Conclusions:** Serotype a is now the most common Hi serotype seen in Alaska, with the highest rates among AN children. Further research is needed to determine long-term sequelae, risk factors, and prevention strategies.

Board 370. Study on the Prevalence of *N. meningitidis* Serogroups and Features of Meningitis Cases in Beijing, China, 2007-2016

D. Zhao, L. Lu, M. Dong
Beijing Center for Disease Control and Prevention, Beijing, China

Background: *Neisseria meningitidis* is recognized as a significant public health problem. *N. meningitidis* is classified into 12 serogroups whose relative prevalence varies considerably with time and geographic location. Before 2006, the majority of cases were caused by

serogroup A strains in Beijing. In 1984 and 2006, Beijing EPI introduced serogroup A meningococcal polysaccharide vaccines, serogroup A and C meningococcal polysaccharide vaccines respectively. A study on the prevalence of *N. meningitidis* serogroup and features of meningitis in Beijing would supply evidence for meningitis control and prevention. **Methods:** Data on reported meningitidis cases from 2007 to 2016 were collected from the National Notifiable Infectious Disease Reporting Information System in China. All laboratory-confirmed cases, which were identified by isolation or PCR, were chosen for descriptive analysis. **Results:** There were 33 laboratory-confirmed cases in Beijing from 2007-2016. The proportion of meningococcal infections with group A, C, B, W135, and X were 33.3%, 30.3%, 12.1%, 3.0%, and 3.0%, 18.2% laboratory-confirmed cases could not be identified by serogroup. The proportion of meningococcal infections with group A declined year by year (from 55.6% in 2007 into 33.33% in 2010, and no cases since 2011). The proportion of meningococcal infections with group C increased year by year (from 11.11% in 2007 to 50% in 2015). Otherwise, meningococcal infections with group B cases were reported in 2009 (2 cases), 2012 (one case), and 2015 (one case). Most meningococcal infections with group A (81.8%) or group C (90.0%) were in patients >15 years old. Seventy-five percent of patients with group B meningococcal infections were 6-35 months old. Group A patients' main clinical features included fever (38-39°C, 54.5%), neck rigidity (90.9%), petechial or purpuric (81.1%), headache (81.1%), nausea (72.7%) and vomiting (72.7%). Group C patients' main clinical features included fever (38-39°C, 60.0%), petechial or purpuric (75%), and neck rigidity (60%). Group B patients' main clinical features included fever (≥39°C,75.0%), neck rigidity (75%), disturbance of consciousness (75%), vomiting (75.0%), and petechial or purpuric (50%). **Conclusions:** The relative prevalence varied from serogroups A to serogroups C, and most children (those <15 years old) could be protected from meningitis because of EPI in Beijing. Serogroup B cases were reported, but no vaccine is available against serogroup B meningococci in China.

Board 371. Outbreak of Bacterial Meningitis in Mali Associated with a New Sequence Type of *Neisseria meningitidis* Serogroup C Clonal Complex 10217

I. Guindo[1], Y. Sanogo[2], S. Diarra[3], A. Retchless[2], M. Abdou[3], S. Coulibaly[3], M. Maiga[4], H. Chang[2], J. Vuong[2], A. Acosta[2], R. Novak[2], X. Wang[2]
[1]Institut National de Recherche en Santé Publique, Bamako, Mali, [2]Meningitis and Vaccine Preventable Diseases Branch, Division of Bacterial Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Institut National de Recherche en Santé Publique, Bamako, Mali, [4]Direction Nationale de la Sante, Bamako, Mali

Background: Between week 8 and week 10 of the 2016 meningitis season, Mali reported a localized outbreak of meningococcal meningitis in the health district of Ouélessébougou (215,775 inhabitants), located about 80 kilometers south-east of the capital Bamako. In total, 39 suspected meningitis cases were reported, with a case fatality rate of 15.3%. This report uses whole genome sequencing (WGS) to describe the molecular features of the causative strain. **Methods:** Suspected meningitis cases were reported through case-based surveillance in Mali. Culture and rt-PCR were performed on available CSF specimens at the National Reference Laboratory (INRSP). *Neisseria meningitidis* isolates were analyzed at CDC by WGS and multilocus sequence typing (MLST), and characteristics were compared with those of meningococcal serogroup C isolates collected in the African region. **Results:** Thirty-nine suspected meningitis cases were reported from 8 villages in Ouélessébougou district, half (18) from Dialakoro and Sicoro alone. Of 29 CSF specimens analyzed, 22 (75.8%) tested positive for bacterial meningitis pathogens, of which 16 (72.7%) were *Neisseria meningitidis* (Nm). Nm serogroup C (NmC) was identified in 14 specimens, representing the most predominant serogroup (87.5%), followed by NmW (1) and Nm strain of undetermined serogroup.(1). Other pathogens detected were *Streptococcus pneumoniae* (5) *and Haemophilus influenzae* (1). Eight NmC isolates were recovered and characterized by WGS. All isolates had identical FetA, PorA, and PorB types and belonged to ST-12446, which is very similar (matching at 6/7 loci) to ST-10217, a strain that caused a large epidemic in Niger in 2015. Both ST-12446 and ST-10217 belong to the same clonal complex (10217). **Conclusions:** A localized NmC outbreak in Ouélessébougou district Mali was caused by an emerging ST-12446 strain, which possibly diverged from the ST-10217 strain recently reported in the African region. The emergence of the new ST of NmC in the African meningitis belt further highlights the need for molecular surveillance in the region. The virulence of this new ST should be investigated in comparison to the ST-10217 strain that recently caused massive outbreaks in Niger and Nigeria.

Board 372. Investigation of Suspected Pertussis Outbreak in Kunar Province, Afghanistan, March 2016

H. Bakhshi, F. Arifi
Ministry of Public Health, Kabul, Afghanistan

Background: Pertussis is sporadically reported in Afghanistan, with 1,497 cases recorded in 2012 by the United Nations, but data are sparse and unreliable. On March 7, 2016, the elders of a remote village of Kunar province of Afghanistan reported cases of illness to the local surveillance officer, who suspected pertussis. A multidisciplinary team was assembled to identify and prevent further cases in two villages, Jeegal and Nakenar, which appeared to be involved. **Methods:** A suspected case was defined as cough lasting at least 14 days with one of following: paroxysms of coughing or inspiratory whoop or tussive vomiting. The team conducted face to face interviews with each case and reviewed vaccination records. **Results:** Over a six-day time period of 7-12 March, we identified 100 (60 male and 40 female) cases and 4 deaths. The illness onset date was from 1st of February. Median patient age was 4 years (range: 1 month- 45 years). The attack rate was 7.6% overall (10 per 1000 population) and was 6.9, 2.2, 0.1 and 0.2 percent among ages 0-5, 6-10, 11-15 and > 16 years groups, respectively. Via a brief random survey of households, vaccination coverage was determined to be 60%. All cases received erythromycin. To prevent further transmission, 134 children (aged 45 days to 5 years) received a first dose of Penta and OPV vaccination and the last case occurred May 12. Health education on prevention of pertussis was delivered to elders of the villages. **Conclusions:** The vaccination coverage was low. Jeegal and Nakenar villages are remote and insecure. Thus, the team could not vaccinate all individuals who would benefit from vaccination, possibly explaining the lingering onset of cases until May 12. Until security improves in Afghanistan, cases of vaccine preventable illness, including pertussis, will continue.

Board 373. Geographic Variation in Invasive Pneumococcal Disease (IPD) Following Six Years of 13-Valent Pneumococcal Conjugate Vaccine (PCV13) Use in the United States

R. Gierke[1], M. Farley[2], W. Schaffner[3], A. Thomas[4], A. Reingold[5], L. Harrison[6], R. Lynfield[7], J. Rowlands[8], S. Petit[9], M. Barnes[10], C. Smelser[11], C. Whitney[1], T. Pilishvili[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Emory University and Atlanta VAMC, Atlanta, GA, USA, [3]Vanderbilt University, Nashville, TN, USA, [4]Oregon Public Health Division, Portland, OR, USA, [5]University of California, Berkeley, Berkeley, CA, USA, [6]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [7]Minnesota Department of Health, St.Paul, MN, USA, [8]New York State Department of Health, Albany, NY, USA, [9]Connecticut Department of Public Health, Hartford, CT, USA, [10]Colorado Department of Public Health and Environment, Denver, CO, USA, [11]New Mexico Emerging Infections Program, Santa Fe, NM, USA

Background: Thirteen-valent pneumococcal conjugate vaccine (PCV13) was recommended for children aged <5 years in February 2010 and for adults aged ≥65 years, in series with 23-valent polysaccharide vaccine (PPSV23), in August 2014. We evaluated geographic differences in PCV13 impact on invasive pneumococcal disease (IPD) among children (direct effects) and adults (indirect and direct effects) 6 years after the pediatric introduction across 10 sites participating in Active Bacterial Core surveillance (ABCs). **Methods:** IPD cases (isolation of pneumococcus from sterile sites) were identified through ABCs during July 2007–June 2016. Isolates were serotyped by Quellung or whole genome sequencing and grouped as either PCV13-type, PPSV23-unique, or non-vaccine type. Percent changes in IPD incidence were estimated as one minus rate ratio and 95% confidence Intervals (95% CI) between pre-PCV13 (2007-2008) and post-PCV13 (2015-2016) periods, by site, age group, and serotype group. Vaccination coverage data for PCV13 were obtained from the National Immunization Survey. **Results:** Of 11,132 cases identified, 1,108 (10%) were in children <5 years and 3,729 (34%) in adults ≥65 years. Reductions in overall IPD rates ranged from 89% (95%CI 64-97) in California to 52% (95%CI 30-67) in Georgia among children <5 years, and from 47% (95%CI 30-60%) in New York to 12% (95%CI -36-44%) in California among adults ≥65 years. Reductions in PCV13-type IPD rates ranged from 93% (95%CI 79-97%) in Minnesota to 68% (95%CI 44-82%) in Georgia among children <5 years, and from 74% (95%CI 63-82%) in Minnesota to 29% (95%CI -41-64%) in California among adults ≥65 years. No significant increases were noted in IPD caused by non-PCV13 types. In 2016, vaccination coverage for ≥ 3 doses of PCV13 by age 19-39 months ranged from 90% in California to 96% in Georgia and Minnesota. **Conclusions:** Reductions in overall and PCV13-type IPD incidence among children and adults were observed for all ABCs sites; however, the magnitude of these reductions varied across the 10 sites and not all reductions were significant. No evidence of serotype replacement was noted at any of the sites. Differences in disease trends by state are not likely to be explained by the relatively small differences in 3-dose coverage by state.

Board 374. Impact of 13-Valent Pneumococcal Conjugate Vaccine (PCV13) on Invasive Pneumococcal Disease in Connecticut

S. Shore[1], S. Petit[1], C. Marquez[1], D. Santoro[2], M. Cartter[1]
[1]Epidemiology and Emerging Infections Program, Connecticut Department of Public Health, Hartford, CT, USA, [2]Katherine A. Kelley State Public Health Laboratory, Connecticut Department of Public Health, Rocky Hill, CT, USA

Background: Invasive pneumococcal disease (IPD) is a leading cause of pneumonia, sepsis, and meningitis. Incidence of IPD has dramatically decreased since the introduction of the 7-valent pneumococcal conjugate vaccine (PCV7) in 2000. Routine immunization with PCV13 was recommended for children <5 years of age in 2010 and for adults aged ≥65 years in late 2014, in series with the 23-valent polysaccharide vaccine (PPSV23). We evaluated PCV13 impact on IPD in Connecticut. **Methods:** IPD cases (sterile site isolates) were identified through Active Bacterial Core Surveillance (ABCs). Isolates were serotyped and classified as PCV13 (including type 6C due to cross-reactivity), PPSV11 (serotypes unique to PPSV23), or non-vaccine types (non-PCV13 or NVT (<5 and ≥65 years of age, respectively)). To assess effects attributable to vaccination we examined trends from 2008 to 2016 overall and for high risk age groups (<5 and ≥65 years of age). **Results:** From 2008 to 2016, 3,004 cases of IPD were identified of which 2,765 (92%) had an isolate available for serotyping. Incidence (cases per 100,000) decreased by 49% overall (13.3 in 2008 to 6.8 in 2016), by 60% in cases <5 years of age (17.6 to 7.0), and by 47% in cases ≥65 years of age (38.8 to 20.5) ($p<0.01$ for each trend). Incidence of PCV13-type disease decreased by 75% overall (7.2 in 2008 to 1.8 in 2016), by 90% in cases <5 years of age (11.1 to 1.1), and by 70% in cases ≥65 years of age (20.9 to 6.3) ($p<0.01$ for each trend). In contrast, incidence of PPSV11-type among cases ≥65 years of age remained stable. From 2008 to 2016, incidence of non-PCV13-type and NVT IPD remained stable overall and in cases <5 and ≥65 years of age. Incidence of type 35B IPD increased by 150% (0.2 in 2008 to 0.5 in 2016; $p<0.01$), with most of the increase in cases ≥65 years of age. Increases in other individual serotypes were not significant. **Conclusions:** In Connecticut, routine pediatric immunization with PCV13 has significantly reduced rates of IPD in children and unvaccinated adults, indicating rapid direct and indirect vaccine effects. Continued routine administration of PCV13 to adults ≥65 years of age has the potential to directly decrease IPD even further. Continued observation of IPD is needed to monitor potential changes in disease burden that may emerge in PCV13 and non-PCV13 serotypes.

Board 375. Long-Term Impact of 10-valent Pneumococcal Conjugate Vaccine (PCV10) Introduction on Carriage of Vaccine Serotype and Antimicrobial-Resistant Pneumococci among Children Less Than 5 Years Old in Mozambique, 2012-2016

S. Valenciano[1], F. Lessa[1], B. Moiane[2], A. Chaúque[2], S. Massora[2], F. Pimenta[1], H. Mucavele[2], J. Verani[1], M. Carvalho[1], C. Whitney[1], N. Tembe[2,3], B. Sigaúque[2,3]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Centro de Investigação em Saúde da Manhiça, Maputo,

Mozambique, [3]Instituto Nacional de Saúde, Ministério de Saúde, Maputo, Mozambique

Background: Antimicrobial-resistant (AMR) pneumococci are a public health threat. Pneumococcal carriage precedes invasive disease, with HIV being a major disease risk factor. Mozambique introduced PCV10 into its infant immunization program in 2013. We evaluated the impact of PCV10 on carriage of vaccine-type (VT) and AMR pneumococci. **Methods:** We conducted three cross-sectional carriage surveys among HIV-infected and -uninfected children aged 6 weeks to 59 months: one pre-PCV introduction (2012-2013 [baseline]) and two post-PCV (2014-2015 [post 1] and 2015-2016 [post 2]). Nasopharyngeal swabs were collected and cultured. Isolates were serotyped by Quellung and underwent antimicrobial susceptibility testing. Non-susceptible isolates were defined as those with intermediate or full resistance to the antibiotic tested using CLSI 2018 breakpoints. We used log-binomial regression to estimate declines in VT-carriage over two time periods: baseline to post 1 [period 1] and post 1 to post 2 [period 2]. We compared prevalence of AMR pneumococci between baseline and post 2. **Results:** We enrolled 720 children at baseline, 911 at post 1, and 1208 at post 2. Overall VT-carriage declined from 35.3% at baseline to 24.3% at post 1 to 17.7% at post 2. After adjusting for age and HIV status, VT-carriage declined by 31.0% (95%CI: 20%–41%; P<0.001) during period 1 and by 26.8% (95%CI: 13%–38%; P<0.001) during period 2. Baseline VT-carriage was similar for HIV-uninfected (36.0%, 110/306) and -infected children (34.8%, 144/414). In HIV-uninfected children, VT-carriage declined by 34.3% (95%CI: 17%–48%; P<0.001) during period 1 and by 38.1% (95%CI: 19%–53%; P<0.001) during period 2, while for HIV-infected children significant VT-carriage decline was only observed during period 1 (28.7%, 95%CI: 13%–42%; P<0.001). Among 757 isolates from HIV-uninfected children, erythromycin-non-susceptible pneumococci declined from 13.8% (34/246) to 8.2% (42/511; P=0.02). Resistance did not change significantly among isolates from HIV-infected children. **Conclusions:** PCV10 introduction was associated with reductions in carriage of VT- and AMR-pneumococci in Mozambique, especially in HIV-uninfected children. PCV10 is an important intervention for prevention of carriage and illness due to AMR-pneumococci.

Board 376. Effectiveness of Pneumococcal Vaccines against Invasive Pneumococcal Disease among US Medicare Beneficiaries Aged 65 Years and Older

O. Almendares[1], S. Nanduri[1], R. Warnock[2], X Wu[2], S. McKean[2], J. Kelman[3], M. Farley[4], W. Schaffner[5], A. Thomas[6], A. Reingold[7], L. Harrison[8], C. Holtzman[9], J. Rowlands[10], S. Petit[11], M. Barnes[12], C. Smelser[13], B. Beall[1], C. Whitney[1], T. Pilishvili[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Acumen LLC, Burlingame, CA, USA, [3]Centers for Medicare and Medicaid Services, Washington D.C., DC, USA, [4]Emory University and Atlanta VAMC, Atlanta, GA, USA, [5]Vanderbilt University, Nashville, TN, USA, [6]Oregon Public Health Division, Portland, OR, USA, [7]University of California, Berkeley, CA, USA, [8]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [9]Minnesota Department of Health, St. Paul, MN, USA, [10]New York State Department of Health, Albany, NY, USA, [11]Connecticut Department of Public Health, Hartford, CT, USA, [12]Colorado Department of Public Health and Environment, Denver, CO, USA, [13]New Mexico Emerging Infections Program, Santa Fe, NM, USA

Background: PCV13 and PPSV23 in series were recommended for all US adults >65 years in late 2014. We evaluated the effectiveness of this recommendation against invasive pneumococcal disease (IPD) among Medicare beneficiaries >65 years old. **Methods:** We linked IPD cases in persons ≥65 years, identified through Active Bacterial Core surveillance (ABCs) during 2015-2016, to records for Centers for Medicare and Medicaid Services (CMS) beneficiaries. Case isolates were serotyped and classified as PCV13 (including type 6C due to cross-protection), PPSV23, or non-vaccine types. We excluded cases with non-continuous enrollment in Medicare, long-term care residence, and missing census tract data. Controls identified through CMS were matched to cases on age, census tract of residence, and length of Medicare enrollment. We obtained vaccination and medical histories through Medicare records. Vaccine effectiveness (VE) was estimated as one minus the odds ratio for vaccination with PCV13 only or PPSV23 only versus neither vaccine using conditional logistic regression, adjusting for sex and underlying medical conditions. **Results:** Of 2,246 IPD cases, 1,017 (45%) were matched to Medicare parts A/B beneficiaries. After exclusions, 699 cases and 10,152 matched controls (n=10,152) were included in the analysis. More cases than controls were of non-white race (16% vs. 11%), had ≥1 chronic medical condition (88% vs. 58%), and had ≥1 immunocompromising condition (54% vs. 32%). PCV13 (+6C) and PPSV23-type IPD accounted for 164 (23%; [88 cases, 12% serotype 3]) and 350 (50%) cases, respectively. Fourteen percent of cases vs 18% of controls received PCV13 vaccine only, 22% of cases vs 21% of controls received PPSV23 only, and 8% of cases and controls received both vaccines. VE against PCV13+6C types for those receiving PCV13 only was 47% (95%CI 4, 71%); VE was 26% (95%CI -58, 65%) against serotype 3 and 67% (95%CI 11, 88%) against other PCV13-types (+6C). VE against PPSV23-unique types was 15% (95%CI -16, 37%) for those receiving PPSV23 only. Neither vaccine showed effectiveness against non-vaccine types. **Conclusions:** PCV13 showed moderate overall effectiveness in preventing IPD caused by PCV13 (including 6C) vaccine types, effectiveness may be lower for serotype 3 than for other PCV13 types. PPSV23 showed limited effectiveness against serotypes unique to that vaccine.

Board 377. Come and Take it: Why Vaccine Advocates Are Losing the Battle in Texas

C. Blackburn
Texas A&M University, College Station, TX, USA

Background: The anti-vaccine movement has been making headlines across the country. In 2017 Minnesota experienced a large measles outbreak because vaccination rates within a Somali community dropped by more than 50% due to targeting from anti-vaccine groups. While the anti-vaccine movement is contributing to the reemergence of vaccine-preventable diseases nationwide, Texas is witnessing exponential increases in the number of parents claiming philosophical exemptions to vaccination. As the state of Texas teeters on the edge of the herd immunity threshold for a number of diseases, vaccine advocates appear to be losing the battle. This paper examines what makes the anti-vaccine movement so strong in Texas and provides recommendations for how to counter its influence. **Methods:** This paper analyzes data on philosophical exemptions in the state of Texas over the last 15 years to show how the number of philosophical exemptions claimed in the state has increased. It also chronicles the rise of the anti-vaccine movement in the state. **Results:** Over the last 13 years there has been

a 19-fold increase in the use of philosophical exemptions in the state of Texas. This is partly related to Andrew Wakefield, the discredited author of the *Lancet* paper claiming the MMR vaccine caused autism, making his home in Austin and continuing to pursue his anti-vaccine message, but it is greater than one variable. In Texas, anti-government individuals have joined the movement in droves. This unique element has made the movement particularly strong in the state. **Conclusions:** The anti-vaccine movement is gaining ground in Texas, even as other states are seeing a drop in the number of parents refusing the vaccinate. This paper analyzes the trend and provides recommendations on how to counter the Texan anti-vaccine movement.

Board 378. Analysis of Measles Immunity Level in Permanent Population in Beijing, 2017

Z. Zhujiazi
Beijing Municipal Centre for Disease Control and Prevention, Beijing, China

Background: The elimination of measles in China was proposed by WHO Western Pacific Region in 2012, so an effective immune barrier in the population must be established to terminate virus transmission. A survey of measles antibody levels can be used to predict the epidemic trend of measles, assess the level of immunity in the population, and provide a scientific strategy for measles elimination. So we launched an investigation of measles antibody level in permanent population in Beijing, China. **Methods:** A total of 2144 objects from 10 age groups, who had been living in Beijing for over 6 months, were selected from urban and rural areas in Beijing in 2017.Demographic characteristics, history of measles and vaccine immunization were investigated by questionnaire.5 ml blood sample of each subject was collected and Measles IgG antibody was measured by ELISA. **Results:** Positive rate of measles antibody was 79.8% (1711/2144) and standardized positive rate was 84.6%. Median of antibody was 773.4IU/L. Positive rate and median of measles antibody were significantly different between population from different age groups (χ^2=358.046, P<0.01; H=232.71, P<0.01). Antibody positive rate and median were lowest in the <1 year age group, which were separately 34.4% (74/215) and 130.6IU/L; and highest in the 1-4 years age group (94.1%(206/219), 1475.6 IU/L) and 40- years age group (90.1%(191/212), 1600.8IU/L). Antibody positive rate and median in permanent population, which were separately 80.3% (862/1074) and 787.8IU/L, approximated those in migrant population, which were 79.4% (849/1070) and 766.0IU/L (χ^2=0.278, P=0.598; U=551067.500, P=0.101). Antibody positive rate and median in population with vaccination history, which were separately 88.7% (790/891) and 888.9IU/L, were higher than those population without vaccination history and people whose history unknown (10.0%(14/140), 81.7 IU/L;81.5% (907/1113), 767.7 IU/L). The difference showed statistical significance (χ^2=468.621, P<0.01; H=287.448, P<0.01). **Conclusions:** The immunity level of permanent population in Beijing has not yet reached the level of measles elimination. measles antibody level among the children aging 1-4 years old was high enough to prevent outbreak and epidemic of measles. However, we should try our best to strengthen the measles antibody level among the babies younger than 1 year old and the adult aging between 15 and 40 years old.

Board 379. A Coverage Survey of Measles-Containing Vaccination among Healthcare Workers in Beijing

Z. Zhujiazi
Beijing Municipal Centre for Disease Control and Prevention, Beijing, China

Background: In order to control the epidemic of measles and the spread of the virus in the hospitals, the health administration department of China suggested that employees of the medical institutions should be vaccinated measles containing vaccine (MCV). So we investigate the coverage rate of measles containing vaccine (MCV) among healthcare workers (HCWs) in Beijing, 2016. **Methods:** Typical sampling was used to choose HCWs from 15 hospitals of Beijing for collecting their demographic information, measles disease history and MCV immunization. **Results:** 591 HCWs, 84(14.2%) ever had measles, and 507 (85.8%) never had measles or their disease history was unknown, in which 48.5%(246/507) were vaccinated with MCV before employed. Among 261 HCWs who did not receive MCV or whose immunization were unknown before employed, the MCV coverage rate was 18.4% (48/261) after employed. In those who still did not receive MCV after employed, 67.1% (143/213) did not know the immunization activities in hospitals. **Conclusions:** The MCV coverage is still very low among HCWs in Beijing, and the implementation effect of immunization for HCWs is not good. We suggest the development of a specific guideline for measles prevention and control in hospitals.

Board 380. Impact of Exclusion on Measles Transmission in Childcare Settings, Minnesota, 2017

K. Como-Sabetti, E. Laine, B. Christianson, J. Griffith, H. Omar, J. Heath
Minnesota Department of Health, St. Paul, MN, USA

Background: CDC and AAP recommend susceptible individuals exposed to measles be excluded from high-risk settings (school, childcare, and healthcare) while potentially infectious. A measles outbreak occurred in Minnesota in 2017 with 75 cases; 91% were unvaccinated children and 70% attended childcare. **Methods:** If a measles case attended childcare while infectious, childcare providers submitted a center roster, daily attendance records, and MMR history for all attendees to the Minnesota Department of Health. Childcare attendees without an MMR were considered susceptible and excluded from childcare and school for 21 days after exposure. We assessed the impact of timely exclusion on disease transmission by comparing the median number of childcare-associated cases (cases resulting from childcare exposure) and epi-linked cases (cases linked to the childcare center but not necessarily exposed at the center). **Results:** Eleven childcare exclusion events (3 centers had >1 case, 2 centers had exclusion twice) were included in the analysis. A total of 1776 children attended these childcare centers. Thirty-one percent of children were susceptible to measles (range 11%-43%). Median time from exposure to exclusion was 11 days (range 8 – 21 days). The number and proportion of susceptible attendees at childcare centers with long (>11 days from exposure to exclusion) and short (≤ 1 days from exposure to exclusion) time to exclusion were similar. Childcare exclusion events with long time to exclusion were associated with more childcare-associated and epi-linked cases compared to childcare events with short time to exclusion (median 6 vs 0 cases, range 0-3 cases, X^2=6.49, p=0.01; median 11 vs 0 cases, range 1-41 cases, X^2=6.49, p=0.01 respectively). From childcare events with long time to exclusion, an additional 7 childcare centers and 2 schools were exposed to measles cases compared to an

additional 2 childcare centers exposed from centers with short time to exclusion. **Conclusions:** Among childcare centers with more timely exclusion implementation, there were fewer secondary and epi-linked cases and fewer additional schools and childcare centers impacted. Although exclusion required extensive public health resources and was difficult for families, timely exclusion decreased measles transmission and was an important outbreak control strategy.

Board 381. Measles Outbreak Investigation in Killi-Qadirabad District, Noshki, Baluchistan (15 September to 21 October 2017)

M. Waheed, A. Saeed
FELTP Pakistan, Quetta, Pakistan

Background: On 18 October 2017, media reported 11 deaths and more than 40 suspected measles cases in Killi-Qadirabad (population=4715; 849 of those are younger than 5 years of age), UC Mengal (population=19500) district Noshki. **Methods:** Cases were defined as any resident of Killi-Qadirabad district Noshki with high grade fever and maculopapular rash and having any of following, conjunctivitis, coryza, or cough from 15 September to 21 October 2017. Active case finding, routine immunization (RI) survey of 34 houses randomly selected and a descriptive study was conducted, data was analyzed for time, place, and person. **Results:** A total 36 cases were identified (overall AR= 0.76%) and 12 deaths (CFR=33.3%) verified by verbal autopsy. The most affected age group (n=9) was 0-12 months with AR=9.6%., Males were most affected 67% (n=24). Conjunctivitis 77.8% (n=28), diarrhea 27.8% (n=10), cough 91.7% (n=33), pneumonia 25% (n=9), and coryza 88.9% (n=32) were most frequent symptoms. Most common reason for not being vaccinated was misbeliefs about vaccination 29.8% (n=20). During RI survey for different vaccine coverage, 77.6% (n=52) were vaccinated for BCG/OPV-0, 40.2% (n=27) for pentavalent I/pneumococcal I/OPV-I, 31.3% (n=21) for pentavalent II/pneumococcal II/OPV.II, 19.4% (n=13) for pentavalent III/pneumococcal III/OPV.III, 16.4% (n=11) for measles I and 7.4% (n=5) for measles II. Three serum samples were positive out of 4. **Conclusions:** Most probable cause of measles outbreak was low RI coverage, illiteracy, and homemade remedies based on cultural myths. A total of 3823 children were vaccinated in mop up. The team recommended to strengthen RI, EPI should plan refresher courses, validated micro plan, outreach team sessions, weekly zero reporting, monitoring on monthly basis, and social mobilization.

Board 382. Measles Outbreak Investigation of Union Council, Taimoorabad District, Quetta, Pakistan, 2017

S. Riaz, A. Saeed
Field Epidemiology and Laboratory Training Program, Quetta, Pakistan

ackground: Despite availability of an effective vaccine, measles is still a major cause of morbidity and mortality in lower-middle income countries. On 13 April 2017, a suspected measles outbreak was reported from Union Council Taimoorabad, District Quetta to the provincial disease surveillance and response unit. A team was formulated to confirm the outbreak and assess its magnitude and determinants and to make control measures and recommendations to prevent future outbreaks. **Methods:** A case was defined as any child younger than 10 years of age and aresident of UC Taimoorabad with non-vesicular maculopapular rash and fever or cough or coryza or conjunctivitis from 30 March to 14 April 2017. Active case finding was done. Information regarding illness status, symptoms, onset of illness, treatment, and routine vaccination coverage in community was collected along with reasons for not getting vaccinated. Five blood samples were collected. **Results:** A total of 18 suspected measles cases were identified through active case finding and among them 5 were laboratory-confirmed cases. Mean age of cases was 33.7 months (range 04-60 months). A total of 67 %(n= 12) were females. The most affected age group was 0-4 years (83 %; n=15) (attack rate = 8.6%). The most frequent symptoms were rash 100 %(n=5), fever 100 %(n=5), and cough 60 %(n=3). Complications developed were ARI (n=4;22.2%) and diarrhea (n=2; 11.1%). Vaccine efficacy could not be calculated because everyone in the community was not immunized. Main reasons being Afghan refugees' refusal families**.** **Conclusions:** The measles outbreak was most probably due to non-immunization status because of cultural and religious beliefs. Mop-up vaccination activities in UC & adjoining areas along with community sensitization for importance of routine immunization. Vitamin A capsules were also given to the affected children. Awareness campaigns regarding routine vaccination were recommended to prevent future outbreaks. VPD surveillance system strengthening with increased outreach vaccination activities were recommended

Board 383. Circulating Vaccine-Derived Poliovirus Type1 Outbreak Response in Lao People's Democratic Republic, 2015-2017

C. Pathammavong[1], D. Mekonnen[2]
[1]National Immunization Program, Vientiane, Lao People's Democratic Republic, [2]World Health Organization, Vientiane, Lao People's Democratic Republic

BBackground: Lao People's Democratic Republic (Lao PDR) was certified as polio-free in October 2000. Between October 2015 and January 2016, 11 confirmed cases of circulating VDPV1 (cVDPV1) and 25 positive contacts were detected in three provinces of Lao PDR. All confirmed cases were from Hmong ethnic community. **Methods:** Detailed epidemiological investigation of the identified acute flaccid paralysis (AFP) cases was carried out as part of enhanced AFP surveillance in the country. An immunization response activity was initiated by the Ministry of Health within 72 hours after confirmation of the first case. A total of 10 Supplementary Immunization Activities (SIA) were conducted between October 2015 and January 2017. Based on the findings of the epidemiological investigation, the beneficiaries in these SIAs ranged from children less than 15 years of age in the first 8 rounds and below 5 years in the last 2 rounds. A rapid convenience monitoring (RCM) was conducted in each of the SIAs to monitor the quality of implementation of these SIAs. **Results:** The reported coverage of these SIAs ranged between 87% and 101%, which resulted in reaching to more than 20 million target beneficiaries. The active involvement of village chiefs, village health volunteers and community leaders ensured effective social mobilization and communication activities during the SIAs. Considering effective population immunity from the quality SIAs and improvement in the quality of AFP surveillance since the detection of the outbreak, the independent outbreak response assessment team in March 2017 concluded the cessation of cVDPV1 transmission in Lao PDR. **Conclusions:** The government of Lao PDR has demonstrated their highest level of commitment and leadership to interrupt the cVDPV1 transmission. It will be critical to sustain the quality of AFP surveillance and immunization activities to maintain the polio-free status.

Board 384. Enhanced Surveillance in the Context of Poliovirus Importation Risk in Lebanon, 2013-2017

N. Ghosn[1], H. Abou Naja[1], R. Louis[1], M. Karasneh[2], M. Sharaf[3], G. Riedner[4], W. Ammar[1]
[1]Ministry of Public Health, Beirut, Lebanon, [2]National Polio Laboratory, Amman, Jordan, [3]World Health Organization, Damascus, Syrian Arab Republic, [4]World Health Organization, Beirut, Lebanon

Background: Lebanon had been declared polio-free since 2002. In 2003, following a single imported polio case, national campaigns contained the outbreak. Since 2013, poliovirus importation risk increased. Risk factors are linked to Syrian crisis: population influx to Lebanon, outbreaks of wild poliovirus 1 in 2013-2014 and circulating vaccine-derived poliovirus 2 (cVDPV) in 2017. There was urgent need to enhance surveillance with the objective of timely detection of poliovirus for timely containment response. **Methods:** Case definitions follow those of WHO for poliovirus. Case detection includes passive reporting, weekly zero-reporting, active surveillance, in addition to community reporting in settings where vulnerable population lives. Case investigation includes data and specimen collection, follow up, and classification. If hot case, specimens are collected from contacts and rapid coverage survey is conducted in neighborhood. Healthcare professionals and out-reach volunteers are sensitized via annual training sessions and advocacy materials. Coordination is enhanced with immunization team and UN partners. Poliovirus environmental surveillance is initiated from selected sewage plants with monthly sampling. Virological culture is conducted in WHO accredited laboratories in Egypt and Jordan. Results are archived in national database. Weekly bulletin is disseminated via official website and mailing list. **Results:** From 2013 to 2017, 382 acute flaccid paralysis (AFP) cases and 583 contacts were detected and investigated. From 2013 to 2017, national indicators improved: non-polio AFP rate under 15 years old from 2/100000 to 4/100000, and adequate specimen collection from 45% to 80%. Cases were 76% Lebanese, 20% Syrian, and 3% Palestinian. Laboratory results detected 31 Sabin-like (SL) and 51 non-polio enterovirus (NPEV) among cases and contacts. All cases were polio-discarded. From 2016-2017, 31 environmental samples were collected from 3 sites and showed 48% SL(1/3) and 42% NPEV. **Conclusions:** Despite the presence of large Syrian population exceeding a million, no wild poliovirus neither cVDVP was detected in Lebanon. Such result is due to enhanced immunization activities. Still, there is a need to maintain high level of surveillance and coordination and to explore strategies for continuous sensitization of healthcare professionals.

Board 385. An Update from Hospital-Based Surveillance for Rotavirus Gastroenteritis among Young Children in Bangladesh, July 2012 to June 2017

S. Satter[1], N. Aliabadi[2], P. Gastañaduy[2], W. Haque[1], A. Mamun[3], M. Flora[4], K. Zaman[1], M. Rahman[1], J. Heffelfinger[2], S. Luby[5], E. Gurley[1], U. Parashar[2]
[1]icddr,b, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [3]BC Centre for Disease Control, Vancouver, Canada, Vancouver, BC, Canada, [4]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh, [5]Center for Innovation in Global Health, Stanford University, USA, Stanford, CA, USA

Background: In preparation for the introduction of a rotavirus vaccine into the routine immunization program of Bangladesh in 2018, we report data from five years of active hospital-based rotavirus surveillance which began in July 2012. **Methods:** We enrolled and collected fresh stool from every fourth child < 5 years admitted with acute gastroenteritis (AGE) at 8 participating surveillance hospitals. Rotavirus infections were detected by enzyme immune assay. Twenty-five percent of rotavirus isolates were genotyped. **Results:** We found that 64% (4,832/7,562) of children < 5 years of age admitted with AGE had evidence of rotavirus infection. The majority (57%) of patients with rotavirus infection were <12 months of age. The most common strains were G1P8 (43%), G12P8 (15%) and G9P8 (9%); 11% of children had mixed infection. G3P[8], which has not been reported in Bangladesh since 2001, was documented for the first time in our surveillance system. **Conclusions:** The high burden of rotavirus-associated hospitalizations highlights the potential value of rotavirus vaccination in Bangladesh. Continued surveillance is important for monitoring the impact of vaccination.

Board 386. Whole Genome Sequencing of Rotavirus Strains Causing Outbreaks in California, USA, in the Post-Licensure Vaccine Era

R. Gautam[1], T. Huynh[2], C. Pan[2], A. Chen[2], R. Burke[1], N. Barin[3], C. Bock[4], D. Chang[4], G. Han[5], J. Holguin[3], R. Quenelle[5], J. Tate[1], D. Wadford[2], U. Parashar[1], M. Bowen[1]
[1]Division of Viral Diseases, Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, [2]California Department of Public Health—Viral and Rickettsial Disease Laboratory, Richmond, CA, USA, [3]Long Beach City Health Department, Long Beach, CA, USA, [4]San Mateo County Public Health, Policy & Planning, San Mateo, CA, USA, [5]Santa Clara County Public Health Department, San Jose, CA, USA

Background: Rotavirus (RVA) is the leading cause of gastroenteritis in children <5 years of age with an estimated 215,000 deaths per year globally. The G12 G genotype associated with P genotypes P[6] or P[8] has emerged as the 6th most prevalent RVA genotype in children. RVA outbreaks in adults are reported infrequently and are mostly associated with genotype G2P[4]. In 2017, 7 RVA outbreaks involving 375 cases distributed among a day care facility, a school, a pediatric long-term care facility and 4 adult long-term care facilities were reported from California, USA. Twenty-seven available samples from these outbreaks were submitted by the California Department of Public Health to the Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA, for RVA strain characterization and next generation sequencing (NGS). **Methods:** At CDC, confirmatory RVA detection was performed by NSP3 qRT-PCR and Rotaclone EIA assays. RVA strains were characterized by qRT-PCR genotyping assays and NGS using an Illumina MiSeq. **Results:** Six of the 7 2017 California outbreaks were caused by RVA genotype G12P[8] and 1 was caused by genotype G2P[4]. Out of 27 samples tested, 21 samples genotyped as G12P[8], 3 samples as G2P[4], 1 as G12P[NT] (NT = nontypeable), 1 as G2P[NT] and 1 as GNTP[NT]. NGS of 16 G12P[8] strains revealed that they possessed the full genomic constellation G12-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1 and exhibited 99.3% - 100% nucleotide sequence identity, suggesting that the G12P[8]-associated outbreaks were caused by the same or nearly identical strains. NGS of 2 G2P[4] samples from an adult long-term care facility outbreak revealed that they possessed the full genomic constellation G2-P[4]-I2-R2-C2-M2-A2-N2-T2-E2-H2 and were 100% identical, indicating infection caused by the same strain. **Conclusions:** This is the first report of investigating multiple RVA outbreaks using whole genome sequence data obtained by NGS. Analysis of whole genome sequences

of G12P[8] and G2P[4] RVA genotypes causing outbreaks concluded that same or almost identical strains caused infection in all outbreaks. Next generation sequencing data will facilitate our understanding of molecular epidemiology of RVA strains and possibly can be used to elucidate the mechanism of vaccine escape for RVA strains causing outbreaks in immunized populations.

Board 387. Rubella Infection in an Unvaccinated Pregnant Woman--Johnson County, Kansas

T. Wallin, C. Walls
Johnson County Department of Health and Environment, Olathe, KS, USA

Background: Rubella, which is subclinical in up to half of all infections, was declared eliminated from the US in 2004, although transmission commonly occurs in many parts of the world. On December 14, 2017, the Johnson County Department of Health and Environment received a phone call from an elementary school reporting a pregnant mother of one of the students was diagnosed with rubella and was taking her unvaccinated child to the doctor. **Methods:** The patient was interviewed and medical records reviewed. Serum was collected on December 12 and sent to a commercial laboratory for IgM testing; IgG testing was subsequently performed. Specimens were forwarded to the Centers for Disease Control and Prevention (CDC) for avidity testing. She presented to two emergency rooms, family care provider, and attended work prior to her diagnosis. Healthcare workers and contacts at these locations were followed up with to determine immunization and pregnancy status. **Results:** The unvaccinated, 18-week pregnant, patient was rubella IgG negative during first trimester prenatal testing. Symptoms began December 6, consisting of a burning, itchy rash, fever, cough, coryza, and congestion. She had no travel history nor contact with any symptomatic individuals. Her unvaccinated brother visited her during the exposure window after returning from a trip to India; he was diagnosed with poison ivy. The patient's lab results were IgM and IgG positive with low avidity, indicating recent infection. Contacts of the patient were evaluated and public health interventions implemented; the patient's unvaccinated daughter was immunized on December 14 and excluded from school. A hospital employee was unvaccinated thus excluded from work. **Conclusions:** Rubella can have serious consequences when contracted during pregnancy, particularly in the first trimester. This occurrence of rubella was in an unvaccinated pregnant woman in her second trimester with no history of travel. The source of the infection was the patient's brother, which was confirmed by IgG positive testing with low avidity by the CDC.

Board 388. Withdrawn

Board 389. Epidemiological Study of Herpes Zoster (Shingles) in Qatar, 2012-2016

H. Al-Romaihi, N. Ganesan, S. Al Thani, S. Nadeem
Ministry of Public Health, Doha, Qatar

Background: Herpes zoster is an acute infectious viral disease caused by reactivation of varicella zoster virus. Increasing incidence globally has been documented although the availability of research data is limited. More than 90% of affected adults are older than 20 years of age but the most commonly affected group are adults between 60-70 years of age. We present surveillance data for a period of five years (2012-2016) to look at the epidemiological pattern of shingles in Qatar. **Methods:** Herpes zoster infection is a notifiable communicable disease in Qatar. The study included herpes zoster cases from January 1 2012 and December 31 2016. The data collected include demographic variables such as age sex, nationality, and month of onset illness. Our study measures the trends in the epidemiology of the disease and incidence rates by age group. **Results:** A total of 1867 cases were notified during the study period. Herpes zoster incidence rate decreased from 9.8 to 4.6 per 100,000 person-years, whereas its incidence peaked to 36.0 per 100,000 person-years in the year of 2017. The incidence of herpes zoster infection increased with age; the incidence was highest in people over 50 years of age (42.4 cases per 100,000 person years) as compared to other age groups. Reported incidence of herpes zoster was higher among men (79.8%) than women (20.2%). The magnitude of occurrences of HZ cases increased in 2016 due to population increase as a consequence of importation from other countries. Seasonal variation of HZ infection was higher in the spring and summer than in winter months. **Conclusions:** In Qatar, herpes zoster infections are transmitted more frequently in men than in women. Its incidence increases with age; high risk groups includes those over 50 years of age. Cases are reported more in the spring and summer. Herpes Zoster vaccination drives during the winter will be more beneficial.

Surveillance II

Board 390. Strengthening Local and Regional Infectious Disease Control in the South of the Netherlands Using a Secure Web-based Dashboard for Real-time Data Exchange

H. ter Waarbeek[1], C. Kara-Zaitri[2], R. ter Schegget[3], A. Rietveld[4], K. Ohrimenko[5], C. Hoebe[6]
[1]Public Health Service South Limburg, Heerlen, Netherlands, [2]inFact, Shipley, United Kingdom, [3]Public Health Service Brabant Southeast, Eindhoven, Netherlands, [4]Public Health Service Hart voor Brabant, s'Hertogenbosch, Netherlands, [5]inFact, Shipley, Netherlands, [6]Caphri Maastricht University, Maastricht, Netherlands

Background: The ongoing occurrence of infectious disease outbreaks demonstrates the importance of real-time surveillance and rapid detection for adequate infectious disease control at both national and regional levels. This need is ideally fulfilled with software systems allowing on one hand daily data entry at the local level, and on the other hand automatically providing a facility for harvesting and sharing key data in a structured, secure and timely manner between public health services (PHS). **Methods:** All six PHSs in the south of the Netherlands (almost 4 million inhabitants) joined forces on a one-year project piloting a secure real-time custom-built infectious disease dashboard for strengthening regional infectious disease control. Each PHS already uses the same real-time web-based software suite for management disease notifications. **Results:** The HPZoneDashboard South-Netherlands provides an aggregate view on real-time data from all 6 PHSs using various filters: what (case, contact, exposed person, outbreak, enquiry), which location (PHS), which infection (disease), when (time period), and where (context, e.g. daycare center, care home). Shared data are based on an agreed common (anonymised) minimal data set presented in tabular, graphical and geographical (GIS) views. Automated disease trigger alerts derived from weekly historical data analysis are shown in traffic light colours with warning and action lines. **Conclusions:** The automated dashboard provides the PHSs with useful real-time local and regional data analysis reports. Regional infectious disease control and epidemiological research have been enhanced using the embedded features including a flexible query facility of the

dashboard for early detection of possible outbreaks, monitoring diseases trends and exploring associations. The dashboard has improved best practice and cooperation among the PHSs and underpinned data quality, consistent data registration and legal agreements. During the next three-year follow-up project, the PHSs will also explore possibilities for antimicrobial resistance surveillance, cross-border cooperation with Flanders, Belgium and roll-out towards national surveillance and control.

Board 391. Surveillance Outbreak Response Management and Analysis System (SORMAS®-open)—mHealth-Implementation for Integrated Disease Surveillance and Response in 15 Federal States of Nigeria, 2017/18

G. Krause[1], O. Adeoye[2], C. Arize[3], P. Nguku[4], F. Oyiri[3], K. Schlinkmann[1], B. Silenou[1], M. Strysewske[4], D. Tom-Aba[1], M. Wahnschaffe[4], C. Ihekweazu[5]
[1]Helmholtz Centre for Infection Research, Braunschweig, Germany, [2]Nigerian Centre for Disease Control, Abuja, Nigeria, [3]Nigeria Centre for Disease Control, Abuja, Nigeria, [4]African Field Epidemiology Network, Abuja, Nigeria, [5]Nigerian Centre for Disease Control, Abuja, Germany

Background: The Integrated Disease Surveillance and Response (IDSR) System, propagated in Africa, is limited to unidirectional reporting and hardly includes response management: Reporting occurs on paper and is being manually aggregated into digital spreadsheets at level of local government areas (LGA/districts). We developed SORMAS (Surveillance Outbreak Response Management and Analysis System), a mobile health information system, to allow health facilities (HF), laboratories and public health departments (PHDepts at LGA, state and national level) to coordinate control measures and exchange epidemiological information digitally. **Methods:** Using the Design Thinking approach we developed disease specific process models for the following 10 diseases in accordance with IDSR: cerebrospinal meningitis (CSM), cholera, dengue fever, Ebola virus disease, highly pathogenic avian influenza, lassa fever (LF), measles, monkeypox (MPX), plague, and yellow fever; plus an adaptable process model for emerging diseases (www.sormas.org). We built 11 user-specific interfaces and dashboards (for hospital informants, laboratory officers, rumor officers, surveillance officers, surveillance supervisors, case supervisors, contact supervisors, contact officers, and incident command centers at state, national and international level). Software development is open source (https://github.com/hzi-braunschweig/SORMAS-Open), based on Java EE server Payara and PostgreSQL database. The mobile app runs natively on Android tablets, desktop version is web based using Vaadin framework. **Results:** From November 2017 to March 2018 we deployed SORMAS in Nigeria in response to a MPX-outbreak in 8 states, a CSM-outbreak in 3 additional states and a LF-outbreak in another 3 states. For MPX and LF contact-follow-up is being managed through SORMAS. Additionally a pilot implementation includes all 80 private and public HFs in 2 LGAs of Kano state. Altogether this results in continued use of SORMAS by 83 HFs, 20 laboratories and 171 PHDepts from 155 LGAs of 16 states covering a population of 36 million. **Conclusions:** SORMAS enabled HFs for digital case based surveillance and proved to be deployable on short notice even in responding to a disease (MPX) not previously part of IDSR. Based on this positive experience the Nigerian Centre for Disease Control strives to implement SORMAS throughout the country.

Board 392. I-Lab: Countrywide Implementation of an Automated Platform for the Collection and Reporting of Laboratory Data for Improved Preparedness and Response to Outbreaks in Senegal

M. Dia[1], P. Sokhna[2], P. Diallo[1], N. Steenkeste[3], L. Delorme[4], L. Fofana[5], E. Cour[2], P. Guinot[2], G. Vernet[6], E. Penrose[6], F. Babin[3], A. Sow[1]
[1]Laboratory Directorate, Ministry of Health, Dakar, Senegal, [2]PATH, Dakar, Senegal, [3]Mérieux Foundation, Lyon, France, [4]Mérieux Foundation, Vientiane, Lao People's Democratic Republic, [5]Mérieux Foundation, Dakar, Senegal, [6]Mérieux Foundation USA, Washington, DC, USA

Background: Improving systems for epidemiological surveillance of infectious diseases in West Africa is a well recognized priority for global health. The quality and relevance of the paper-based monthly reports common in the region are often compromised by incomplete reports, lack of timely submission, and the human error and time lag inherent in manual data entry. These factors make paper-based reports poorly suited for timely surveillance systems. **Methods:** The District Health Information Software version 2 (DHIS2) is an open-source software platform for reporting, analysis, and dissemination of data that has now been adopted in more than 60 countries as an integral part of national health information systems that can help countries meet the requirements of the IHR. Here, we showcase successes of DHIS2 adoption in the clinical laboratories of Senegal. Using this open-source platform, laboratories across the country have been able to enter data on 11 notifiable diseases via a mobile phone or computer, which are then captured on a centralized internet server with the capacity to rapidly produce a variety of reports. **Results:** As of December 2017, 118 laboratories have been trained in the use of the tool, and 91 (77%) laboratories are utilizing the software to transmit complete weekly reports, of which 72 (61%) do so without any external prompting or support. The weekly reports comprise information on clinically suspected cases as well as diagnostic methods used for confirmation/elimination. Approximately 35 laboratories have capacity for microbial culture, and 24 of these conduct routine antimicrobial susceptibility testing; culture results and resistance profiles are systematically captured in DHIS2 when available with a dedicated monthly report. **Conclusions:** Thanks to this improved e-health tool, the frequency and reliability of laboratory-based surveillance data has greatly increased, and enabled improved reporting on disease trends from the Senegalese Ministry of Health to the WHO. This laboratory based surveillance system will accelerate the reaction time in the case of epidemic threat and contribute to global health security. The impact of this improvement on the reduction of the number of priority disease cases needs to be evaluated. This approach could be replicated in other countries to improve epidemiological surveillance capacity in the region.

Board 393. The Epi Info™ Mobile Vector Surveillance System

R. Levine[1], A. Islam[1], D. Impoinvil[1], M. Lamtahri[1], J. Aponte[1], R. Stafford[2], S. Agnihotri[1], M. Burrows[1], A. Lenhart[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Self, Atlanta, GA, USA

Background: The 2016 Zika virus outbreak highlighted capacity gaps of many vector surveillance programs to rapidly conduct mosquito surveillance for supporting vector control measures. Many countries employed generalized vector control, based on patchy or out-of-date

surveillance data, which prevented them from more effectively and efficiently targeting their vector control efforts aimed at reducing the spread of disease. **Methods:** CDC developed a mobile application for vector surveillance and data analysis, using existing free Epi Info™ software. The new Epi Info™ mobile vector surveillance system allows users to enter vector surveillance and control data directly in the field. The field component consists of five modules: 1) Trapping (multi-day activities), 2) Collection (single day activities), 3) Bioassays (insecticide resistance monitoring), 4) Insecticide longevity monitoring, and 5) Vector control interventions and studies. GPS coordinates, GPS signal accuracy, elevation, dates, and times are automatically collected. These field-collected data sync with the cloud upon the mobile device's detection of a wireless connection or phone network, and are immediately uploaded and analyzed. The analysis mode of the system automatically calculates relevant vector indices, places locations on maps, and presents users with graphical representations of trends by location, all of which can also be filtered by dates of interest. **Results:** The system was piloted and optimized in Haiti, Dominican Republic, Trinidad and Tobago, and Sierra Leone, and is now freely available on Google Play for android mobile devices in English, Spanish, French, and Portuguese. From its initial release in November 2017, it has been downloaded over 1000 times worldwide and trainings have involved vector surveillance leaders from over 15 countries. **Conclusions:** The Epi Info™ mobile vector surveillance system requires minimal set-up and configuration and eliminates the need for paper-based vector surveillance. The near real-time availability of results improves data-driven vector control decisions, which increases the efficacy and efficiency of public health responses to vector-borne diseases.

Board 394. Improving Infectious Disease Surveillance in West Africa through Standardized Platforms Permitting Molecular Epidemiologic Investigations and Reporting Disease Emergence

J. Diclaro[1], J. Eisner[2], J. Ake[3]
[1]US Navy, Jacksonville, FL, USA, [2]Henry M. Jackson Foundation (HJF), Bethesda, MD, USA, [3]US Army, Silver Spring, MD, USA

Background: The Joint West Africa Research Group (JWARG) is a multinational collaboration improving frontline surveillance strategies in West Africa by delivering a platform of standardized clinical and laboratory methods for disease detection and molecular epidemiologic investigations. As a Global Health Engagement for improving health systems capacity in Nigeria, Ghana, and Liberia, the JWARG provides a foundation for early warning of emerging infectious disease threats reported to Ministries of Health and ultimately the World Health Organization and Centers for Disease Control for outbreak response. **Methods:** In 2016, the JWARG strategy introduced clinical trial conduct and initiated clinical laboratory development in coordination with pathogen detection laboratory technologies to 13 hospitals and research laboratories in Nigeria, Ghana, and Liberia. To build sustainable partnerships while improving research skillsets, 21 clinical and laboratory training events were led by global infectious diseases experts from academia and partner militaries. Web-hosted data services include informatics pipelines for sequence and molecular analysis with results communication and sharing across regional and international partners. **Results:** The JWARG is a regional network of clinical and laboratory professionals informed and trained to conduct frontline biosureveillance for patients presenting with febrile illness at their clinics. Nigeria sites activated in September 2017 and have 36 participants enrolled as of February 2018. With standardized clinical and laboratory methods, results for 30+ pathogens can integrate into regional phylogeographical models of pathogen evolution and infection dynamics critical for molecular epidemiologic investigation, such as long distance translocation of pathogens by travel. **Conclusions:** The JWARG improves host-nation infectious disease surveillance capability, analysis and reporting while strengthening the regional research network in West Africa. By transferring technology for pathogen detection and establishing a regional trained workforce to conduct clinical surveillance, the JWARG is not only primed to prevent a repeat of the 2013-15 Ebola outbreak but other emerging and ignored infectious diseases in West Africa.

Board 395. EpiCore: Crowdsourcing Epidemic Intelligence across the Globe to Verify Outbreaks Faster

N. Divi, A. Crawley, M. Libel, M. Smolinski
Ending Pandemics, San Francisco, CA, USA

Background: With automated disease detection systems on the rise, verifying actual outbreaks from the digital 'noise' is a critical, but arduous task. EpiCore is a robust global community of human, animal, and environmental health professionals committed to verifying disease outbreaks. EpiCore's online platform launched in November 2015, and operates under a simple premise: connecting health professionals to a system with early alerts on health threats in their area and allowing them to validate those threats—leads to faster, accurate outbreak verification. **Methods:** Through a secure online platform, EpiCore *Requestors* review reports of potential outbreaks in humans or animals from disparate sources and then use EpiCore to send requests for information (RFI) to *Responders* for verification of the signal. EpiCore *Responders* combine their expertise and knowledge of on-the-ground realities to quickly verify or discard early indicators of an outbreak to help expedite outbreak verification. They respond to *Requestors*, who assimilate responses and share their findings with the global disease surveillance community. EpiCore *Responder* applications are vetted to ensure they possess necessary expertise to contribute to the platform. **Results:** As of January, 2018, EpiCore has over 2,000 members that span 144 countries. During the first year since EpiCore's launch, ProMED moderators used EpiCore to post over 500 requests for information to volunteers with a response rate of over 70%. EpiCore is providing real-time updates to RFIs and the average time to response is less than 1.5 days. **Conclusions:** With its broad geographical distribution of members and high response rate, EpiCore is poised to enable verification of potential outbreak signals faster. By improving situational awareness and de-escalating rumors, EpiCore is able to reduce the signal-to-noise ratio among disease surveillance data streams. By detecting and verifying outbreaks faster, EpiCore can enable early outbreak response efforts.

Board 396. Participatory One Health Disease Detection (PODD)—Community-Based Reporting for Emerging Infectious Diseases in Thailand

Ekachai Laiya[1], Sakulrat Pattamakaew[1], Lertrak Srikitjakarn[1], Surasing Wisarurat[2], Somporn Pornwisetsirikul[3], Karoon Chanachai[4], Terdsak Yano[1], Patipat Susumpao[5], Polawat Phetra[5], Pairat Trakarnsirinont[6], Boontuan Kaewpinta[6], Mark Smolinski[7], Jennifer Olsen[7], Adam Crawley[7]
[1]Chiang Mai University, Chiang Mai, Thailand; [2]Public Health and Public Policy Expert, Chiang Mai, Thailand; [3]Bueng Kan Provincial Livestock Office, Bueng Kan, Thailand; [4]Department of Livestock

Development, Bangkok, Thailand; [5]Opendream Co., Ltd., Bangkok, Thailand; [6]Public Health and Public Policy Expert, Chiang Mai, Thailand; [7]Skoll Global Threats Fund, San Francisco, CA, USA

Background: Public engagement plays a crucial role in early identification of both human and animal diseases circulating in the community. Mobile tools and technology can improve the reach and timeliness of reporting of suspected outbreaks. The Participatory One Health Disease Detection (PODD) project was developed at Chiang Mai University using an open source technology platform. This community-owned, event-based surveillance system is now operating in Chiang Mai, Chiang Rai, and Khon Kaen Provinces. **Methods**: Trained volunteers submit suspected outbreak reports, including photos, via the PODD application on their mobile phones. The PODD system then delivers automated outbreak notifications to local villages and authorities in the district public health and livestock offices. A standardized protocol guides alert recipients through the process of vetting reports and initiating and rapid response to both human and animal health threats. **Results**: Since inception over two years ago, the PODD project has developed over 4,600 trained volunteers. In Chiang Mai Province, where the project was initiated, volunteers reported more suspect animal health events in less than 6 months than had been reported throughout the entire province during the previous year, helping to address the issue of underreporting. Over 1,300 reports have been submitted to date, with at least 36 events having been confirmed as potential zoonotic health events. **Conclusions**: As the PODD project continues to expand from Chiang Mai to additional provinces in Thailand, it serves as a model for community-based, One Health reporting approaches that can be adapted and implemented in other geographies. Community ownership, government engagement, and open source technologies have been key success factors.

Board 397. A Novel Syndromic Surveillance System for Travelers' Health in the Caribbean Region

L. Indar, J. Edwin
Caribbean Public Health Agency, Port of Spain, Trinidad and Tobago

Background: The Caribbean is the most tourism dependent region in the world, with over 60 million visitors in 2017.Travel and tourism pose global health security risks via the introduction and spread of disease, as demonstrated by Chikungunya (2013), and Zika (2014). No regional surveillance systems for illnesses in visitors' populations exist in the Caribbean. In 2017, Caribbean Public Health Agency (CARPHA), designed and implemented the Tourism and Health Information System (THiS), a novel web-based application for syndromic surveillance in Caribbean accommodation settings. **Methods:** The THiS system was designed to capture illnesses and trigger responses in real time with real-time data analytics and aberration detection built in. Participation is voluntary. Cases of illness can be reported by ill guests and staff either to hotel administration for data entry or self-reported, via an online questionnaire. Reported symptoms are applied against case definitions to generate the following syndromes: gastroenteritis, fever and respiratory, fever, and hemorrhagic, fever and neurologic, undifferentiated fever, and fever and rash. Data is analyzed in real-time and include syndrome trends over time, gender and age and illness attack rates. Decision-makers (managers, surveillance teams, CARPHA) have immediate access to online reports. Email alerts are generated by the system when illness thresholds are reached. From July 2017, 105 accommodations from 7 countries (Bahamas, Barbados, Belize, Bermuda, Guyana, Jamaica, Trinidad & Tobago, and Turks & Caicos) used THiS. **Results:** Of the 105 accommodations, 39.1% (n=41) registered to participate, accounting for 3738 lodging rooms. Five cases of syndromes from three accommodations in two countries were reported in the THiS. Gastroenteritis and fever & respiratory symptoms were self-reported. Three cases of gastroenteritis were reported from two registered accommodations .The average response rate to weekly emails confirming 'nil' cases was 32.1% (range: 10.5-83.3%). One accommodation reported by email a cluster of 7 cases (2 staff and 5 guests) with possible conjunctivitis. One outbreak was detected. **Conclusions:** This novel surveillance system is critical for improving the capacity of countries to monitor and respond to the spread of infectious diseases and promoting health, safety, and security for visitors and locals in the Caribbean, but it will take time to establish.

Board 398. Assessing Event-Based Surveillance of Zoonotic Disease Reports for Impacts on Human Health

C. McKnight
World Health Organization, Geneva, Switzerland

Background: A broad range of zoonotic disease reports are captured during routine event-based surveillance. These initial reports regarding outbreaks in animal populations can be useful for early detection and monitoring for the potential risk to humans, though the extent of whether animal health events impact the human population is not well established. This study was done to determine how five serious zoonoses reported in animals are associated with events also affecting humans. **Methods:** Using ProMED-mail search archives, all postings were retrieved for reports on Anthrax, Brucellosis, Plague, Rabies, Rift Valley Fever, from 1 January to 31 December 2017. Pro-MED posts were included in the study if the report related to a current disease incident involved either animal species or humans, and occurred in a region (province, state) without a previous report of that zoonosis during the same year. The WHO Hazard Detection and Risk Assessment System (HDRAS) database was then checked using place names and other search criteria to identify any follow-up reports related to disease in humans. **Results:** A total of 186 unique zoonosis disease events reports were identified in 2017, with the greatest number of reports on rabies (n=98), followed by anthrax (n=54), brucellosis (n=18), plague (n=11), and Rift Valley fever (n=5). Among these events, 60% (n=112) reported an event affecting both animal and humans, with the majority related to rabies (n=77); 32% (n=60) were animal events with no human cases recorded during the 6 months following the prior report; and 8% (n=14) were reports which described disease burden in humans without mention of animal exposure. **Conclusions:** The majority of reports mentioned both human and animal infection, in comparison to animal-only events, suggesting a tendency for first reporting events primarily related to humans. Wider reporting of animal disease would be helpful for more complete surveillance of diseases to humans, particularly for rabies and anthrax. Regions with endemic zoonosis disease should regularly laboratory test and report results in the animal population for earlier detection and mitigation of threats to prevent human cases. Further studies are needed to understand how the reporting of other zoonoses, such as avian influenza, is associated for cross-species outbreaks.

Board 399. Real-Time Surveillance of a Canine Rabies Outbreak in a Large Indian Metropolis

I. Banerji[1], N. Panchamiya Jangle[1], A. Vanak[2]
[1]ResQ Charitable Trust, Pune, India, [2]Ashoka Trust for Research in Ecology and the Environment, Bangalore, India

Background: The lack of a systematic surveillance mechanism for canine rabies in India has often been identified as a key hurdle in the control of this dreaded disease. Here we present the implementation of an online animal rescue system for reporting suspected rabies cases. **Methods:** We adapted a custom 24-hour webline that is generally used as a citizen portal for small and large street animal rescue for active surveillance of rabies in street dogs in Pune city, Maharashtra, India. Animals presenting with symptoms such as hyperesthesia, hyperaggression, paralysis of mandible and larynx, inability to swallow, or a history of aggression/ bites were brought into the ResQ rabies ward and isolated on admission. Ante-mortem and post-mortem tests for rabies were conducted using Anigen Rapid Rabies Antigen Test Kit (BIONOTE) and confirmatory RT-PCR or FAT at NIMHANS, Bangalore. **Results:** From September 2017 to February 2018, 118 canine and 1 non-canine cases were reported for suspected Rabies at the ResQ Centre. Of these 65 dogs and 1 bull tested positive using the LFA. Pet dogs and street dogs were reported and tested positive. The differential diagnoses amongst canine cases ranged from head trauma to neuromuscular insufficiencies. The furious form of rabies was more commonly reported (118) but (19) cases also presented the paralytic form. The cases showed a steady rise in numbers as well as geographic spread across the city as the outbreak progressed. **Conclusions:** A systematic reporting system has enabled the detection of an ongoing rabies outbreak in a large metropolis of India. Given the limitations of funding and other resources, outbreak data such as these allow for targeted canine vaccination drives, as well as enhanced PEP awareness. Future plans involve rabies monitoring and detection via a dedicated Dog Bite Helpline, increased rapid response units, and mass education and awareness for the local population.

Board 400. Chagas Disease Surveillance Activities--7 US States, 2017

C. Bennett[1], A. Straily[1], D. Haselow[2], S. Weinstein[2], R. Taffner[2], H. Yaglom[3], K. Komatsu[3], H. Venkat[3], C. Brown[4], P. Byers[5], J. Dunn[6], A. Moncayo[6], B. Mayes[7], S. Montgomery[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Arkansas Department of Health, Little Rock, AR, USA, [3]Arizona Department of Health Services, Phoenix, AZ, USA, [4]Massachusetts Department of Public Health, Jamaica Plain, MA, USA, [5]Mississippi State Department of Health, Jackson, MS, USA, [6]Tennessee Department of Health, Nashville, TN, USA, [7]Texas Department of State Health Services, Austin, TX, USA

Background: Chagas disease has become a concern in the United States due to human populations moving from Latin America where the disease is endemic. An estimated 300,000 people with Chagas disease living in the United States acquired their infections in endemic countries, and an estimated 63 to 315 congenital infections occur annually in the US. The true burden of disease and risk of infection are not fully defined, as Chagas disease is under-recognized partially due to a lack of awareness among healthcare professionals. **Methods:** We reviewed current state-level public health surveillance for Chagas disease in the United States using semi-structured interviews with staff from states in which Chagas disease is listed (or was previously listed) as a reportable condition. Interview questions focused on why the disease was made reportable, how data are collected and utilized to follow up on cases, and if data were collected on at-risk pregnant women, infants born to infected mothers, non-human cases, or triatomine vectors. **Results:** Chagas disease is currently a reportable condition in 6 states (Arizona, Arkansas, Louisiana, Mississippi, Tennessee, and Texas), and previously was reportable in Massachusetts. States implemented surveillance in response to blood donor screening for Chagas disease and to trigger efforts to identify the route of disease transmission. Many states reported primarily chronic cases with little public health response to local transmission since acute cases were infrequently reported. Five states actively distribute surveillance reports to health care providers. Although not asked explicitly, all six states mentioned that they help link physicians to information about appropriate clinical management. States do not conduct surveillance specifically for congenital infections, and no systematic surveillance is directed at non-human cases or vectors. **Conclusions:** Although there are limited opportunities for public health action, Chagas disease surveillance remains important in states with large populations of immigrants or frequent travelers from endemic countries and for states with a risk of local transmission. Surveillance activities help increase awareness among public health professionals and physicians and can assist in linking Chagas cases to treatment to help prevent cardiac and gastrointestinal complications.

Board 401. CHIKRISK: Mapping and Assessment of Chikungunya Risk

A. Anyamba[1], R. Soebiyanto[1], X. Rama[1], K. Linthicum[2]
[1]Universities Space Research Association / NASA Goddard Space Flight Center, Greenbelt, MD, USA, [2]US Department of Agriculture (USDA) - Center for Medical, Agricultural and Veterinary Entomology (CMAVE), Gainesville, FL, USA

Background: There is an increasing concern for reemergence and spread of chikungunya in the last 10 years. The 2013 outbreak and its spread in the Americas has so far resulted in more than 1.7 million suspected cases. This event has demonstrated the importance of readiness in assessing potential risk of the emergence of vector-borne diseases (VBD). Climate and ecological conditions are now recognized as major contributors to the emergence and re-emergence of various VBD including chikungunya. Variations and persistence of extreme climate conditions provide suitable settings for certain disease vector populations to propagate and amplify VBD transmission. **Methods:** We are compiling and geocoding records of locations where chikungunya has occurred since 1980 from publicly available records (Program for Monitoring Emerging Diseases (ProMed-mail), Pan-American Health Organization (PAHO), Armed Forces Health Surveillance Branch (AFHSB) Health Surveillance Updates and literature). This data is combined with climate anomaly data sets (rainfall & temperature) into an analytical framework to determine conditions that lead to chikungunya outbreaks. After characterizing the climatic conditions prior to the outbreaks, we use the resulting relationships to develop mathematical and statistical models to map and monitor areas at risk for chikungunya activity. **Results:** Under the umbrella of Biosurveillance Ecosystem (BSVE), we have developed a prototype climate-based app, CHIKRISK, which will help analysts answer three critical questions: (i) Where has chikungunya activity occurred; (ii) Where it is occurring now; (iii) Which regions are currently at risk for chikungunya. The app has the capability to visualize historical chikungunya activity locations, climate anomaly conditions and chikungunya risk maps. **Conclusions:** The CHIKRisk App is available for various ana-

lysts and public health professionals in customizing response plans. It is also available for use by the Department of Defense for execution of pre-deployment and post-deployment Force Health Protection (FHP) measures. This prototype is a good example of how we can use disease outbreak and climate data to address an issue of global public health concern. It can be potentially extended to other equivalent applications related to Zika and dengue.

Board 402. Examining Foodborne Illness Complaints Online Using the Twitter platform *(Will be displayed with Foodborne Infections posters on Monday)*

K. Sewalk, J. Hawkins, J. Brownstein
Boston Children's Hospital, Boston, MA, USA

Background: The Foodborne Dashboard is an online surveillance platform, which monitors social media data related to foodborne illness. By using social media data from Twitter, public health agencies can monitor foodborne illness cases via Twitter users who complain of illness of symptoms online. Once identified, public health officials can then reach out directly to the user for follow-up information and official reports. Approximately 48 million Americans are affected by foodborne illness each year, but traditional public health surveillance systems only capture a small fraction of these incidents. Very few people choose to seek medical care or report their illness. By using non-traditional surveillance methods with Twitter data, public health agencies can improve surveillance methods by capturing foodborne illness cases that might not otherwise be identified. This platform intends to supplement traditional food illness reporting methods for local health departments in the US by integrating digital data from Twitter. **Methods:** Using a machine-learning classifier, we identify and geo-locate foodborne illness complaints on Twitter. Local health agencies respond to users via Twitter in their jurisdiction to request additional missing information. Twitter users fill out an online report with detailed case information to the local health agency. **Results:** Since 2014, we have collected 1,244,875 classified tweets as food poisoning related in the United States. Through manual classification of tweets, we identified 34,754 tweets as confirmed food-poisoning tweets in the jurisdiction with whom we partner. Of those confirmed classified tweets, we have 6,281 tweets that have been responded to by the local health agencies. In total, we observe 3,147 submitted reports from Twitter users on their foodborne illness experience. **Conclusions:** This information is used to supplement traditional data reporting to best utilize and target inspection resources.

Board 403. Multisite Active Surveillance for Acute Gastroenteritis in Veterans Affairs Hospitals, 2016–17

C. Cardemil[1], A. Kambhampati[2], S. Grytdal[1], M. Rodriguez-Barradas[3], B. Vargas[3], D. Beenhouwer[4], K. Evangelista[4], V. Marconi[5], K. Meagley[5], S. Brown[6], A. Perea[6], H. Browne[7], J. Vinje[1], U. Parashar[1], A. Hall[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]IHRC, contracting agency on behalf of Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Houston VAMC, Houston, TX, USA, [4]Los Angeles VA, Los Angeles, CA, USA, [5]Atlanta VA, Atlanta, GA, USA, [6]Bronx VA, New York City, NY, USA, [7]ORISE, Oak Ridge, TN, USA

Background: Acute gastroenteritis (AGE) causes approximately 179 million illnesses per year in the United States. Viruses are leading causes of AGE, yet the burden and severity of illness attributable to specific AGE pathogens in adult populations are not well understood. In 2016, we implemented a multisite inpatient and outpatient surveillance platform capturing AGE cases and controls in 4 Veterans Affairs hospitals (Atlanta, Bronx, Houston, and Los Angeles) that collectively serve >320,000 patients annually. **Methods:** AGE inpatient cases and age- and time-matched controls were actively identified through prospective screening of admitted patients via standardized case definitions. Eligible and consenting patients were enrolled, interviews conducted, medical charts abstracted, and stool, saliva and blood samples collected. AGE outpatient cases were passively identified through collection of stool samples submitted for routine clinical microbiological diagnostics, followed by medical chart abstraction. All stool samples were tested for 22 pathogens using the FilmArray Gastrointestinal Panel. **Results:** From December 1, 2016, through December 31, 2017, 1,121 patients were enrolled. In the active arm, cases (n=545) and controls (n=304) did not differ by age or sex (92% male for both; median age was 63 and 62 respectively, range 23-94). Norovirus and rotavirus were the most common viral pathogens detected, and prevalence was higher in cases vs controls (norovirus: 5.1% vs 1.3%, $p<0.01$; rotavirus: 2.8% vs 0%, $p<0.01$); other viral pathogens were detected less frequently (sapovirus: 1.1% vs 0.9%, p=1; astrovirus: 0.6% vs 0%, p=0.6; adenovirus: 0.6% vs 0%, p=0.6). 61 intensive care unit (ICU) admissions and 9 deaths were documented among cases, including 1 norovirus-associated death. In the passive arm (n=272), norovirus prevalence was 8.8%, followed by astrovirus (2.2%), sapovirus (1.5%), and rotavirus (1.1%). **Conclusions:** Implementation of a multisite AGE surveillance platform captured a wide spectrum of AGE illness in US veterans including outpatient visits, hospitalizations, ICU stays, and deaths. Norovirus was the leading viral pathogen detected. Ongoing surveillance using this platform will allow for further characterization of the pathogen distribution, serologic response, and associated disease burden of AGE in adults.

Board 404. Surveillance for Acute Gastroenteritis Outbreaks through the National Outbreak Reporting System (NORS), United States, 2009–2016

M. Wikswo, V. Roberts, H. Kisselburgh, K. Fullerton, S. Crowe, A. Hall
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: About 179 million cases of acute gastroenteritis (AGE) occur annually in the United States, although exposure information to guide prevention is generally limited to outbreaks. Data from the National Outbreak Reporting System (NORS) was used to characterize pathogen-specific transmission modes and settings of AGE outbreaks. **Methods:** Finalized data reported to NORS on outbreaks occurring during 2009–2016 were extracted for descriptive analysis. We included outbreaks with a reported AGE etiology and outbreaks of other or unknown etiologies with either ≥50% of cases reporting diarrhea or ≥50% reporting vomiting. Waterborne data for 2015–2016 are preliminary. **Results:** A total of 25,832 AGE outbreaks were reported to NORS during the 8-year study period, resulting in 722,021 reported illnesses (median 17 per outbreak, range 2–2,500), 16,920 hospitalizations, and 925 deaths. Outbreaks were reported by all 50 states, Puerto Rico, and the District of Columbia. The most common mode of transmission was person-to-person (n=16,029, 62%), followed by foodborne (n=6,356, 25%), unknown mode (n=2,733, 11%), waterborne (n=348, 1%), animal contact (n=288, 1%), and environmental contamination (n=78, 0.3%). At least one suspected or confirmed etiology was reported in 20,521 (70%) outbreaks. Norovirus was most common, reported in

15,007 (73%) outbreaks as the sole etiology, followed by *Salmonella* (n=1,744, 9%) and *Shigella* (n=902, 4%). Norovirus was most frequently transmitted person-to-person (n=11,687 outbreaks, 78%) and by food (n=2,189, 15%), and outbreaks occurred primarily in long-term care facilities (n=7,597, 51%) and restaurants (n=1,597, 11%). *Salmonella* was predominantly transmitted through food (n=1,082, 62%) and unknown mode (n=326, 19%), and outbreaks occurred most often in restaurants (n=407, 23%) and private homes (n=331, 19%). *Shigella* was mostly transmitted person-to-person (n=736, 82%) and by unknown mode (n=105, 12%), and outbreaks occurred primarily in day care facilities (n=415, 46%) and schools (n=175, 19%). Waterborne outbreaks were most frequently associated with *Cryptosporidium* (n=158, 47%). **Conclusions:** through NORS highlights the leading etiologies, transmission modes, and settings of reported AGE outbreaks, which can help guide targeted interventions.

Board 405. Geospatial Open Data Platforms to Tackle Hospital-Associated Infections

S. Engel, D. Rabinowitz, J. Bakal, D. Koutsonanos, L. Ganesan, A. Dane
Deloitte, Atlanta, GA, USA

Background: Open data solutions for studying infectious disease are evolving, moving from static data catalogs and specialist visualizations targeting analysts and scientists, towards multiple-dimension web platforms that engage a greater number and diversity of users. These newer platforms are built with the recognition that creating value from open data requires answering users' questions in the context of each user's unique situation. Applying these concepts to surveillance will enable participants to more effectively monitor populations, communicate results, and develop response methods, ultimately driving federal and public health missions to improve capabilities and mitigate disease. **Methods:** Applications exhibiting "Open Data 2.0" concepts provide graphs, charts, data-driven narratives, Application Programming Interfaces, search engine optimization, and journalistic stories that allow for even greater information sharing and insight. These help patients, providers, network administrators, researchers, and policy makers understand population health, outbreak trends, healthcare quality and costs, and many other aspects that drive decisions on response and prevention of infectious disease. **Results:** The CDC Division of Healthcare Quality Promotion (DHQP) are building a solution that embraces Open Data 2.0 concepts, the Antibiotic Resistance Patient Safety Portal. This portal will provide enhanced methods to study and share how Hospital-Associated Infections and Antimicrobial Resistance, Use, and Stewardship vary in risk across the nation, providing data throughout spatially driven mediums to drive intuitive decision-making. Site contents include various data-driven pages, ranging from narratives, or data "stories", to advanced analytical surveillance dashboards, all maintaining dynamic qualities for high levels of user interaction. **Conclusions:** Through implementing the portal, DHQP will broaden types of data provided, organize content in ways that are relevant to both general users and advanced analysts, and attract larger audiences through modern sharing and social engagement techniques. The concepts of the Patient Safety Portal ultimately align with the Division's greater mission to streamline their technological tools internally, and to unify messaging to the public about its programs and achievements.

Board 406. Identification of Facilities at Risk of Receiving Patients Colonized with Emerging Multidrug-Resistant Organisms

M. Kainer[1], R. Octaria[1], R. Slayton[2], P. Paul[2], A. Chan[1], N. Smith[1]
[1]Tennessee Department of Health, Nashville, TN, USA, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA

Background: When patients are admitted over time to multiple healthcare facilities ("patient sharing"), the risk for transmission of multi-drug resistant organisms (MDRO) is increased. We developed an interactive web interface for visualization of the patient sharing network of Tennessee (TN) healthcare facilities to identify facilities at risk of receiving patients with MDRO for public health interventions such as screening admissions. **Methods:** Using the statewide hospital discharge data (HDDS) from 2014 -2016 and aggregated facility-level patient sharing data from the Centers for Medicaid & Medicare Services (CMS) claims and Minimum Dataset (MDS) 2014, we constructed patient-sharing networks through direct patient transfers and total patient transfers including indirect transfers with up to 30, 56, and 365 days of intervening stays in community. HDDS data contains all admissions to 154 TN hospitals and CMS data contains admissions of all CMS fee-for-service beneficiaries to 138 TN hospitals and 327 TN nursing homes. The interactive web interface was developed using the Shiny package in R. **Results:** Authorized users can access the Shiny web application to visualize the patient sharing network of a facility of interest (ego) without having to develop code. Users can tailor visualizations based on the year, data source (HDDS or CMS), length of intervening stays in the community, ego facility, and the lower threshold of the number of transfers. The interface visualizes the ego facility and other facilities that receive or send patients to that facility and the number of transfers between pairs of facilities. A tooltip displays the facility's characteristics. A transfer statistics tab displays facilities that are most at-risk to receive transfers from the ego facility prioritized based on the number of historical transfers in the event of any MDRO transmission or when a novel MDRO mechanism or organism is detected within the ego facility. A download feature allows users to download the spreadsheet summarizing at-risk facilities including facility characteristics and image of ego network visualization. **Conclusions:** The interactive web platform of patient sharing network is likely to assist public health professionals to easily identify facilities at-risk of receiving patients colonized by MDRO from an index facility.

Board 407. Interactive Visualizations of Carbapenem-Resistant Enterobacteriaceae (CRE) Surveillance Data in Tennessee, United States

A. Chan, R. Octaria, P. Talley, M. Kainer
Tennessee Department of Health, Nashville, TN, USA

Background: CRE have been reportable in Tennessee (TN) since 2011; isolates must be sent to the state public health laboratory to confirm carbapenemase production. Easy access to visualizations of CRE surveillance data is a critical component to improve regional response to this urgent threat. **Methods:** CRE were defined as *E.coli*, *Klebsiella*, and *Enterobacter spp.* (big 3 genera) resistant to doripenem, meropenem, imipenem (minimum inhibitory concentrations [MIC] of ≥4 µg/ml) or ertapenem (MIC ≥2 µg/ml, or demonstrated production of a carbapenemase. We compared data from January. 1 through November 30 2016 and 2017. County level aggregate data were displayed in Tableau, a visual tool that allows interactive portrayal of data. **Results:** We utilize Tableau to display up-to-date CRE surveillance data using dashboards.

Dashboards are automatically updated each month, which include case counts by month and within the last 30 and 90 days. Genera and species breakdowns, by county, are available along with the capability to filter data by genus, year of specimen collection, and resistance mechanism. In 2016, 669 cases of CRE were reported; 195 (30%) were carbapenemase-producing (CP-CRE) compared to 2017, in which 212 of 709 CRE (30%) were CP-CRE. The statewide cumulative incidence of CP-CRE was 3.1 and 3.3 cases/100,000 persons during the first 11 months of 2016 and 2017, respectively. For 2016, the distribution of CP-CRE genera was as follows: 43% *Enterobacter*, 10% *E. coli*, and 47% *Klebsiella* compared to 43%, 5%, and 52%, respectively in 2017. The Tableau dashboard highlights CP-CRE hotspots in Southwestern TN, Northeastern (NE) TN, and an emerging hotspot in Middle TN. CP-CRE in Shelby County (Memphis) in both 2016 and 2017 were predominantly *Enterobacter*. Historically, NE TN has been a hotspot of *Klebsiella* CP-CRE but showed a small influx of *Enterobacter* in 2017. There was an increase in CP-CRE in 2017 for Davidson County (Nashville) with 4 *Enterobacter*, *2 E.coli*, and 10 *Klebsiella* CP-CRE compared to 1 *Enterobacter* CP-CRE in 2016. **Conclusions:** CP-CRE continue to be an urgent threat showing remarkably dynamic geographic variation. We have seen a dramatic influx in Davidson County of KPC CP-CRE involving all big 3 genera. Tableau allows users to easily visualize up-to-date surveillance data and identify current trends without the need to code or learn a new system.

Board 408. Development and Implementation of a Cloud-Based Meningitis Surveillance and Specimen Tracking System in Burkina Faso

T. Kiemtore[1], S. Sanou[2], B. Bicaba[1], I. Medah[3], T. Tarbangdo[4], G. Sawadogo[4], A. Diallo[5], R. Novak[5], H. Ake[4]
[1]Direction de la Lutte contre la Maladie, Ministry of Health, Ouagadougou, Burkina Faso, [2]Ministry of Health, Ouagadougou, Burkina Faso, [3]Direction de la Prévention par les Vaccinations , Ministry of Health, Ouagadougou, Burkina Faso, [4]Davycas International, Ouagadougou, Burkina Faso, [5]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Among the 26 meningitis belt countries in sub-Saharan Africa, Burkina Faso has the highest historic burden of meningitis. A member of the MenAfriNet Consortium, it has implemented case-base meningitis surveillance nationally with more than 90% of all suspected meningitis cases having a specimen collected, and contributed critical evidence on meningitis vaccine effectiveness. To address delays in collection of patient information and laboratory results, a cloud-based specimen-tracking and meningitis surveillance platform was developed and implemented (STELaB). **Methods:** STELaB is an online and offline application with a web-interface for surveillance data entry, validation, reporting and visualization. MenAfriNet case investigation forms are completed for patients with suspected meningitis and specimens sent to the laboratory with the forms to be barcoded, scanned into STELaB, and laboratory testing results recorded. Surveillance officers enter patient information from the barcoded case investigation forms which are linked to the specimens. A Help Desk monitors the functionality of the application, resolve technical issues, gather user feedback and improve system performance. **Results:** STELaB was deployed nationally over a six-week period from November-through December 2017. STELaB was installed at 180 sites covering all national, regional, and district level laboratories and surveillance units, each site received software, computer, barcode labels and scanners, and user training. STELaB verifies the availability of data connection to sync sites with a cloud server, data are synced nationally via satellite internet to a local server, and networked to the Ministry of Health via fiber optic cable. Monitoring and evaluation of STELaB during the 2018 season is ongoing, data will be presented on the performance, user feedback, and initial impact of STELaB on the public health system data in Burkina Faso. **Conclusions:** Implementation of STELaB established a national network of laboratories for timely tracking of specimen transport and pathogen confirmation to ensure continued effectiveness of vaccine programs in Burkina Faso. STELaB's novel design and country-driven approach has potential to achieve sustainable real-time data reporting and specimen tracking for the first time in sub-Saharan Africa.

Board 409. Death Certificate Review to Ascertain Additional Deaths among Patients Hospitalized with Invasive Bacterial Infections 90 Days Post-Discharge, Minnesota, 2012-2016

C. Holtzman, R. Lynfield, K. Como-Sabetti, L. Triden, B. Jewell, R. Danila
Minnesota Department of Health, St. Paul, MN, USA

Background: As part of CDC Active Bacterial Core Surveillance (ABCs), the Minnesota Department of Health conducts active population-based surveillance of invasive disease of residents with bacteria isolated from normally sterile body sites, including *Haemophilus influenzae* (HI), *Neisseria meningitidis* (NM), group A *Streptococcus* (GAS), group B *Streptococcus* (GBS), and *Streptococcus pneumoniae* (SP). ABCs methodology captures inpatient mortality data. This analysis estimates the contribution of death certificate data to ABCs disease burden data. **Methods:** We linked death certificates to ABCs cases identified during 2012-2016 to identify additional deaths after hospital discharge. For cases with recurrent infections, only the most recent infection was used. Cause of death (COD) was characterized as non-infectious etiology or infectious etiology. **Results:** We identified 7,042 ABCs cases during 2012-2016, of which 6,538 (93%) were hospitalized; 507 (8%) died before hospital discharge. Upon linking cases with death certificates, we found an additional 336 (5%) cases died ≤ 90 days of hospital discharge, 237 (71%) cases were ≥ 65 years of age (range 0-102 years, median=74 years). 130 (39%) cases had an infectious etiology listed as primary or contributing COD. Sepsis was the most common infectious COD, and 59 (18%) cases listed sepsis, septic shock, or meningitis as COD. Of cases who died after discharge, 60/144 SP (42%), 19/40 GAS (48%), 47/121 GBS (39%), and 4/31 HI (13%) had infectious COD listed. Type of ABCs pathogen causing invasive disease was associated with having an infectious COD listed (p=0.01). Age, clinical presentation, and underlying conditions were not associated with infectious COD. **Conclusions:** Current ABCs data collection methods likely underestimate the true mortality associated with having an invasive infection, particularly among those >65 years. Use of death certificate data can enhance ABCs surveillance. Notably, over one-third of deaths in ABCs cases occurring within 3 months of hospital discharge had an infectious COD. Review of available medical records post-hospitalization for the invasive infection, but closer to the time of death for these cases, may further clarify the role of the ABCs pathogens.

Board 410. Z-POINT: An Adaptable Data System for Outbreak-Related Case Review Designed for the Zika Emergency Response

J. Nahabedian, N. Roth, J. Sims, A. Fulton, S. Ellington, R. Galang
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: In 2016, as part of the Centers for Disease Control and Prevention's (CDC) emergency response to the Zika virus (ZIKV) outbreak, CDC and public health partners established Zika pregnancy and infant registries to monitor pregnancy and infant outcomes among pregnant women with ZIKV infection. During an emergency response, data collection methods are rapid and dynamic, requiring adaptable review systems. Scientists must review collected health data to classify identified outcomes according to standardized surveillance case definitions. To simplify the review process, an adaptable data system was created called the Zika Pregnancy of Interest Navigation Tool (Z-POINT). **Methods:** Z-POINT was created using Microsoft Access and can function as an independent compiled program. Exported data from Zika pregnancy and infant surveillance systems are reformatted in SAS 9.4 and then uploaded into Z-POINT. Z-POINT automatically calculates infant growth percentiles for gestational age and sex based on INTERGROWTH-21st standards and creates concise narrative summaries from hundreds of variables for each case. Reviewers record classification decisions using a form standardized to the CDC surveillance case definitions for Zika-related birth defects. Classification data are then uploaded to the registries and available for analysis. **Results:** Using Z-POINT, CDC scientists have reviewed over 15,000 records. Z-POINT effectively reduced workload for case review by re-formatting data, performing complex calculations, and writing complex clinical data summaries. Ten versions of Z-POINT have been created to interface with multiple surveillance systems demonstrating its ability to be adaptable. **Conclusions:** Z-POINT presents a major advantage to conventional data review methods by displaying hundreds of data fields simultaneously in a manner that can be custom-tailored for reviewers. Z-POINT has allowed for rapid review and analysis of data that has been critical to understanding ZIKV infection during pregnancy and informing clinical guidance for care of affected pregnant women and infants. The adaptability of Z-POINT and its capacity to interface with a variety of systems demonstrates its potential as a valuable tool that can be applied to future emergencies.

Board 411. Integrated Monitoring for Zika-Exposed Persons: Georgia, 2016-2017

A. Feldpausch[1], K. Soetebier[2], S. Feinman[2], S. Brennan[2], A. Thompson[2], T. Graham[2], J. Barton[2], J. Gabel[2], C. Drenzek[2]
[1]University of Georgia, College of Veterinary Medicine, Athens, GA, USA, [2]Georgia Department of Public Health, Atlanta, GA, USA

Background: In 2015, Zika virus emerged as a widespread health threat in the Americas. In January 2016, Georgia Department of Public Health (DPH) epidemiologists received their first call about a traveler with suspected Zika infection. As the outbreak evolved, concerns for pregnant women came to the forefront of the response. It was apparent that an information system was needed to track citizens approved for Zika virus testing that integrated pregnancy data, testing data, and environmental assessments. The Zika Active Monitoring System (ZAMS) was completed in June of 2016 and made active across the state in September 2016. **Methods:** ZAMS was modeled after the Ebola Active Monitoring System (EAMS) developed by DPH in 2014. DPH epidemiologists worked with in-house software developers to create a system to capture a record for each Zika-tested person that included demographics, comments, travel information, symptoms, and laboratory data and results. Developed within the web-based, State Electronic Notifiable Disease Surveillance System (SendSS), the system would facilitate use by multiple epidemiologists state-wide in real-time. Subsequently, the Zika Pregnancy Registry (ZPR), Zika Birth Defects Registry (ZBDR), and a PDF upload for environmental assessments were added, all accessible within a single system. **Results:** Between January 26, 2016 and December 15, 2017, DPH Epidemiology triaged over 10,000 Zika-related inquires, resulting in over 3,600 patients tested at DPH or commercially, all tracked in ZAMS. DPH participates in the US ZPR and ZBDR using data from ZAMS in conjunction with medical records and other DPH record systems. ZAMS data are also used to support decision-making in Georgia Zika protocols, including testing algorithms and environmental follow-up. ZAMS allows more than 20 epidemiologists to track and follow up on patients. **Conclusions:** ZAMS is an effective and user-friendly system for tracking persons being tested for Zika, Zika-positives, and pregnant women with evidence of Zika in Georgia. ZAMS provides a centralized location where DPH personnel from multiple disciplines can share information on cases and access consolidated data on all aspects of Zika case investigation to increase efficiency of communication and follow-up. Utilizing EAMS as a template for ZAMS supported preparedness activities and resourceful use of institutional knowledge.

Genomic and Molecular Epidemiology

Board 412. Genomic Epidemiology of *Salmonella* Mississippi in Australia

L. Ford[1], D. Ingle[1], M. Harlock[2], M. Veitch[2], K. Glass[1], D. Williamson[3], J. Gregory[4], R. Stafford[5], M. Kirk[1]
[1]Australian National University, Canberra, Australia, [2]Department of Health and Human Services Tasmania, Hobart, Australia, [3]University of Melbourne, Melbourne, Australia, [4]Department of Health and Human Services Victoria, Melbourne, Australia, [5]Queensland Health, Brisbane, Australia

Background: *Salmonella* Mississippi is the most commonly notified *Salmonella* serovar in the Australian island state of Tasmania. A case-control study of *S.* Mississippi in Tasmania found that indirect contact with native birds, untreated drinking water, and travel within the state were associated with infection. We investigated *S.* Mississippi in Australia using whole genome sequencing to improve our understanding of the epidemiology and sources of infection. **Methods:** We used national notification data to examine trends in *S.* Mississippi infection in Australia. Population denominator data were obtained from the Australian Bureau of Statistics. We sequenced 12 human isolates from Queensland from 2008-2011 and randomly sampled and sequenced 34 human (2011-2015), 42 animal, and 18 environmental (2000-2016) isolates from Tasmania, and 16 human isolates from residents of other Australian states and territories (2011-2015). Illumina sequence reads were analysed with the "Nullarbor" pipeline using the *Salmonella* Typhimurium LT2 reference genome at the Microbiological Diagnostic Unit Public Health Laboratory. Core genome single nucleotide polymorphisms (SNPs) were used to construct a maximum likelihood phylogenetic tree. **Results:** Between 2000 and 2016, the median notification rate of *S.* Mississippi in Tasmania was 15 cases (range 12-24) per 100,000 population, compared to a notification rate of 0.11 cases (range 0.07-0.16) per 100,000 on mainland Australia. The maximum

likelihood tree showed the 122 isolates clustered into 21 clades, with a median pairwise SNP difference within clades of 106 SNPs (range 32-415). Both human and non-human isolates were included in 16/21 (76%) clades. Strains in humans were clustered together with animals and environmental sources, but there was no clustering by animal species or by time. There was considerable heterogeneity of strains found in animal sources. **Conclusions:** *S.* Mississippi is an important cause of human infection and is found in several animal and environmental sources in Tasmania. The genetic diversity and persistence of strains in these sources suggest that *S.* Mississippi is endemic in the Tasmanian environment. The range of animal and environmental sources makes it difficult to identify control strategies.

Board 413. The Emergence of *Salmonella* Typhimurium DT 160 in Australia among Humans and Sparrows

L. Ford[1], D. Ingle[1], A. Gonçalves da Silva[2], M. Harlock[3], M. Veitch[3], K. Glass[1], D. Williamson[2], M. Kirk[1]
[1]Australian National University, Canberra, Australia, [2]University of Melbourne, Melbourne, Australia, [3]Department of Health and Human Services Tasmania, Hobart, Australia

Background: Ten years after its emergence in New Zealand, the first locally acquired case of *Salmonella* Typhimurium DT 160 (STm160) was reported in Tasmania, Australia in 2008. Since 2008, STm160 has been cultured from wild Tasmanian sparrows and >50 cases from Australian residents, almost all living in Tasmania. We investigated the genetic relatedness of Australian human and animal STm160 isolates, their relatedness to animal STm160 isolates from New Zealand, and examined molecular patterns by time, place and person. **Methods:** Sixty Australian human and 31 Australian animal STm160 isolates, including 19 isolates from sparrows, were whole genome sequenced at the Microbiological Diagnostic Unit Public Health Laboratory. We compared these with 74 published STm160 isolates from animals in New Zealand. Illumina sequence reads were analysed through the "Nullarbor" pipeline. Reads were mapped to the *Salmonella* Typhimurium LT2 reference strain to identify core genome single nucleotide polymorphisms (SNPs) which were used to construct a maximum likelihood phylogenetic tree. We developed hypotheses about the epidemiological relatedness of isolates, and evaluated these with sequence data. **Results:** The maximum likelihood tree showed two distinct clades, with one containing isolates from humans and animals in Australia, and the other containing animals from New Zealand and 7 Australian residents who had reported travel to New Zealand. The median pairwise SNP difference between the Australian and New Zealand isolates was 32 (range 11-69), while the median pairwise SNP difference within both clades was 22 (AU: range 0-59; NZ: range 1-59). Within the Australian clade, isolates over several years from human and animal sources were clustered together. Direct animal contact was reported in 88% (37/42) of human isolates where epidemiological data was available. **Conclusions:** Phylogenetic analysis of whole genome sequence data separated Australian and NZ STm160 isolates in to separate clades. The high relatedness between Australian human and animal isolates suggests a predominantly locally acquired zoonotic infection. This is corroborated by the epidemiological data, and suggests promoting hand hygiene after contact with wild birds and other animals in order to minimize risk of infection.

Board 414. Impact of Population-Based Prospective Whole-Genome Sequencing on *Salmonella* Outbreaks in British Columbia (BC), Canada

K. Meghnath[1], M. Taylor[1], L. Janz[1], L. Hoang[1], A. Paccagnella[1], J. Cutler[2], C. Misfeldt[3], E. Galanis[1]
[1]BC Centre for Disease Control, Vancouver, BC, Canada, [2]Public Health Agency of Canada, Guelph, ON, Canada, [3]Public Health Agency of Canada, Winnipeg, MB, Canada

Background: Prospective whole genome sequencing (WGS) for all *Salmonella* isolates began in Canada in May 2017. This method has provided greater specificity for outbreak detection than the previously-used PFGE and phage-typing. The objective of this study is to describe *Salmonella* clusters and outbreaks that have been detected through WGS, and the impact of WGS on outbreak investigation in BC. **Methods:** BC isolates with wgMLST completed at the National Microbiology Laboratory between May 2017 and Feb 2018 were included. Clusters were defined as isolates with up to 10 allele differences. Provincial clusters included 3 or more BC isolates. National clusters included 2 or more isolates from different provinces/territories, including at least one from BC. BC *Salmonella* outbreak data from 2010 to 2018 was analyzed to determine how the number and types of outbreaks investigated changed before and after the implementation of prospective WGS. **Results:** WGS data is available for 872 BC *Salmonella* isolates. 55.8% of these isolates fall into 92 clusters, and the remaining 44.3% are sporadic. Eighty-four of 92 clusters were national and account for 50.2% of BC isolates. Three of the 84 clusters account for 25% of BC isolates. 8 provincial clusters account for 5.5% of isolates. Between May 2017 and Feburary 2018, BC investigated 15 *Salmonella* outbreaks. This marked an increase from the 2 to11 outbreaks investigated annually between 2010 and 2016. Eight of the 15 outbreaks were national, compared to 0 to 2 in 2010-2018. Of the 15 outbreaks, 14 utilized WGS. Eleven were detected and 3 were confirmed by WGS. Nine of 14 were *S*. Enteritidis, and the remaining 5 were different serotypes. From 2010-2016, 1 to 6 *S*. Enteritidis outbreaks were investigated annually. **Conclusions:** WGS has shown that the majority of BC *Salmonella* isolates fall into national clusters. This has led to an increase in the number of outbreaks investigated; particularly national *S*. Enteritidis outbreaks. WGS shows promise to improve our ability to identify and control *Salmonella* in the population.

Board 415. Whole Genome Sequencing-Based Analysis of a Child Care-Associated *Salmonella* Infantis Cluster with Conflicting Pulsed-Field Gel Electrophoresis Patterns

J. Garfin, M. Decuir, X. Wang, P. Webb, C. Medus, D. Boxrud
Minnesota Department of Health, St. Paul, MN, USA

Background: *Salmonella* Infantis is an uncommon serotype that accounts for 3.9% of *Salmonella* isolates in Minnesota. Pulsed-field gel electrophoresis (PFGE) has historically been the gold standard for the determination of genetic relatedness of enteric pathogens. Recent introduction of Whole Genome Sequencing (WGS) to public health laboratories has provided significantly higher resolution to investigations of outbreak clusters compared to PFGE. In a December 2017 *S.* Infantis outbreak at a Minnesota childcare facility, four distinct PFGE patterns were reported for five isolates which had strong epidemiological linkage. WGS was utilized to address this unusual scenario by compiling data from this outbreak into a retrospective analysis of Min-

nesota *S.* Infantis collected since 2017. **Methods:** The daycare outbreak isolates, along with all *S.* Infantis isolated at MDH since 2017, were sequenced using the Illumina Nextera XT library preparation kit and MiSeq sequencers. All samples had an estimated depth of coverage >40x and average read Q score >30, adhering to PulseNet requirements. High quality single nucleotide polymorphism (hqSNP) analysis was carried out using lyve-SET 1.1.4f, and a heatmap of pairwise SNP comparisons was created using R. **Results:** A total of 58 *S.* Infantis isolates were included in this study. Whole genome hqSNP analyses indicated that all five daycare isolates clustered together with a SNP range of 1-4. Two of the five child care-associated isolates had matching PFGE patterns, each of the other three isolates from the cluster produced unique patterns which differed by 1-2 bands. The SNP differences for isolates not linked to the childcare cluster range from 19-829. Other 2017 *S.* Infantis clusters supported by epidemiological data were also observed via WGS. The likely cause of discordant results from PFGE and WGS was also investigated. **Conclusions:** Despite diverse PFGE patterns, WGS results were consistent with the epidemiological findings in this investigation. WGS has previously been shown to be useful to find subclusters within a single PFGE pattern, but this case study shows that it is also useful to identify clusters that include multiple PFGE patterns, especially those that differ by a small number of bands. If used during routine surveillance, WGS could identify outbreaks that would otherwise be missed by PFGE-based surveillance.

Board 416. Application of Whole Genome Sequencing Analytics to Aid Local Salmonellosis Outbreak Investigation in the Commonwealth of Virginia

K. Libuit, G. Wilson, L. Turner
Division of Consolidated Laboratory Services, Richmond, VA, USA

Background: Multiple cases of gastrointestinal illness were reported following a Chili and Chowder Cook-off event in the Eastern Shore of Virginia in 2017. *Salmonella* serotype Javiana isolates from clinical and food samples were submitted to the Division of Consolidated Laboratory Services (DCLS) for pulsed-field gel electrophoresis (PFGE). Multiple *Salmonella* PFGE pattern types were identified from samples associated with the event and from cases that clustered geographically yet preceded or anteceded the event. The limitations of PFGE DNA fingerprint comparison made it difficult for Virginia Epidemiologists to understand the significance of the different pattern types identified from samples associated with the cook-off and cases before and after the event. **Methods:** Fourteen clinical isolates and one *Salmonella* isolate from a clam chowder sample with known association with the cook-off event, as well as four clinical *Salmonella* isolates unrelated to the event were tested by whole-genome sequencing (WGS) on the Illumina MiSeq DNA Sequencing platform. Taxonomic label verification and read-quality assessments were performed for WGS quality control using a DCLS-developed pipeline (Tredeger) and the CDC PulseNet CG-Pipeline, respectively. Single-nucleotide polymorphism (SNP) analysis was performed using both the FDA CFSAN-SNP and the CDC Lyve-SET pipelines. FigTree and RAxML were used to render dendrograms for the CFSAN-SNP and Lyve-SET output, respectively. **Results:** Tredegar analysis confirmed the taxonomic labels (*Salmonella* ser. Javiana) of all nineteen isolates. Scripts form the CG-Pipeline confirmed high-quality sequences (average Phred score >30, estimated coverage > 30x) appropriate for variant analysis. CFSAN-SNP and Lyve-SET pipelines both showed that all nineteen isolates were within <10 SNP difference, constituting an putative outbreak clade. **Conclusions:** WGS analysis concluded that the differences observed in PFGE pattern types were insignificant to the outbreak investigation based on the genomic relatedness of isolates. Salmonellosis cases that clustered geographically but occurred before or after the event were determined to be closely related to the outbreak strain, leading to further investigations to identify the extent and source of the outbreak.

Board 417. Evidence of Long-Term *Salmonella* Contamination Linked to a Single Restaurant in Michigan

S. Dietrich[1], J. Wholehan[1], K. Jones[1], S. Bidol[1], K. Arends[1], A. Adediran[2], L. Gladney[2], E. Trees[2]
[1]Michigan Department of Health and Human Services, Lansing, MI, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: The public health laboratory in Michigan monitored a rare strain of *Salmonella enterica* ser. Mbandaka spanning 10 years. Most cases were epidemiologically linked to one restaurant indicating a strain persisted on the premises. The strain was first identified by PulseNet pulsed-field gel electrophoresis (PFGE) surveillance. Whole genome sequencing (WGS) was then applied to confirm that the isolates were the same strain, and to assess the evolution of sequences over a period of several years. A specific ser. Mbandaka PFGE pattern was first identified in two isolates in 2008, which were temporally and geographically similar. This pattern was later found in 25 additional isolates through 2017, 1-6 isolates per year though not in each year. The PFGE pattern is highly specific to Michigan, found only a few times in other states according to the PulseNet national database. The great majority of patients clustered geographically in Southwest Michigan. Of the 28 cases with the same PFGE pattern, 21 (75%) were female and 6 (21.4%) were hospitalized. The age range was 1–90 years, with a median age of 68 years. In response to several new cases in 2017, epidemiological investigation determined that all but one had exposure to a specific restaurant. A common food or other source could not be identified. **Methods:** WGS was applied to all 6 isolates from 2017 and 17/21 earlier isolates dating back to 2008. High quality single nucleotide polymorphism (hqSNP) analysis (github.com/lskatz/lyve-SET/v.1.1.4f) identified two clades. **Results:** All but one of the 2017 isolates and two isolates from 2015-16 formed a tight clade within 1-6 SNPs. The rest of the pre-2017 isolates formed a second clade within 0-14 SNPs. The two clades differed by 14-24 SNPs with the 2017 clade branching out from the pre-2017 clade. One isolate from a 2017 case reporting no exposure to the restaurant differed from the rest by 84-110 SNPs. **Conclusions:** This study indicates that hqSNP profiles are discriminating and stable enough to link cases from a single source outbreak over a period of 10 years. Slight differences in subtypes among the earlier isolates could be due to evolution of the strain over time. The combination of both laboratory and epidemiological data is necessary to produce the needed evidence to establish interpretation criteria for WGS and link cases with each other and to a possible source.

Board 418. Are Georgia's Non-Typhoidal *Salmonella* Isolates Joining the (Antimicrobial) Resistance?

H. Dishman, M. Tobin-D'Angelo, T. Parrott
Georgia Department of Public Health, Atlanta, GA, USA

Background: More than 2000 cases of non-typhoidal *Salmonella* (NTS) are reported annually in Georgia (GA). Any antimicrobial resistance was detected in 27 (20%) GA NTS isolates submitted to the

National Antimicrobial Resistance Monitoring System (NARMS) in 2015. The proportion of resistance among NTS isolates has increased nationally and international travel may be a risk factor. Infections with resistant NTS may result in more hospitalizations and be more difficult to treat. The Georgia Public Health Laboratory (GPHL) performed whole genome sequencing (WGS) on approximately 1000 selected NTS isolates in 2016 and 2017. We sought to describe sequence-based markers for resistance along with epidemiologic characteristics for a subset of NTS-infected case-patients. **Methods:** GPHL performed WGS using the PulseNet Nextera XT Library Preparation on the Illumina Miseq on 61 2016 and 2017 NTS isolates. WGS results were analyzed utilizing the CLC Genomics Workbench 11.0 (https://www.qiagenbioinformatics.com); its antibiotic resistance database was used to detect antimicrobial resistance genes among a convenience sample of sequenced NTS isolates. Resistance data were merged with NTS epidemiologic data, including hospitalization status, outbreak association, and travel history. **Results:** Sixty-one NTS isolates representing 31 unique serotypes were analyzed. Five (8%) isolates showed any genetic markers for antimicrobial resistance. Resistance markers for more than 1 drug were present in three (5%) isolates. Hospitalization occurred among 26/56 (46%) cases with no resistance and 1/5 (20%) cases with resistance; only 1 death occurred (NTS isolate had no resistance genes). Four (7%) cases with no resistance and no cases with resistance reported international travel. Two cases with no resistance were outbreak-associated. **Conclusions:** This is the first time that markers for antimicrobial resistance among GA NTS isolates were evaluated with corresponding epidemiologic data. Using CLC Genomic Workbench to detect antimicrobial resistance among future NTS isolates from outbreak, international travel, or hospitalized cases could prove useful. Future analyses may be more timely and focused on a specific outbreak or may include a larger sample size and a broader range of exposure variables including previous antimicrobial use.

Board 419. Use of Whole Genome Sequencing during a Multistate Outbreak of Multidrug-Resistant *Campylobacter jejuni* Linked to Pet Store Puppies

L. Joseph[1], L. Francois Watkins[1], J. Chen[2], K. Tagg[2], C. Bennett[2], M. Laughlin[1], L. Koski[3], R. Silver[3], L. Stevenson[4], S. Robertson[1], M. Nichols[1], H. Pouseele[5], H. Carleton[1], K. Hise[1], R. Aubert[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]IHRC, Inc., Atlanta, GA, USA, [3]ORISE, Oak Ridge, TN, USA, [4]CAITTA, Inc., Herndon, VA, USA, [5]Applied Maths, Sint-Martens-Latem, Belgium

Background: *Campylobacter jejuni* is a leading cause of bacterial illness in the United States. Pulsed-field gel electrophoresis (PFGE) has been used for *Campylobacter* surveillance and outbreak investigation; however, we are implementing whole genome sequencing (WGS) for surveillance/outbreak investigation. In 2017, CDC and state health departments investigated a multistate outbreak of campylobacteriosis linked to pet store puppies. We used whole genome multi-locus sequence typing (wgMLST) to link outbreak-associated human and canine *C. jejuni* isolates and used WGS data to predict the antimicrobial susceptibility of these isolates. **Methods:** Human and canine *C. jejuni* isolates were sequenced using the Illumina MiSeq. wgMLST analysis of the sequences was performed in BioNumerics 7.6. ResFinder 3.0 was used to determine the predictive resistance from the sequences. Antimicrobial susceptibility testing (AST) was performed using the broth microdilution method. PFGE was performed on a subset of isolates using the PulseNet *Campylobacter* protocol and the patterns were analyzed in BioNumerics 6.6.10. **Results:** The wgMLST analysis differentiated epidemiologically linked isolates from PFGE-indistinguishable sporadic isolates and separated the outbreak isolates into three clades. Clade 1 contained four clinical isolates from four states. Clade 2 contained 11 clinical isolates from six states. Clade 3 contained 18 clinical isolates from 11 states and nine canine isolates from two states. Five PFGE patterns were produced by isolates in clades two and three. All isolates were multidrug resistant using WGS data that was confirmed by AST. **Conclusions:** Our study showed that wgMLST analysis provided greater resolution and epidemiological concordance compared with PFGE during this outbreak investigation. Predicted resistance results were comparable to AST and were available in real-time. This study demonstrated the power of WGS data for linking outbreak-associated *C. jejuni* isolates and determining the antimicrobial resistance profiles of these isolates in a single workflow.

Board 420. Genetic Diversity in Non-O157 Shiga Toxin-Producing *Escherichia coli* (STEC) and Clustered Regularly Interspaced Palindromic Repeat (CRISPR) Spacer Variation

H. Blankenship[1], R. Mosci[1], J. Rudrik[2], S. Manning[1]
[1]Michigan State University, East Lansing, MI, USA, [2]Michigan Department of Health and Human Services, Lansing, MI, USA

Background: STEC is a leading cause of foodborne infections in the U.S. While O157:H7 is commonly associated with illness, non-O157 serotypes have increased in frequency from clinical samples. The CRISPR spacers are thought to contain information regarding genomic elements and bacteriophages that have entered the cell. However, the CRISPR region does not actively acquire spacers in STEC, presenting an ideal target for further assessing the diversification of isolates along with multi-locus sequence typing (MLST). We therefore sought to examine genetic variation among non-O157 isolates collected in Michigan, which is important given that Michigan is not included in the FoodNet surveillance system. **Methods:** Clinical STEC isolates were obtained from the MDHHS via sentinel surveillance in 2001-2005 (n=41) and active surveillance in 2010-2014 (n=380). Whole genome sequencing was performed and genomic elements were extracted for serotyping (O and H antigen), MLST and CRISPR analysis through the use of bioinformatic scripts, CRISPRFinder and Geneious. Phylogenetic analysis performed using the Neighbor-joining algorithm and the unweighted pair group method with arithmetic mean (UPGMA) with Jaccard similarity coefficient. **Results:** The frequency of isolates comprising the "big-six" non-O157 serogroups was similar in 2001-2005 (73.2%) and 2010-2014 (72.4%), while 11 and 24 additional serogroups were detected in these time periods, respectively. MLST identified 7 of the 22 serogroups to belong to different STs located on different branches of the Neighbor-joining phylogeny. A total of 23 unique CRISPR spacer profiles were found in the subset of 41 strains evaluated. The UPGMA tree defined 9 unique clusters based on CRISPR profiles and exhibited similar clustering of strains as identified in MLST analysis. Two CRISPR spacers, 231 and 317, were isolated from 62.4% of strains regardless of serogroup and ST. **Conclusions:** This data highlights the high degree of diversity among STEC isolates linked to clinical infections over a long period of time, and demonstrate that CRISPR profiling can be used to further discriminate strains along with MLST. Understanding the genetic diversity of non-O157 strains associated with disease is required to help identify characteristics and lineages associated with disease and to identify new ways to combat infections.

Board 421. Genomic Concordance of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Clinical and Colonization Isolates from US Army Trainees with Skin and Soft Tissue Infection

E. Millar[1], G. Rice[2], C. Schlett[1], E. Elassal[1], R. Cer[2], K. Frey[2], T. Hamilton[2], M. Ellis[3], K. Bishop-Lilly[2], D. Tribble[1], J. Bennett[4]
[1]Infectious Disease Clinical Research Program, Department of Preventive Medicine and Biostatistics, Uniformed Services University of the Health Sciences, Bethesda, MD, USA, [2]Biological Defense Research Directorate, Naval Medical Research Center, Ft. Detrick, Frederick, MD, USA, [3]College of Medicine and Life Sciences, University of Toledo, Toledo, OH, USA, [4]Department of Medicine, Uniformed Services University of the Health Sciences, Bethesda, MD, USA

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of skin and soft tissue infection (SSTI). Military recruits are at increased risk for MRSA SSTI and colonization. The intrahost relatedness between MRSA clinical and colonization isolates among individuals with SSTI is incompletely understood. **Methods:** From 2010-2012, we conducted a prospective case-control study of SSTI among US Army Infantry trainees at Fort Benning, enrolling as cases those who presented to the troop medical clinic with purulent SSTI. Clinical swabs were collected from cases with purulent SSTI. Colonization swabs of the nasal, oral, inguinal, and perianal regions were collected at the same visit. *S. aureus* culture and susceptibility was performed by standard methods. DNA extraction of all isolates was performed using the Wizard Kit (Promega) and libraries were produced using the Nextera XT DNA Library Preparation Kit (Illumina). Libraries were sequenced on an Illumina MiSeq (2x300 base-pair). Single nucleotide variant (SNV) data were analyzed using the Bacterial and Archaeal Genome Analyser. USA300 strain TCH1516 was selected as the reference. **Results:** Of 74 trainees with MRSA SSTI, 19 (25.7%) were colonized with MRSA at the time of clinical presentation. The most frequent diagnoses were purulent cellulitis (73.7%) and abscess (57.9%), with the majority (63.2%) of infections occurring on the lower extremities. A total of 36 MRSA colonization isolates were identified. The frequency of colonization by anatomic site was as follows: inguinal region (33%), nares (30%), perianal region (22%), and throat (14%). Ten (52.6%) individuals were colonized at more than one anatomic site; two (10.5%) individuals were colonized at all four anatomic sites. The overall median (range) number of SNVs among MRSA colonization isolates was 123 (83-19,382). At the intrahost level, the median (range) number of SNVs between clinical and colonization isolates was 17 (1-19,396). There were no significant differences in the intrahost relatedness of clinical and colonization isolates when stratified by anatomic site. **Conclusions:** Genomic characterization of MRSA clinical and colonization isolates among military trainees with SSTI revealed limited intrahost diversity (i.e. high degree of strain relatedness), suggesting that single acquisition events account for MRSA colonization and infection in this population.

Board 422. The European Survey of Carbapenemase-Producing Enterobacteriaceae (EuSCAPE) Reveals Widespread Emergence of Carbapenem Resistance in Diverse Genomic Backgrounds of *Klebsiella pneumoniae*

S. David[1], S. Reuter[2], S. Harris[3], C. Glasner[4], V. Cohen[1], S. Argimon[1], T. Feltwell[3], T. Giani[5], M. Aspbury[6], G. Rossolini[5], E. Feil[6], H. Grundmann[2], D. Aanensen[1]
[1]Centre for Genomic Pathogen Surveillance, Cambridge, United Kingdom, [2]Freiburg University Medical Centre, Freiburg, Germany, [3]Wellcome Sanger Institute, Cambridge, United Kingdom, [4]University of Groningen, Groningen, Netherlands, [5]University of Florence, Florence, Italy, [6]University of Bath, Bath, United Kingdom

Background: Carbapenemase-producing *Enterobacteriaceae* (CPE) are listed by the World Health Organization amongst the top priority bacterial pathogens for which new antibiotics are needed. To investigate their diversity, spread and resistance dynamics, we analyzed genomes of 1717 *K. pneumoniae* isolates collected by 244 hospitals in 32 countries during a six-month European survey of CPE (EuSCAPE). 944/1717 (55.0%) and 773/1717 (45.0%) were submitted as carbapenem-resistant and –susceptible, respectively. **Methods:** All isolates were sequenced using Illumina HiSeq. A core gene alignment was used for phylogenetic analysis. Sequence types (ST) and the presence/absence of carbapenemase genes were determined including *Klebsiella pneumoniae* carbapenemase, New Delhi metallo-beta-lactamase 1-like, Verona integron-encoded metallo-beta-lactamase and oxacillinase 48-like genes. The resistance plasmid repertoire was characterized using PacBio sequencing of >80 isolates with evidence of unique carbapenemase backgrounds, followed by mapping of all Illumina reads to the newly sequenced plasmids. **Results:** Carbapenemase-producing isolates are distributed widely across the phylogeny and interspersed amongst susceptible isolates. However, 436/651 (67.0%) carbapenemase-producing isolates belong to 5 clonal "high-risk" STs (11, 15, 101, 258, 512), which harbor a variety of carbapenemase-containing plasmids. We found strong geographical clustering of carbapenem-resistant isolates e.g. 445/944 (47.1%) resistant isolates are most similar to another isolate from the same hospital. By combining our data with public genomes, we have mapped the international spread of the epidemic ST258/512 lineage and propose a cutoff for the number of single nucleotide polymorphisms (SNP) that discriminate institutional outbreaks. **Conclusions:** This study demonstrates numerous independent emergences of carbapenem resistance in *K. pneumoniae* mediated by horizontal transfer of diverse plasmids. The finding of different resistance plasmids within single "high-risk" STs highlights the importance of genetic background in determining success. Spread of resistance is deeply connected to movement of people, who travel more within rather than between countries and are referred within national healthcare networks.

Board 423. A Longitudinal Birth-Cohort Study for Norovirus Infections in Children ≤2 Years of Age From Resource-Constrained Communities in Peru

P. Chhabra[1], S. Rouhani[2], H. Browne[3], M. Kosek[2], P. Peñataro Yori[2], M. Salas[4], M. Olortegui[5], J. Vinje[6]
[1]Synergy America, Inc, Atlanta, GA, USA, [2]Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, USA, [3]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [4]AB PRISMA, Investigacion Biomedica, Iquitos, Peru, [5]AB PRISMA,

Investigacion Biomedica, Iquitos, Peru, [6]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Malnutrition affects nearly 20% of children in the developing world. Enteric pathogens play a crucial role in developing malnutrition. There is little information on the relationship between malnutrition, norovirus infections, and the role of genotype or immunotype cross-protection after norovirus infections in young children. **Methods:** Methods: From January 2010-February 2014, 304 children in rural Peru were enrolled within the first 17 days of life and followed up to 24 months of age. Home visits were done twice weekly and stool samples were collected from all participants each month until 1 year of age and at 15, 18, 21, and 24 months of age while diarrheal stools were collected from each episode of diarrhea (n=y). Routine and diarrheal stool samples from 294 children were tested for norovirus GI/GII by RT-qPCR followed by sequence-based dual genotyping (region B-C) of positive samples. **Results:** In total, 241(82%)/294 children had at least one episode of norovirus diarrhea. Out of 4031 samples, 1298 (32.2%) tested positive for norovirus. GII infections were more common (972 [74.8%] /1298) that GI infections (271 [20.8%]). GI and GII mixed infections were identified in (55(4.2%)/1298) samples. Of 1298 norovirus positive samples, 1075 (83%) samples were genotyped by dual-typing assay. Multiple different dual-genotypes including 10 GI (GI.P1-GI.1, GI.P2-GI.2, GI.P3-GI.3, GI.P4-GI.4, GI.P5-GI.5, GI.P6-GI.6, GI.P7-GI.7, GI.P8-GI.8, GI.P9-GI.9 and GI.Pd-GI.3) and 21 GII (GII.P2-GII.2, GII.P4New-Orleans(NO)-GII.4NO, GII.P7-GII.5, GII.P7-GII.6, GII.P7-GII.7, GII.P8-GII.8, GII.P13-GII.17, GII.P16-GII.3, GII.P17-GII.17, GII.P22-GII.5, GII.P23-GII.23, GII.P24-GII.24, GII.P25-GII.25, GII.Pe-GII.17, GII.Pe-GII.4NO, GII.Pe-GII.4Sydney, GII.Pe-GII.4, GII.Pe-GII.7, GII.Pg-GII.1, GII.PNA1-GII.NA1, GII.PNA2-GII.NA2, and GII.PNA4-GII.17) genotypes were detected. GII.4 was the predominant genotype circulating. Re-occurrence of norovirus infection with same genotype was found as early as 5 month after the date of first infection. **Conclusions:** These data demonstrate that children in this cohort were exposed to multiple different genotypes within the first 2 years of life. These data suggest that a future norovirus vaccine that includes only 1 GI and 1 GII genotype may not be effective in malnourished children in resource-constrained communities.

Board 424. Outbreaks of Acute Gastroenteritis Associated with a Re-emerging GII.P16/GII.2 Norovirus in the 2016/17 Season in China

M. Jin[1], Y. Ao[1], J. Wang[1], X. Cong[1], X. Sun[1], A. CaliciNet China[2], Z. Duan[1], L. Li[1], L. Pang[1], J. Li[1]
[1]National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China, [2]Local CDCs, Beijing, China

Background: While the GII.4 noroviruses have been predominant worldwide for the past decades, two epidemics were caused by rarely detected variants in China recently. During 2014/2015 winter season, a new GII.17 variant emerged and surpassed the GII.4 virus in causing significantly increased outbreaks. It is very important to establish a sensitive norovirus surveillance network for the prevention and control of the norovirus epidemics in China. **Methods:** CaliciNet China, the outbreak surveillance network for noroviruses, was launched in 2016 to monitor the epidemiology and molecular characteristics of norovirus outbreaks, and to identify the emerging strains associated with norovirus outbreaks in China. The model of four-level network (national-provincial-municipal-district) labs has been developed and 10 network labs has been developed and certified as members of CaliciNet China in the first year. **Results:** During October of 2016 and September of 2017, 277 outbreaks were submitted to CaliciNet China. The outbreaks occurred in childcare center (57%), school and community (39%) and other settings (4%). The outbreak peak was different in Guangdong (December), Jiangsu (February) and Beijing (March). A total of 249 (89.9%) outbreaks were typed as GII.P16/GII.2, which first emerged in October 2016. Phylogenetic analysis suggests that this reemerging GII.P16-GII.2 lineage most likely evolve from the GII.P16-GII.2 (2011-2012) virus. Sequence analysis, saliva-binding profile, and crystal structure suggests the lack of antigenic and HBGA binding changes of the viruses. The minor changes in the nonstructural protein might have driven the pandemic of this GII.P16-GII.2 virus. **Conclusions:** CaliciNet China is a good tool to improve surveillance capacity for norovirus outbreaks. The re-emerging GII.P16/GII.2 recombinant became dominant for norovirus outbreaks in China in 2016/2017. Continuous surveillance is needed to explore the epidemiologic, clinical, and evolutionary characteristics of this GII.P16-GII.2 strain and new variant of other genotypes.

Board 425. Emerging Norovirus Recombinant Strains Causing Outbreaks in the United States

L. Barclay, J. Cannon, A. Phillips, J. VInjé
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Noroviruses are the most frequent cause of epidemic acute gastroenteritis in the United States. Since 2009 outbreak surveillance is conducted by CaliciNet, which collects limited epidemiologic info and genotype data. Traditionally, noroviruses are genotyped by amplifying sequences of a partial region of the capsid gene. However, in recent years several recombinant strains have emerged which prompted us in June 2016 to implement a new polymerase-capsid typing scheme nationwide to better understand the frequency and clinical importance of recombinant noroviruses. **Methods:** A new laboratory protocol to obtain polymerase and capsid typing was performed on samples, retrospectively and prospectively by the CaliciNet laboratories. Updated and new typing data were uploaded to CaliciNet. CaliciNet data were downloaded into Microsoft Excel and analyzed with Microsoft Excel and R. **Results:** From September 2013 through February 2018, 3,768 confirmed norovirus outbreaks were submitted to CaliciNet. GII.4 Sydney viruses caused 58% of the outbreaks during the study period. In 2013, most GII.4 Sydney viruses harbored a GII.Pe polymerase and in November 2015 a new GII.4 virus emerged which had a GII.P16 polymerase. This new recombinant virus caused 60% of all GII.4 outbreaks in 2015-2016 and 93% in the 2016-2017 season. Several other genotypes that circulated were also associated with more than one polymerase type. GII.P16 polymerase sequences associated with co-circulating GII.2 and GII.4 Sydney viruses during September 2016-February 2018 were nearly identical, suggesting common ancestry. Other common genotypes, each causing 4-19% of outbreaks in a season, included GI.3, GI.5, GII.2, GII.3, GII.6, GII.13, and GII.17 Kawasaki. **Conclusions:** Acquisition of alternative RNA polymerases by recombination is an important mechanism for norovirus evolution and a phenomenon that occurs more frequently than previously recognized in the United States. Continued molecular surveillance of noroviruses, including typing of both polymerase and capsid genes, is important for monitoring emerging strains in our continued efforts to reduce the overall burden of norovirus disease.

Board 426. Distinguishing Circulating Type 2 Vaccine-Derived Polioviruses (VDPVs) from Immunodeficiency-Associated VDPVs

K. Zhao[1], J. Jorba[1], J. Shaw[1], J. Iber[1], Q. Chen[1], K. Bullard[2], O. Kew[1], C. Burns[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]IHRC, Inc., Atlanta, GA, USA

Background: The Global Polio Eradication Initiative has reduced the number of annual paralytic polio by >99.9%, from an estimated 350,000 cases in 1988 to 22 wild poliovirus (WPV) cases and 91 circulating vaccine-derived poliovirus (cVDPV) cases in 2017. These case numbers suggest that the risk of infection with VDPV strains outweighed the risk of infection with naturally occurring WPV in 2017. As all poliovirus circulation must be detected and interrupted, public health response to cVDPV, which is transmitted from person to person, differs significantly from response to virus that replicates in individuals with primary immunodeficiency (immunodeficiency-associated VDPV [iVDPV]). cVDPV outbreaks require a community immunization response, whereas iVDPV chronic infections require careful patient monitoring and appropriate individual treatment. **Methods:** To support poliovirus outbreak response, particularly for type 2 VDPV, we previously investigated the genetic distinctions between cVDPV2 and iVDPV2 complete VP1 capsid coding region sequences using a comparative genomic approach and statistical modeling. In this study, we extended this analytic approach to complete capsid sequences. **Results:** We observed that simple genetic measurements of nucleotide and amino acid substitutions are sufficient for distinguishing highly divergent iVDPV2 from cVDPV2 sequences, but are insufficient to make a clear distinction between the two categories among less divergent sequences. **Conclusions:** Genetic variations between cVDPV2 and iVDPV2 may reflect differences in viral micro-environments, host-virus interactions, and selective pressures during person-to-person transmission compared with chronic infections in immunodeficient patients. We present quantitative approaches using genetic information as a surveillance tool for early detection of cVDPV outbreaks.

Board 427. Genetic Characterization of Parapoxviruses (PPVs) Circulating in Sheep, Goats, and Dromedary Camels in Eastern Sudan, 2016

A. Khalafalla
Abu Dhabi Food Control Authority (ADFCA), Abu Dhabi, United Arab Emirates

Background: Parapoxviruses (PPVs) are zoonotic viruses, which belong to the family *Poxviridae.* For decades PPVs have been known to cause contagious ecthyma in different animal species around the world. Outbreaks of contagious ecthyma have been frequently reported in sheep, goat, and camels the Sudan. However, little is known about the PPV circulating in animals sharing the same pasture and whether a cross-species transmission exists or the infection is caused by genetically different PPV species. **Methods:** PCR was utilized to amplify the B2L gene of the PPV directly from clinical specimens collected from sheep, goats, and dromedary camels affected with contagious ecthyma in eastern Sudan in 2016. Representative PCR products (two each from sheep *[SPPV]*, goats *[GPPV],* and camels *[CPPV]*) were sequenced and subjected to genetic analysis. **Results:** BLAST search revealed that the studied SPPV and GPPV isolates belong to the ORFV species of the PPV genus while the CPPV isolates are closer to the *Pseudocowpox virus* (PCPV) species. The SPPV isolates shared 99.08% nucleotide sequence intragroup identity, 96.88 - 97.27% identity with the GPPV isolates, yet 92.51 - 93.62 % identity with the CPPV isolates. On the phylogenetic tree the SPPV and the GPPVs grouped in one branch together with Orf virus (ORFV) from goats and reindeer, while the CPPVs clustered close to PCPVs from cattle and the other CPPVs published earlier. **Conclusions:** The present study uncovered that the CPPV circulating in eastern Sudan is closely related to the PCPV, but genetically distant to ORFV that affecting sheep and goats in the same environment. The ORFVs that originate in sheep and goats in this geographic area displayed minimal interspecies genetic variation. The investigation helps in our understanding of the diversity of PPV strains in Sudan and their association with other strains globally.

Laboratory Capacity

Board 428. Clinical Diagnostic "Lab-in-a-Pack" for Disease Surveillance and Outbreak Response in LMICs

V. Meka, M. Leffler, J. Fluder, A. Waite
USAID, Washington DC, DC, USA

Background: Many low- and middle-income countries (LMICs) do not have sufficient capacity to address disease outbreaks. Laboratory infrastructure is often inadequately equipped and understaffed. As observed during the Ebola, Zika, and plague outbreaks, this can result in a time lag from sample collection to testing to diagnosis that can be weeks, if not months. Such delays can mean the difference between an outbreak and an epidemic. It is therefore vital to equip health workers with clinical diagnostic tools that will enable them to screen individuals and take prompt actions to prevent disease transmission. Mobile lab concepts have been piloted previously in LMICs with limited success. To increase the chances of adoption, USAID used the principles of Human Centered Design (HCD) to create new concepts of "lab-in-a-pack." **Methods:** Literature review and interviews with experts in infectious diseases, outbreak response, and laboratories shed light on previously piloted mobile labs. Principles of HCD were applied to gain a nuanced understanding of workflows and design criteria across a variety of settings. The "lab-in-a-pack" concepts were developed through a combination of expert interviews and co-design workshops with end users in India. **Results:** Two promising "lab-in-a-pack" design concepts were created: Portable Pack and Mobile Pack. The Portable Pack is a stackable, modular design that can be set up quickly and serves as a temporary stationary lab. It can be transported using a dolly and is built to enable response teams within LMICs to deploy a functional lab to the location of a contagious disease outbreak. The Mobile Pack is a lab inside of a backpack that is built for individual health workers to carry for extended periods and support their surveillance activities. Both concepts allow point-of-care testing and access to power and cellular connectivity. **Conclusions:** There was consensus among experts and end users on the need for a rapidly deployable clinical diagnostics laboratory that can be used both during a disease outbreak and routine surveillance in LMICs. The "lab-in-a-pack" concepts bring clinical laboratory capabilities where they are needed, and will not only help with diagnosis and disease confirmation, but will also support clinical testing to assess patient prognosis. The concepts are available to interested innovators seeking to further the advancement of a mobile clinical diagnostic laboratory.

Board 429. Establishment and Use of Field Forward Diagnostic Laboratories and Assays for Viral Pathogens during Outbreaks

G. Olinger[1], L. Presser[1], A. Parsons[2], P. Matero[3], D. Roberts[4], K. Yeh[1]
[1]MRIGlobal, Gaithersburg, MD, USA, [2]BIA Diagnostics, Colchester, VT, USA, [3]Aatos Consulting & Training, Vantaa, Finland, [4]MRIGlobal, Palm Bay, FL, USA

Background: Clinical viral assays are often designed to be conducted in well-established and controlled laboratory environments. Unfortunately, outbreaks, especially those caused by high consequence viral pathogens occur in regions of the world that have limited or no laboratory capabilities. The result is a mix of laboratories with capabilities ranging from point of care assays to retrofitted laboratory spaces. The most desired approach is often modifying existing laboratories or small buildings by physical means or by practices that allow for safety requirements needed to conduct viral diagnostic tests. On the other end of the spectrum, laboratory capability continues to be brought closer to the patient. Mobile and field transportable laboratories have long been used by military and defense, law enforcement, environmental monitoring, and health related agencies. With the advent of technology that has enabled the use of diagnostic instruments in the field, in addition to transportation capabilities to rapidly deliver these assets and services, mobile and field units have served to further extend networks of existing, fixed laboratories. **Methods:** The purpose of this poster is to present an objective review of laboratory capability and assays that enable rapid diagnosis of patients during an outbreak in austere conditions. The work is presented through our team's case history and review of literature that include various international partner response efforts from the 2014-2016 Ebola virus outbreak. **Results:** Our results include an examination and comparison of the respective cost and sustainment challenges of operating and maintaining retrofitted or mobile laboratories. **Conclusions:** Lessons learned and recommendations for the practical use and deployment of these important assets during an outbreak will be addressed in conclusion.

Board 430. Utilizing Local Collaborations to Gain Capacity in Bioinformatics

W. Manley[1], N. Blouin[2], V. Chhatre[2], K. Sondgeroth[3], L. Fink[4], J. Sevinsky[4], N. Hull[1], S. Buss[1]
[1]Wyoming Public Health Laboratory, Cheyenne, WY, USA, [2]University of Wyoming, Laramie, WY, USA, [3]Wyoming State Veterinary Laboratory, Laramie, WY, USA, [4]Colorado Department of Public Health and Environment, Denver, CO, USA

Background: In 2016 the Wyoming Public Health Laboratory (WPHL) utilized AMD funding to establish a collaboration with the University of Wyoming's, INBRE Bioinformatics Core (UWIBC) for bioinformatics training and support. WPHL has whole genome sequencing (WGS) capacity but no internal bioinformatics expertise, whereas UWIBC has bioinformatics expertise and no internal WGS capacity. The Wyoming State Veterinary Laboratory (WSVL) regularly works with both WPHL and UWIBC. Collaboration between all three facilities naturally arose as a consequence of the formalized WPHL-UWIBC relationship. **Methods:** The WPHL received human derived specimens for identification or further typing of bacterial pathogens. Bacterial identification was performed via biochemical analysis and / or 16S rDNA sequencing. WGS of enteric pathogens was conducted using PulseNet protocols and the MiSeq instrument. The WSVL received specimens from animals for pathologic investigation and / or identification of bacterial pathogens. Bacterial identification was performed via biochemical analysis and / or MALDI-TOF mass spectrometry. When necessary, WSVL referred isolates to WPHL for WGS analysis. The WPHL shared Fastq files with UWIBC from Illumina's BaseSpace and sequences were uploaded to NCBI. UWIBC performed sequence assembly and analysis. Assembled sequences were queried in GenBank and findings shared with both WPHL and WSVL. **Results:** An investigation launched by the WSVL resulted in identification of *Pasturella multocida* in two domesticated Bison calves. Via the collaborative effort the organism was able to be linked to a strain from domestic turkeys. Cases of *Salmonella* and *Campylobacter* in humans and animals have also been linked via the collaboration. **Conclusions:** Facilities that lack internal bioinformatics expertise can exploit regional resources to obtain the support externally. The collaboration between the WPHL and the UWIBC has resulted in enhanced capabilities for the State of Wyoming. The WPHL is able to refer to the UWIBC for bioinformatics analysis and expertise, and utilize UWIBC staff for development of internal bioinformatics knowledge. Additionally, a One-Health framework has been established in the state of Wyoming via collaborations between the WPHL, WSVL and UWIBC.

Board 431. Building Next-Generation Sequencing Capacity in Ghana--Successes, Challenges, and Future Directions

R. Marine[1], N. Ntim[2], K. Attiku[2], C. Walker[1], W. Gatei[1], P. Rota[1], M. Oberste[1], W. Ampofo[2], A. Balajee[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Department of Virology, Noguchi Memorial Institute for Medical Research, Accra, Ghana

Background: Public health laboratories worldwide are keen to adopt next-generation sequencing (NGS) methods for surveillance and rapid characterization of pathogens during outbreaks. In Ghana, the Noguchi Memorial Institute for Medical Research (NMIMR) is a reference laboratory for polio, rotavirus, and influenza surveillance, and provides additional testing capabilities for the national public health laboratory. NMIMR acquired an NGS platform in October 2016, but lacked the expertise needed to prepare samples and analyze resulting data. As part of CDC's Global Health Security Agenda activities, the Division of Viral Diseases provided technical assistance and training to NMIMR towards building a working core NGS laboratory. **Methods:** A three-tiered approach was used for building NGS proficiency. First, NGS experts from CDC visited NMIMR to discuss priority NGS projects and formulate a training schedule. In July 2017, two scientists from the Virology Department at NMIMR travelled to CDC for a three-week training in NGS laboratory procedures and data analysis. NGS reagents were provided by CDC as part of the capacity building effort. In September 2017, a two-week training course was held on-site at NMIMR for a larger cohort of scientists. **Results:** Feedback from pre- and post-training surveys indicated that hands-on training with validated laboratory protocols and bioinformatics exercises, using previously generated viral NGS data, were helpful for learning NGS procedures. In addition, six enterovirus (EV) isolates from acute flaccid paralysis cases in Ghana were successfully sequenced during the NMIMR on-site training. These genomes provide increased knowledge on circulating EVs, and included a genotype (EV-B84) for which few sequences have been reported. Challenges met during the training program in Ghana included a lack of reliable internet access for analysis of NGS data, and effective remote support for technical/mechanical troubleshooting. **Conclusions:** The progress demonstrated provides evidence

that NGS activities can be sustained at NMIMR through mentorship by CDC and other partners, and incremental expansion of capacity. Future NGS projects include investigation of specimens where standard diagnostic assays could not identify an agent, such as unexplained acute hemorrhagic fever syndromes and suspected zoonotic infections.

Board 432. FoodCORE Centers Demonstrate Improvements in Isolate Testing during a Shift in Laboratory Techniques for Enteric Disease Surveillance

F. Roldan, E. Sillence, A. Newton, G. Biggerstaff
Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: In 2009, CDC started the Foodborne Diseases Centers for Outbreak Response Enhancement (FoodCORE) program to improve the completeness and timeliness of laboratory, epidemiology, and environmental health activities for foodborne disease surveillance and outbreak response. Laboratory subtyping of *Salmonella*, Shiga toxin-producing *Escherichia coli* (STEC), and *Listeria* (SSL) is one critical piece to detecting and solving foodborne disease outbreaks. Public health laboratories in the United States are moving to primarily using whole genome sequencing (WGS) as it is more precise and offers greater detail than traditional subtyping methods like pulsed-field gel electrophoresis (PFGE). However, PFGE is being maintained while the transition to WGS occurs. **Methods:** Centers submit SSL isolate/specimen-based metrics biannually to evaluate completeness and timeliness of surveillance and subtyping data. In Year 6 (Y6, 1/1/2016–12/31/2016), centers pilot-tested a set of expanded SSL metrics to capture percent of primary isolates with WGS/PFGE results (completeness) and time from sequencing/completion of PFGE to upload to a national database (timeliness). The expanded metrics went into effect in Year 7 (Y7, 1/1/2017–12/31/2017). **Results:** From the start of Y6 to July 2017, centers reported a total of 14,471 primary SSL isolates/isolate-yielding specimens and maintained the percentage of SSL isolates with complete PFGE information at 94.6%. WGS completeness varied by pathogen. During Y6, WGS was performed on 40.2% of *Salmonella*, 64.2% of STEC, and 97.7% of *Listeria* isolates. Among all SSL isolates, the proportion with WGS information increased from 45.2% in Y6 to 86.2% during 1/1/2017–7/31/2017. From the start of Y6 to July 2017, the average time from completion of PFGE to upload to a national database stayed constant at 2.4 days; the average time from sequencing to upload to a national database decreased from 12.0 days to 9.0 days. **Conclusions:** As centers transition from PFGE to WGS, they continue to maintain timeliness and completeness of PFGE while demonstrating improvements in enteric disease outbreak surveillance and response activities using WGS, leading to faster and more complete investigations to help stop the spread of enteric diseases.

Board 433. Withdrawn

Board 434. Performance of NIC, Afghanistan, for Isolating and Sharing Influenza Virus Isolates during 2015-17

Nasir Stanikzai
Central Public Health Laboratories/CPHL-MoPH, Kabul, Afghanistan

Background: Influenza surveillance was re-initiated in 2014 in Afghanistan by establishing nine (9) sentinel sites that collect specimens and epidemiological data on weekly basis from severe acute respiratory illness (SARI) and influenza-like illness (ILI) cases. NIC Kabul was established and recognized by WHO in 2009 with the support of US-NAMRU-3. However, it was non-functional since 2012 for virus isolation after the NAMRU-3 support had ended. Virus isolation work was re-initiated in September 2015 and NIC for the first time isolated and shipped three influenza virus isolates in December 2015 to WHO CC in CDC Atlanta on its own efforts. **Methods**: Altogether between December 2015 and September 2017, 35 influenza virus isolates, 1 non-influenza virus (unidentified), and 120 original samples were shipped to the WHO CC in 7 shipments. All influenza virus isolates sent to WHO CC were reconfirmed, and studies showed that these circulating viruses matched with globally circulating influenza viruses and were sensitive to the common antivirals. CDC also isolated two additional influenza-A (H3N2) isolates in MDCK-SIAT-1 cell line. Isolates in all were influenza-A (H1N1, pdm09) - 14, influenza-A (H3N2) - 5, influenza-B (Victoria lineage) – 11, and influenza-B (Yamagata lineage) - 7 isolates. With this, a database of circulating influenza virus isolates has been documented in Afghanistan. NIC also tested specimens received in 2015-17, by Real Time PCR (1421 samples in 2015, 3123 in 2016 and 2179 in 2017 15 November) and no unsubtypeable influenz-A results were detected in the country. **Results**: Afghanistan NIC passed WHO proficiency EQAP panels with 100% scores for 2015, 2016 and 2017. Results were uploaded in global influenza databases of FluNet, FluID, and EMFLU regularly. Currently, a fully independent and functional NIC is in place for Afghanistan although there are many challenges in addition to the security situation in the country. **Conclusions**: Afghanistan NIC passed WHO proficiency EQAP panels with 100% scores for 2015, 2016 and 2017. Results were uploaded in global influenza databases of FluNet, FluID, and EMFLU regularly. Currently a fully independent and functional NIC is in place for Afghanistan although there are many challenges in addition to the security situation in the country.

Board 435. Lebanese NIC Roadmap: Achievement and Future Improvement Plan

M. AlBuaini[1], N. Jammal[1], L. Mroueh[1], P. Zalloua[1], F. Abiad[1], P. Mrad[2], A. Rady[2], N. Ghosn[3], W. Ammar[3]
[1]Rafic Hariri University Hospital, Beirut, Lebanon, [2]World Health Organization, Beirut, Lebanon, [3]Ministry of Public Health, Beirut, Lebanon

Background: The National Influenza Center (NIC) was established in 2015 at Rafic Hariri University Public Hospital. NIC objectives are to analyze clinical specimens for influenza, contribute to national preparedness plan, and contribute to the Global Influenza Surveillance Network. The NIC benefited from World Health Organization (WHO) support under Pandemic Influenza Preparedness framework. In 2017, WHO assessment mission highlighted activities to move forward for external quality control and initiation of virologic culture. **Methods:** NIC capacity was enhanced via trainings and development of procedures for better laboratory practice. Nasopharyngeal and oropharyngeal swabs were collected from patients meeting WHO case definition of severe acute respiratory infection, from 12 sentinel hospitals. Specimens were conserved in viral transport media. At NIC, specimens were extracted by high pure viral nucleic acid kit, and tested on ABI 7500, using CDC kits for Influenza virus real-time-polymerase chain reaction (PCR) influenza A/B types, influenza H3/H1 pdm09 subtypes, and influenza B lineage genotypes. Results were shared with surveillance team and sentinel hospitals via paper then via electronic platform. Mechanism was set to share positive isolates with WHO Collaborat-

ing Centers (WHO-CC). NIC staff was certified for specimen transportation and shipment as per International Air Transport Association Regulations. **Results:** Since January 2015 to February 2018, the NIC tested 3292 clinical specimens for influenza. 94% were from sentinel hospitals, 6% from critical patients and <1% related to A(H5N1) poultry outbreak containment. Sixteen percent of PCR tests were influenza positive. Among the positive samples, 46% were influenza A and 54% B. Of the samples positive for influenza A, 69% were A(H3N2) and 31% A(H1N1) pandemic2009. Of the samples positive for influenza B, 23% were Yamagata, 2% Victoria, and 75% not typed. Results were shared with WHO via FLUNET platform. The number of shared isolates with WHO-CC was 9 in 2016, 4 in 2017 and 10 in 2018. In January 2018, 5 isolates were timely shared before WHO Vaccine Composition Meeting. **Conclusions:** Progressively, the NIC is fulfilling needed indicators: conducting PCR tests, sharing data and isolates.

Board 436. Expanding a Trans-Atlantic Quality Assurance Laboratory Mentor Program

M. Warren[1], L. Igboh[2], P. Blevins[3], H. Charest[3], S. Emery[2], J. Getchell[3], E. Reisdorf[3], D. Sowa[4], N. Tavakoli[3], A. Tate[1], K. Wu[2]
[1]Association of Public Health Laboratories, Silver Spring, MD, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]APHL, Silver Spring, MD, USA, [4]CDC, Freetown, Sierra Leone

Background: In July 2017, the Centers for Disease Control and Prevention (CDC) and the Association of Public Health Laboratories (APHL), with collaboration from the World Health Organization Regional Office for Africa (WHO AFRO), held a kick-off meeting in Kigali, Rwanda, to establish a 2nd iteration of the Influenza Laboratory Quality Assurance Mentoring Program. The program was modeled off of an initiative pairing APHL consultants with national influenza laboratories in Europe. The primary goal of the mentorship is to help laboratories that are not currently WHO National Influenza Centers (NIC) achieve WHO NIC recognition while implementing a quality monitoring system (QMS) that can be applied to testing for other respiratory pathogens. **Methods:** APHL selected 11 mentors from CDC and public health laboratories with influenza and quality management expertise. Laboratories from ten African countries were selected as mentees based on their activities pursuing WHO NIC recognition and needs for quality assurance laboratory strengthening. Mentors and countries developed a QMS action plan feasible to accomplish one year. Action items were selected from multiple sources including the WHO NIC Terms of Reference and recommendations from previous laboratory assessments addressing quality management weaknesses. **Results:** Mentor pairs established regular communication and document progress on QMS action plans. Mentors, APHL and CDC convened quarterly calls to share challenges and lessons learned. Participants utilized an electronic document library to share procedures and documents. Biosafety training was identified as a consistent training gap; a regional course is planned for August 2018 to address this need. **Conclusions:** Mentors-mentee relationships are supporting accelerated progress toward countries' identified goals and priorities. After 1 year notable progress has been made to strengthen laboratory systems through quality assurance and help improve capacity for public health response to emerging infectious diseases, improving overall global health security.

Board 437. The US Centers for Disease Control and Prevention-Supported National Laboratory Strengthening Initiative in India

S. Kabra[1], D. Garcia[2], M. Dwivedi[2], I. Roy[2]
[1]The National Centre for Disease Control, Delhi, India, [2]Division of Global Health Protection (DGHP), Centers for Disease Control and Prevention (CDC), Center for Global Health (CGH), Delhi, India

Background: Laboratory confirmation is essential for disease surveillance and rapid public health response. India has >700 districts but many lack adequate diagnostic capacity within government labs despite high disease burden. To allow clinicians to practice evidence-based medicine and produce reliable data for laboratory-based surveillance, India's National Centre for Disease Control (NCDC) in collaboration with U.S. CDC developed a national laboratory strengthening initiative (NLSI) for district hospital and government medical colleges. NCDC and CDC partnered with the Indian Association of Medical Microbiologists (IAMM) to pilot the initiative in four states: Gujarat, Tamil Nadu, Jharkhand and Madhya Pradesh. **Methods:** We implemented a stepwise approach of: 1) advocacy meetings in each state with state health leadership; and 2) baseline assessment of all government district hospital and medical college labs using teams composed of national and state lab experts using the World Health Organization tools (S-LAT and F-LAT) adapted to the Indian context. **Results:** From September 2016 to January 2018, 160 district hospitals and medical colleges were assessed. We observed low compliance in five major areas – quality assurance (11%), biorisk management (BRM, 18%), diagnostic capacity (18%), training (33%), networking and sample referral (34%). To address these deficiencies, a total of 1,242 lab persons were trained/re-trained including 647 on quality management systems (QMS), 251 on BRM, 206 on basic microbiology techniques, and 222 on specimen transport. **Conclusions:** Based on gaps identified, trainings were provided on basic lab techniques, QMS and BRM among other topics. The government of India has now ordered expansion of this initiative to all states, beginning with developing 30 model labs across the country. To best drive NLSI, Government of India is also drafting a National Strategic Plan for upgrading district/state level public health labs. The strategic plan will include a roadmap for a tiered laboratory network involving regional and apex disease diagnostic labs for efficient specimen referral. The plan will also address stepwise quality improvement towards accreditation, BRM capacity building, training and provisions for adequate equipment, supplies and human resources.

Board 438. Laboratory Mapping in India: A Joint Initiative of the US Centers for Disease Control and Prevention and Indian Association of Medical Microbiologists

D. Garcia[1], M. Dwivedi[1], I. Roy[1], B. Sherwal[2]
[1]Division of Global Health Protection (DGHP), Centers for Disease Control and Prevention (CDC), Center for Global Health (CGH), Delhi, India, [2]Indian Association of Medical Microbiologists, Delhi, India

Background: Diagnostic and biorisk management (BRM) capacities of government and non-government laboratories in India are largely un-inventoried. The U.S. CDC and the Indian Association of Medical Microbiologists (IAMM) collaborated to map labs of public health importance to identify diagnostic and BRM gaps, and to facilitate a re-

ferral system for specimen transport. **Methods:** A list of 1,400 laboratories was created from infectious disease publications in India, publications/policy statements from the Indian government, survey reports, public health programs, established lab networks of India, directories of Medical Council of India (MCI) and National Accrediting Board for Testing and Calibration of Laboratories (NABL). A questionnaire to self- report diagnostic and BRM capacities was sent to each lab; several labs were also visited to verify or collect data from new labs. Data were entered into a web-based database linked to an android application designed to mark the geographic location of each lab. **Results:** Among 1,400 laboratories, 314 (22%) have been mapped. These include 98 district public health labs, 94 medical college labs, 65 private diagnostic labs, 54 research labs and 3 veterinary labs. Sixty-eight percent of mapped labs have a BSL2 facility; 14.6% were using proper PPE and 28.7% were following waste management guidelines. Access control was present in 27.1% of labs and 2.2% labs had biosecurity awareness; 1.6% labs provided secure storage of pathogens. The diagnostic capacity was low. Diagnostic capacity for endemic zoonotic diseases (anthrax, brucellosis, leptospirosis, etc.) were found <10% of labs. While higher testing capacity was found for cholera (43.9%), malaria (29%), diphtheria (13.7%) and human seasonal influenza (11.1%). Only 11% of labs have molecular diagnostic capacity. Approximately 36% of the private labs and 15% of the public labs were accredited. Only 11% (35/314) of labs had molecular diagnostic capacity. **Conclusions:** Principle gaps of laboratories surveyed in India exhibited inadequate BRM abilities and poor diagnostic capacities for the majority of priority infectious diseases including zoonotic diseases endemic to India. Once completed, the database will be utilized for efficient specimen referral systems to facilitate early detection of pathogens of high consequence and rapid intersectoral response.

Late Breakers

Board LB-60. Estimating the Burden of Waterborne Disease in the United States

S. Collier, L. Deng, K. Benedict, K. Fullerton, J. Yoder, V. Hill, M. Beach
CDC, Atlanta, GA, USA

Background: One of the greatest public health achievements of the last century, the routine treatment of drinking water, has led to a safe, reliable water supply being used in many complex ways that can affect disease transmission. Additionally, increased leisure time has led to more recreational water use. Waterborne disease and outbreaks continue to occur in the United States. An estimate of the burden of waterborne disease in the United States, that is, the total number of illnesses, hospitalizations, and deaths, is needed to direct prevention activities and set public health goals. **Methods:** We estimated the number of domestically acquired waterborne illnesses, emergency department visits, hospitalizations, and deaths, quantified the direct healthcare costs and 95% credible intervals (95% CrI) of emergency department visits and hospitalizations due to 19 infections in the United States in 2014. We used a series of disease-specific multipliers to adjust the documented number of cases of each disease for under-reporting and under-diagnosis, proportion domestically acquired, and proportion attributed to waterborne transmission. **Results:** The diseases included in this analysis caused 6.8 million illnesses (95% CrI 3.7 M-11.6 M) in 2014, 580,000 emergency department visits (95% CrI 360,000-840,000), 120,000 hospitalizations (95% CrI 90,000-150,000), 7,000 deaths (95% CrI 4,000-9,000), and incurred more than $5 billion in direct healthcare costs for hospitalizations and emergency department visits. The most common causes of domestic waterborne illness in 2014 included otitis externa and norovirus. The most common, and costly, causes of waterborne hospitalizations in 2014 were infections with organisms associated with premise plumbing systems (non-tuberculous mycobacterial infections [NTMs], *Pseudomonas pneumonia* and septicemia, and Legionnaires' disease) at an annual cost above $2 billion. **Conclusions:** These results represent the first estimate of the burden of waterborne disease in the United States that encompasses all water exposures, not just drinking water. Results demonstrate the importance of premise plumbing pathogens such as NTMs and *Pseudomonas*. The results of this estimate will be vital in prioritizing resources, informing policy makers directing CDC's waterborne disease prevention efforts.

Board LB-61. Responding to a Large Norovirus Outbreak at a University Complicated by a Water Main Break, Connecticut 2018

T. Rabatsky-Ehr[1], P. Gacek[1], Q. Phan[1], E. Milardo[1], C. Nishimura[2], D. Noel[2], M. Cartter[1]
[1]State of Connecticut, Department of Public Health, Hartford, CT, USA, [2]State of Connecticut, Department of Public Health Laboratory, Rocky Hill, CT, USA

Background: On April 20, the Connecticut DPH was notified of 40 gastrointestinal (GI) illnesses among university students during the prior 24 hours. The university had two campus locations (A and B) each with a cafeteria; 1400 students were housed in six residence halls. An additional 4000 commuters attend classes on one or both campuses. A large water main break occurred on April 24, resulting in a lack of portable water on Campus B. DPH assisted the university to determine magnitude of illness, likely cause(s), and implement control measures. **Methods:** A self-administered online questionnaire was distributed to university members. A case was defined as vomiting or diarrhea (>2 stools in 24 hours) in a respondent with onset in the previous 2-weeks. A case-control analysis using cases with onsets during April 19-21 was conducted to identify possible food exposures. We conducted food worker (FW) interviews and onsite environmental assessments of food service venues. DPH laboratory tested stool specimens. **Results:** Among the 6516 university members, 1743 (27%) completed the survey; 384 (22%) cases were identified in students (25%), faculty (9%), and staff (10%). Median age was 20 years (range18-63); 68% were female; 51% lived on-campus (77% on Campus A). Illness was associated with eating any burrito (OR 7.5-21.4, $p<0.0001$) or wrap (OR 4.8-10, $p<0.0001$) from Campus A cafeteria during April 16–19; additionally having lettuce (OR 5.4-17.0, $p<0.0001$) or tomato (OR 3.6-7.4, $p <0.0001$-0.003) on any burrito or lettuce (OR 9.8-17.7, $p <0.0001$) or tomato (7.9-28, $p<0.0001$) on a sandwich or wrap from Campus A cafeteria during April 16–19 was associated with illness. Norovirus (NoV) GII was confirmed in 7 students and 8 of 20 FWs. Fourteen (33%) of 43 FWs interviewed reported GI illness. Improper glove use and inadequate handwashing were observed; an effective EPA-registered sanitizer was not used in the cafeteria until April 25. **Conclusions:** A large NoV outbreak occurred among a university community during April 2018. Most cases likely occurred initially through foodborne transmission. Person-to-person contact and exposure to contaminated environments likely played a role further propagating the outbreak. Both the university and external food service company struggled with timely and effective environmental cleaning.

Board LB-62. Viral Metagenomic Analysis of Stool Specimens from Undiagnosed Cases Acute Gastroenteritis in Children

H. Zaraket[1], A. Ezzeddine[1], K. Alasnari[2], A. Althani[3], E. Abu Baker Abd Farag[4], H. Yassine[3]
[1]American University of Beirut, Beirut, Lebanon, [2]Hamad Medical Center, Doha, Qatar, [3]Qatar University, Doha, Qatar, [4]Ministry of Public Health, Doha, Qatar

Background: Acute gastroenteritis constitutes a significant health burden worldwide especially in children in developing countries. Viruses are considered the major etiologies of diarrhea in children; however, bacteria and parasites are also important causes. Despite the advances in molecular diagnosis, many outbreaks remain unsolved using conventional methods. Metagenomic analysis of viruses in specimens from these outbreaks might provide a diagnosis and may potentially identify novel agents. **Methods:** We used a virus enrichment protocol coupled with Illumina High Throughput Sequencing using stool specimens to investigate 10 undiagnosed cases of gastroenteritis in children under the age of 5 years in Qatar. The obtained sequences were analyzed for virus content after subtracting host and bacterial sequences. Consensus sequences longer than 100 nucleotide bases in length were analyzed using BLAST and hits with an E-value of 10e-5 or less were considered true. **Results:** Preliminary analysis of 93 million sequence reads obtained from 3 samples, with an average of 30,000,000 reads per sample, revealed that 13% of the reads potentially mapped to a viral genome. Several viruses were identified in the specimens. These included three viruses that are commonly associated with gastroenteritis (adenovirus, rotavirus, and norovirus). In addition, viruses (influenza A virus and coxsackievirus A) that cause other non-enteric illnesses but have been shown to shed in stool were also detected. Sequences mapping to poliovirus were also identified in the stool specimens of two children; however, these were likely associated with polio vaccination, which is implemented in Qatar. Furthermore, cucumber green mottle mosaic virus was commonly retrieved in all specimens and is likely to be associated with food consumption. Full analysis of the 10 samples along with 5 specimens from children previously diagnosed with norovirus and rotavirus will be presented. **Conclusions:** Viral metagenomics provide a promising approach for investigating undiagnosed outbreaks of gastroenteritis.

Board LB-63. Outbreak of Acute Diarrheal Disease by *E. coli* Pathogen in Mass Event in Brazil, a Case-Control Study, Brasília, 2018

I. Grando[1], S. Almeida[1], M. Ruy[2], T. Vieira Segatto[2], M. Lavocat Nunes[3], J. Percio[1]
[1]Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Surveillance and Response to Emergencies in Public Health, Program of Training in Epidemiology Applied to Services of the Single Health System, Brasilia, Brazil, [2]Secretary of Health, Secretariat of Epidemiological Surveillance of the Federal District, Brasilia, Brazil, [3]Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Surveillance and Response to Emergencies in Public Health, Brasilia, Brazil

Background: The first National Health Surveillance Conference (CNVS) took place in Brazil–a mass event that took place in Brasília (Distrito Federal) between February 28 and March 2, 2018. In this event, real-time monitoring of medical care, which identified a probable outbreak of acute diarrheal disease (ADD). Research was carried out with the purpose of describing the cases and analyzing factors associated with ADD. **Methods:** A case-control study (1: 2) was performed during CNVS. A case was defined as a patient with diarrhea and control was defined as a person who did not seek treatment for diarrhea during the event period. To collect data, a questionnaire was prepared with clinical and epidemiological variables, including the list of foods offered at the event (lunch, snacks and dinner). For the analysis, Chi-square or Fisher's exact statistical tests were used for categorical variables, and Student t or Kruskal-Wallis for the quantitative variables. The measure of effect used was the odds ratio (OR), considering the 95% confidence interval (95% CI). Multivariate analysis was performed through stepwise logistic regression, calculating the adjusted odds ratio (ORA) and 95% CI. The critical error for statistical significance was considered 5%. **Results:** Twenty case-patients with ADD and 40 controls attended during the timeframe were investigated; most had an with onset of symptoms on 27 and 28/02/2018 (n = 17);. Of the cases, 12 (60%) were female (p-value: 0.27); and the mean age was 49.8 (± 12.59) years (p-value: 0.19). In addition to diarrhea, the main symptoms reported were abdominal pain (80%), colic (70%), and nausea (60%). Stool samples were collected from six patients and tested positive for *E. coli.* Two samples were genotyped and were positive for STEC (shiga toxin producing *E. coli*). In the event, the only food that was statistically associated with the cases of ADD was carrots cooked with meat (OR: 1.76; ORA: 11.29; 95% CI: 1.64 - 77.50; p-value: 0, 01). **Conclusions:** An outbreak of ADD occurred caused by E. coli STEC, a foodborne microorganism found mainly beef products. Prevention and control measures, such as good practices in food preparation and preservation, especially in collective feeding kitchens as in mass events, were recommended.

Board LB-64. First National Conference on Health Surveillance in Brazil, Monitoring of Medical Care in Real Time-New Strategies and Experiences in Mass Event.

I. Grando[1], S. Almeida[1], M. Ruy[2], T. Vieira Segatto[2], M. Lavocat Nunes[3], J. Percio[1]
[1]Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Surveillance and Response to Emergencies in Public Health, Program of Training in Epidemiology Applied to Services of the Single Health System, Brasilia, Brazil, [2]Secretary of Health, Secretariat of Epidemiological Surveillance of the Federal District., Brasilia, Brazil, [3]Ministry of Health, Secretariat of Health Surveillance, Department of Surveillance of Communicable Diseases, General Coordination of Surveillance and Response to Emergencies in Public Health, Brasilia, Brazil

Background: Mass events concentrate an extraordinary flow of people, which can cause public health risks, such as outbreaks. In Brazil, between February 28 and March 2, 2018, in Brasilia, Federal District, the 1st National Conference on Health Surveillance took place, where the monitoring of medical care was performed by using the method of collecting data in real time with devices with the objective of characterizing the profile of patients and identifying potential threats to public health. **Methods:** We included all people who sought medical attention at the event. Data were collected in a semistructured questionnaire in Epi Info™ 7.2 using mobile devices that were synchronized with a

Microsoft Azure, an online cloud whose data were accessed remotely by health managers and research teams using the Dashboard tool of Epi InfoTM 7.2. Data were analyzed by descriptive statistics. **Results:** Of the 1,830 people who participated in the event, 181 sought medical attention (incidence: 98/1000 participants). On February 28, there were 100 visits and the highest incidence of the period (50/1000 visits). The majority of those served came from the states of São Paulo (10.7%), Rio de Janeiro (9.6%), and Bahia (7.3%). Of the total, 94% were participants and the rest were workers att the event; 111 (61%) were female. The median age was 49 (range: 36 to 56) years of age. Of the visits, 175 (97%) were due to a clinical complaint and six (3%) due to trauma. The main signs and symptoms were headache (42.5%), malaise (22.1%), and nausea (10.5%). There were 20 patients with diarrhea, of these, stool samples were collected from 6 and were positive for *E. coli* producing shiga toxin - STEC. Regarding the evolution of the attendances, there were two transfers and no deaths. **Conclusions:** The monitoring of the medical attendance related to the mass event allowed the knowledge of the health situation of the participants as well as the identification of a probable outbreak of diarrheal disease, confirmed by an epidemiological investigation carried out by the field team. A case-control study was conducted to identify the food associated with diarrhea and it was recommended to perform real-time monitoring for other mass events.

Board LB-65. Natural History of Astrovirus- and Sapovirus-associated Gastroenteritis in Children Visiting the Emergency Department

G. Tarr[1], R. Zhuo[2], B. Parsons[2], X. Pang[3], B. Lee[2], L. Chui[3], S. Ali[2], S. Freedman[1]
[1]University of Calgary, Calgary, AB, Canada, [2]University of Alberta, Edmonton, AB, Canada, [3]Provincial Laboratory for Public Health, University of Alberta, Edmonton, AB, Canada

Background: Astrovirus (AsV) and sapovirus (SaV) had been underappreciated as causes of gastroenteritis until the recent increased use of molecular diagnostic testing. However, longitudinal studies of the natural history of AsV and SaV gastroenteritis are lacking. Better characterization of the type, duration, and severity of symptoms is necessary. **Methods:** APPETITE (Alberta Provincial Pediatric EnTeric Infection TEam) is a prospective cohort study of children <18 years old with ≥3 episodes diarrhea and/or vomiting in 24 hours. Children were enrolled from December 2014 through May 2018, during an emergency department (ED) visit at either of two large Children's Hospitals in Alberta. All APPETITE participants were tested by xTAG® Gastrointestinal Pathogen Panel (Luminex), bacterial culture, and an in-house RT-PCR assay for 5 gastrointestinal viruses, including AsV and SaV. Parents/guardians provided data on symptoms, medications, and potential exposures at enrollment and 14 days. We compared the natural histories of AsV and SaV to that of norovirus (NoV). **Results:** Rectal swabs and/or stool samples from 2590 children (of 2632 enrolled) were tested: AsV was detected in 84 (3.2%), SaV in 229 (8.8%), and NoV in 655 (25%) children. Vomiting occurred in 85%, 93%, and 98% in AsV, SaV, and NoV cases, respectively; diarrhea occurred in 94%, 83%, and 77%. The median maximal vomiting episodes per day was 5 (IQR 3, 7), 7 (IQR 4, 10), and 7 (5, 12) for AsV, SaV, and NoV cases, respectively; median maximal diarrheal episodes per day was 5 (IQR 4, 9.5), 4 (IQR 3, 7), and 4 (IQR 3, 7). Median duration of vomiting was 3 days (IQR 2, 7), 3 days (IQR 2, 6), and 2 (IQR 1, 4) for AsV, SaV, and NoV cases, respectively; median diarrhea duration was 6 days (IQR 3.75, 8), 5 days (IQR 3, 8), and 5 (IQR 2, 7). Among cases with vomiting at presentation, it had resolved within 3, 4, and 3 days in 80% of AsV, SaV, and NoV cases, respectively. For those presenting with diarrhea, it had resolved in 80% of cases within 7 days for all three viruses. **Conclusions:** Among children visiting the ED with acute gastroenteritis, the natural history of AsV and SaV are similar to one another, as well as to NoV. These data provide a clearer picture than previously available of the duration and intensity of cardinal gastroenteritis symptoms associated with AsV and SaV infections.

Board LB-66. Use of Digital Channels Facilitates Active Case Finding Following a Foodborne Botulism Exposure Event—Alaska, 2018

A. Tiffany[1], K. Helfrich[2], K. Krings[3], E. Achee[3], L. Castrodale[2], J. McLaughlin[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Alaska Division of Public Health, Section of Epidemiology, Anchorage, AK, USA, [3]Alaska Division of Public Health, Section of Public Health Nursing, Bethel, AK, USA

Background: During 1950-2016, all 366 cases of foodborne botulism reported in Alaska for which source food was identified were associated with consumption of traditional Alaska Native foods. On March 21, 2018, the Alaska Section of Epidemiology received a report of a hospitalized patient experiencing diplopia, photophobia, and dry mouth four days after attending a community event. The patient had purchased and consumed salad containing rendered seal oil from an unregistered booth at the event. Leftover salad provided by the patient tested positive for type E botulinum toxin, meeting the definition of a probable case. We investigated to raise botulism awareness and to identify additional cases. **Methods:** We used digital channels (i.e., social media and event organizer's website) to immediately disseminate botulism food exposure risk and prevention messages, and an online survey for event attendees ~1 week after the case was reported. The survey could be completed anonymously and asked about event attendance, salad consumption, and self-reported symptoms. **Results:** Ninety-one people responded; seventy-five (82%) attended the event. Among 35 (47%) who purchased salad, 12 (34%) shared salad with persons outside their household. Salad was eaten the purchase day by 23 (66%) persons, 4 (11%) did not know what happened to the salad, and 1 (3%) reported not consuming the salad. Seven (20%) reported saving salad in a resealable plastic bag or lidded plastic container; among these seven, one stored salad in the freezer, four in the refrigerator, one outside, and one on a counter. Seven of the 35 reported illness ≤1 week after the event. Five persons reported symptoms; nausea, abdominal pain, and fatigue were reported by four. One person also reported dry mouth, dizziness and muscle weakness. Four reported seeking medical attention; no additional persons received a botulism diagnosis. **Conclusions:** Use of digital channels enabled dissemination of exposure information and facilitated active case finding. Although no additional cases were identified, four respondents reported symptoms that might have represented mild botulinum intoxication. The sale of food from unregistered booths will be discouraged by the organizer at future events and messages about methods for safe preparation and storage of traditional foods have been shared with the community.

Board LB-67. ClinEpiDB: The Clinical Epidemiology Database Resource

B. Lindsay[1], J. Brestelli[1], B. Brunk[1], D. Falke[2], D. Helb[1], J. Kissinger[2], D. Roos[1], S. Shah-Simpson[1], C. Stoeckert[1]
[1]University of Pennsylvania, Philadelphia, PA, USA, [2]University of Georgia, Athens, GA, USA

Background: Population-based epidemiological studies provide new opportunities for innovation and collaboration among researchers addressing pressing global health concerns; however, open access to study data pose many challenges. ClinEpiDB (https://clinepidb.org), launched in February 2018, is an open-access online resource enabling investigators to maximize the utility and reach of their data and to make optimal use of data released by others. **Methods:** ClinEpiDB was developed using the existing infrastructure of EuPathDB (https://eupathdb.org), a collection of databases that cover 170+ eukaryotic pathogens, along with relevant free-living and non-pathogenic species and select pathogen hosts, which provides a sophisticated search strategy system that enable complex interrogations of underlying data. Currently, data integration for ClinEpiDB has occurred or is in process for NIH-supported International Centers for Excellence in Malaria Research (ICEMR), the Gates Foundation-supported Malnutrition and Enteric Diseases Network (MAL-ED), and the Global Enteric Multicenter Study (GEMS) projects. In the process of data integration, a unified semantic web framework has been used to describe data generated from these studies. The ICEMR projects used comprehensive surveillance data to elucidate interactions between malaria parasites, their mosquito vectors, and human hosts. The MAL-ED and GEMS projects studied the etiology, incidence, and impact of childhood enteric disease in low-income countries. **Results:** Over 1500 different data variables about participants, their associated anthropometry, demographics, and disease episodes were collected in these clinical epidemiology studies. Query results can be statistically analyzed and graphically visualized via interactive web applications launched directly in the ClinEpiDB browser, providing insight into distributions and exploratory associations with any observational covariates. **Conclusions:** The ClinEpiDB resource will continue to grow with integration of new datasets, enhanced tool development and significant user outreach and education.

Board LB-68. Carbapenem-Resistant Enterobacteriaceae Surveillance in Wisconsin: The First Eleven Months of the Antibiotic Resistance Lab Network (ARLN)

M. Lasure[1], A. Valley[1], N. Shrivastwa[2]
[1]Wisconsin State Laboratory of Hygiene, Madison, WI, USA, [2]Wisconsin Division of Public Health, Madison, WI, USA

Background: Carbapenem-resistant Enterobacteriaceae (CRE) infections are associated with a high mortality rate. Carbapenemases that confer resistance might be encoded on plasmids and transferred between bacterial strains. For these reasons, carbapenemase-producing CRE (CP-CRE) are a clinical and public health concern. During 2010, the Wisconsin State Laboratory of Hygiene (WSLH) began receiving CRE isolates on a voluntary basis, and expanded testing to include antimicrobial susceptibility testing (AST) and carbapenemase screening during July 2017. The objective of this study was to characterize CRE within the state of Wisconsin through the first eleven months of testing. **Methods:** Isolates were submitted from clinical and reference laboratories across Wisconsin. Isolate identification was confirmed using MALDI-TOF. AST was determined using broth microdilution and interpretations were based on current CLSI breakpoints. CRE was defined as an isolate resistant to at least one carbapenem (doripenem, ertapenem, imipenem, meropenem) or positive for a carbapenemase either through phenotypic screening or molecular detection. CP-CRE were identified through resistance mechanism testing using PCR following a positive on a phenotypic screening test, the modified carbapenem inactivation method (mCIM). **Results:** WSLH tested 632 Enterobacteriaceae, 316 (51.4%) of which were confirmed to be CRE. The most common CRE species was *Enterobacter cloacae* complex (44.6%), followed by *Klebsiella pneumoniae* (17.4%), and *E. coli* (11.4%). CP-CRE comprised only 16.8% of the CRE isolates with the majority (85.0%) being KPC. The majority of CP-CRE isolates came from the Southeastern public health region (71.7%). Among the Southeastern region 59.6% of submitted isolates were CRE and 22.2% of those tested positive for CP-CRE. While most CP-CRE were from the "Big Three" genera (*Klebsiella*, *Enterobacter*, *E. coli*), 13.2% were from others including *Citrobacter*, *Proteus*, and *Providencia*. **Conclusions:** Although Wisconsin remains a low-incidence state, the Southeastern region has significant CRE and CP-CRE burden. Continued CRE and CP-CRE surveillance is warranted.

Board LB-69. Epidemiology of Bloodstream Infections and Antimicrobial Resistance in Adult, Pediatric, and Neonatal Intensive Care Units in a Regional Referral Hospital, Guatemala, 2016-2018

H. Maldonado[1], R. Gonzalez[1], A. Roldán[1], C. Galicia[2], E. García[2], M. Cortés[2], B. Park[3], N. Gupta[3], A. Espinosa-Bode[4], J. Bryan[4]
[1]Centro de Estudios en Salud, Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Hospital Regional de Cuilapa, Cuilapa, Santa Rosa, Guatemala, [3]Division of Healthcare Quality Promotion, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Division of Global Health Protection, Central American Regional Office, Centers for Disease Control and Prevention, Guatemala, Guatemala

Background: Healthcare-associated infections (HAI) and antimicrobial resistance result in increased morbidity and mortality. In Guatemala, the burden of HAIs and severity of outcomes is poorly described; improved surveillance can help inform prevention measures. **Methods:** During February 2016–January 2018, we conducted intensive care unit (ICU)-based surveillance for bloodstream infections (BSI) and central line-associated BSI (CLABSI) in neonatal (NICU), pediatric (PICU), and adult (AICU) units in a regional teaching hospital in Cuilapa, Santa Rosa, Guatemala. A dedicated nurse collected clinical and laboratory data using a standardized protocol adapted from the U.S. National Healthcare Safety Network. **Results:** Overall, 493 cases were reported; 458 (93%) were CLABSI. Pooled mean BSI rates in the NICU, PICU, and AICU were 18.2, 11.6, and 15.4 per 1000 patient-days, respectively. Pooled mean CLABSI rates were 38.6, 22.6, and 23.7 per 1000 catheter days, respectively. The proportion of pathogens differed by ICU type: NICU (n = 270): *Klebsiella spp.* (64%), *S. aureus* (14%), and *Pseudomonas spp*. (5%), and *Candida spp* (4%); PICU (n=103): *Klebsiella spp.* (32%), *S. aureus* (18%), Non-fermentative gram-negative bacilli (NFGNB) (16%), *Candida spp*. (13%), *E. coli* (6%); AICU (n = 118): NFGNB (24%); *Klebsiella spp* (20%), *S. aureus* (20%), *Candida spp*. (8%), CoNS (7%), *E. coli* (5%). Among all *Klebsiella spp.,* 97% were resistant to ceftriaxone, 67% to imipenem, 64% to ciprofloxacin, 78% to amikacin, 50% to fosfomycin. All *S. aureus* isolates were resistant to methicillin. Case-fatality rates by organism were 41%

(*Klebsiella spp.)*, 32% (*S. aureus)*, 66% (NFGNB), and 60% (*Candida spp).* **Conclusions:** In this regional teaching hospital, HAI burden was substantially high and associated with concerning antimicrobial resistance and adverse outcomes, highlighting an important need for infection prevention and control and antibiotic stewardship. Standardized surveillance provides quality data to better define target populations and pathogens for priority interventions and a platform to measure the impact of those interventions on patient outcomes.

Board LB-70. Point Prevalence and Epidemiology of Antimicrobial Use in Nursing Homes, New Haven and Hartford Counties, Connecticut, 2017

P. Clogher[1], K. Srinivasan[2], M. Maloney[3], J. Meek[1]
[1]Connecticut Emerging Infections Program, New Haven, CT, USA, [2]Yale School of Public Health, New Haven, CT, USA, [3]Connecticut Department of Public Health, Hartford, CT, USA

Background: Concern about the role nursing homes (NH) play in transmission of antimicrobial resistant organisms has prompted the rollout of antimicrobial stewardship (AS) in NH. However, data on antimicrobial use (AU) from U.S. NH are limited. In 2017, the CDC's Emerging Infections Program (EIP) conducted a point prevalence survey to determine AU, Healthcare Associated Infection (HAI) and (AS) practices in NH in 10 EIP sites including Connecticut (CT). **Methods:** NH in New Haven and Hartford counties in CT were randomly selected to participate in a 1-day AU point prevalence survey as part of a larger study of AU, HAI and AS practices; participation was voluntary. For NH residents receiving antimicrobial drugs (AD) on the survey day, EIP staff reviewed available medical records to collect the AD route, rationale, infection site(s) and treatment (tx) duration. AD were categorized using the World Health Organization Anatomical Therapeutic Chemical classification system. Data were analyzed in SAS 9.4. **Results:** Of 1299 residents in 11 NH, 128 (10%) received ≥1 AD on the survey day (AD range 1-2, 87% monotherapy). Of 148 total ADs, 78% were administered for tx of an active infection and 22% for prophylaxis (ppx). Most AD (87%) were administered by the oral/enteral route and most (89%) were antibacterials. The top infection sites and proportion of each site treated for ppx included urinary tract (28%, 24%), respiratory tract (21%, 16%), skin/wound (20%, 21%), gastrointestinal tract (10%, 21%), and bone/joint (10%, 21%). Median duration of therapy for active infection was 8 days (range 1-730) versus 59 days, (2-1656) for ppx. Skin/wound and urinary tract sites had the longest single ppx tx duration at 1656 and 558 days. Fluoroquinolones (16%), tetracyclines (12%) combination penicillins (11%), combination sulfonamides (10%), and first generation cephalosporins (9%) ranked highest in use. **Conclusions:** On a given day, 10% of residents in surveyed NH received ≥1 AD. Notably 28% of AD ordered were for urinary tract infection. AD were frequently used for long-term ppx, with a high proportion prescribed for months or years. AD in classes associated with emergence of antibiotic resistance due to indiscriminate use were common. These findings suggest unnecessary AD use occurs in NH and supports new requirements that NH implement AS programs.

Board LB-71. Recent Increase in Colistin-Resistant Acinetobacter Infections at a Tertiary Care Center in Pakistan

N. Nasir, F. Sharif, R. Mansoor, S. Ahmed, B. Jamil, F. Mahmood
Aga Khan University, Karachi, Pakistan

Background: Acinetobacter is an important nosocomial pathogen and a major cause of morbidity and mortality in hospitalized patients. The use of intravenous colistin increased with the emergence of carbapenem resistant multi-drug resistant Acinetobacter- and carbapenem-resistant Enterobacteriaceae. Recently, colistin resistant strains of Acinetobacter were reported from different parts of the world. We are describing a case series of 18 patients with colistin resistant Acinetobacter over a span of 4 years with only three cases reported between 2014 to 2015 and an alarming increase in number of cases to 15 between 2016 to 2017. **Methods:** Patients with any clinical specimen positive for colistin resistant Acinetobacter between 2014 - 2017 were identified from the hospital's microbiology records. Three cases were isolated between 2014 and 2015, six cases in 2016 and 9 cases in 2017. Data on patients' demographics as well as clinical data was collected retrospectively on a structured proforma from the hospital medical records. **Results:** Mean age of the patients was 50 ± 18 years. Fifteen (83.3%) out of the 18 patients were male. Acinetobacter pneumonia was the most common diagnosis in n=13(72.2% of the patients). Nine (50%) of the patients developed sepsis. In addition to colistin resistance, carbapenem and amikacin resistance was documented to be 94% and 61% respectively. Colistin- and carbapenem-based combinations were used to treat all patients with a mean antibiotic duration of 20 ± 10 days. Median length of hospital stay was 25 days (range 8 - 61), with 14 patients (77.8%) requiring ICU admission. Eight (44.4%) of the patients expired and only 6 (33.3%) achieved microbiological eradication. **Conclusions:** Infections due to colistin-resistant strains of Acinetobacter are rapidly increasing, have limited antimicrobial treatment options, and are associated with poor outcomes.

Board LB-72. Evaluation of The Impact Of Antimicrobial Hand Towels On Hand Contamination With *Escherichia coli* Among Mothers in Nyanza Province, Kenya, 2011-2012

S. Kim[1], A. Brown[1], J. Murphy[1], J. Oremo[2], Q. Rob[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Safe Water and AIDS Project, Kisumu, Kisumu, Kenya

Background: Poor hand hygiene contributes to diarrhea in developing countries. Handwashing with soap reduces diarrhea risk, but drying hands on contaminated towels can compromise the benefits of handwashing. In response to the challenge of keeping hands clean, an antimicrobial hand towel was developed, shown to be efficacious in the laboratory, but not adequately tested in the field. **Methods:** We evaluated the effectiveness of an antimicrobial towel in two, double-blinded randomized crossover trials among the same 125 mothers with children (age < 5y) in Kenya. In trial 1, we randomly assigned mothers to use either the treated towel or an identical placebo towel and made surprise home visits at random times each week for 3 weeks to test hands for *Escherichia coli* through fingertip rinses in sterile water, then switched towel types in the two groups and repeated 3 weekly rounds of *E. coli* testing. In a second trial, we used fingertip rinses to compare *E. coli* contamination of maternal hands immediately following 3 handwashing/drying procedures: soap and water + treated towel, water only + treated towel, and soap and water + air dry. **Results:** Our study found

no difference in the level of *E. coli* contamination on maternal hands by type of towel used during trial 1 (odds ratio for treated vs untreated towel: 1.14, 95% confidence interval 0.83-1.56). In trial 2, compared to mothers using the standard method of handwashing with soap and water + air drying, there were no differences in maternal *E. coli* hand contamination among those who used soap and water + treated towel or water only + treated towel. **Conclusions:** Use of antimicrobial hand towels did not prevent *E. coli* contamination of mothers' hands in Kenyan households during random testing and offered no advantages over standard handwashing and drying practices. Handwashing with soap and clean water and drying with clean towels are recommended.

Board LB-73. Combating Antimicrobial Resistance: Utility of Antimicrobial Combination Therapy and / or β–Lactamase Inhibitors

G. Matar, B. El-Hafi, N. Salloum, A. Abou Fayad, G. Araj
American University of Beirut, Beirut, Lebanon

Background: The range of antimicrobial agents that can be used to treat bacterial infections is becoming limited with the constant increase in antimicrobial resistance (AMR). Several genetic factors underlie AMR, including β-lactamase-encoding genes such as $bla_{CTXM-15}$ that confers resistance to third-generation cephalosporins, and bla_{OXA-48}, bla_{NDM-1}, and bla_{KPC-2} that confer resistance to carbapenems. Remaining treatment approaches for such resistant infections include antimicrobial combination therapy and the use of β-lactamase inhibitors. This study assesses the molecular effects of such treatment approaches on antimicrobial resistant Enterobacteriaceae clinical isolates in vitro and in vivo. **Methods:** Nine clinical Enterobacteriaceae isolates were included in the study. One harboring $bla_{CTXM-15}$, one harboring bla_{OXA-48}, one harboring bla_{KPC-2}, two harboring bla_{NDM-1} and $bla_{CTXM-15}$, and four harboring bla_{OXA-48} and $bla_{CTXM-15}$. Minimal inhibitory concentrations were determined for carbapenems with avibactam, Ca-EDTA, and relebactam. Synergism between antibiotic combinations was determined by in vitro and in vivo studies when using colistin with several antibiotics. In vitro and in vivo gene expression levels were done on these combinations with and without inhibitors. **Results:** Antimicrobial synergism was mostly detected between colistin and meropenem, fosfomycin, or tigecycline. The use of meropenem, imipenem, and ertapenem with the selected β-lactamase inhibitors restored isolate susceptibility in 100%, 87.5%, and 25% of the cases. Survival studies revealed a significant high survival rate in mice receiving antimicrobial combination therapy with β-lactamase inhibitors as compared to the controls. Overall gene expression levels of resistance genes were variable depending on treatment. **Conclusions:** Combination therapy along with β-lactamase inhibitors proved to be highly efficient in determined in vitro and in vivo survival studies. The threat of antibiotic resistant bacterial infections remains viable; however, different approaches to therapy are available.

Board LB-74. Medicine Quality and Antimicrobial Resistance

D. Bempong[1], M. Levy[1], W. Kaplan[2], F. Umaru[1]
[1]US Pharmacopeia, Rockville, MD, USA, [2]Boston University, Boston, MA, USA

Background: Consumption of poor quality medicines is associated with adverse health including treatment failure. Poor quality medicines are common in countries with weak regulatory systems. There is the need to determine if there is a link between poor quality medicines and the development and spread of resistance. This is needed to support advocacy efforts on the danger of the emergence of antimicrobial resistance (AMR) due to substandard medicines. The presentation will summarize what is known at present about the linkage between medicine quality and AMR and provide suggestions for further research. **Methods:** We searched for publications between January 2000 to April 2017 in English, French, Spanish, and Portuguese in PubMed, Excerpta Medica Database (EMBASE), Cumulative Index to Nursing and Allied Health Literature (CINAHL), Thomson Reuters Web of Science, POPLINE (One Source), and the Latin American Literature on Health Sciences (LILACS). A total of 1869 titles and abstracts of studies were initially screened and 180 studies were selected and further reviewed. **Results:** The literature search revealed that sub-therapeutic plasma levels of an active ingredient may result from use of poor quality medicine and that sub-therapeutic dosing could create the necessary selection pressure for AMR. The relationship between sub-therapeutic dosing and consequent resistance has been established using mathematical modelling, in-vivo non-human animal models, sub-therapeutic dosing of farm animals, patient outcomes across clinical data, and laboratory studies of poor quality and non-bioequivalent antimicrobials. **Conclusions:** Field evidence is limited and insufficient to definitely prove poor quality medicines are contributors to resistance but observational/clinical research has established a relationship between sub-therapeutic dosing in humans and consequent resistance. Our logic would suggest that one needs to demonstrate the link between various types of poor quality medicines—falsified, substandard or degraded- and sub-therapeutic dosing, and at that point, in our view, the "dots will be connected" between poor-quality medicines and AMR.

Board LB-75. Evaluation of Candidate Diagnostic Culture Media for ESBL *E. coli* in Environmental Samples as a One Health Indicator System for Global Antimicrobial Resistance Surveillance

M. Sobsey[1], A. Koltun[1], T. Chai[1], M. Jacob[2]
[1]University of North Carolina, Chapel Hill, NC, USA, [2]North Carolina State University, Raleigh, NC, USA

Background: The World Health Organization (WHO) seeks a harmonized, culture-based indicator system and methodology for rapid detection and quantification of important antimicrobial resistant (AMR) bacteria of health concern. The WHO indicator system proposes integrated monitoring for the presence and concentrations of extended-spectrum-β-lactam resistant (ESBL) *Escherichia coli* (E-Ec) in environmental hotspots, along with their presence in clinical (human fecal) and animal agriculture (specifically poultry cecal) samples. Candidate E-Ec-selective agar media need to be evaluated rigorously for performance in environmental samples. **Methods:** Six candidate ESBL agar media, including three generics (MacConkey agar with and without an *E. coli*-specific chromogen and Tryptone bile glucuronide [TBX] agar) and three commercial (CHROMAgar ESBL, Hi-Crome ESBL, and Chromatic ESBL), were evaluated simultaneously by analyzing successive samples of municipal wastewater and poultry waste (by spread plate methods) and urban surface waters (by membrane filter methods). Data for the different media were statistically compared for each sample type and overall based on E-Ec detection frequency, concentration, and the proportion of total *E. coli* that were ESBL resistant. Presumptive E-Ec colony isolates were confirmed by MALDI-TOF MS speciation and VITEK AST analyses. Results for each medium were assessed and compared for diagnostic effectiveness based on sensitivity, specificity, positive predictive value (PPV), neg-

ative predictive value (NPV) and overall diagnostic efficiency (ODE) **Results:** Overall, there were differences among candidate media for direct detection and quantification of E-Ec in these samples. Based on rank order of mean and median E-Ec concentrations, specificity, sensitivity, PPV, NPV and ODE, TBX was most effective in detecting E-Ec in all samples. TBX and MacConkey agar supplemented with cefotaxime and an *E. coli*-chromogen were more effective for ESBL *E. coli* detection than the other media tested. **Conclusions:** TBX-and MacConkey-based culture media were most effective for E-Ec detection and quantification in an integrated One Health global AMR surveillance system.

Board LB-76. Combating Antimicrobial Resistance by Utilizing Novel Antibiotics from Soil and Marine Microorganisms in Lebanon

A. Abou Fayad, D. Itani, M. Miari, A. Tanelian, G. Matar
American University of Beirut, Beirut, Lebanon

Background: Antimicrobial resistance (AMR) is emerging at an alarming rate as mortality due to resistant pathogens could rise to 10 million per year by 2050. Since AMR is against all clinically utilized antibiotics, finding novel antimicrobials with unexploited targets remains the main goal worldwide. Soil microorganisms produce natural products as a significant number of drugs in clinical use are derived from these metabolites. Actinomycetes and Myxobacteria are soil dwelling microorganisms that produce secondary metabolites to be screened for antibacterial activity. More than 80% of clinically utilized antibiotics are either natural products or natural product-derived molecules such as vancomycin, teicoplanin, daptomycin, and tetracycline. This study aims to isolate and identify novel antimicrobials from Actinomycetes and Myxobacteria. **Methods:** Soil samples were collected from several areas in Lebanon. Samples were serially diluted for Actinomycetes isolation and boiled for Myxobacteria extraction, then plated on suitable media. Colonies obtained were purified and subjected to genomic DNA extraction then 16s rRNA analysis. Novel isolates were tested for their antimicrobial activity against Gram-positive *Bacillus subtilis* (ATCC 6051), *Staphylococcus aureus* (ATCC 29213, Newman, N315), *Enterococcus faecalis* (ATCC 19433), and *Enterococcus faecium* (DSMZ 17050), and Gram-negative *Escherichia coli* (ATCC 9637), *Klebsiella pneumoniae* (DSMZ), *Pseudomonas aeruginosa* (ATCC 27853, MEXAB), and *Acinetobacter baumannii* (ATCC 15308). **Results:** Strain isolation and cultivation yielded a number of novel isolates whose extracts demonstrated strong antibacterial activity against pathogens including MRSA, VRE, and *Escherichia coli* (ATCC 9637). **Conclusions:** Our efforts now focus on purifying these compounds, elucidate their structures and study their mode of action.

Board LB-77. The Emerging Fungal Pathogen *Candida auris* Contains Cell Wall Mannans That Exhibit Unique Structural Features Not Found in Other Fungi

M. Kruppa[1], D. Lowman[1], Z. Ma[1], Y. Jiao[1], B. Graves[1], P. Rice[2], J. Meis[3], M. Netea[4], D. Williams[1]
[1]East Tennessee State University, Johnson City, TN, USA, [2]University of Colorado, Denver, CO, USA, [3]Canisius-Wilhelmina Hospital, Nijmegen, Netherlands, [4]Radboud University Medical Center, Nijmegen, Netherlands

Background: *Candida auris* is a multi-drug resistant fungal pathogen that is an emerging public health threat. *C. auris* is difficult to identify, difficult to treat, and it persists for prolonged periods in healthcare environments. Mannans and glucans are major components of the fungal cell wall and are essential to the survival of fungi. Very little is known about the structure and composition of these cell wall carbohydrates in *C. auris*. **Methods:** In this study, we isolated and characterized mannans and glucans from seven clinical strains and one reference strain of *C. auris*. Mannan and glucan structure were elucidated by 1-D and 2-D solution-state ^{1}H NMR as well as ^{31}P decoupled ^{1}H NMR. We referenced the mannan and glucan from the seven clinical isolates to *C. auris* KCTC17810. **Results:** All of the *C. auris* mannans exhibit two unique acid labile Mα1-PO_4 side chains that, to the best of our knowledge, have not been observed in other fungal mannans. In addition, the reference strain KCTC17810 and strain 10-05-12-52 2014 have acid stable and acid labile portions with structural fragments that differ from the other six mannans and from each other. Strain KCTC17810 contains only Mα1-PO_4 side chains in the acid labile portion and side chains in the acid stable portion that are not end-capped with β-(1-2)-linked mannosyl repeat units. Strain 10-05-12-52 2014 contains a Mβ1-2Mα1-PO_4 side chain in addition to Mα1-PO_4 side chains in the acid labile portion and side chains in the acid stable portion that do not contain α-(1-3)-linked mannosyl repeat units. All *C. auris* mannans interacted with rhDectin2 and rhMMR and their affinities were higher than those for *C albicans* SC5314 yeast mannan. *C. auris* glucans did not show any unique structural features. **Conclusions:** We conclude that as expected the *C. auris* cell wall contains both mannan and glucan. Mannan from all *C. auris* strains showed unique structural features when compared with other fungal mannans. The unique structural features of *C. auris* mannan may be useful in the development of new and novel diagnostic and/or therapeutic approaches for this emerging fungal pathogen.

Board LB-78. Efficacy of Dettol Antiseptic Liquid for Inactivation of Ebola-Makona Virus Suspended in an Organic Load – a Targeted Hygiene Intervention for Reducing Virus Spread

T. Cutts[1], S. Theriault[1], R. Nims[2], J. Rubino[3], M. Ijaz[3]
[1]Canadian Science Centre for Human and Animal Health, Winnipeg, MB, Canada, [2]RMC Pharmaceutical Solutions, Inc., Longmont, CO, USA, [3]RB, Montvale, NJ, USA

Background: There have been 34 Ebola virus disease outbreaks since the initial emergence of the Ebola Zaire strain in 1976. The most significant outbreaks occurring between 2014-2016, along with the 2018 Ebola outbreak in the Democratic Republic of Congo, have refocused efforts of public health agencies and the World Health Organization toward identifying approaches to reduce the spread of the disease. Targeted hygiene should play an important and integral role in accomplishing this goal. **Methods:** The efficacy of Dettol Antiseptic Liquid (DAL) was evaluated per ASTM E1052-11 for inactivating Ebola-Makona virus (EBOV/Mak) within an organic load in suspension. Three batches of the product were evaluated at three concentrations each (1:10, 1:20, and 1:40), with contact times of 0.5, 1, 5, and 10 minutes. An initial virus titer of ~7 $\log_{10}$ tissue culture infectious $dose_{50}$ ($TCID_{50}$) was exposed to DAL at ambient temperature. Survival of virus below the limit of detection of the $TCID_{50}$ assay was ruled out by inoculating T-75 flasks of Vero E6 cells with 500 µL of undiluted neutralized test sample after each contact time and scoring the cultures for cytopathic effect after 14 days. **Results:** At all DAL dilutions tested, the titer of infectious EBOV/Mak virus was reduced by ~5 $\log_{10}$ within one minute. Detectable virus was still present at the 30-second time point, but >4 $\log_{10}$ reduction in titer was observed for each DAL

dilution. Surviving virus was not detected using the flask inoculation method in samples subjected to DAL for 5 or 10 minutes, regardless of the dilution of the product evaluated. **Conclusions:** The rapid and substantial reduction of Ebola-Makona virus afforded by this commercially available product suggests that it may be useful as part of targeted hygiene for preventing the spread of infectious virus during Ebola virus disease outbreaks.

Board LB-79. Investigation of Zika Virus Transmission in a Laboratory Setting

K. Sandhu, C. Brown, M. Osborne, L. Madoff, S. Hennigan, K. Chen, H. Nguyen, Y. Gonzalez-Chase, K. Tran, G. Gallagher, S. Smole, A. DeMaria
Massachusetts Department of Public Health, Boston, MA, USA

Background: With only five cases reported since 1963, Zika virus (ZIKV) transmission in the laboratory is rare. The route of transmission is usually unknown with one documented needle-stick exposure. In 2017, an employee working with ZIKV in a commercial laboratory presented for care with headache, arthralgias, myalgias, fatigue, and a rash. The employee tested positive for ZIKV by a commercial PCR assay prompting a public health investigation. **Methods:** A comprehensive interview tool collected information on possible exposures, including travel, sexual contact, blood transfusion, organ transplant, and occupational activities. Additional laboratory testing was conducted at the Massachusetts State Public Health Laboratory to confirm the employee's infection and to assess exposure to ZIKV in other laboratory employees. **Results:** A convalescent sample was collected 18 days after symptom onset and was ZIKV PCR negative, but IgM antibody positive with a PRNT titer for Zika antibody ≥ 1:1280 (dengue 1 and 2 negative). Semen tested positive for the presence of ZIKV RNA. The employee denied travel to any areas with ZIKV transmission, sexual partners, blood transfusion, and organ transplantation within the six months prior. At work, the employee reported pouring large volumes of high-titer ZIKV outside of a biosafety cabinet but within a BSL-2 laboratory. The recommended PPE, including double gloves, gown, booties, plastic face shield, and goggles, were reportedly used. Neither facemasks nor respirators were worn. The investigation indicated that laboratory tasks could have caused droplet splashes of ZIKV including on and under the face shield. No other employee at the laboratory tested positive for ZIKV. **Conclusions:** Laboratory transmission of ZIKV through droplet contact with mucous membranes appears highly likely. This case suggests that prior to initiating laboratory work: 1) risk assessments should be performed ensure that the appropriate biosafety precautions and control measures are instituted; and 2) baseline serological status should be documented. Manipulating large quantity volumes and/or high titer preparations of arboviruses may warrant a shift from BSL-2 to BSL-3 practices. Given the potential for subsequent sexual transmission of a laboratory-acquired infection, stronger guidance for containment recommendations may be warranted.

Board LB-80. Implementation of Next Generation Sequencing Technology for HIV Resistance Determination and Genotyping

M. Rowlinson[1], J. Blanton[1], M. Schimenti[1], B. Bennett[1], S. Fordan[1], J. Sanders[2], E. Spencer[2]
[1]Florida Department of Health, Bureau of Public Health Laboratories, Jacksonville, FL, USA, [2]Florida Department of Health, Bureau of Communicable Diseases, Tallahassee, FL, USA

Background: Early HIV diagnosis and timely patient care is essential. The Florida Department of Health (FDOH) Bureau of Public Health Laboratories (BPHL) performs the fourth-generation HIV algorithm, for identification of acute and established HIV-1 infections and clinical management testing including HIV-1 viral load, CD4 testing, and genotyping, in line with a "test and treat" approach. As ongoing improvements are made, BPHL worked with the FDOH HIV/AIDS Section to evaluate next generation sequencing (NGS) for HIV genotyping. **Methods:** HIV genotyping for detection of resistance is performed by Sanger sequencing, ViroSeq HIV-1 Genotyping assay (Abbott Laboratories). NGS was performed on a MiSeq with Nextera XT (Illumina). NGS involved targeted sequencing of DNA (protease, reverse transcriptase [RT] and integrase genes), produced from HIV-positive specimens. Analysis was performed using the SmartGene IDNS® 5 (SmartGene) curated pipeline that includes Stanford University's Genotypic Resistance Interpretation Algorithm. An interpretation cut-off of 5% was used to detect minority resistant variants. Consensus sequence was provided to the HIV/AIDS Section. **Results:** BPHL performed ViroSeq HIV-1 Genotyping and NGS on 53 samples. A proficiency testing sample was tested for comparison. Concordance was seen for common mutations. NGS identified additional mutations not detected by Sanger. NGS also identified mutations present in a lower percentage of the population sampled (i.e. minority variants). **Conclusions:** BPHL has NGS infrastructure established; however, NGS continues to be a challenging technology. Extraction and RT-PCR steps are crucial for generating high-quality DNA, and data interpretation is dependent on pipelines and databases. NGS is more sensitive than Sanger in the detection of minority variants and can detect rare or uncommon HIV subtypes. The SmartGene pipeline and database is a trusted means of data analysis and can store sequences and conduct comparative analyses for epidemiological purposes. Ultimately, NGS will be performed on all newly identified HIV cases diagnosed at BPHL to improve initiation of appropriate anti-retroviral therapy.

Board LB-81. Utilizing TaqMan Array Card (TAC) to Study the Etiology of Community-acquired Pneumonia among Hospitalized Adults in Hunan Province, China

Y. Zhang[1], N. Liu[2], Z. Xie[2], J. Kleana[3], J. Milky[3], J. Rainey[1], Y. Huang[4], Z. Xu[4], Z. Xie[4], B. Wolff[3], J. Winchell[3], C. Van Beneden[3], Z. Duan[2]
[1]United States Centers for Disease Control and Prevention, Beijing, China, [2]China Centers for Disease Control and Prevention, Beijing, China, [3]United States Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Chenzhou Renmin Hospital, Chenzhou, China

Background: Identifying the etiology of community-acquired pneumonia (CAP) is important for clinical treatment and public health surveillance. TAC is a detection tool capable of simultaneously detecting over 21 pathogens. To identify the potential etiology of CAP among hospitalized adults, we implemented a prospective case-control study in Chenzhou, Hunan province, China. **Methods:** Between December

2013 to March 2015, we enrolled patients aged >18 years, hospitalized with an acute (≤7 days) respiratory infection with cough and fever. We enrolled controls from healthy hospital visitors matched to cases by age group, catchment area, and month of onset. Nasopharyngeal and oropharyngeal swabs were collected from cases and controls and tested by TAC. Influenza A viruses were subtyped by conventional real-time PCR. We generated descriptive statistics and odds ratios to estimate the probable etiology of CAP. **Results:** We enrolled 537 cases and 216 controls. Among cases, 414 (77.1%) were aged 18-49 years and 310 (57.8%) were male. The pathogens most frequently detected in cases were influenza A (n=206, 38.4%), *Haemophilus influenzae* (n=92, 17.1%), *Streptococcus pneumonia* (n=59, 11.0%), and rhinovirus (n=55, 10.3%). No pathogens were detected in 123 (23.0%) cases. More than one pathogen was detected from 174 (32.5%) cases, most frequently involving influenza A and *H. influenzae*. Among influenza A viruses, 48 (23.8%) were subtyped as H1pdm and peaked during January to March 2014; 149 (73.8%) were identified as H3 and peaked in June and July 2014. Both influenza virus A (38.4% vs 3.7%, OR=16.18, 95%CI=7.82-33.49) and B (15.7% vs 0%) were more likely to be detected from cases than controls, consistent with true infection. There was no statistical difference in the positive rate between cases and controls for *H. influenzae*, *S. pneumoniae*, rhinovirus, and other pathogens. **Conclusions:** Influenza A viruses were likely to be the major cause of CAP in adults in Chenzhou, Hunan province during the study period. TAC cards were beneficial in quickly detecting the pathogens of CAP; however, additional work is needed to better differentiate between colonization and infection.

Board LB-82. One Thousand Bacterial Genomes in One Week: Microfluidics for Molecular Epidemiology

G. Lagoudas[1], P. Blainey[2], S. Kim[3]
[1]MIT, Cambridge, MA, USA, [2]Broad Institute and MIT, Cambridge, MA, USA, [3]Broad Institute, Cambridge, MA, USA

Background: High-throughput and low-cost whole genome sequencing (WGS) of bacterial pathogens has the potential to transform clinical microbiology and infection control through high-volume surveillance of patient bacterial specimens. However, sample preparation of bacteria for sequencing is more resource intensive, costly, and logistically complex than DNA sequencing, providing a serious barrier for large-scale studies (100s – 1000s of isolates). **Methods:** We developed a procedure to prepare thousands of bacterial isolates for sequencing at the scale of 1000 samples in 7 days. Based on a microfluidic device developed in our lab, we implemented an improved operating protocol that increased throughput by an order of magnitude and extensively validated a protocol for device reuse without contamination. The new procedure produces DNA libraries for sequencing from an input of whole cells and allows a single operator to process 1000 samples in 7 days (or 144 samples/8 hours) using only four small devices and small quantities of reagents. **Results:** The microfluidic sample preparation produced DNA libraries that were reproducible and of comparable quality to libraries from a standard benchtop preparation method. We applied this method to prepare and sequence 3000 methicillin-resistant Staphylococcus aureus (MRSA) isolates collected from study subjects in a clinical trial studying the impact of an MRSA decolonization protocol. Using WGS data, we identified 45 different MRSA sequence types and determined that samples were resistant to an average of 4.5 antibiotics (range 1-9). **Conclusions:** Our microfluidic platform fully integrates bacterial DNA isolation and library construction to enable high-throughput bacteria WGS. This platform supports very large clinical studies and surveillance efforts, as shown through our sequencing of 3000 MRSA isolates. This technology can facilitate routine infection control efforts and support clinical and epidemiological studies.

Board LB-83. A Thousand Assays in One Night: Detecting Over >150 Genotypes of Picornaviruses from 11 Divergent Genera through Microfluidic Real-time RT-PCR

T. Ng[1], S. Rogers[1], A. Montmayeur[2], A. Nix[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]CSRA International, Atlanta, GA, USA

Background: Picornaviruses can cause a spectrum of diseases including respiratory infections, gastroenteritis, meningitis, acute flaccid paralysis, myocarditis, hepatitis, and neonatal sepsis. The picornaviruses of public health interest, the enteroviruses, hepatovirus and parechoviruses, are conventionally detected by qualitative reverse transcription, real-time PCR (RT-rPCR) targeting conserved RNA sequences in the 5' nontranslated region (5'NTR). The contribution of other recently described human and primate picornavirus genera (*Salivirus, Kobuvirus, Cosavirus, Cardiovirus, Senecavirus, Teschovirus, Sapelovirus,* and *Lesavirus*) to human disease burden is not understood. A high-throughput method is needed for simultaneous detection of the growing number of picornaviruses in humans and animals. **Methods:** Based on all available GenBank sequences, we have designed qualitative probe-based (TaqMan™) consensus 5'NTR RT-rPCR assays for 11 picornavirus genera. Application in a microfluidic PCR platform (Fluidigm) allows the simultaneous detection of all 11 genera (≥23 species and >150 genotypes). **Results:** Serial dilution experiments of 11 different picornavirus RNA confirmed that the microfluidic format has a limit of detection comparable to that of conventional RT-rPCR. Our experiments also confirmed that this microfluidic pan-picornavirus RT-rPCR approach successfully detected all available enterovirus (108/113 types) and parechovirus (16/17 types) genotypes. Less than 12 hours turn-around time is needed for a run with approximately 700 reactions (72 samples for 12 assays). **Conclusions:** This microfluidic PCR provides high-throughput, simultaneous detection of multiple picornaviruses, with significant time and labor savings versus the current-conventional RT-rPCR platforms. This platform will facilitate higher efficiency in large-scale pan-picornavirus surveillance in human and animal clinical samples.

Board LB-84. A Reference-Free, Alignment-Free Approach for Epidemiological Outbreak Investigations and Clinical Microbiology of Fungal Pathogens

K. Etienne, C. Huang, F. Vannberg
Georgia Institute of Technology, Atlanta, GA, USA

Background: Whole genome sequencing (WGS) and bioinformatics analyses used in molecular typing has become the cornerstone of epidemiology and clinical microbiology allowing for complete genome capture providing insight to strain variations important for etiology in emerging outbreaks; surveillance; and drug treatment. For fungal pathogens, these approaches involve generating a reference genome, which can be difficult given the limited availability of complete fungal reference genomes; performing multiple sequence alignment (MSA); and producing a phylogenetic tree. Workflows that alleviate MSA comparisons (alignment-free methods), specifically, using kmers (sequences of length k) have been investigated in bacterial and viral genomics, however it has yet to be tested and validated for fungal ge-

nomics. Additionally, a minimal set of maximally informative kmers can be instrumental in surveillance and clinical settings. **Methods:** A collection of 200 isolate WGS sequences representing 3 major fungal outbreaks was used for analysis. Briefly, a reference was generated/evaluated for each outbreak, subjected to MSA, SNP identification, followed by phylogenetic tree generation. For the kmer-based analysis, kmers were generated from sequences using an appropriate kmer length and denoising parameters, evaluated using a rapid alignment/reference free software, followed by a clustering analysis. Phylogenetic trees from each approach was compared for consistency. Informative kmers were derived for database creation and tested using blinded isolates. **Results:** Clustering results from the k-mer based tree had >95% concordance with SNP-based trees given appropriate data denoising and k-mer length. The kmer database accurately identified each outbreak set. **Conclusions:** These results suggest that kmer-based methods are comparable to SNP based methods with the additional advantage of speed that can be used in real-time analysis. This approach will greatly benefit fungal epidemiology and surveillance by mitigating the need for considerable resources to process fungal genomic data and extensive bioinformatics expertise.

Board LB-85. Developing Capacity for Whole Genome Sequencing in PulseNet International Laboratories

J. Concepción-Acevedo[1], H. Carleton[1], S. Stroika[1], A. Sabol[1], L. Joseph[1], M. Freeman[1], K. Hise[1], K. Kubota[2], I. Chinen[3], J. Campos[3], E. Pérez[4], A. Smith[5], R. Kumar[6], C. Nadon[7], E. Ribot[1], P. Gerner-Smidt[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Association of Public Heath Laboratories, Silver Spring, MD, USA, [3]National Institute of Infectious Diseases ANLIS, Buenos Aires, Argentina, [4]World Health Organization, PAHO, Washington, DC, MD, USA, [5]National Institute of Communicable Disease, Johannesburg, South Africa, [6]Central Public Health Laboratories, Ministry of Health, Muscat, Oman, [7]Public Health Agency Canada, Winnipeg, MB, Canada,

Background: PulseNet International is a global network dedicated to laboratory-based surveillance for foodborne bacteria. The network is comprised of laboratories in seven regions: Africa, Asia Pacific, Canada, Europe, Latin America and the Caribbean, the Middle East, and the United States. The mission of PulseNet International is to implement standardized molecular subtyping methods and share information in real-time with regional and national laboratories to support surveillance and outbreak response. For over 20 years, pulsed-field gel electrophoresis (PFGE) has been the primary method used by PulseNet International to identify and investigate foodborne outbreaks. Laboratories are now replacing traditional microbiology and subtyping methods, including PFGE, with next generation sequencing technology. Whole genome sequencing (WGS) has shown superior sensitivity, specificity and more timely resolution to outbreak clustering compared with traditional methods. PulseNet International is in the process of developing, validating, and issuing standard analysis procedures and establishing standardized nomenclature to facilitate data exchange and comparison. **Methods:** The PulseNet International vision is the standardized use of WGS to identify and subtype foodborne bacterial pathogens worldwide, replacing traditional methods to strengthen preparedness and response, reduce global social and economic disease burden, and save lives. **Results:** Training is the foundation for the success of PulseNet activities. PulseNet supports the transition to new methods by training microbiologists on standardized laboratory and WGS analysis methods. So far, more than 30 public health scientists working in international laboratories have been trained on the laboratory and analysis methods. **Conclusions:** PulseNet laboratories in all regions are making progress building their WGS laboratory and analysis infrastructure by acquiring sequencers, updating their BioNumerics licenses and training their public health scientists. Access to the bioinformatics tools needed to analyze data and lack of IT capacity are the main challenges for the region. PulseNet International is working on placing WGS analysis tools in the public domain and developing guidelines to support global WGS implementation.

Board LB-86. Contribution of HIV Molecular Data to Understanding an HIV Epidemiologic Investigation – West Virginia, 2017

M. Ocfemia[1], J. Cope[1], D. Wills[2], V. Hogan[2], C. Agnew-Brune[1], M. Evans[1], N. Panneer[1], W. Hoffman[2], H. Bradley[1], B. Hoots[1], P. Weidle[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]West Virginia Department of Health and Human Resources, Charleston, WV, USA

Background: During August–November 2017, in response to an increase in HIV diagnoses primarily among men who have sex with men in rural southern West Virginia, an epidemiologic investigation identified 70 HIV-infected persons (47 with HIV diagnosed in 2017 and 23 before 2017) and determined epidemiologic linkages based on named sex or needle-sharing partners. To assess rapidity of transmission and scope of the situation, we analyzed HIV sequence data to identify infections that were closely related. **Methods:** We analyzed HIV-1 pol sequences generated from provider-ordered drug resistance testing available for West Virginia residents using a computational tool, HIV-TRACE. We conducted pairwise sequence comparisons to identify molecular linkages (genetic distance of ≤0.005 substitutions/site) and molecular clusters of ≥2 linked sequences. We compared the molecular linkages with the named partner linkages identified during the investigation. **Results:** As of April 2018, HIV sequences were reported for 473 persons, including sequences for 36 (51%) of the 70 HIV-infected persons identified. All 36 persons had ≥1 molecular linkage, and 20 (56%) of the 36 had a molecular linkage to a named partner. Ten molecular clusters were identified, of which only one contained more than 3 persons. The large molecular cluster contained 19 persons: 16 (44%) of the 36 mentioned above and 3 persons not named during the investigation. **Conclusions:** In this epidemiologic investigation of a large HIV transmission network in rural southern West Virginia, HIV molecular data revealed the presence of a large molecular cluster and several smaller ones, indicating recent and rapid transmission. The large molecular cluster contained persons identified during the investigation and additional persons not previously identified. HIV molecular data can supplement epidemiologic data by providing evidence of recent transmission and improving the understanding of the scope of transmission.

Board LB-87. PA-Led Implementation of a Co-Located HIV/HCV/MAT Program in an FQHC in Rural Idaho: A Proactive Approach to Reduce Infectious Disease Outbreaks in the Context of the Opioid Crisis

H. Schaper
Health West Inc., Pocatello, ID, USA

Background: Reflecting on the CDC analysis of contributors to the 2015 HIV/HCV outbreak in Indiana, we identified similar risk profiles in 8 communities served by an FQHC in rural Idaho. Experience in a RW HIV clinic and training through the AETC provided a PA impetus to propose and implement a program to reduce risk of incident HIV and HCV infections, while addressing the need for MAT services in rural areas impacted by opioid dependence. **Methods:** Literature review identified RFs for IVU, HIV, and HCV infection, and data supporting efficacy of co-location of HCV treatment with MAT services to improve treatment adherence. Operations were observed at one FQHC treating HCV, and another offering MAT services. Online review of public health, HRSA, and other resources identified relevant policies and procedures guiding opioid and naloxone prescription, rapid HIV and HCV testing, MAT clinic operations, and linkage to care protocols. Policies were adapted to reflect FQHC's organizational requirements. Program design and patient handouts presented to 4 IVUs, and feedback was incorporated to optimize accessibility of MAT/HIV/HCV services. The final program, based on a model of integrated medical and behavioral healthcare and clinical pharmacy services, was presented to interested parties, approved by FQHC leadership, and implemented in May 2018. PA obtained DATA 2000 Waiver to prescribe Suboxone, and participation in ECHO programs on HIV, HCV, and opioids augments the team's medical knowledge and access to specialty consultations not otherwise available to rural, uninsured, and vulnerable patients. **Results:** Using a diverse set of resources, a PA developed and implemented a comprehensive program to increase diagnosis and treatment of HIV and HCV, as well as reduce incident infections through addressing treatment needs of IVUs. Through colocation of HIV, HCV, and MAT services in an FQHC, several barriers to access have been reduced. Adherence and outcome data are actively being collected. **Conclusions:** Addressing the syndemic of HIV and HCV in the context of a national, primarily rural, opioid crisis will require novel--but not necessarily revolutionary--approaches to the delivery of services. Sharing organizational processes among PCPs in rural and underserved communities may be an efficient way to mitigate the risk of new HIV and HCV outbreaks.

Board LB-88. Deaths with Possible Infectious Etiologies among Persons with Reported Alcohol, Opioid, or Illicit Drug Use, 2016-2018

S. Reagan-Steiner[1], S. Holzbauer[2], A. Denison[1], S. Lathrop[3], J. Bhatnagar[1], V. Singh[4], R. Mody[2], R. Lynfield[5], W. Shieh[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, St. Paul, MN, USA, [3]University of New Mexico, Albuquerque, NM, USA, [4]Midwest Medical Examiner's Office, Anoka, MN, USA, [5]Minnesota Department of Health, St. Paul, MN, USA

Background: Use of opioids, alcohol, and illicit drugs (substance use [SU]) is an increasing public health problem, and a risk factor for fatal infections. We performed a descriptive analysis of deaths among persons ≥14 years of age with reported SU for which autopsy tissues were submitted to CDC's Infectious Diseases Pathology Branch (IDPB) during January 2016--May 2018 to assess the frequency of possible infectious causes of death. **Methods:** IDPB received formalin-fixed autopsy tissues from health departments in collaboration with medical examiners/coroners (ME/C) and pathologists when infectious disease testing was not performed, or was negative or inconclusive. At IDPB, evaluation included routine histopathology, immunohistochemical (IHC), and molecular testing. Data were abstracted from submitted medical and autopsy records. Descriptive analysis by demographic, clinical, and pathologic features, and test results was performed. SU was defined as report of alcohol misuse/abuse, or misuse/abuse or toxicologic evidence of opioids or illicit drugs. **Results:** IDPB received autopsy tissues from 402 deaths; 104 (26%) had reported history of SU. These 104 cases were received from 19 jurisdictions, including 65% from Minnesota or New Mexico, which perform ME/C-based surveillance for infectious disease-related deaths. Median age of those who died was 59.5 years, 63% were men, 77% had other medical comorbidities, and 77% died before hospitalization. Substances reported included alcohol (51%), opioids (38%), and >1 substance (45%). Common clinical/pathologic syndromes were respiratory (57%), neurologic (15%), and multisystem (including endocarditis) (14%). Sixty-seven (65%) had possible infectious etiologies identified, including infections with non-pyogenic *Streptococcus* species (including *S. pneumoniae*) (27 cases), *Staphylococcus aureus* (10), influenza viruses (4), *Mycobacterium tuberculosis* (4), and free-living amoeba (4). **Conclusions:** IDPB identified pathogens of public health importance in deaths among persons with possible SU. Routine surveillance for infectious disease-related deaths, particularly those that fall under ME/C jurisdiction, could lead to a better understanding of the full spectrum of harms contributing to premature mortality in this population.

Board LB-89. Development of Shigellosis-Related Health Communication Materials: Results of a Qualitative Study among Gay, Bisexual, and Other Men Who Have Sex with Men (MSM)

A. Garcia-Williams[1], E. Wright[2], E. Townsend Respress[2], E. Caruso[1], S. Evener[2], K. Jacobson[2], R. Kachur[1], A. Bowen[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Georgia State University, Atlanta, GA, USA

Background: Since the 1970's there have been reports of shigellosis spread through sexual activity among MSM. There are growing concerns about the emergence of antimicrobial-resistant shigellosis, and clusters of resistant shigellosis have been reported among MSM. As part of a comprehensive approach to prevention and control of shigellosis among MSM, health communication can be used to raise awareness and promote healthy behaviors. We report on the results of a qualitative study that we used to develop shigellosis-related health communication materials for MSM. **Methods:** Six, hour-long, focus groups were conducted in Atlanta, GA among 24 self-identified MSM. Participants ranged in age from 21 to 59, and 63% were Black or Latino. A semi-structured interview guide was used to facilitate a discussion about preferences for shigellosis-related health communication materials. **Results:** Preferred location for health communication materials included virtual (e.g., social media, dating apps/sites), and physical locations (e.g., clubs/bars, bath houses, gyms, clinics). Participants reported that materials should be "funny, engaging," saying, "Make it catchy so people will think 'Oh! I need to look that up later.'" They emphasized that content must be short and simple, with some describing existing materials as having "Too. Much. Text." Stigma was

a concern, with one respondent saying existing material "sends another message to the gay community that we're dirty." Participants recommended focusing materials on behaviors, and not on populations, saying shigellosis "is an issue for everyone." **Conclusions:** Shigellosis-related health communication materials for MSM should be short, simple, and eye-catching, and should encourage information seeking. Care is needed to ensure materials are inclusive and not stigmatizing. Preliminary health communication materials developed as a result of these focus groups will be discussed.

Board LB-90. Assays for the Detection of Bacteria and Viruses Involved in Urinary Tract Infections and Profiling their Antibiotic Resistance

P. Brzoska, I. Pagani, N. Fantin, S. Patel, K. Varma, E. Diamond, N. Puri, K. Li
Thermo Fisher Scientific, South San Francisco, CA, USA

Background: Urinary tract infections (UTIs) are commonly caused by the gram-negative bacteria *Escherichia coli*, *Klebsiella pneumoniae* and the gram-positive *Staphylococcus saprophyticus* and *Enterococcus faecalis*. Other less frequent bacteria causing UTIs are *Morganella morganii*, *Acinetobacter baumanii*, *Citrobacter freundii* and others. Some viral and fungal pathogens also have been associated with UTIs. **Methods:** A bioinformatic assay design pipeline was developed to enable the design of specific and sensitive detection assays taking under consideration genome sequences of 80,000 bacterial species deposited at NCBI. The panel is based on the TaqMan® assay platform and was designed to allow the specific detection of these pathogens on the microfluidic OpenArray® platform. **Results:** Using this assay design pipeline, we developed a comprehensive panel of real time PCR assays to detect different bacteria, viruses, and fungi involved in UTIs. UTI infections are often resistant to antibiotic treatment. Carbapenem-resistant and extended spectrum beta lactamase-harboring bacteria are most commonly found in UTIs. We also designed and developed a panel of TaqMan® assays to detect genes conferring antibiotic resistance. We focused on beta lactamases and included detection assays for a wide variety of different members of this group, including the OXA, PER, NDM, CTX, and other beta lactamases. Assays for predictive identification of vancomycin resistance and quinolone resistance are included. **Conclusions:** We designed a panel of sensitive and specific TaqMan® assays that allows the identification of UTI associated microorganisms and their antibiotic resistance genes on the microfluidic OpenArray® system.

Oral Presentation Abstracts

01. Detection and Diagnosis

3:30-5:00 pm Grand Ballroom A/B

The Association between Precipitation, Temperature, and the Detection of Viruses in Six Community Groundwater Supplies in Minnesota

S. Gretsch, A. Koskey, K. Smith, T. Robinson
Minnesota Department of Health, St. Paul, MN, USA

Background: Conditions surrounding viral contamination of groundwater are not well understood. As studies indicate viruses are present in groundwater more frequently than previously thought, it is important to understand the factors that influence viral contamination in order to better protect groundwater sources and prevent waterborne illness. **Methods:** From May 2015-April 2016, weekly drinking water source samples were collected from six community groundwater supplies and tested for a suite of human enteric viruses and pepper mild mottle virus (PMMV) via qPCR. Hourly precipitation totals were obtained from the National Centers for Environmental Prediction stage IV quantitative precipitation estimate, which produces a 4-kilometer precipitation grid. The average of the four closest grid points to each well was used to estimate cumulative precipitation and occurrence of an extreme precipitation event (>90%) in the 24, 48, 72, and 168 hours prior to sample collection. Median precipitation totals were compared using the Kruskal-Wallis test. **Results:** Of the 306 water samples collected, 33 (11%) were positive for a virus. The median viral concentration was 2.1 genomic copies (gc) per L (range, <0.01 to 17.5 gc L^{-1}). Samples that were positive for PMMV were more likely to be collected when the ground was frozen than samples that were positive for a human enteric virus (13 of 19 samples vs. 3 of 14 samples, $p = 0.013$). Excluding the 72 samples collected when the ground was frozen, samples with a human enteric viral detection had a median cumulative precipitation of 1.47 mm (range, 0.00 to 54.0 mm) 24 hours prior to sample collection compared to 0.00 mm (range, 0.00 to 73.9 mm) for samples with no detection ($p = 0.070$). This association did not remain when looking at cumulative precipitation 48, 72, and 168 hours prior to sample collection. This association was also not observed when comparing samples with PMMV detections. **Conclusions:** Precipitation and temperature conditions prior to human enteric virus and PMMV detections were different, suggesting that these two classes of viruses have different pathways into groundwater. Precipitation occurring in the 24 hours prior to sample collection was most associated with human enteric virus detections, indicating that contamination occurs quickly follow precipitation events.

A Comparison of Reference-based and Reference-free Binning Tools for *Salmonella enterica* Subtyping Directly from Stool

J. Shay[1], H. Carleton[2], A. Huang[2]
[1]Association of Public Health Laboratories, Silver Spring, MD, USA, [2]Enteric Diseases Laboratory Branch, United States Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Culture-independent diagnostics are becoming more prevalent, meaning cultures may no longer be available for public health surveillance. We need new, high-resolution techniques to subtype and characterize foodborne pathogens directly from stool. One approach to do this is shotgun metagenomics of stool DNA. Multiple bioinformatics tools tout strain-level resolution from shotgun metagenomic data. We tested the applicability of three such tools to foodborne bacterial disease surveillance: MIDAS (reference-based), MaxBin (reference-free), and MetaBAT (reference-free). **Methods:** Each tool was assessed using shotgun metagenomic data from disease-state stools and computationally produced mock community data. Stool samples from fifteen patients in two similar *Salmonella enterica* outbreaks in 2013 were compared with matching isolate sequence data. Mock community data sets, produced by randomly selecting 39 species from a manually curated list of 334 bacterial species described as being found in stool in at least one peer-reviewed publication, were analyzed. Single nucleotide variants (SNVs) were detected using MIDAS, and were detected from MaxBin and MetaBAT output by aligning contigs to a reference using Mauve. **Results:** Thirteen of the fifteen disease-state stools had sufficient coverage of *S. enterica* for the MIDAS SNV calling pipeline (ranging from 6.6x to 250x). MIDAS phylogenetic trees correctly separated samples from two similar outbreaks with high support values (>0.99), but trees produced using MaxBin or MetaBAT output did not separate the outbreaks with any of the assembly tools tested. Each tool identified *S. enterica* SNVs in the mock communities with high precision (>0.96), but MaxBin and MetaBAT had higher sensitivity than MIDAS when using multiple mock samples (>0.96 vs. <0.41). **Conclusions:** Published tools for strain characterization from metagenomics need to be assessed for the unique circumstances of enteric pathogen surveillance. MIDAS was able to use metagenomic data to cluster outbreak samples consistently with isolate and epidemiological data, but MaxBin and MetaBAT were not. Each tool correctly identified *S. enterica* in mock communities and identified SNVs with high precision. Future directions include testing these tools on more real and mock outbreak data sets.

Development of a Human Pathogen-Specific Sequencing Assay for the Detection of Unknown Infection

J. Chen[1], F. Ge[2]
[1]Alaska State Public Health Virology Laboratory and University of Alaska Fairbanks, Fairbanks, AK, USA, [2]University of Alaska Fairbanks, Fairbanks, AK, USA

Background: The application of next generation sequencing (NGS) technology in infectious disease diagnosis is largely hindered by the fact that pathogenic sequences, especially viral, are often scarce in human clinical specimens. This obstacle leads to the requirement of subsequent deep sequencing and extensive bioinformatics analysis in order to find the rare pathogenic sequences in a sea of background host sequences. This is like "search for a needle in a haystack". **Methods:** We developed a method called "Preferential Amplification of Pathogenic Sequences (PATHseq*)", that can be used to greatly enrich pathogenic sequences in a sequencing library. This method does not require prior knowledge of the pathogen or presumption of infection and thus provides a fast and target-independent approach to identify known and unknown human pathogens. The PATHseq method uses a set of minimal length oligonucleotides, called "non-human" primers, that does not match to the sequences of the most abundant human transcripts. Instead of using random primers for the construction of sequencing libraries, the PATHseq method employs these minimal length "non-human" primers, which in turn, preferentially amplify non-human, presumably pathogenic sequences. **Results:** As a proof

of principle study, we developed a computer program to generate a set of 88 8-mer oligonucleotides that do not match the sequences of the top 2,000 most abundant human transcripts. The application of this set of oligos in replacement of random primers in the construction of sequencing library can eliminate most of the human transcripts from final sequencing library, greatly increasing the percentage of pathogenic sequences. We employed the PATHseq method for the investigation of an unknown infection from a clinical specimen with bronchitis & pulmonary inflammation and successfully identified a new variant of *Streptococcus pneumonia.* **Conclusions:** Using PATHseq method, we can generate a panel of minimal length (8-10 mer) "non-human" oligos that do not match to the most abundant human transcripts. We aim to develop a human pathogen-specific sequencing system that would provide at least 1,000-fold more efficiency than current NGS system. The success of this technology has the potential to fundamentally change the current practice in clinical infectious disease diagnostics. *PATHseq method is pending US and international patent.

Antimicrobial Resistance Genotypes Are Consistent with AMR Phenotypes in NARMS Isolates

M. Feldgarden[1], W. Klimke[1], A. Prasad[1], D. Haft[1], V. Brover[1], J. Folster[2], A. McCullough[2], P. McDermott[3], G. Tyson[3], S. Zhao[3], U. Dessai[4], J. Haro[4], C. Morales[5], M. Simmons[5], G. Tillman[4], J. Wasilenko[5]
[1]NCBI/NLM/NIH, Bethesda, MD, USA, [2]CDC/OID/NCEZID, Atlanta, GA, USA, [3]FDA/CVM, Silver Spring, MD, USA, [4]USDA/FSIS, Washington, DC, USA, [5]USDA/FSIS, Athens, GA, USA

Background: Antimicrobial resistance (AMR) is a major public health problem. To assist researchers in finding AMR genes within genomes, NCBI developed AMRFinder, which has been integrated into NCBI's Isolates Browser (www.ncbi.nlm.nih.gov/pathogens). **Methods:** To assess the accuracy of AMRFinder, we measured the consistency between our predicted AMR genotypes and reported resistance phenotypes from 6,242 National Antimicrobial Resistance Monitoring System (NARMS) *Salmonella enterica*, *Campylobacter* spp., and *Escherichia coli* isolates collected from animals, and food. Isolates were tested against the standard NARMS test panels, with a subset of resistant isolates tested against additional antibiotics. Resistance was identified using NARMS cutoffs. **Results:** Out of 94,679 susceptibility tests performed, 97% were consistent with predictions based on the acquired resistance genotypes. Within *S. enterica*, 97% of susceptibility tests were consistent with the predicted resistance genotype. Aztreonam and fluoroquinolone resistance in *S. enterica* were poorly predicted; *S. enterica* isolates with several different beta-lactamase families also displayed decreased susceptibility to amoxicillin-clavulanic acid. In *C. coli* and *C. jejuni*, respectively, 98% and 99% of susceptibility tests were consistent with the predicted resistance genotype when resistance via point mutation was incorporated, as fluoroquinolone and macrolide resistance were not associated with acquired AMR genes, but with point mutations. We also compared gene names generated by AMRFinder to those generated by Resfinder, a widely-used tool, yielding 1,292 different gene name. In five cases, Resfinder provided a more accurate gene name than AMRFinder (e.g., *fosA7* instead of *fosA*). In 979 cases, Resfinder overspecified the gene name (e.g., a novel OXA allele was called as OXA-61), and in 248 instances, Resfinder misidentified the AMR gene name (e.g., OXA-489 was called as OXA-61). **Conclusions:** AMRfinder had high consistency with AMR predictions based on acquired AMR genes. In addition, relative to a widely-used tool, AMRFinder rarely misidentified AMR gene symbols. Based on these results, AMRFinder appears to be an accurate AMR gene detection system.

Prevalence and Assessment of Risk Factors Associated with Antibiotic Resistance Genes (ARGs) among Children Under 5 in Informal Urban Maputo, Mozambique

A. Wood[1], D. Berendes[2], J. Knee[1], R. Nala[3], J. Brown[1]
[1]Georgia Institute of Technology, Atlanta, GA, USA, [2]Waterborne Disease Prevention Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]MISAU: Mozambican Ministry of Health, Maputo, Mozambique

Background: Antimicrobial resistance (AMR) is a growing public health threat that remains poorly characterized outside clinical settings. We examined AMR gene (ARG) prevalence and concentrations as a constituent of the gut microbiome among children aged 2 months to 5 years living in informal urban settlements (slums) of Maputo, Mozambique. **Methods:** ARGs conferring resistance to beta-lactam (BLA-TEM), chloramphenicol (FloR), quinolone (QnrB), sulfonamide (Sul1), and tetracycline (TetA) antibiotics, as well as a mobile genetic element (IntI1), were assessed by droplet digital PCR in the 400 stool specimens collected. **Results:** Among the 200 specimens processed to-date, 98% were positive for TetA, 64% for QnrB, 59% for FloR, and 96% for Int1. Within children, ARG concentrations varied by up to 5 $\log_{10}$ gene copies. On average, TetA and Int1 concentrations were similar, and were approximately 3 $\log_{10}$ gene copies higher than QnrB or FloR. Approximately 78% of children in 2015 were positive for ARGs. One year later, 78% of children with no change in sanitation facilities, compared to 92% of children living in compounds that received a septic tank during that period, were positive for ARGs. Preliminary associations between age and ARG concentrations were not significant. Further analyses will include assessment of associations with environmental conditions and behaviors from concurrent surveys and correlations between enteric pathogen detection and ARG concentrations in stool. **Conclusions:** ARG prevalence was demonstrated across classes of antibiotics. Data from these analyses will provide evidence of both within-host and environmental risk factors for ARG transmission in this setting, further clarifying potential roles for the environment in influencing AMR in children's gut microbiomes.

Rapid, Specific, and Cost-effective Identification of Zika Virus from Fixed Tissues of Congenital and Pregnancy-Associated Infections using a Novel Pyrosequencing-Based Assay

J. Bhatnagar, L. Estetter, D. Rabeneck, A. Paulino, S. Reagan-Steiner, R. Martines, G. Hale, W. Shieh, S. Zaki
Infectious Diseases Pathology Branch, Division of High-Consequence Pathogens and Pathology, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Zika virus (ZIKV) infection during pregnancy can cause microcephaly and is associated with pregnancy loss. Laboratory diagnosis of ZIKV is challenging for pregnancy-associated infections due to a short duration of viremia. Prolonged detection of ZIKV RNA in placental, fetal, and neonatal brain tissue has been reported. Tissue-based RT-PCR and pyrosequencing can improve and expand diagnostic opportunities for ZIKV infection, particularly when serum RT-

PCR or serologic testing is negative due to testing performed outside the optimal testing window. **Methods:** We have developed a ZIKV pyrosequencing-based RT-PCR (PSQ) assay and evaluated RNA extracted from formalin-fixed, paraffin embedded (FFPE) tissues from 60 case-patients, including placental/fetal tissues from 53 women, and brain tissues from 7 infants with microcephaly who died. In tissues of all case-patients (received during January 2016 to August 2017), ZIKV was previously identified by conventional RT-PCR and Sanger sequencing. Results of PSQ assay were also compared with ZIKV *in-situ* hybridization (ISH) performed on infant/fetal tissues. Specificity of PSQ assay was evaluated by testing various negative controls (n=40). **Results:** The PSQ assay detected and sequence-confirmed ZIKV in tissues from all 60 case-patients. All negative controls tested negative. The PSQ assay detected ZIKV RNA in various tissue: infant brains (n=7), placenta/umbilical cord of women (n=53) with various pregnancy outcomes (13 had first trimester and 10 second/third trimester pregnancy losses, 30 had live-born infants), and fetal brain/kidneys (n=5). The average time-frame from maternal ZIKV symptom onset (40/60 case-patients) to detection in tissues was 3.7 months. In PSQ assay positive brains, ZIKV RNA was also localized by ISH. By PSQ, results can be obtained in 1 day and in half the cost of Sanger sequencing. **Conclusions:** The PSQ assay can be a valuable diagnostic tool for rapid, specific, and cost-effective detection of ZIKV in tissues of congenital and pregnancy-associated infections. Tissue-based assays extend the timeframe for ZIKV detection and provide insights into viral tissue tropism and replication.

02. Seasonal Influenza and RSV

3:30-5:00 pm International Ballroom A/B/C

Assessing the Burden of Respiratory Syncytial Virus (RSV) within a Community-based Prospective Birth Cohort

J. Kubale[1], G. Kuan[2], L. Gresh[3], S. Ojeda[3], E. Azziz-Baumgartner[4], N. Sanchez[3], R. Lopez[5], A. Balmaseda[5], A. Gordon[1]
[1]Department of Epidemiology, School of Public Health, University of Michigan, Ann Arbor, MI, USA, [2]Sócrates Flores Vivas Health Center, Ministry of Health, Managua, Nicaragua, [3]Sustainable Sciences Institute, Managua, Nicaragua, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]National Center for Diagnosis and Reference, Ministry of Health, Managua, Nicaragua

Background: RSV causes substantial morbidity and mortality among children worldwide, commonly through severe lower respiratory tract infections accompanied by bronchiolitis and pneumonia. While RSV burden among hospitalized children has been relatively well characterized, fewer data exist about the burden of RSV among infants in the community. **Methods:** To assess the burden of incident RSV among infants, we conducted a prospective birth cohort study following children in Managua, Nicaragua from 0-2 years of age. Weekly contact was kept through home visits, and parents recorded infant health information in daily symptom diaries. Respiratory samples were taken from infants meeting the testing definition of fever or history of fever, using nasal and oropharyngeal swabs and tested for RSV using RT-PCR. A GEE Poisson model was used to calculate incidence rates, and account for correlation between repeated measures. **Results:** A total of 833 infants participated in the study between September 2011, and study conclusion in September 2016. Incidence of RSV across the five-year study was 250 cases per 1000 person-years (95%CI: 226.0, 276.2). However, incidence varied widely across age groups with the youngest infants (aged 0 to < 2 months) displaying the lowest rate of 93 per 1000 person-years (95%CI: 48.5, 177.2). Incidence increased in those aged 2 to < 6 months (145 per 1000 person-years, 95%CI: 103.7, 202.0), and peaked among infants aged 6 to <12 months of age (352 per 1000 person-years, 95%CI: 300.8, 413.0), before decreasing to 250 per 1000 person-years (95%CI: 215.4, 289.7) among infants ≥ 12 months. **Conclusions:** We found a substantial burden of RSV among children aged < 2 years in this community-based study. Further analysis is underway to characterize the burden of severe RSV in the cohort, examine risk factors that affect time to first RSV infection and severity, and characterize RSV re-infection.

Respiratory Syncytial Virus Deaths in Minnesota, 2006 - 2017

E. Bye[1], S. Holzbauer[1], C. Lees[2], K. Martin[1], H. Friedlander[1], K. Como-Sabetti[1], A. Strain[1], S. Reagan-Steiner[3], R. Lynfield[1]
[1]Minnesota Department of Health, St. Paul, MN, USA, [2]Dakota County, Apple Valley, MN, USA, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Respiratory syncytial virus (RSV) is a common cause of pediatric lower respiratory tract infections and can cause severe morbidity. Since 1996, unexplained deaths evaluated by medical examiners that may have an infectious cause are reportable to the Minnesota Department of Health's (MDH) Unexplained Deaths Project (UNEX). Cases <50 years old without significant comorbidities are

prioritized. MDH began severe acute respiratory illness (SARI) and population-based, laboratory-confirmed RSV surveillance (RSVS) in hospitalized patients in 2013 and 2014, respectively. We described RSV-associated deaths (RADs) reported through UNEX, SARI, or RSVS and death certificate (DC) review. **Methods:** During 2006-2017, RADs were defined as: 1) laboratory-confirmed RSV deaths detected through UNEX, SARI, or RSVS (including those who died <30 days of discharge); or, 2) RSV listed as a cause of death on DCs. As part of routine SARI and UNEX surveillance, clinical specimens were collected during hospitalization or autopsy. RSV was detected at MDH using PCR or at CDC using PCR and/or immunohistochemistry. **Results:** We identified 132 RADs through UNEX (49), SARI (14), RSVS (23), and DC (46). Of these, 92 (70%) were white and 75 (57%) were male. Median age was 31 years (range 0-97); 33% were <2 y/o, 14% 2-17 y/o, 7% 18-49 y/o, 14% 50-64 y/o, 11% 65-74 y/o, and 22% ≥75 y/o. Seventy percent of RADs occurred in a hospital, 19% at home, 10% in a long-term care facility, 2% were unknown and 70% had ≥1 comorbidity. Comorbidities varied by age; 33% of RADs <2 y/o had a comorbidity versus 95% ≥18 y/o. Congenital heart defects (18%) and prematurity (18%) were most commonly reported for RADs in <6 month olds compared to neurologic disorders (15%) and immunocompromising conditions (IC) (15%) for RADs in 6 month olds-17 y/o. For 18-49 y/o, the most commonly reported comorbidity was chronic lung disease (CLD) (56%); for 50-64 y/o, IC (50%); for 65-74 y/o, CLD (67%) and cardiovascular diseases (CVD) (67%); and for ≥75 y/o, CVD (59%). Smoking was noted for 30% of RADs ≥18 y/o. **Conclusions:** RADs are an underappreciated cause of death in adults and unexpectedly, 30% of deaths occurred outside the hospital. Comorbid conditions were common and type of comorbidity varied by age group. Additional studies are needed to further define risk factors and inform prevention measures to decrease RADs.

The Economic Impact of Influenza Hospitalizations on Families in Lao PDR

A. Xeuatvongsa[1], J. Mott[2]
[1]National Immunization Program, Vientiane, Lao People's Democratic Republic, [2]USCDC, Bangkok, Thailand

Background: Lao PDR purchases influenza vaccines for specific target groups but is considering expansion of the vaccine to children. We estimated the cost of laboratory-confirmed influenza hospitalizations by age to inform future cost-benefit evaluations for possible vaccine program expansion. **Methods:** From 5/2015 to 9/2017, we interviewed 2,118 hospitalized patients who met the World Health Organization (WHO) case definition for severe acute respiratory infection (SARI) and tested them by RT-PCR for influenza virus infection. Participants were from four provincial hospitals, including the capital city of Vientiane. Patients or their caregivers were interviewed by trained nurses to estimate direct and indirect costs associated with the illness event within 24 hours of admission, and at follow up 14 days after discharge. Direct costs were defined as in-hospital direct medical costs (clinical management, clinical laboratory costs, transportation, pharmaceuticals, and supportive care) and non-medical expenditures (food and lodging). Indirect costs included lost income of the patient and/or caregivers who of patients during illness, and child care services. Results were stratified by age groups < 2, 2-4, 5-19, and >= 20 years. Costs were converted from Lao Kip to US dollars at an exchange rate of $1 dollar to 8,000 Lao Kip. **Results:** Of the 2,118 SARI cases, 253 (11.2%) tested positive for influenza; 65 (25.7%) for influenza A/pdmH1N1, 68 (26.9%) for A/H3N2, and 120 (47.4%) for influenza B. Of the influenza positive cases, 74 (29.2%) were aged < 2, 59 (23.3%) 2-4; 58 (22.9%) 5-19; and 62 (24.5%) >= 20 years. The median total direct and indirect costs per hospitalization were $98 (Interquartile range [IQR] =70, 142). Of total costs, 93.9% were direct costs and 78.7% of patients paid out of pocket. Total costs by age were $87 (14, 768); $84 (26, 1301); $92 (27, 1012); and $133 (35, 2754) for age groups <2, 2-4, 5-19, and >=20 years, respectively. One third of persons with influenza had a family monthly household income of less than $125/month (and the median per capita income in Lao PDR was $137/month). **Conclusions:** An influenza hospitalization costs about 71% of the median per capita monthly income of Lao PDR. These data will aid Lao PDR in future cost effectiveness evaluations and expansion decisions for the vaccine program.

Effect of 9- to 16-day Holiday Breaks on the Time Courses of Seasonal Influenza Outbreaks in a School Population: ORCHARDS – Wisconsin 2014-2018

J. Temte[1], S. Barlow[1], M. Goss[1], E. Temte[1], L. Comp[1], Y. Zheteyeva[2], A. Uzicanin[2]
[1]University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]NCEZID - U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Breaks in K-12 school sessions have been postulated as nonpharmacologic means to reduce influenza transmission within schools. Using data from a longitudinal study in a Wisconsin school district, we assessed effects of 9- to 16-day planned school closures (winter and spring holidays) on student absenteeism and influenza cases during five successive outbreaks of seasonal influenza that coincided with these breaks over a 42-month period. **Methods:** The Oregon Child Absenteeism due to Respiratory Disease Study (ORCHARDS) is a prospective study of absenteeism and influenza in students, aged 4-19 years, in Oregon, WI, that began 9/02/14. Absenteeism due to influenza-like illness (a-ILI)—reported fever plus a respiratory symptom (cough, sore throat, nasal congestion, runny nose)—was assessed daily. Students with ILI were visited at home to collect symptom data and pharyngeal swabs for influenza PCR and multiplex PCR testing starting 1/05/17. We compared a-ILI, PCR-confirmed-influenza cases identified through home visits, and medically-attended influenza (MAI) in the community for 3-week periods immediately before and after planned breaks using the paired t-test. **Results:** Five seasonal influenza outbreaks occurred during the study period: A[H3N2] followed by B in 2014/2015, combined A[H1N1]/B in 2015/2016, combined A[H3N2]/B in 2016/2017, and A[H3N2] in 2017/2018. All outbreaks overlapped planned school breaks (two winter and three spring breaks), with initial school cases detected 3 to 6 weeks before the breaks. Absenteeism (a-ILI) decreased by an average of 52.6% (16.3 vs. 7.7 absences/day; t=3.35; p=.029; range: 22.3—73.2%), following planned breaks. Laboratory-confirmed influenza among students, decreased by an average of 58.7% (23 vs. 9.5 cases; t=4.90; p=.016; range: 40.4—100%). Community MAI cases showed a non-significant 17.5% decline (37.8 vs. 31.3 cases; t=0.45; p=.678). **Conclusions:** Breaks of 9 to 16 days were followed by significantly reduced levels of absenteeism due to ILI and laboratory-confirmed influenza cases in schoolchildren. These results suggest the potential of short school breaks to reduce within-school transmission. Further research is needed to explore whether these breaks modulate the dynamics of seasonal influenza outbreaks in the surrounding community.

Correlation between Hospitalized Influenza and Invasive Methicillin-Resistant *Staphylococcus aureus* Infections in Minnesota, 2010 – 2017

O. Arogbokun[1], C. Bernu[1], B. Abidoye[2], K. Como-Sabetti[1], M. McMahon[1], R. Lynfield[1]
[1]Minnesota Department of Health, St. Paul, MN, USA, [2]Yale University School of Forestry and Environmental Studies, New Haven, CT, USA

Background: Secondary bacterial infections are known to occur among influenza patients and can result in pneumonia and increased mortality. The Minnesota Department of Health conducts surveillance for hospitalized influenza and invasive methicillin-resistant *Staphylococcus aureus* (iMRSA) in Hennepin and Ramsey Counties as a part of the Emerging Infections Program. We used surveillance data to determine the correlation between hospitalized influenza cases and iMRSA during influenza seasons (October 1– April 30). **Methods:** Influenza cases were hospitalized patients with laboratory-confirmed influenza. iMRSA cases had infections with MRSA isolated from a normally sterile site (e.g., blood, cerebrospinal fluid). Cases were restricted to Hennepin and Ramsey County residents with cases identified during influenza seasons from October 1, 2010 to April 30, 2017. Cases were assigned *MMWR* weeks based on specimen collection date. Using STATA (v14), the correlation between the number of influenza cases and the number of overall iMRSA cases, and separately iMRSA pneumonia cases, were assessed in weekly time periods with the Granger causality test. **Results:** A total of 4,003 influenza and 897 iMRSA cases were included. The number of influenza cases were marginally associated with an increase in the overall number of iMRSA cases (Wald X^2=3.378, p=0.066); an increase in 1000 cases of influenza cases predicts 7 iMRSA cases the following week. Influenza cases were compared to iMRSA pneumonia cases (n=118). The number of influenza cases were associated with an increase in the number of iMRSA pneumonia cases (Wald X^2=17.025, p=0.001); the correlation is best described with a 2-week lag where an increase in 1000 influenza cases predicts an increase of 5 iMRSA pneumonia cases 2 weeks later. **Conclusions:** Granger causality tests are commonly used in economic models but have not been routinely applied to infectious diseases. Using the Granger causality test, we were able to predict increases in the number of iMRSA and iMRSA pneumonia cases due to increases in hospitalized influenza. Results of this analysis demonstrate the potential usefulness of the Granger causality test to predict disease occurrence.

Homotypic and Heterotypic Protection from Influenza Infection in Children

A. Gordon[1], S. Ng[1], G. Kuan[2], L. Gresh[3], S. Ojeda[3], N. Sanchez[3], R. Lopez[2], A. Balmaseda[2], E. Harris[4]
[1]University of Michigan, Ann Arbor, MI, USA, [2]Ministry of Health, Managua, Nicaragua, [3]Sustainable Sciences Institute, Managua, Nicaragua, [4]University of California, Berkeley, Berkeley, CA, USA

Background: Influenza causes substantial morbidity and mortality worldwide, especially among children. In tropical and developing countries, less is known about the burden and epidemiology of seasonal influenza. **Methods:** To examine the incidence of influenza, characterize risk factors for infection and disease severity, and investigate determinants of reinfection, we are conducting a prospective cohort study in children aged 0 to 14 years in Managua, Nicaragua. All children are provided with primary medical care through the study, and data from each visit is systematically recorded. Children meeting the study definition of a possible influenza case are tested for influenza virus by real-time RT-PCR following CDC protocols. **Results:** Between January 1, 2011, and December 31, 2015, ~1,700 children participated each year in the cohort study. Overall incidence of influenza during the 5-year period was 14.3 cases per 100 person-years (95% CI: 13.4, 15.1; range 8.1 to 22.8). Incidence of influenza varied by age, ranging from 21.2 cases per 100 person-years in children <2 years of age to 8.6 cases per 100 person-years in children aged 9-14 years. The effective reproductive number of each seasonal epidemic ranged from 1.2 to 1.4. Forty-eight percent of the cohort participants had at least one RT-PCR confirmed clinical influenza infection over the 5-year period. Homotypic protection lasting at least three years was observed for both influenza A H1N1pdm and H3N2 infections, with odds ratios of 0.08 (95% CI: 0.01, 0.58) and 0.33 (0.14, 0.75), respectively. No significant homotypic protection was observed with influenza B between seasons. Within-season heterotypic protection was detected between influenza types with odds ratios ranging from 0.17 (95% CI: 0.04, 0.73) to 0.50 (95% CI: 0.3, 0.81) depending on the length of time between heterotypic peaks. **Conclusions:** We found a significant burden of influenza, with an incidence of 14.3 cases per 100 person-years. The basic reproductive number for our seasonal influenza epidemics was within the range of those observed for seasonal influenza in temperate settings. Homotypic protection of at least 3 years was observed for both H1N1pdm and H3N2 infections. Heterotypic protection was observed within influenza seasons, but not across years. We are currently updating these findings to include the 2017 influenza season as well as to examine the duration of protection.

03. Evolving Challenges

3:30-5:00 pm International Ballroom D

Increasing Incidence of Invasive Nontyphoidal *Salmonella* Disease in Queensland, Australia, 2007-2016

A. Parisi[1], J. Crump[2], R. Stafford[3], K. Glass[1], B. Howden[4], M. Kirk[1]
[1]Australian National University, Canberra, Australia, [2]University of Otago, Dunedin, New Zealand, [3]Queensland Health, Brisbane, Australia, [4]University of Melbourne, Melbourne, Australia

Background: Although nontyphoidal *Salmonella* has emerged as a major cause of bloodstream infections worldwide, evidence from high-income countries is very scarce. In Australia, salmonellosis is a key cause of foodborne disease and rates of infection have increased over the last decade. Notification rates of *Salmonella* in tropical areas of Australia are amongst the highest in the industrialized world, but there has been little focus on invasive infections. **Methods:** We analyzed data on reported cases of invasive nontyphoidal *Salmonella* disease (iNTS) for Queensland from 2007-2016. We defined a case of iNTS disease as an episode of *Salmonella* isolated from blood, cerebrospinal fluid or other normally sterile site. We analysed data by sex, age group, and geographical area to examine trends and identify most common iNTS serotypes. For spatial analysis, we used 19 statistical areas, level 4 (SA4) as defined by the Australian Bureau of Statistics. **Results:** There were 995 cases of iNTS disease, with majority detected in blood (92%). *Salmonella* Virchow was responsible for 25% of all iNTS disease, while *Salmonella* Typhimurium was responsible for 20%. Among each of the serotypes, the proportion of infections that were invasive was highest for Choleraesuis (67%) and Dublin (38%). Notification rates peaked among infants (<1 year) and during the summer months. The iNTS notification rate in 2016 was 2.99 cases per 100,000 population (95% confidence interval 2.5-3.48), which was 41% higher than in 2007 (test for trend, $p < 0.001$). Notification rates by statistical areas ranged between 0.15 and 2.98 per 100,000 population, except for outback Queensland where the rate was 17.3 cases per 100,000 (95% CI 14.5–20.1). **Conclusions:** We observed an increasing trend of iNTS disease in Queensland. Although notification rates are lower than those in developing countries, the high disease burden in young children and remote areas represents an important public health risk that requires future investigation.

Medical Examiner–Investigated Fungal Deaths, Minnesota 2012-2017

S. Holzbauer[1], S. Lockhart[2], S. Reagan-Steiner[2], A. Strain[3], J. Palm[3], J. Christensen[3], R. Mody[1]
[1]Centers for Disease Control and Prevention/Minnesota Department of Health, Saint Paul, MN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Minnesota Department of Health, Saint Paul, MN, USA

Background: Infectious disease surveillance does not typically capture all cases occurring in a population, including fatal infections that go undiagnosed. Since 1996, unexplained deaths that appear to have an infectious etiology among persons with no significant underlying conditions investigated by a medical examiner (ME) are reportable to the Minnesota Department of Health (MDH) Unexplained Critical Illness and Death Project (UNEX) to aid in understanding the array of pathogens causing deaths. Because fungal infections can be hard to diagnose and few are reportable, UNEX is uniquely positioned to discover undetected fungal-related deaths. We describe fungal deaths detected by UNEX since 2012. **Methods:** We summarized UNEX cases investigated during 2012–2017. As part of UNEX surveillance, cases were defined as deaths that had infectious hallmarks and were not provider-explained. Autopsy and death scene investigations were used to guide testing at MDH and the Centers for Disease Control and Prevention (CDC) for an etiologic agent. Clinical samples were collected at autopsy. Fungal pathogens were detected at CDC using immunohistochemistry and PCR. **Results:** We investigated 378 UNEX cases; 152 (40%) had a pathogen identified. Fungal organisms were identified in 5 (3%) cases, including *Candida glabrata* detected in a 37 year-old female with bronchopneumonia; *Histoplasma capsulatum* in a 38 year-old male with necrotizing lymph nodes and coronary artery arteritis; *Candida albicans* in a 28 year-old female with tracheitis and necrotizing pneumonia; *Saccharomyces cerevisiae* in a 34 year-old male with necrotizing pulmonary granulomas; and *Candida* sp. in a 61 year-old diabetic male with suppurative pneumonia and necrotizing fasciitis. Two decedents had bacterial and/or viral co-infections and two had a history of substance abuse. **Conclusions:** UNEX surveillance in collaboration with MEs enables case-based investigations to establish potential infectious etiologies for otherwise unexplained deaths. Fungal detections were rare and *Candida* sp. accounted for the majority of those detected. Although some of these detections could represent colonization, the histological findings support the presence of true infection. Similar programs should be considered in other states as resources allow to assist in identification of new and emerging pathogens.

A Cause for Concern: *Candida auris* Fungemia in Critically Ill Patients

R. Petrossian, J. Shakil, D. Zapata, D. Wisa, R. Shah, V. Persuad, M. Rajabbik
Flushing Hospital Medical Center, New York, NY, USA

Background: Candidemia is a common concern in critically ill patients associated with a high morbidity. *Candida auris* is a new global health concern due to its resistance to multiple classes of antifungal medication and unknown virulence. Experiences range from asymptomatic colonization to fungemia. Over 200 cases have been identified in the United States with limited information regarding candidemia. **Methods:** Critically ill patients diagnosed with *C. auris fungemia* were included in our retrospective review. *C. auris* was confirmed by culture or polymerase chain reaction (PCR). **Results:** Specimens from 53 patients in our facility grew *C. auris*. 24 of which were found to be colonized on surveillance cultures. Of those, 29 were diagnosed with *C. auris* infection and 7 were candidemic. Ages ranged from 35 to 94, and 5 patients were females and 2 were males. All received broad spectrum antibiotics, central venous catheters, mechanical ventilation, vasopressors and 3 had surgical intervention prior to fungemia. All isolates were resistant to fluconazole and amphotericin. Four patients expired despite treatment of co-morbidities and fungemia. Three achieved culture conversion. Two patients received fluconazole prior to sensitivity results and all patients received micafungin. Three patients treated successfully received a minimum 15 days course. Two cases were misidentified. **Conclusions:** Candidemia is associated with mortality rates of 35 to 71%. Our review shows comparable mortality rates despite the limited sample size. *C. auris* exposure, broad spectrum antibiotic use, surgery, diabetes, critical illness and central venous catheters were identifiable risk factors. Guidelines recommend treating moderately ill patients with invasive candidiasis with fluco-

nazole and reserve echinocandins for the critically. High clinical suspicion is key in diagnosing *C. auris* due to frequent misidentification. We recommend treatment with echinocandins if *C. auris* is a concern. Twp patients whose isolates were misidentified expired despite subsequent treatment with micafungin. Confirmatory testing with cultures, PCR and strict infection control measures are recommended if there is any suspicion for *C. auris*.

Antibody Responses among MERS-CoV Infected Patients in Saudi Arabia

H. Al-Abdely[1], C. Midgley[2], K. Alanazi[1], A. Alkhamis[1], S. Trivedi[3], G. Abedi[3], S. Lester[3], O. Abdalla[4], A. Tamin[2], M. Mohammed[4], X. Lu[2], H. Algarni[4], S. Sakthivel[5], R. Alhakeem[1], H. Jokhdar[1], S. Ghazal[6], A. Assiri[1], J. Watson[2], S. Gerber[2], N. Thornburg[2]
[1]Ministry of Health, Riyadh, Saudi Arabia, [2]Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]IHRC, Inc., contracting agency to the Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Ministry of Health, Riyadh, GA, USA, [5]Battelle, contracting agency to the Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]Prince Mohammed Bin Abdulaziz Hospital, Riyadh, Saudi Arabia

Background: Serologic responses among patients with Middle East respiratory syndrome coronavirus (MERS-CoV) infection are incompletely understood. We sought to compare antibody responses in MERS survivors and patients who died. **Methods:** MERS-CoV infected patients were enrolled at a single hospital during August 1, 2015 – August 31, 2016. We periodically collected serum specimens for serologic analysis and MERS-CoV molecular testing. Specimens were diluted (1:400) and screened by ELISAs detecting antibodies that recognize the spike (S) and nucleocapsid (N) proteins; OD values >0.15 and >0.20 were considered positive for the S and N ELISA, respectively. Sera with detectable antibodies were subsequently titered in both ELISAs, and tested by microneutralization (MNt) assay. MERS-CoV RNA was detected by real-time RT-PCR targeting upE, N2 and N3; viral loads were estimated using upE Ct values. We conducted interviews and chart abstractions to identify illness onset and outcome. For analysis, we included specimens collected during weeks 2 – 8 post-onset. **Results:** Serum specimens (n = 66) were available from 23 patients; 10 died. Specimens were collected from survivors during day (d) 8 – d50 post-onset (n = 34, median = d18), and during d7 – d45 (n = 32, median = d18.5) among those who died. During weeks 2 – 3 of illness, 8/11 survivors had seroconverted (had detectable antibodies in ≥1 specimen) by N ELISA, but only 6/11 and 5/11 had seroconverted by S ELISA and MNt, respectively. By comparison, 7/7 deceased patients had seroconverted by MNt and N ELISA during weeks 2 – 3, but only 4/7 had detectable S ELISA responses. For two patients who died, S ELISA responses were still below the limit of detection at d27 and d45; all other patients still enrolled beyond week 3 had seroconverted in all assays. MERS-CoV RNA was detected in the sera of 5 patients who died; among the 7 specimens collected from these patients after week 3 of illness, all had detectable MNt responses and 5 still had detectable RNA (≤6.6 x 10^3 genome copies/ml). **Conclusions:** Our findings suggest that N ELISA responses may precede S ELISA responses in some individuals. Patients who died elicited early and robust MNt responses, but this was not sufficient to clear virus. These findings might have implications for diagnostics, vaccine development and antibody therapeutics.

Enhanced Environmental Surveillance for Avian Influenza A(H7N9), A(H5), and A(H9) Viruses in Guangxi, China, 2017-2018

T. Chen[1], Y. Song[2], J. Yang[1], M. Lin[3], Y. Tan[3], M. Chen[3], W. He[3], D. liu[4], T. Huang[4], X. Zhao[4], X. Wang[5], Z. Li[6], C. Greene[2], J. Kile[7], R. Zhang[2], D. Wang[1]
[1]Chinese National Influenza Center, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing, China, [2]Influenza Division, United States Centers for Disease Control and Prevention, Beijing office, Beijing, China, [3]Guangxi Autonomous Regional Center for Disease Control and Prevention, Nanning, China, [4]Chongzuo City Center for Disease Control and Prevention, Guangxi, Chongzuo, China, [5]Longzhou Center for Disease Control and Prevention, Chongzuo, Guangxi, Chongzuo, China, [6]Pingxiang Center for Disease Control and Prevention, Chongzuo, Guangxi, Chongzuo, China, [7]Influenza Division, United States Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: After the largest epidemic reported of human infections with avian influenza A(H7N9) virus during the 2016-2017 season, China launched poultry vaccination with a bivalent H5/H7 vaccine in September 2017. In December 2017, we initiated enhanced environmental surveillance to assess circulation of avian influenza viruses in live poultry settings at the China-Vietnam border. **Methods:** We collected environmental samples from12 live poultry markets (LPMs) and 8 poultry farms in two counties in Guangxi Autonomous Region from December 2017-April 2018. LPMs selected included all in townships bordering Vietnam plus the largest LPMs in the two counties. For LPMs, we randomly selected up to 5 poultry stalls per LPM, and collected swabs on visibly dirty surfaces for different poultry-related activities: on trucks used for poultry delivery, fecal droppings, drinking water samples, bloody sewage samples, feather-removal machines, and chopping boards. For poultry farms, we randomly selected two different locations and collected swabs on trucks used for poultry delivery, fecal droppings, drinking water samples, and egg shells. Samples were transported to a national influenza network laboratory and tested for avian influenza H5, H7 and H9 viruses by real-time reverse transcription PCR, and later transported to the National Influenza Center for full gene sequencing and hemagglutination assay testing. **Results:** From December 4, 2017, to February 2, 2018, 2911 environmental samples were collected from 12 LPMs, 2 poultry farms and 4 back-yards with poultry. Preliminary PCR analysis of the samples indicate that none (0%, upper 95% CI: 0.2%) were positive for H7, 186 (6%, 95% CI: 5-7%) were positive for H5, and 815 (26%, 95% CI: 25-28%) were positive for H9 viruses. The proportion of samples positive for any influenza A was highest in LPMs (56%, 95% CI: 54-57%), and lowest in backyard farms (22%, 95% CI: 16-28%) ($p<0.05$). For sample type, the highest proportion positive (76%, 95% CI: 72-80%) was from bloody sewage associated with the slaughter process, while the lowest was from egg shells (9%, 95% CI: 3-14% [$p<0.05$]). **Conclusions:** As of February 2, 2018, we did not detect any A(H7) virus from environmental samples in selected LPMs and poultry farms in Guangxi. Avian influenza viruses H9 and H5 continue to circulate, with highest proportions of positive samples detected in bloody sewage samples from LPMs.

Nationwide Prevalence of the Chagas Disease Parasite, *Trypanosoma cruzi,* in Government Working Dogs and Associated Cardiac Health Abnormalities

A. Meyers[1], M. Ellis[2], J. Purnell[1], L. Auckland[1], M. Meinders[3], J. Sanders[3], A. Saunders[1], S. Hamer[1]
[1]College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA, [2]College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO, USA, [3]Office of Health Affairs, Department of Homeland Security, Washington, DC, USA

Background: Infection with the protozoan parasite *Trypanosoma cruzi* causes Chagas disease, a potentially deadly heart disease of humans and animals. Chagas disease is increasingly recognized in the southern U.S., where triatomine vectors transmit the parasite among wildlife and domestic dogs with occasional spillover to humans. Clinical outcome in canines is uncertain, but infections range from asymptomatic to causing acute death or chronic heart disease. The Department of Homeland Security trains thousands of working dogs to provide detection and security functions across the country. We hypothesized that *T. cruzi* infection is greatest in dogs working in the southern states where triatomine vectors occur, and that cardiac rate and rhythm abnormalities would occur more commonly in infected than uninfected dogs. **Methods:** In 2015-17, we sampled 1,660 working dogs from 43 states and used indirect fluorescent antibody tests, immunochromatographic assays, and RT-PCR to determine infection prevalence. We applied a 24-hour, ECG Holter monitors to 42 dogs including 24 *T. cruzi*-infected and 18 uninfected dogs. Additionally, we measured serum concentrations of cardiac Troponin I (cTnI), a biomarker of cardiac injury. **Results:** We detected an overall infection prevalence of 7.3% with nearly equal infection between dogs in the north and the south. This finding suggests that mandatory canine training in the south prior to deployment, where dogs may encounter vectors, is a risk factor for infection. Overall, we found that 75.0% (18/24) of the seropositive dogs had one or more EGG abnormalities, which was significantly higher ($p<0.001$) then the 5.6% (1/18) of seronegative dogs with ECG abnormalities. Similarly, the average cTnI levels of seropositive dogs (0.071 ng/mL) was significantly higher than the average cTnI levels in a subset of seronegative dogs (n=10, 0.017 ng/mL, $p=0.015$), indicating that cardiac injury was more severe in positive dogs. **Conclusions:** Despite a century of research since discovery, the associations between *T. cruzi* infection and disease outcome are not completely understood in humans or dogs. Understanding the epidemiology and pathology of *T. cruzi* infection is critical for implementing disease control measures and managing the health of these high-value working dogs.

04. Late Breakers II

3:30-5:00 pm International Ballroom E

Nationwide Outbreak of Listeriosis Associated with Ready-to-Eat Processed Meat Products, South Africa

J. Thomas, N. Govender, K. McCarthy, N. Ramalwa, A. Smith, N. Tau, S. Williams, G. Ntshoe, M. Rakgantso, N. Page, M. Allam, A. Ismail, P. Sekwadi, R. Mathebula
National Institute for Communicable Diseases, Johannesburg, South Africa

Background: While listeriosis cases have been reported from the African continent, listeriosis outbreaks are not readily recognized or investigated in this region. We investigated a nationwide listeriosis outbreak during 2017-2018 in South Africa, which is the largest ever recorded worldwide. **Methods:** Cases with laboratory-confirmed Listeria monocytogenes infection from 1 January 2017 to 19 June 2018 were included. Epidemiologic, trace-back, and environmental investigations were conducted. **Results:** 1,053 cases including 212 deaths were reported. Multilocus sequence typing (MLST) of 628 clinical isolates using whole genome sequencing (WGS) determined that 571/628 (91%) isolates belonged to L. monocytogenes sequence type 6 (ST6). Age groups most affected were neonates (41%), followed by 15-49 year-olds (32%), who were likely at greater risk than expected due to pregnancy and HIV. Investigation teams interviewed 109 case-patients; 39 were ST6, 8 were non-ST6, and ST was not available for 47. Consumption of polony (a widely consumed ready-to-eat [RTE] processed meat product similar to bologna) was significantly associated with illness in outbreak-related cases. Trace-back investigations following the identification of ST6 as the cause of febrile gastroenteritis in children attending a crèche led to identification of the outbreak source. ST6 was isolated from polony and several RTE processed meat products produced at a single facility, and from the facility's processing environment. ST6 isolates from the RTE processed meat products, processing environment, and outbreak-related cases were highly related, showing <10 single nucleotide polymorphism (SNP) differences. Following recall of the implicated products, the number of cases rapidly declined. The recalled products had been exported to several other African countries; a suspected outbreak-related case was reported from Namibia, but was non-ST6. **Conclusions:** WGS proved invaluable for outbreak investigation and source identification. The trend towards mass production of processed food in South Africa coupled with weak food safety legislation and enforcement poses an ongoing risk for listeriosis outbreaks.

Post-Hurricane Leptospirosis Case Increase in Puerto Rico, October – December 2017

I. Schafer[1], R. Galloway[1], A. Artus[1], R. Stoddard[1], C. Rodriguez[2], M. Santiago[2], R. Cuevas-Ruiz[2], S. Reagan-Steiner[1], S. Zaki[1], A. Hoffmaster[1], W. Bower[1], H. Walke[1], C. Deseda[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Puerto Rico Department of Health, San Juan, Puerto Rico

Background: Leptospirosis, a potentially fatal bacterial zoonosis caused by *Leptospira* species and spread by the urine of infected animals, can cause outbreaks after hurricanes and flooding. It is endemic in Puerto Rico, which reported 45-73 cases annually from 2014–2016. After two hurricanes struck Puerto Rico in September 2017, an increase in suspected leptospirosis cases was reported. **Methods:** All

specimens from suspected case-patients submitted to the Puerto Rico Department of Health (PRDH) for leptospirosis testing post-hurricane were sent to CDC for testing by PCR (blood, urine, serum) and/or Microscopic Agglutination Test (MAT) serology and/or tissue Immunohistochemistry (IHC). Cases were classified using the Council for State and Territorial Epidemiologists leptospirosis case definition. Patient information was obtained from specimen submission forms. **Results:** CDC tested specimens from 712 patients with illness in the 3 months post-hurricane (through December 31, 2017), identifying 85 leptospirosis cases (54 confirmed, 31 probable). Among the 85 case-patients, 14 (16.5%) deaths were reported (9 confirmed, 5 probable), mean age was 48.8 years (range 10-92 years), and 66/83 (79.5%) were male. Patient specimens were submitted from hospitals in 6/7 regions: Metro (25.9%), Arecibo (27.1%), Ponce (14.1%), Bayamón (11.8%), Mayagüez/Aguadilla (9.4%), and Caguas (10.6%). Cases were confirmed by PCR alone (28, 51.9%), MAT alone (22, 40.7%), PCR and MAT (2, 3.7%), IHC alone (1, 1.9%), and PCR/MAT/IHC combined (1, 1.9%). Species-specific PCR identified both *L. interrogans* (n=19) and *L. kirschneri* (n=2) as causative species. **Conclusions:** The number of leptospirosis cases identified in Puerto Rico in the 3 months after the September 2017 hurricanes is over twice the number reported each October–December in 2014–2016, and more than the total annual cases reported in 2014–2016. However, diagnostic testing and case reporting behaviors by physicians before and after September, 2017 may have differed. Rapid detection of leptospirosis case increases enables early case identification and treatment in the affected area and in evacuees, which can decrease illness severity.

Active Surveillance for Rabies in Animals in Vietnam, 2016 – 2017

L. Nguyen[1], M. Phan[1], T. Nguyen[2], C. Tran[3], T. Nguyen[2], T. Nguyen[4], D. Nguyen[4], D. Nguyen[1], R. Wallace[3], B. Jesse[3], J. Doty[3], E. Pieracci[3], L. Orciari[3], D. Pham[1]
[1]Department of Animal Health of Viet Nam, Ha Noi, Viet Nam, [2]Sub-department of Animal Health of Phu Tho Province, Phu Tho, Viet Nam, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]National Centre for Veterinary Diagnosis, Ha Noi, Viet Nam

Background: Between 2011 and 2016, on average, annually 92 people died of rabies and 400,000 people needed medical treatment and rabies post-exposure prophylaxis (PEP) in Vietnam. In Phu Tho province, a total of 86 rabies outbreaks with 114 infected dogs were reported and 45 people died of rabies. **Methods:** Between January 2016 and December 2017, dog bite events were reported to local animal health staff (AHS); then, AHS collected information about locations of animals involved in the bite events and a unique patient identification number that links the health record. AHS conducted an animal rabies and community bite investigation and, when rabies was suspected, collected appropriate brain samples. These events occurred within 24 hours of the initial report. Collected samples were tested at the national laboratory using both direct fluorescent antibody and real-time PCR. **Results:** In total, 604 dog bite events were fully investigated, with 593 bitten people. 71.7 % events were reported by public health staff (PHS), compared with 15.1% events reported by AHS; public community and slaughters reported just more than 13%. Records from dog bite facilities showed a 26% increase in PEP demand after the program was implemented, likely reflecting an increase in detection of rabies exposures and initiation of PEP. In total, 226 samples collected from rabies suspect dogs were tested and 78 (34.5%) were positive with rabies virus. **Conclusions:** This pilot program was successfully implemented and detection of rabid dogs increased in Phu Tho province. If PEP decisions were dependent upon the investigation findings, it may be possible to more efficiently distribute rabies PEP to persons with a true exposure risk. As 71.7 % dog bite events were reported by PHS, it is critical to have a One Health approach to rabies investigations and effective communication between the human and animal health sectors; expansion of this active surveillance model to other provinces will likely help to reduce risk of rabies in Vietnam.

High Tetanus Burden among Men — Uganda, 2017

R. Casey[1], J. Nguna[1], O. Toliva[2], P. Tanifum[4], J. Lubwama[4], B. Zhu[4], A. Kisakye[5], E. Kabwongera[6], R. Tohme[7], B. Dahl[7], A. Ridpath[7], H. Scobie[7]
[1]Epidemic Intelligence Service, Global Immunization Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uganda National Expanded Program on Immunization, Kampala, Uganda, [4]Centers for Disease Control and Prevention, Uganda, Kampala, Uganda, [5]World Health Organization, Uganda, Kampala, Uganda, [6]UNICEF, Uganda, Kampala, Uganda, [7]Global Immunization Division, Centers for Disease Control and Prevention, Atlanta, GA, USA

Background: Worldwide, Uganda has one of the highest reported incidences of non-neonatal tetanus (non-NT), which can have a case-fatality ratio (CFR) approaching 100% without medical intervention. In Uganda, infants and reproductive-age women are offered tetanus toxoid-containing vaccine (TTCV), but older children and adult males are not provided the three TTCV booster doses recommended by the World Health Organization. Analyses of reported data in the District Health Information System (DHIS2) identified a lower CFR (18%) and a lower proportion of cases among males (47%) than expected. We conducted a field investigation to evaluate whether reported non-NT data reflects the true disease burden for Uganda. **Methods:** Across all four regions of Uganda, we selected 26 facilities (14 hospitals, 12 health centers), including 20 reporting high numbers of non-NT cases and 6 reporting zero cases. We compared the number of non-NT cases identified in facility registers with the number reported to DHIS2 during January 1, 2016 – June 30, 2017. For identified cases, we abstracted data from patient records, including medical history and outcome. **Results:** Among 482 non-NT inpatient cases reported to DHIS2 from hospitals visited, 342 (71%) were identified in facility registers, despite some missing registers. Males comprised 283 (83%) of case-patients identified. Of 145 cases with available inpatient records, 134 (92%) were clinically confirmed tetanus; among these, CFR was 54% and 22% had unknown outcome. Fourteen cases were identified at two hospitals reporting zero cases. Among >4,000 non-NT cases reported from health centers visited, only 3 cases were found in registers; the remainder were recording or data entry errors. **Conclusions:** A substantial number of tetanus cases and deaths occur in Uganda, especially in hospital inpatient settings. The high non-NT burden in men and high CFR indicate the need to add TTCV booster doses to protect all individuals across the life-course. The observed instances of under-reporting and over-reporting indicate the need for DHIS2 data quality improvement activities.

Novel Use of Syndromic Surveillance Data to Identify when *Candida auris* Carriers Present to Emergency Departments — New York City, 2018

D. Bloch[1], K. Murray[1], H. Parton[1], M. Lash[1], G. Airall-Simon[1], M. Antwi[1], S. Clark[1], G. Hrusa[2], M. Kratz[1], H. Kubinson[1], P. Del Rosso[1], D. Weiss[1]
[1]New York City Department of Health and Mental Hygiene, Queens, NY, USA, [2]New York City Department of Health and Mental Hygiene, New York, NY, USA

Background: *Candida auris* is a globally emerging resistant yeast causing health care-associated outbreaks. Outpatient *C. auris* carriers presenting to health care facilities unrecognized could introduce the yeast to new health care environments. About half of the *C. auris* cases in the United States were diagnosed in New York City (NYC). The New York State Health Department refers known outpatient *C. auris* carriers to the NYC Health Department for case management, and we interview carriers to identify facilities where they usually receive care, then inform those facilities of their patients' carrier status. We piloted a novel application of syndromic surveillance data to identify when *C. auris* carriers present to NYC emergency departments (EDs) or urgent care clinics (UCCs). **Methods:** We retrospectively queried ED and UCC syndromic surveillance data from January 1, 2016 – February 26, 2018 to identify possible visits by *C. auris* carriers using three identifiers: date of birth, sex, and home zip code. We investigated whether each signal of a unique patient-facility combination (PFC) represented the patient of interest via facility infection control practitioner interview and review of Regional Health Information Organization data. We calculated positive predictive value (PPV) and noted PFCs not previously identified by carrier interview. On February 27, 2018, we automated an hourly query of the syndromic database and investigated within 1 business day whether a signal represented a patient of interest and whether facility staff were aware of the *C. auris* status. **Results:** A retrospective query for 24 outpatient *C. auris* carriers yielded 42 PFC signals for 18 patients visiting 24 facilities on 140 occasions. We confirmed that 27 PFC signals identified patients of interest (64% PPV). Five confirmed PFCs were newly identified. Prospectively, 20/22 signals over 2.5 months identified patients of interest (91% PPV). Staff at facilities with prospective signals reported being aware of the *C. auris* status, yet on 2 occasions had not implemented *C. auris* precautions before our call. **Conclusions:** The use of syndromic surveillance data to rapidly identify and alert health care staff when *C. auris* patients present to EDs and UCCs can be expanded to other communicable diseases (e.g., lost to follow-up tuberculosis cases).

A Mathematical Model of the Transmission of Middle East Respiratory Syndrome Coronavirus in Dromedary Camels (*Camelus dromedarius*)

A. Dighe[1], T. Jombart[1], M. Van Kerkhove[2], N. Ferguson[1]
[1]MRC Centre for Outbreak Analysis and Modelling, Imperial College London, London, United Kingdom, [2]WHO Health Emergencies Programme, Geneva, Switzerland

Background: Middle East Respiratory Syndrome Coronavirus (MERS-CoV) remains an emerging disease threat, with regular reports of human cases on the Arabian Peninsula, driven by recurring camel-to-human transmission events. A prophylactic vaccine under development has been found to greatly reduce shedding in dromedaries, but there are major gaps in our quantitative understanding of the epidemiology of MERS-CoV in dromedary populations that need to be addressed to inform the development of evidence-based animal vaccination strategies. **Methods:** After reviewing publicly available data on camel demography and epidemiology of MERS-CoV in camels, we developed a stochastic, age-structured mathematical model of MERS-CoV transmission in single homogeneous camel populations, and between coupled sub-populations. **Results:** We show that if immunity is completely protective against future infection, a basic reproduction number (R_0) of 6 reproduces reported patterns of age-stratified seroprevalence observed in camel populations sampled in the Arabian Peninsula and Northern Africa. If immunity offers only partial protection, we estimate that R_0 is approximately 3. In large modelled populations where transmission persists long-term, epidemics are predicted to have an annual periodicity driven by seasonal births. Allowing reinfection (due to partial immunity) enhances persistence but disease extinction by chance is still expected in well-mixed populations of less than 1,000 animals. Hence, we predict that single herds are unlikely to be able to sustain MERS-CoV transmission. Using a meta-population model of multiple coupled small populations, we show that transmission can persist in the population as a whole due to random reintroduction of virus into populations in which transmission has previously ceased via animal movements. **Conclusions:** We conclude that the R_0 of MERS-CoV in camels is in the range 3-6, indicating moderate transmissibility. A meta-population model of MERS-CoV transmission reproduces the long-term persistence of MERS-CoV in camel populations in Africa and the Arabian Peninsula and may be useful for simulating camel vaccination strategies.

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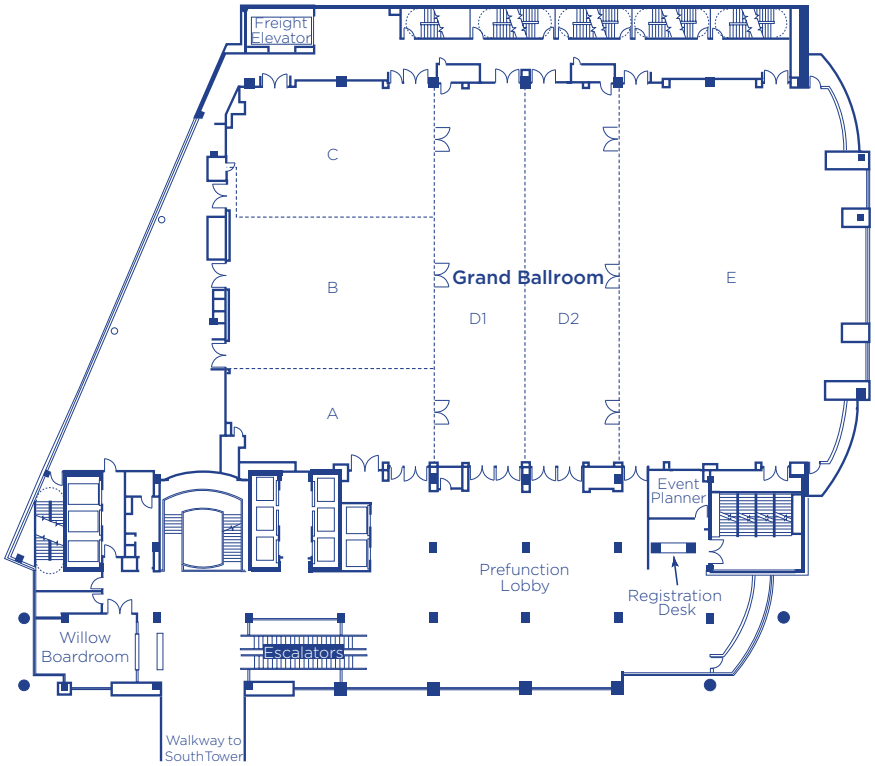
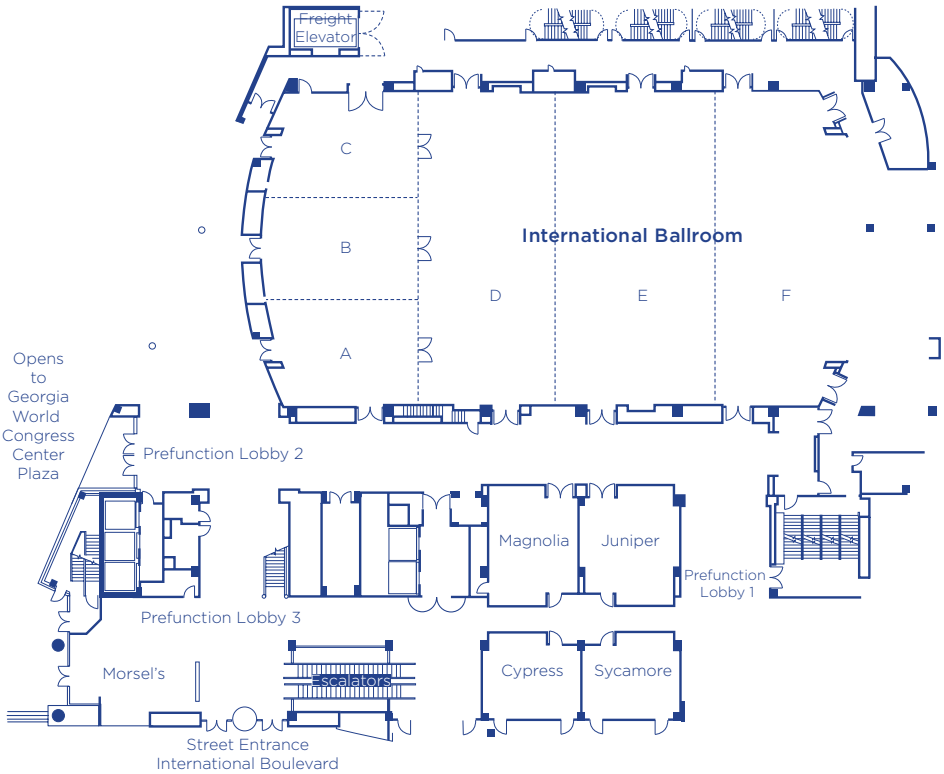
Floor Plans

CNN North Tower M4 Grand Ballroom Level



CNN North Tower M2 International Ballroom



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