
# International Conference on Emerging Infectious Diseases 2022 Poster and Oral Presentation Abstracts

Emerging Infectious Diseases is providing access to these abstracts on behalf of the ICEID 2022 program committee (http://www.iceid.org), which performed peer review. ICEID is organized by the Centers for Disease Control and Prevention and Task Force for Global Health, Inc.

Emerging Infectious Diseases has not edited or proofread these materials and is not responsible for inaccuracies or omissions. All information is subject to change. Comments and corrections should be brought to the attention of the authors.

*Suggested citation*: Authors. Title [abstract]. International Conference on Emerging Infectious Diseases 2022 poster and oral presentation abstracts. Emerg Infect Dis. 2022 Sep [*date cited*]. http://www.cdc.gov/EID/pdfs/ICEID2022.pdf

## Monday, August 8, 2022

## Poster Session 1 Abstracts

**12:30 PM – 1:30 PM**

**Grand Hall**

## COVID-19 and SARS-CoV-2

### Poster 1. Anti-SARS-Cov-2 Antibody in COVID-19 Positive Patients: Scope and Limitation

**R. Raihan**[1], S.A. Hassan Abdullah[2], S. Islam[3], M. Murshed[4], G. D. Harun[5], T. Aktar[4], N. Jubaida[6], M. Ul Anwar[7]
[1]US Bangla Medical College, Dhaka Bangladesh, [2] South Asia Field Epidemiology & Technology Network (SAFETYNET), Bangladesh, [3]American Society of Microbiology (ASM), Bangladesh, [4] Holy Family Red Crescent Medical College, Dhaka, Bangladesh, [5]Icddrb, Dhaka, Bangladesh, [6]Armed Forces Institute of Pathology Bangladesh, [7]Dhaka University, Bangladesh
**Background**: The ongoing pandemic of coronavirus disease 2019 (COVID-19) has shattered the entire world with 4.55 million deaths. In order to develop proper containment strategy, there is a pressing need to develop insights about the real proportions of SARS-CoV-2 infected persons among total population of any country or community. Although the role of antibody assay system has been of no help for diagnosis of SARS-CoV-2 infection, the utility of antibody testing for epidemiological purposes remains an open field. **Methods**: In this study, we used three different commercial SARS-CoV-2 antibody kits to develop insights about the utility of these kits in Bangladesh perspective. We selected 161 PCR-confirmed SARS-CoV-2-infected patients and checked their SARS-CoV-2 antibody presence at 3 time points - 5th, 8th and 14th day after primary diagnosis of the infection. **Results**: Among the 161 participants, 83% were male, majority (80%) aged below 50 years and 68.83% were symptomatic. On the day 5th and 8th of PCR positivity, 47.0%-58.0% and 66.5%- 83.0% patients' antibody (IgM/IgG) was positive respectively, which reached between 82.6%- 93.0% on day 14th after the COVID-19 diagnosis. Conclusions: We observed higher antibody positivity rate along with the time irrespective of the kits used. Results imply that antibody kits might be useful for epidemiological studies. This can also be used to detect the infection at the later stage of the disease process after two weeks when PCR or antigen test is negative.

### Poster 2. Implementation of an Adaptive Event-based Surveillance System through a Network of Drug Dispensing Outlets to Enhance Detection of COVID-19 Cases in Communities in Dar es Salaam, Tanzania, 2020

**H.L. Mohamed**[1], D. Faini[1], L. Ngailo[2], C. Munishi[1], R. Mutayoba[2], R. Mpembeni[1], M. Mponela[3], M.F. Jalloh[3], P. Mmbuji[3], W. Gatei[3], L. Subi[4], E. Kwesi[4], M. Bakari[1], J.M. Mghamba[1,4]
[1]Muhimbili University of Health and Allied Sciences, Dar es Salaam, Tanzania, [2]Amref Health Africa, Dar es Salaam, Tanzania, [3]Tanzania Country Office of the US Centers for Disease Control and Prevention, Dar es Salaam, Tanzania, [4]Ministry of Health, Community Development, Gender, Elderly and Children, Dodoma, Tanzania
**Background:** Tanzania reported its first case of COVID-19 on 16th March 2020. Cases quickly spread across multiple regions in the country; however, Dar es Salaam region remained the epicenter of the outbreak. To increase rapid detection of suspected COVID-19 cases and link them to rapid response teams (RRTs), we designed an adaptive event-based surveillance system through an existing network of Accredited Drug Dispensing Outlets (ADDOs) in Dar es Salaam. **Methods:** Between 23rd April and 18th May 2020, we conveniently selected 103 ADDOs from Kinondoni and Ilala municipalities in Dar es Salaam. Clients presenting with respiratory symptoms or influenza-like illness (ILI) and seeking symptom relieving medication were screened using the COVID-19 suspect case definition. Those meeting the criteria were requested for consent to provide mobile contact information and subsequently linked with designated COVID-19 RRTs for further investigation and SARS-CoV-2 testing. **Results:** Out of the 103 ADDOs in our network, 52 (50.5%) of them were from Ilala and 51 (49.5%) were from Kinondoni. A total of 75 clients from 69 ADDOs were suspected of COVID-19 or ILI. Common symptoms reported were fever (81%, 61/75), cough (73%, 55/75), and sore throat (60%, 45 /75). Majority of clients (73%) refused to provide their contact information, which hindered linkages with RRTs for further investigation. Based on qualitative data obtained from the ADDO administrators, clients' refusal to provide contact information was largely due to fear of getting quarantined in designated government facilities. **Conclusion**: Early in the COVID-19 outbreak in Tanzania, we demonstrated the feasibility and utility of ADDO surveillance as an adaptive event-based surveillance strategy that can be used to rapidly detect cases from the community. However, fear of quarantine posed a major challenge to

linking suspect cases to response teams. Strong community engagement is required to facilitate optimal cooperation and timely public health action.

### Poster 3. Routine Media Monitoring for COVID-19 Early Warning and Contextual Assessment in the WHO European Region

**L.E. MacDonald**, L. Hernandez-Garcia, J. Pires, J.T. Pukkila
Health Emergency Information and Risk Assessment (HIM), WHO Regional Office for Europe, Copenhagen Ø, Denmark

**Background**: Under the International Health Regulations (2005), the WHO Regional Office for Europe's (WHO EURO) early warning surveillance aims to achieve timely detection and appropriate management of all health emergencies of international concern across European Member States (MSs). In order to rapidly detect emerging COVID-19 issues during the COVID-19 pandemic, media monitoring for COVID-19 signals and events was implemented as a component of WHO EURO's epidemic intelligence activities. **Methods:** Using the Epidemic Intelligence from Open Sources (EIOS) system, open-source media were filtered using advanced text search algorithms and built-in system filters, to collate relevant reports. Reports were screened daily against pre-established relevancy criteria, adjusted to the regional pandemic situation, and registered into an interactive signal tracking tool. With geocoding, signals and events were then mapped to an internal facing COVID-19 media dashboard, which allowed for visualization of trends across WHO EURO MSs, by time and signal type. **Results:** Over a 12-month period 5245 relevant signals were detected through EIOS out of 155 787 screened media reports (3.4%), with 280 signals identified through other sources. The majority of reports were from the United Kingdom (14%), Spain (9%), France (7%), Italy (5%) and the Russian Federation (4%), and described changes in epidemiological trends (41%), signals of health system pressure (21%) and outbreak or clusters of interest (18%). The volume and type of signals varied by mentioned country, likely reflecting national media interest, publicly released information and freedom of press. **Conclusions:** Initial evaluations of the surveillance system identified solutions to improve geographical representativeness through adaptive search strategies, which also thereby improved system timeliness and usefulness. Daily signal summaries were distributed to internal stakeholders for immediate situational awareness, and individual reports provided COVID-19 contextual information for internal risk assessment and information products.

### Poster 4. An Investigation on Epidemiological Characteristics of COVID-19 — District West Karachi, March — December 2020

**A. Hussain**, M.A. Syed
Field Epidemiology Laboratory Training Pakistan, Health Department, Government of Sindh, Karachi, Pakistan

**Background:** The first COVID-19 case of district West Karachi has been identified through laboratory-based surveillance (LBS) on 18 March 2020. This novel respiratory disease was started from Wohan, China in December 2019. Due to rapid transmission, soon it had converted into pandemic. This was the first opportunity when local laboratories started to share COVID-19 data on daily basis to health department, Sindh. This study has highlighted the epidemiological characteristics of COVID-19 cases reported through LBS. **Methods:** With the start of pandemic, health department of Sindh made obligatory to designated public and private laboratories to report COVID-19 (positive PCR test) cases for the chief minister portal (CMP) on daily basis. From CMP data is shared to district level rapid response team (RRT), which investigate the cases, conduct contact tracing, on call follow-ups and recommend lockdowns. In this descriptive study, statistical analysis of COVID-19 reported cases from March to December 2020, was accomplished utilizing Epi Info version-7. Nasal swabs from 21347 suspected cases were tested for corona virus. **Results:** A total of 7,587 COVID-19 cases were reported through LBS. Mean age was 38.8 years (SD=15.3). Males (n=5,496, 72.4%) were predominantly affected. The most affected age group was 21-30 years (n=2,255, 29.7%). The 1,337 (17.6%) cases were hospitalized. The 4,545 (59.9%) cases were with fever, while 4,122 (54.3%) had respiratory symptoms. The case specific mortality was 3.1% (n=239), which was common among 61-70 years age group (n=74, 30.9%) and with comorbidity (n=155, 64.8%). The risk factors identified for death were age above 50 years (aOR=25.23, 95% CI: 18.78, 33.90), being hospitalized (aOR=4.56, 95% CI: 3.63, 5.74) and previous history of comorbidity (aOR=6.63, 95% CI: 5.52, 7.97). **Conclusion:** Coronavirus had infected the individuals of district West Karachi without considering the age and gender. However, COVID-19 mortality was high among older age group. Thus, after healthcare professionals, elderly should be vaccinated promptly. Management of comorbidities should be consulted with the experts. Moreover, LBS should be engaged in other infectious disease as well.

### Poster 5. Evaluation of an Abbott BinaxNOW Rapid Antigen Tests for SARS-CoV-2 Infection Using Self-collected and Healthcare Provider-collected Anterior Nasal Swabs in an Emergency Department Setting — Puerto Rico, December 2020–April 2021

**J.M. Wong**[1], A. Martinez-Quiñones[1], J. Cepeda Ramos[1], L. Hernandez-Mercado[1], J. Robles-Cedeno[1], H.R. Volkman[1], R. Tosado-Acevedo[1], J. Perez-Padilla[1], L.E. Adams[1], J. Bertrán-Pasarell[2], D. Sainz de la Peña[2], C. Oliveras García[3], J.L. Muñoz-Jordán[1], L. Sánchez-González [1], V. Frasqueri[3], V. Rivera-Amill[3], M.A. Rolfes[4], G. Paz-Bailey[1]

[1]Dengue Branch, Centers for Disease Control and Prevention, San Juan, Puerto Rico, USA, [2]Auxilio Mutuo Hospital, San Juan, Puerto Rico, USA, [3]Ponce Health Sciences University/Ponce Research Institute, Ponce, Puerto Rico, USA, [4]Epidemiology and Prevention Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background**: Antigen-based diagnostics for SARS-CoV-2 using self-collected swabs (SCS) are widely used because of their rapid turnaround time and low resource requirements. Test performance in real-world settings and comparison of SCS to healthcare provider collected swabs (HPCS) requires further evaluation. **Methods**: From December 2020 to April 2021, Abbott BinaxNOW COVID-19 Ag Card testing was introduced at two emergency departments in an enhanced surveillance system in Puerto Rico. Study staff enrolled patients with fever, cough, or dyspnea within 7 days, and collected nasopharyngeal swabs for testing using the CDC 2019-Novel Coronavirus (2019-nCoV) Real Time RT-PCR Diagnostic Panel. BinaxNOW tests with HPCS were offered at both sites according to the hospital's COVID-19 screening policy and test availability. At one site, study staff offered participants ≥21 years a supervised SCS BinaxNOW test after collection of the HPCS. For this evaluation, we included participants with a valid RT-PCR result and a BinaxNOW result by either collection technique within 7 days of symptom onset and using RT-PCR as the reference standard, calculated sensitivity, specificity, concordance, and discordance with 95% confidence intervals (CI) by the exact binomial method. **Results**: Among 522 participants enrolled during December 2020–April 2021, 249 (48%) had a BinaxNOW test within 7 days of symptom onset of whom 129 (52%) had a HPCS only, 69 (28%) had an SCS only, and 51 (20%) had both. Among the 249 participants with a BinaxNOW test, the median age was 34 (IQR 15–58) years and the median days from symptom onset to testing was 2 (1–4). The HPCS had a sensitivity of 79.2% (19/24; 95% CI 57.9–92.9%) and a specificity of 100% (156/156; 97.7–100%). The SCS had a sensitivity of 84.1% (37/44; 69.9–93.4%) and a specificity of 100% (76/76; 95.3–100%). In participants with both a HPCS and a SCS, 50/51 (98.0%; 89.6%–100%) had concordant results with only 1/51 with a negative HPCS, a positive SCS, and a positive RT-PCR. **Conclusions**: In this small study, the BinaxNOW COVID-19 Ag Card was highly specific, and results from SCS were comparable to HPCS. For symptomatic persons presenting to care within 7 days of symptom onset, SCS may be an acceptable method of specimen collection to reduce healthcare provider occupational exposure to SARS-CoV-2.

### Poster 6. Using Voluntary Contact Diaries to Understand University Campus Employee Contact Patterns

**S.S. Johnson**, K.C. Jackson, M.S. Mietchen, E.T. Lofgren
Washington State University, Pullman, WA, USA

**Background:** The COVID-19 pandemic has proven a difficult challenge for colleges and universities across the country. While students are learning in-person and virtually, employees -faculty, staff, graduate students, etc.-might be required to work on campus, especially if teaching. Student transmission is the focus for many testing programs, leaving employee contact networks and student-employee transmission understudied. **Methods:** We conducted an anonymous, voluntary online contact diary survey for faculty and staff of a PAC-12 university on their contact patterns both within and outside the university during the COVID-19 pandemic. Surveys were deployed when classes were virtual and when they were in-person. Participants were asked about the individuals they've encountered, the type and location of the interactions, and what COVID-19 precautions were taken – if any. Participants were also asked general questions about their location and COVID-19. Finally, participants from the first survey were asked to try and recall the same type of questions on a similar day from a year ago, prior to the COVID-19 pandemic. **Results:** Of the approximately 500 total responses, 75% worked primarily on the main campus. The mean number of contacts during the first survey period was 2 per respondent, with a standard deviation of 7. The second survey period had an increase from the first survey period, but not as high as pre-pandemic interactions. The first survey period had immediate family relations (43%) as the primary type of contact followed by colleagues and students (19%). The second survey and pre-pandemic period flipped this, with colleagues and students being the primary type of contact (>48%). **Conclusions:** These results suggest that, even while effectively social distancing, there is substantial out of home contact for university faculty and staff. Once in-person teaching resumed, employee contacts substantially rose but did not rise to pre-pandemic levels, further suggesting a potential increase in student-employee and employee-employee transmission as universities resume to more pre-pandemic

interactions. Understanding specific contact patterns and using these parameters will potentially demonstrate how transmission for future and current outbreaks could be further mitigated and reduced on campus.

### Poster 7. Cross-Sectional Study on SARS-COV-2 in Health Professionals at a Reference Hospital for Infectious Diseases, São Paulo - Brazil

**A.F. Ribeiro**, R.F. Cavalin, G. Bianchi, T. Nasser, N. Cavalcante, A. Souza, J.A. Lindoso, A. Losacco, R. Sobreira, M.A. Campos, L. Duarte, A.P. Santos, e Work Group
Instituto de Infectologia Emílio Ribas, Sao Paulo, Brazil

**Background:** The Instituto de Infectologia Emílio Ribas is a reference hospital for infectious diseases, especially COVID-19. From January 2020 to June 2021, 7128 suspected cases of flu-like illness were reported, with 34.3% confirmed by COVID-19. In the same period, 3479 cases of severe acute respiratory syndrome were reported, with 87.2% confirmed by COVID-19, 95% by laboratory criteria. The aim of the study was to analyze the prevalence of antibodies to the SRAS-COV-2 virus in health professionals. **Methods:** A cross-sectional study was carried out with a random sample of professionals, categorized into 4 categories: physician, nursing, other health professionals and administrative employees. A cross-sectional study was carried out with a random sample of professionals, categorized into 4 categories: physician, nurse, other health professionals and administrative employees. Professionals answered a structured questionnaire on google forms, with sample collection for serology. Pearson's chi-square test was performed. **Results:** A total of 292 questionnaires were answered, being 33.2% nurses, 25.7% physicians, 28.4% administrative employees and 12.7% other health professionals. A total of 233 serological tests were performed, 79.8% in 2020. The result of serology for SARS-COV-2 was reactive in 21.5%, ranging from administrative employees, 15.5%, nursing 21.4%, physicians 25, 5% and other professionals 29.0%, p=0,3890. The following are some risk factors analyzed with serology results: contact with covid (p = 0.079), number of people working in the same environment (p = 0.487), procedures that generate aerosol (p = 0.4591), working in another health service (0.001), use of urban transport (p = 0.144) and number of people eating together (0.305), use of surgical mask x N95 (0.456). **Conclusions**: There was a prevalence of 21.5% of SARS-COV among health professionals, with no statistical difference between the categories. There was a greater proportion of reactive serology among professionals who worked in more than one health service.

### Poster 8. Factors Associated with Early Uptake of COVID-19 Vaccination among Healthcare Workers in Azerbaijan, 2021

**J. Doran**[1,2,*], N. Seyidov[3*], S. Mehdiyev[3], G. Gon[2,4], E. Kissling, T. Herdman[1], J. Suleymanova, A.P. Couthino Rehse, R. Pebody[2], M.A. Katz[2], G. Hagverdiyev[3]
[1]UK Field Epidemiology Training Programme, UK Health Security Agency, London, UK, [2]High Threat Pathogen Team, Health Emergencies Program, World Health Organisation Regional Office for Europe, Copenhagen, Denmark, [3]Centre of Public Health and Reforms of the Ministry of Health, Baku, Azerbaijan, [4]London School of Hygiene and Tropical Medicine, London, United Kingdom
*These authors contributed equally to this publication and share first authorship

**Background:** In Azerbaijan, an upper-middle income former Soviet Union country with a population of 10 million people, the COVID-19 vaccination campaign began on January 18th, 2021, for healthcare workers (HWs) using CoronVac. Understanding factors associated with vaccine uptake among HWs is essential to advancing the vaccine campaign and containing the pandemic. **Methods:** We used enrolment-data from an ongoing study of COVID-19 vaccine effectiveness among HWs in Azerbaijan. We assessed independent variables, including demographics, occupational factors and acceptance of the COVID-19 vaccine by calculating crude odds ratios. Factors associated with uptake of the COVID-19 vaccine at the univariate level (defined as p-value <0.1) were iteratively inserted into a stepwise forward multivariable-regression model and retention was based on the model with the lowest Akaike information criterion. **Results:** From May 17-July 17, 2021, we enrolled 1,575 HWs at 7 hospitals; at enrolment, 73% had at least received one dose of CoronaVac and 67% had received two doses of CoronaVac. Of the 1575 participants enrolled in the study, the majority were female (93%), the mean age was 47 years (range: 21-72), and most participants were doctors (31%) and nurses (45%) (Table 1). Almost two-thirds (59%) of participants reported having no underlying clinical conditions. Most HWs believed the COVID-19 vaccine was safe (62%) and effective (47%). In the multivariable analysis, increased vaccine uptake was associated with older age (OR: 1.8; 95% CI: 1.09-2.86); having received the influenza vaccine in 2019-20 (OR: 2.3; 95% CI: 1.67-3.2); and working in a patient-facing role (OR: 1.41; 95% CI: 1.1-1.84). Lower vaccine uptake was associated with fair or poor self-assessed health status (OR: 0.49; 95% CI: 0.31-0.81); previous infection with COVID-19; (OR: 8.98; 95% CI: 6.7-11.9); and lack of perception that the vaccine was safe (OR: 0.25; 95% CI: 0.13-0.49). **Conclusions:** We found relatively high early vaccine uptake among HWs enrolled in a VE study in Azerbaijan. Vaccine uptake among HWs in Azerbaijan should

be increased by targeting younger HWs, HWs in non-patient facing roles and HWs with poor self-assessed health, and by emphasizing vaccine safety.

### Poster 9. Evaluation of the Impact of SARS-CoV-2 Nucleocapsid Mutations on Antigen Detection by Rapid Diagnostic Tests

**M.A Rodgers**[1], X. Luo[1], S. Cherukuri[1], G.A. Cloherty[1], A. Leeman[2], A. Palmer[2], L. Rogers[2], B. Dragoo[2], S. Muszynski[2], D. Noblesmith[2], S. Gardner[2], A. Snipe-Bushey[2], A. Kill[2], S. Kovacs[2], S. Gregory[3], T. Rae[3], A. Kar[3], J. Hartnett[3], C. Marohnic[3], L. Schurig-Briccio[3], D. Christensen[3], J. Moore[3], B. Tieman[3], A.S. Muerhoff[3], P.M. Hemken[3]

[1]ID Core Research, Abbott Laboratories, Abbott Park, IL, USA, [2]Abbott Rapid Diagnostics, Abbott Laboratories, Westbrook, ME, USA, [3]Biologics Discovery, Abbott Laboratories, Abbott Park, IL, USA

**Background**: The ongoing evolution of SARS-CoV-2 presents a challenge for diagnostic tests, which must keep pace with detection of new variants as they emerge and spread globally. In particular, antigen tests provide a frontline defense against the SARS-CoV-2 pandemic and must be continually tested for performance with emerging variants. While variants of concern are primarily defined by mutations in the spike protein, the mutations that would impact nucleocapsid detection of these strains by antigen tests are not often noted. **Methods**: To evaluate the impact of nucleocapsid mutations found in circulating SARS-CoV-2 strains, recombinant proteins were prepared that carry mutations identified in clinical specimens for testing on two lateral flow rapid antigen tests: Panbio COVID-19 Ag Rapid Test Device (Panbio) and BinaxNOW COVID-19 Ag (Binax). Mutations tested individually or in combinations included: D63G, R209I, R203K, G204R, R203M, A220V, M234I, P365S, A376T, Q229H, D348Y, E367Q, S235F, D377Y, and a wildtype (WT) Wuhan reference control. These mutations represent the unique nucleocapsid sequence profiles of several circulating lineages: B.1.1.7, B.1.617.1, B.1.617.2, B.1.617.3, B.1.618, AY.1, AY.2, P.2, B.1.526, B.1.526.1, B.1.526.2, and a panel of strains from Italy. Lateral flow antibodies were also evaluated with western blots and a research use automated high-throughput immunoassay on the ARCHITECT instrument. **Results**: Western blotting with the lateral flow antibodies confirmed detection of all mutant and WT recombinant antigens (rAg). Application of these same antibodies in an ARCHITECT immunoassay confirmed detection at a sensitivity equivalent to the WT control for all mutant rAgs tested. Serial dilutions of the rAg panel were also detected at an equivalent sensitivity to WT on the Panbio and Binax rapid antigen tests. **Conclusions**: These results demonstrate that the mutations in this study do not directly impact detection by the Panbio or Binax rapid antigen tests. Continued vigilance and monitoring of additional variants as they emerge will be critical to ensuring accurate diagnosis of SARS-CoV-2 infections with rapid antigen tests targeting nucleocapsid.

### Poster 10. Infection Prevention and Control Situation during COVID-19 Pandemic in Selected Tertiary Care Hospitals in Bangladesh: Results from WHO Infection Prevention and Control Assessment Framework

**G.D. Harun**[1], S.A. Sumon[1], Z. Hassan[1], S. Mah-E-Muneer[1], A. Rahman[2], S.A.H. Abdullah[3], S. Islam[1,4], A.R. Styczynsk[5]

[1]Programme on Emerging Infections, Infectious Diseases Division, icddr,b, Dhaka, Bangladesh, [2]Communicable Disease Control, Directorate General of Health Services, Bangladesh, [3]Consultant, SafetyNet, Bangladesh, Dhaka, Bangladesh, [4]University of New South Wales, Sydney, Australia, [5]Division of Infectious Diseases and Geographic Medicine, Stanford University, Stanford, CA, USA

**Background:** Infection prevention and control (IPC) in healthcare settings is a global priority for preventing hospital-acquired infection (HAI). WHO has developed the Infection Prevention and Control Assessment Framework (IPCAF) to measure current IPC activities, resources, and gaps at the facility level. This study aimed to assess the existing IPC practices of selected tertiary care hospitals in Bangladesh during the COVID-19 pandemic using IPCAF to explore its strengths and weaknesses. **Methods:** A total of eleven tertiary-care hospitals of 300-1200 bed capacity were assessed from September to December 2020. The IPC focal person of the hospital was interviewed. Descriptive analysis was performed. The IPCAF score was calculated based on WHO eight core components, each of which had a score of 100. Based on the total score, the hospitals were categorized into four distinct IPC levels- Inadequate, Basic, Intermediate, and Advanced. **Results:** The median IPCAF score was 321 out of a total score of 800. Three-fourths (73%) of the hospitals met the criteria for 'Basic' IPC level and two hospitals were categorized as 'Intermediate' level. None of the hospitals had an IPC surveillance system with reliable surveillance case definition to tract clinically-defined infections. More than half (55%) of the hospitals did not have defined IPC guidelines, training, and education programs. In 35% of hospitals, health workers have never or rarely received any IPC training. Most (90%) of hospitals did not have any active IPC monitoring and audit system. Inadequate staffing and workload were found in half of the hospitals. More than two-thirds (72%) of hospitals had

functional hand hygiene stations, but sufficient toilets were available only in 37% of hospitals. **Conclusions:** In the majority of sampled hospitals, IPC activities and structures are at a BASIC level, demonstrating inadequate practices to ensure the safety of healthcare workers, patients, and visitors. In particular, overcrowding poses an immediate threat to patient safety in the setting of widespread SARS-CoV-2 transmission. Quality improvement programs and feedback mechanisms should be implemented to strengthen all IPC core components, particularly around IPC surveillance and guidelines.

### Poster 11. A Cluster of SARS-COV-2 Infections among Workers in a Factory Making Personal Protective Equipment – Buikwe District, Uganda, 2020

**A. Byaruhanga**[1], E. Katana[1], A. Ndyabakira[1], S. Nabatanzi[1], L. Bulage[1], D. Kadobera[1], A. Riolexus Ario[1,2]
[1]Uganda Public Health Fellowship Program, Ministry of Health, Kampala, Uganda, [2]Uganda National Institute of Public Health, Kampala, Uganda

**Background:** In September 2020, a cluster of severe acute respiratory syndrome coronavirus 2 (SARS- COV-2) infections was reported among workers at a factory making personal protective equipment (Factory X) in Buikwe District, Uganda. The factory had previously instituted risk reduction measures, including mandatory wearing of masks and hand sanitizing at all entry points. We investigated the cluster to establish the magnitude and determine factory-related exposures associated with transmission. **Methods:** We defined a confirmed case as a positive RT-PCR test for SARS-COV-2 infection in a Factory X worker during August-September 2020. We defined a control as a Factory X worker with a negative RT-PCR test for COVID-19 during August-September 2020. We identified cases through records at the health facility at Factory X. We selected controls randomly from Factory X departments with cases. We conducted a case-control study using a semi-structured, standardized questionnaire to compare exposures between cases and controls, using a randomly selected subset of cases from the line list. We conducted informal qualitative interviews with facility staff to understand compliance to prevention measures and used an environmental assessment checklist to identify factory-specific risk factors for infection. **Results:** We identified 163 cases from 18 August-14 September 2020; none died. The factory attack rate was 10.9/100 workers. The engineering department was the most affected (attack rate=29.8/100 persons). In the case-control study with 75 cases and 75 controls, lack of mask use (AOR=13.5, 95% CI 2.4-75.8) and working in the engineering department (AOR=5.9, 95% CI 2.3-15.8) were associated with infection. **Conclusions:** This cluster of SARS-COV-2 infections was associated with failure to use masks and working in poorly ventilated and/or congested areas. We recommended development of Standard Operating Procedures to ensure adherence to face mask use and provision of adequate windows and doors by factory management.

### Poster 12. Israel COVID -19 Readiness and Resilience Exercise - Lessons Learned - 2020-2021

**K. Muhsen**[1], D. Cohen[1], C. McNeil[2]
[1]Department of Epidemiology and Preventive Medicine, School of Public Health, Sackler Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel, [2]Ending Pandemics, San Francisco, CA, USA

**Background**: Reevaluating response plans is essential to ensuring readiness and resilience to the COVID-19 pandemic challenges. The During Action Review and Tabletop (DART) methodology provides a unique opportunity for retrospective and prospective assessment to inform adaptive response. Israel was pioneer in introducing COVID-19 vaccinations (December-2020), leading to substantial declines in COVID-19 rates. Israel experienced 4 COVID-19 surges, the last ~5-6 months after the first vaccine campaign, caused by the Delta variant and waning immunity, which triggered the introduction of COVID-19 booster vaccination (July-30 2021). We evaluated Israel's readiness and resilience. **Methods:** A DART analysis was conducted between January to June 2021. During the retrospective stage, a role-based questionnaire and discussions were undertaken in a participant-led review of the response, focusing on epidemiology and surveillance, risk communication, and vaccines. The prospective stage included tabletop exercises to evaluate short to long-term simulated scenarios. **Results**: Participants emphasized the pivotal role of Israel globally by sharing experience related to vaccination. Perceived strengths included multi-sectoral collaboration between the Ministry of Health, healthcare providers, and other organizations, stretching capacities, expanding laboratory workload, establishing/maintaining surveillance, the vaccine prioritization plan, strong infrastructure including computerized databases that enabled real-life assessment of vaccine uptake and impact. Challenges included changing case definitions early on, insufficient staffing. Patient and contacts quarantine was challenging among underprivileged communities. Risk communication approaches need to focus on creating norms in behavior. Trust issues and limited cooperation were noted especially among ethnic and religious minorities. To ensure continued improvement in readiness and resiliency, participants recommended establishing a nationally-deployed system for bringing in and acting upon feedback from the field, especially risk communication and vaccines. **Conclusions**: DART approach enabled successful evaluation of COVID-19 pandemic response in Israel,

appraised strengths and weaknesses, and led to concrete recommendations for adjusting responses to the chronic pandemic phase and future similar events.

### Poster 13. *Withdrawn*

### Poster 14. Physical and Mental Health Condition of Hospitalized COVID-19 Patients in a Dedicated COVID-19 Hospital in Bangladesh

**S. Islam,** I. Haque, A. Chowdhury, G.D. Harun
Department of Public Health, Faculty of Allied Health Science, Daffodil International University, Dhaka, Bangladesh

**Introduction:** Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic has triggered the globe in 2020. The pandemic has squeezed the physical, mental, livelihood and economic activities both infected and non-infected population of the world. Infected and hospitalized people were severely distressed both physically and mentally with the disease. This study aimed to assess the physical and mental health condition of hospitalized COVID-19 patients in a dedicated COVID-19 hospital in Bangladesh. **Methods:** This cross-sectional study was conducted among 101 laboratory-confirmed COVID-19 hospitalized patients of a dedicated COVID-19 Hospital in Dhaka city of Bangladesh from 1 July to October 2020. Hospital Anxiety and Depression Scale (HADS) was used to assess the mental health condition. Multivariable logistic regression was performed for patient-perceived recovery with age, sex, ethnicity, body mass index (BMI), co-morbidities, and severity of acute illness as co-variates. Factor analysis was applied to assess mental health. Data were analyzed by SPSS Statistics software 22.0 (Armonk, NY: IBM Corp). **Results:** A total of 101 laboratory-confirmed COVID-19 patients were enrolled. Three fourth (75%) of cases admitted hospital with mild symptoms, followed by 15% severe and 10% with moderate symptom. Overall, the median age of the participants was 37 years (IQR: 31-53); more than 80% of these patients were under 60 years. More than half of the patients (52.4%) had at least one co-morbidity, including hypertension in 35 (34%), diabetes mellitus in 22 (21.4%) and ischemic heart disease in 10 (9.7%) patients. There was significant association with severity and age and comorbid condition (p=0.02). According to HADS scale data, one third (33%) had severe and 47% had moderate anxiety and depression. Anxiety and depression were significantly associated with age, socio economic status and having a full time attendant (p=. <0.05). Severe anxiety and depression found highly significant association (p=0.001) with COVID-19 severity and outcome. **Conclusions:** The study suggests that mental health counseling is crucial beside treatment for the better health outcome and early recovery. The policy makers and hospital authority should take these findings for better COVID-19 treatment and management.

### Poster 15. Contact Tracing and Community-based Surveillance for COVID-19 Using Health Assistants, Masindi District, Uganda

**B.O. Amodan**[1,2], I. Akusekera[1], G. Amanya[1], J. Namayanja[1], D. Kadobera[1], A. Driwale[2], L. Bulage[1], A.R. Ario[1,2], J.R. Harris[3]
[1]Uganda Public Health Fellowship Program, Kampala, Uganda, [2]Ministry of Health Uganda, Kampala, Uganda, [3]Division of Global Health Protection, Centers for Disease Control and Prevention, Kampala, Uganda

**Background**: On 1 May 2020, the first COVID-19 community case in Uganda was detected in Masindi District, Uganda. The case-patient, a policeman, reportedly had an extremely high number of contacts. Although national-level healthcare workers had previously conducted all contact tracing in Uganda, this approach was considered unfeasible in this situation. In order to meet this requirement, Health Assistants (HAs) in Masindi District were trained to conduct active COVID-19 surveillance. We compared the costs of deploying central-level and local-level responders. **Methods**: We worked with the Masindi District Task Force to identify 31 HAs, who we trained for 2 days on COVID-19 contact tracing and community-based surveillance (CBS). We established a CBS system involving local leaders and village health teams (VHTs) who supported the HAs to trace and monitor all contacts each day. We determined and compared response costs between the use of 31 HAs and 10 national-level epidemiologists for this work. **Results**: HAs identified 729 contacts to the case-patient. Each HA visited or telephoned 20-25 contacts daily for 14 days after their last exposure to the case-patient. Only four (<1%) contacts were lost to follow-up. All contacts tested negative for SARS-CoV-2 on Day 14. The new CBS system received and investigated 531 separate community alerts for suspected cases unlinked to the index case. Using HAs vs national-level epidemiologists reduced the 14-day response costs by 70% ($8,300 vs $2,500). **Conclusion**: Local training on contact tracing and CBS enabled a less costly approach to alert response, contact tracing, and control of COVID-19 at the district level. Decentralized use of HAs to conduct contact tracing and CBS can increase community and district ownership of COVID-19 response.

### Poster 16. Nonpharmaceutical Interventions and Changes in Reported COVID-19 Cases and Community Mobility during Ramadan and Eid-al-Fitr – 14 Middle Eastern countries, April 23 – June 3, 2020

**M. Al-Shawaf**, K.C. Coy, C. Jones, G. Fox, L. Erickson-Mamane, S. Hillis, K.R. Victory, A.J. Hakim
COVID-19 Response Team, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Muslims around the world observed Ramadan and Eid al-Fitr differently in 2020 in response to the COVID-19 pandemic. Countries implemented nonpharmaceutical interventions (NPIs) to reduce the spread of COVID-19. Reports from Middle Eastern countries show different approaches to NPI implementation. **Methods:** We explored the relationship between daily percent change in COVID-19 cases and daily average percent change in community mobility with NPIs during Ramadan and Eid al-Fitr, April 23–June 7, 2020, in 14 countries (Afghanistan, Bahrain, Egypt, Iraq, Jordan, Kuwait, Lebanon, Libya, Oman, Pakistan, Qatar, Saudi Arabia, United Arab Emirates, and Yemen). Epidemiologic data came from Johns Hopkins University COVID-19 Data Repository and mobility data from Google Community Mobility Reports. NPIs included stay-at-home orders, curfews, mosque closures, non-essential business closures, and gathering restrictions. Daily changes in cases and mobility were estimated and compared between groups of countries that implemented these NPIs and those that did not. Cases and community mobility were assessed with a 10-day lag. **Results:** Among the 14 countries, 5 implemented stay-at-home orders, 9 implemented curfews, 5 implemented non-essential business closures, 12 implemented gathering restrictions of any size, and 8 implemented mosque closures during Ramadan. During Eid al-Fitr, 5 countries implemented stay-at-home orders and 8 implemented curfews. During Ramadan, all restrictions except mosque closures were associated with lower daily percentage increases in cases, while stay at home orders, non-essential business closures, and mosque closures were associated with a greater reduction in daily mobility. Neither stay at home orders nor curfews were associated with either daily percent change in new cases or daily average percent change in mobility. **Conclusions:** Understanding the ways NPIs and COVID-19 case trends and mobility interact could be useful in periods of expanded mitigation efforts and policy planning moving forward, especially in areas where vaccination is not widely available.

### Poster 17. Bayesian Estimation of Multisystem Inflammatory Syndrome in Children (MIS-C) Cases Reported within COVID-NET Catchment Areas by Capture-Recapture — 10 states, April – December 2020

**L.D. Zambrano**[1], L. Meng[1,2], A. Miller[1], H. Pham[1], F. Havers[1], C. Taylor[1], M. Newhams[3], M. Patel[1], M. McMorrow[1], L. Feldstein[1], S. Godfred-Cato[4], E. Belay[5], J.Y. Abrams[5], A. Randolph[3], C.E. Rose[4], A.P. Campbell[1]
[1]National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]General Dynamics Information Technology, Inc., Falls Church, VA, USA, [3]Department of Anesthesiology, Critical Care, and Pain Medicine, Boston Children's Hospital, Boston, MA USA, [4]National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Multisystem inflammatory syndrome in children (MIS-C) is characterized by hyperinflammation and multisystem organ involvement in persons aged <21 years with onset 2–6 weeks after SARS-CoV-2 infection. CDC's MIS-C national surveillance system enables passive reporting of MIS-C cases from all U.S. jurisdictions. Merging and de-duplication of data across multiple surveillance platforms using capture-recapture methods can help improve accuracy of MIS-C incidence. **Methods:** This analysis included reports from three systems: 1) CDC's MIS-C national surveillance system; 2) COVID-NET, which includes hospitalized patients of all ages with laboratory-confirmed SARS-CoV-2 infection within pre-specified catchment areas, and 3) Overcoming COVID-19, which includes children admitted with MIS-C across 61 hospitals. To identify unique MIS-C cases reported within 10 selected COVID-NET catchment areas, we de-duplicated children reported through each system from April 1–December 31, 2020, by birth date, admission date (+/- 4 days), 4-digit ZIP code or county, state, and sex. Bayesian log-linear models were fit to account for dataset dependence. The preliminary estimated number of cases was obtained through weighted averages of model estimates, with weights computed as the inverse of the deviance information criterion. **Results:** Among the 378 total cases reported within 10 targeted COVID-NET catchment areas, 316 (83.6%) were reported through MIS-C national surveillance, 160 of whom were also reported through either Overcoming COVID-19 or COVID-NET. Preliminary analysis yielded an estimated MIS-C population of 507 cases (95% uncertainty interval (UI): 413.73 – 783.07), indicating that a multiplier of 1.34 (95% UI: 1.09 – 2.07) could be used to estimate MIS-C incidence from MIS-C national surveillance data across these COVID-NET catchment areas. **Conclusion:** These methods will enable calculation of population-based MIS-C incidence rates among children with SARS-CoV-2 infection, given that COVID-NET hospitalization data can be more broadly

extrapolated to estimate SARS-CoV-2 burden within catchment areas and at different points in time. These methods have wide applicability to surveillance of other post-COVID conditions since universal and standardized data collection may not be established.

### Poster 18. Closing Gaps in Policies, Preparedness, and Emergency Response in East Mediterranean Region during COVID-19 Pandemic

H.Y. Hussain
University of Baghdad, Baghdad, Iraq

**Background**: Operating insightful policies in place, preparedness plan at hand and conceptual framework of emergency response. Is a pre response milestone linked to rapidly accelerate the scaling up of their capacities for the prevention and early detection of, and rapid response to, coronavirus disease 2019 (COVID-19). Identifying currently existing structural and functional gaps in policies, preparedness and emergency response domains at east Mediterranean region, and inspiring closure approached to similar. **Methods**: Revising national response lay out at different countries EMR, national epidemiological and statistical reports, and literature review for the relevant publish articles at regional and international level, by utilizing key word search strategy at different search engines after carefully applying selection and refining criteria. Results: The study revealed that there are significant structural and functional gaps needs to be closed urgently aiming to improve regional response and reduce the morbidities, mortalities and other socio- economic consequences. Gaps can be outlined as follow : Partnership and coordination : Establish a regional incident support management team (IMST) to monitor country level activities, facilitate coordination with counterpart IMSTs in WHO headquarters and country offices, and mobilize resources. Strengthen multispectral coordination, and Global Outbreak Alert and Response Network (GOARN. Conduct quick mapping of human resource needs for the implementation of national plans. Activate emergency operation centers at national and subnational levels to better coordinate the response. Points of entry and IHR (2005): weakness of technical guidance and building up technical capacity in relation to IHR in the region, Epidemiology and health information management: closing gaps at the level of standardizing and disseminating case definition, case investigation, data collection, timely notification, and risk assessment. Isolation and case management: Infection prevention and control: Support countries to provide IPC training and capacity building. Assist countries to strengthen triage and isolation capacity. Rapid response teams: activate/reactivate the multidisciplinary rapid response teams (RRTs) and ensure the RRTs are in place at country and regional level & Coordinate with GOARN Laboratory diagnostics: standard operating procedures for specimen collection, management and transportation for COVID-19 diagnostic testing. Technical support, kits & material availability Risk communication and community engagement: implement national emergency risk communication and community engagement strategies and/or action plans for COVID-19 Operations support and logistics: At regional, national and local levels ensuring the remote peripheries. **Conclusions**: Structural and functional gaps are currently existing in EMR and burdening the regional response.

### Poster 19. Timeliness Assessment of COVID-19 Media Monitoring as Contributor to SARS-CoV-2 Variants Surveillance in the WHO European Region

**L. Hernandez-Garcia,** L.E. MacDonald, T. Amar, J.T. Pukkila
Health Emergency Information and Risk Assessment (HIM), WHO Regional Office for Europe, Copenhagen, Denmark

**Background:** There is limited evidence of the value of monitoring non-traditional information for early warning during COVID-19 pandemic, and no reported evidence of the timeliness and usefulness of these data for rapid detection of SARS-CoV-2 variants of concern (VOC) emergence compared to other surveillance data. Since the identification of first VOC in December 2020, targeted media monitoring (MM) was developed for both detection of newly emerging variants across the WHO European Region and epidemiological trends in VOC transmission. Surveillance system attributes (timeliness and usefulness) were assessed retrospectively to demonstrate the value and performance of VOC MM. **Methods:** Upon identification of the first VOC in the WHO European Region, epidemic intelligence activities were adjusted to monitor non-traditional surveillance data for VOC early warning. Open-source reports were screened daily according to a pre-defined selection criteria. Variants signals trends over time for all variants and its geographical distribution were analyzed. Timeliness of this surveillance strategy was assessed for VOCs by comparing MM to other EBS activities, over a 10-month period of time. Trends in first signal type (initial suspicion vs official statement) and epidemiological context were also assessed. **Results:** During the

period Oct 2020-July 2021, 1 082 signals were detected with a focus on SARS-CoV-2 variants, this is 24.9% of all COVID-19 signals and 2.3% of screened articles under variants specific search strategy. Most signals involved a VOC (76%), while 6.4% involved a novel or not-yet defined variant or mutation. Initial results for timeliness analysis showed the majority of first detections of Alpha VOC were detected by MM activities earlier than through other EBS activities. A case study of information evolution of Alpha VOC emergence in the UK was carried out, seeing early detection of signals suggesting change in transmission patterns in Kent area in early December, prior to its classification as VOC on 19th Dec. **Conclusions:** MM activities proved to be a useful and timely information source for SARS-CoV-2 variants surveillance in collaboration with other formal reporting systems in the WHO European Region, particularly among those countries with less robust surveillance systems or low sequencing capacity.

### Poster 20. Number of Deaths Averted as a Result of COVID-19 Vaccination Programmes in the WHO European Region between December 2020 and August 2021

**M.M.I. Meslé**[1], J. Brown[1], P. Mook[1], J. Hagan[1], R. Pastore[1], N. Bundle[2], G. Spiteri[2], G. Ravasi[2], N. Nicolay[2], N. Andrews[3], T. Dykhanovska[4], J. Mossong[5], M. Sadkowska-Todys[6], R. Nikiforova[7], F. Riccardo[8], H. Meijerink[9], C. Mazagatos[10], J. Kyncl[11], J. McMenamin[12], T. Melillo[13], S. Kaoustou[14], D. Lévy-Bruhl[15], F. Haarhuis[16], R. Rich[17], M. Kall[18], D. Nitzan[1], C. Smallwood[1], R. Pebody[1]

[1]World Health Organization (WHO) Regional Office for Europe, Copenhagen, Denmark, [2]European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden, [3]Public Health England, London, UK, [4]Public Health Centre of the Ministry of Health of Ukraine (UPHC), Kyiv, Ukraine, [5]Health Directorate, Luxembourg, Luxembourg, [6]National Institute of Public Health (NIH) – National Research Institute, Warsaw, Poland, [7]Latvian Centre for Disease Prevention and Control, Riga, Latvia, [8]Instituto Superiore di Sanità, Rome, Italy, [9]Norwegian Institute of Public Health, Oslo, Norway, [10]Institute of Health Carlos III, Madrid, Spain, [11]National Institute of Public Health, Prague, Czech Republic, [12]Public Health Scotland, Glasgow, UK, [13]Ministry of Public Health, Valletta, Malta, [14]National Public Health Organization, Athens, Greece, [15]French Public Health Agency, Paris, France, [16]Sciensano, Brussels, Belgium, [17]Israel Ministry of Health, Jerusalem, Israel, [18]Public Health England, London, UK

**Background**: Since December 2019 over 1.3 million SARS-CoV-2 related fatalities were recorded in the WHO European Region, with 90.6% in those aged ≥60 years. The rapid development and administration of novel vaccines across countries of the European Region has been very diverse. We aim to estimate the number of lives saved in those aged ≥60 years since the start of vaccination in countries with available data. **Methods:** We adapted methods previously applied to influenza to first estimate the number of deaths a country could have expected without any vaccination programmes using the observed weekly reported death counts and vaccination coverage. We then calculated the number of lives saved from COVID-19 vaccination in 33 countries from December 2020 to August 2021 for those aged ≥60 years and where possible, in three age groups (60-69 years, 70-79 years and ≥80 years). **Results:** The complete vaccination coverage in those aged ≥60 years was 77% in the countries considered, ranging from 13% to 100% per country. We estimated that vaccination averted 296,673 deaths (44% of expected deaths, country range: 1 to 92%), with the largest number of fatalities averted seen in those aged ≥80 years (185,023 fatalities averted). The overall expected mortality rate in the absence of a vaccination programme was calculated to be 554.2 per 100,000 population, compared to the observed 309.1 per 100,000 population. **Conclusions:** The largest impact was experienced in countries where implementation was early and wide reaching. Other countries experienced more limited effects of vaccination because their programme was implemented more slowly or given the effective use of non-pharmaceutical interventions. These findings should encourage member states where complete vaccination coverage is below 50% in older adults to further increase their coverage in order to save the most lives. Our calculations did not estimate the indirect effect of vaccination due to reduction in transmission, which is one limitation of this analysis.

### Poster 21. Pakistan COVID -19 Readiness and Resilience Exercise and the Way Forward – 2020-2021

**S. Mursalin**[1], A. Zaeer[2], C. McNeil[3]

[1]Pak One Health Alliance, Lahore, Pakistan, [2]University of Health Sciences, Lahore, Pakistan [3]Ending Pandemics, San Francisco, CA, USA

**Background:** To assess its country's readiness and resiliency, Pakistan One Health Association (POHA) conducted a During Action Review and Tabletop Exercise (DART) from November 2020–January 2021. DART provided retrospective evaluation of strengths and gaps in current response and prospective testing of future scenarios. In February 2020, COVID-19 was first detected in Pakistan. By December 2020, Pakistan had >450,000 cases and

>10,000 deaths. These figures alarmingly rose to 1,144,000 confirmed cases with 25,000 deaths by August 2021. As scientists understood COVID-19 was likely to persist, a policy shift from emergency mode to enhancing resilience was desired. With support from Ending Pandemics and local stakeholders, POHA conducted DART for an in-depth analysis of readiness and resilience for Pakistan and Punjab Province. **Methods:** Public health epidemiologists, laboratorians, animal health specialists, emergency responders and communicators, and Airport Response Team/point-of-entry responders participated in the retrospective analysis consisting of a role-based questionnaire and participant-led analysis. Participants engaged in a remote, multisector tabletop exercise looking at scenarios three months, six months, and three years in advance to explore readiness for situations including vaccine resistance, variants, internet outages, economic recessions, and limited surge capacity. Participant-led discussion of findings led to recommendations. **Results:** Participants identified self-sufficiency in manufacturing, centralized response, political commitment, and uniform risk communication as key strengths. Recommendations included increasing rural healthcare access; strengthening long-term fiscal and policy support; building lab capacity and public-private partnerships; leveraging FELTP to increase One Health response; and developing mass vaccination plans. **Conclusions:** A combined retrospective and prospective approach using DART was adopted by provincial and national experts to recommend planning priorities for improving readiness and resiliency to meet future challenges from the COVID-19 pandemic and other health emergencies. DART found centralized national response coupled with well-structured operational plans are critical for provincial level logistics, communication, and epidemiology response.

### Poster 22. The Caribbean Public Health Agency (CARPHA)'s Regional Response to the COVID-19 Pandemic

**L. Indar,** S. Kissoondan, J. St. John
Caribbean Public Health Agency, Port-of-Spain, Trinidad & Tobago

**Background:** Proximity, porous borders, and interconnectedness of CARPHA Member States (CMS), coupled with dependence on travel and tourism provide opportunities for the seamless and enhanced spread of COVID-19 and its variants in the Caribbean. **Methods:** The Caribbean Public Health Agency (CARPHA), the sole public health agency in the region, is leading the Caribbean's public health response to COVID-19 from a regional health perspective, through multifaceted, disease emergency preparedness and response activities. These include coordination with Heads of Government, Ministers and Chief Medical Officers, regional and international agencies, epidemiological surveillance and response, technical guidance and support, laboratory testing, support to vaccination programs, risk communication, capacity building and COVID-19 Health Round s, operational research and proactive measures for a healthier, safer return to tourism. **Results:** As of September 30, 2021, CARPHA has produced: 10 regional mandated documents, 197 situation reports, 64 technical guidelines on testing, surveillance, prevention, and safe reopening, 106 dashboards, 39 vaccine updates and significant findings from CARPHA's vaccine acceptance survey. A total of 83 webinars were conducted with 13,478 persons trained from 76 countries via COVID-19 Health Rounds and 82,995 samples have been received from CMS for COVID-19 testing. Specifically for travelers' health, CARPHA has developed regional tools such as the measurable and verifiable Caribbean Travelers Health Assurance Stamp (awarded based on training and surveillance) and the Mobile App, with 88 awardees and 683 active installations respectively, as well as the real time Tourism and Health early warning Information System (with 737 business registered) www.carpha.org. **Conclusions:** Despite the Caribbean's vulnerabilities and the health inequalities, CARPHA continues to prioritize the health, safety, and protection of the region from public health threats, especially, infectious diseases. Through its multifaceted, multiagency approach, CARPHA remains committed to support its CMS through its coordinated, regional response to the COVID-19 pandemic.

### Poster 23. Participatory Surveillance – How a National Hotline was Instrumental in the Response to COVID-19 in Cambodia

**L. Sovann**[1], S. Sok[1], C.S. Lan[2], K. Chheang[2], N. Divi[3], M. Smolinski[3]
[1]Cambodia CDC, Phnom Penh, Cambodia, [2]InSTEDD iLab Southeast Asia, Phnom Penh, Cambodia, [3]Ending Pandemics, San Francisco, CA, USA

**Background:** In 2016, a national hotline in Cambodia was re-designed to expand public reporting of health threats directly to national health authorities. This participatory surveillance tool was developed as a collaboration between local technologists and the Ministry of Health (MoH) with the goal of ensuring accessibility to all persons in

Cambodia regardless of literacy or access to technology. The InSTEDD iLab Southeast Asia, a technology company in Phnom Penh, built and maintained the hotline using a free, open-source tool called Verboice. A partnership between the MoH and Telecom Cambodia enables equitable national access. The hotline is staffed 24/7 with identified threats responded to by health authorities. Philanthropic funding supported the hotline pilot; in 2020, the MoH took ownership and covers infrastructure costs. **Methods:** Hotline utilization between January 2016 and October 2021 was analyzed. The hotline was modified in April 2020 to support contact tracing which was analyzed separately. **Results:** Between 2016 and 2019, the system received an average of 342 calls per day, with 20–30 events per month triggering immediate action by health authorities. During March 2020, the system began receiving up to 18,000 calls per day, identifying 90% of early COVID-19 cases and providing timely information to the public. Once modified to enable contact tracing, the hotline sent up to 12,000 auto calls/day with a total of 760,000+ contact tracing calls between March 2020 and August 2021. **Conclusions:** Countries benefit from participatory surveillance systems operating year-round that can quickly scale to meet demands during health emergencies like COVID-19 and be adapted to assist present needs such as contact tracing. The hotline is a cost-effective means of early detection that is being shared across human and animal health ministries in Cambodia and serving as a model for replication in Tanzania and Vietnam.

### Poster 24. Assessment of Adverse Events Following COVID-19 Immunization in Greater Kampala, Uganda, June 2021

**A. Komakech**[1,2], J. Kamulegeya[3], J. Izudi[2], E.J. Nsubuga[1], B. Kwesiga[1,4], D. Kadobera[1,4], L. Bulage[1,4], P. Nakamya[1], A.R. Ario[1,4]

[1]Uganda Public Health Fellowship Program, Kampala, Uganda, [2]Clarke International University, Kampala, Uganda, [2]World Health Organization, Kampala, Uganda, [4]Uganda National Institute of Public Health, Kampala, Uganda

**Background:** Tracking of adverse events following immunization (AEFIs) is important for evaluating vaccine safety. During March 2021, Uganda began COVID-19 vaccination using the Astra-Zeneca vaccine. We assessed AEFIs in Greater Kampala, Uganda to track the safety of the new vaccine. **Methods:** We used vaccination registers to identify persons who received ≥1 dose of the AstraZeneca COVID-19 vaccine during March 10-April 30, 2021. AEFIs were defined as an untoward medical occurrence after immunization (not necessarily causally related to the vaccine). Serious AEFIs were defined as any event considered life-threatening or resulting in hospitalization. We extracted telephone contacts for a systematic random sample of vaccinated individuals and conducted phone interviews with those who consented to collect data on demographics and details of AEFIs where they occurred. **Results:** Among 374 subjects interviewed, mean age was 41 years (IQR=28-54); 176 (47%) were female. Of these, 235 (63%) received only one dose and 139 (37%) received two doses. In total, 516 AEFIs occurred in 286 (77%) individuals, including in 255 (68%) individuals after the first dose and in 45 (32%) individuals after the second. The most common AEFIs were redness/pain/itching at the injection site (34%) and headache (32%). In total, 35 vaccination events (6.8%) resulted in medical care-seeking and six (1.2%) were classified as serious, involving vomiting/diarrhea (3), headache (2), and difficulty in breathing (1). Persons aged 20-50 years (AOR:3.6, 95% CI: 2.2-6.2) were more likely to develop AEFIs than those aged ≥50 years. **Conclusion:** Most individuals experienced ≥1 AEFI. Serious AEFIs occurred after approximately one in 100 vaccination events. Younger age (<50 years) was associated with AEFIs. We recommend prospective studies to fully understand adverse events following AstraZeneca COVID-19 vaccination in Uganda.

### Poster 25. National SARS-CoV-2 Strain Surveillance – High-Throughput Next-Generation Sequencing Wet Laboratory Processing

**M. Sheth**[1], M.L. Bentz[1], A. Burgin[1], M. Burroughs[1], M.L. Davis[1,4], K. Dillon[2], S. Le[3], J. Madden[1], S. Nobles[1], J. Padilla[1,4], L.A. Rowe[5], B. Dhwani[6], K. Knipe[3], D. Howard[3], Y. Unoarumhi[1], Strain Surveillance and Emerging Variants Working Group[7], Core Operations Outbreak Response and Support Laboratory[8], Specimen Triage and Tracking Team[8], J Lee[1]

[1]Biotechnology Core Facilities Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Integrated Life Sciences, University of Georgia, Athens, GA, USA, [3]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]ASRT Incorporated, Atlanta, GA, USA, [5]Department of Microbiology, Tulane National Primate Research Center, Covington, LA, USA, [6]Office of Advanced Molecular Detection, Centers for Disease Control and Prevention, Atlanta, GA, USA, [7] COVID-19 Laboratory and Testing Task Force, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]Division of Scientific Resources, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** The COVID-19 pandemic has caused widespread negative impacts on public health. Sequencing and characterization of SARS-CoV-2 positive specimens is needed for surveillance to monitor changes in viral genetic

diversity over time. The Centers for Disease Control and Prevention and the Association of Public Health Laboratories started the National SARS-CoV-2 Strain Surveillance (NS3) program in the US in December 2020. The objective of this program is to gather laboratory confirmed SARS-CoV-2 positive diagnostic specimens from all 64 US public health jurisdictions for genomic surveillance. We describe the high-throughput laboratory workflows being used to generate the data for this nationwide surveillance program. **Methods:** The laboratory workflow comprises the following steps: receipt and accessioning of specimens, total nucleic acid extraction, compatible library preparation and next-generation sequencing (NGS) on the Illumina Novaseq, analysis of sequence data and submission of sequences to public repositories. The reagents, automated liquid handlers, laboratory information management system integration, and downstream analysis have all been optimized to consistently generate high quality sequence data while efficiently processing up to 1200 specimens per week. Quality control measures that identify potential sequence cross contamination or other issues along the workflow and in the sequence data are also included. **Results:** Submission of random specimens from different jurisdictions has represented geographic, demographic, and viral diversity over time. The implementation of automation, specimen tracking, workflow optimizations and quality control measures have made the laboratory workflow more efficient and productive over time. To date 20,000 SARS-CoV-2 positive specimens have been processed and sequenced with 85-90% of samples per plate passing our quality control standards. The average turnaround time from specimen receipt to data submission is currently 21 days. **Conclusion:** This lab workflow provides a framework for NGS preparedness and response that can be implemented in any public health emergency response and adapted across public health laboratories of various sizes and experience.

### Poster 26. Modelling the Transmission Dynamics of SARS-CoV-2 in the Dominican Republic

**E. Finch**[1], E.J. Nilles[2,3], A.J. Kucharski[1]
[1]Centre for Mathematical Modelling of Infectious Diseases, London School of Hygiene & Tropical Medicine, London, UK, [2]Harvard Humanitarian Initiative, Cambridge, MA, USA, [3]Brigham and Women's Hospital, Boston, MA, USA
**Background:** During the COVID-19 pandemic, there has been limited modelling analysis of underlying SARSCoV-2 transmission dynamics in the Caribbean region, as well as more widely in the Global South. In particular, very few studies have incorporated the multiple data streams needed to distinguish between key drivers of epidemic dynamics. In this study, we combined available data streams for the Dominican Republic within a transmission dynamic modelling framework to understand the role of population immunity, non-pharmaceutical interventions, and population mobility in driving transmission. **Methods:** We synthesized publicly available data streams for the Dominican Republic including surveillance data published by the Ministry of Health, Google COVID-19 Community Mobility Reports, and information on non-pharmaceutical interventions from the Oxford COVID-19 Government Response Tracker. We also incorporated novel population-representative serological data, sampling between June and September 2021. We then used an age-structured compartmental model to reconstruct unobserved SARS-CoV-2 transmission dynamics in the Dominican Republic between 1st January 2020 and the end of July 2021. **Results:** Comparing the available data streams, we found that changes in population mobility alone could not explain the epidemic trajectory of the COVID-19 pandemic in the Dominican Republic, in contrast to several high-income countries where population mobility and COVID-19 dynamics in surveillance data were highly correlated. We found the model was best able to capture the timing of peak dynamics in the first year of the epidemic in a scenario where substantial levels of immunity to SARS-CoV-2 had accumulated, particularly in younger age groups, alongside broader behaviour changes. **Conclusions:** Available evidence suggests COVID-19 epidemic dynamics in the Dominican Republic were driven both by a combination of accumulating population immunity, as well as changes in population mobility during the first year of the pandemic. Accounting for these factors will be crucial for making better predictions about the future epidemic trajectory.

### Poster 27. Putting COVID-19 Cases on Surveillance Screen in High Mountain Population of Gilgit-Baltistan, Pakistan, 2020

**Malika Saba**[*1],**Sumara Baig**[*2], Saleem uddin[3], Syed M. Shah[4,5,6]
[1]Health Department, Gilgit Baltistan, [2]Field Epidemiology and Laboratory training program Pakistan (FELTP-Pakistan), Islamabad, Pakistan, [3]Health Department, Gilgit Baltistan, [4]Institute of Public Health, College of Medicine and Health Sciences, United Arab Emirates University, Al Ain, UAE, [5]Zayed Centre for Health Sciences, UAE University, Al Ain, UAE, [6]Department of Family Medicine, Aga Khan University, Karachi, Pakistan
**Background:** COVID-19 pandemic originated in China, linked to Pakistan through the China Pakistan Economic Corridor (CPEC) passing through the high mountain villages of Gilgit Baltistan. This study aimed to describe the COVID-19 cases identified through the active surveillance system, initiated by the local government. **Methods:** A

descriptive cross-sectional study design was employed to describe the COVID-19 cases identified between 1st March and May 31st, 2020.All suspected cases were confirmed through genetic sequencing analysis of lower respiratory tract samples. Socio-demographic characteristics of confirmed cases were analyzed using descriptive statistics. Epidemiological trend was described by epidemiological curve. Geo temporal distribution of cases was analyzed using color coded maps, while manual spot maps were designed to identify the areas having high prevalence. **Results:** We identified a total of 711 COVID-19 cases. The first case was identified on 1st March 2020.The mean age of study subjects was 37 (SD±18) years and the age ranged (0.6-89 years). High proportions (69.7%) were males. The results revealed that among the positive cases (N=711) a majority of confirmed cases were aged 15-30years (32.7%), and most affected occupation was service industry 10.2%.All ten districts of Gilgit-Baltistan were affected. Among districts, district Gilgit accounted highest 35.5% of cases followed by 22.2%, 15.04%, and 10.2% in Astore, Nagar, and Skardu district respectively. The overall prevalence of COVID-19 in GB was 50 cases per hundrend thousand of population.The highest prevalence of 13.1% in district Nagar followed by district Astore ( 12.6%). The overall recovery of COVID -19 cases in Gilgit Baltistan was 69.7%. The overall case-fatality was 1.54%, above 61 years age group had the highest case fatality rate of all age groups at 9.5%. **Conclusion:** All ten districts has been affected by COVID-19; district Nagar has highest prevalence of 13.1% . Most affected age group was between 15-30 years (mean 37 and mode 30). The mean age of expired subjects was 62 (SD±17.4) years and the age ranged (28-85 years). Among them 27% were female and 73% male, with pre-existing, co-morbid conditions such as hypertension, cardiovascular disease, asthma, renal insufficiencies, and COPD.

### Poster 28. Evaluation of the Effect of Community Dialogue Meetings on Self-Interest, Willingness to Receive, and Attitude towards COVID-19 Vaccine among District Leaders in Western Uganda, May 2021

**E.J. Nsubuga**[1], A. Komakech[1], B.O. Amodan[1], D. Kadobera[1,2], B. Kwesiga[1,2], L. Bulage[1,2], F. Banage[3], A. Fitzmaurice[3], J.R. Harris[3], P.J. Elyanu[4], A.R. Ario[1,2]
[1]Uganda Public Health Fellowship Program, Ministry of Health, Kampala, Uganda, [2]Uganda National Institute of Public Health, Kampala, Uganda, [3]United States Centers for Disease Control and Prevention, Kampala, Uganda, [4]Baylor College of Medicine Children's Foundation, Kampala, Uganda
**Background:** Widespread COVID-19 vaccine uptake is necessary for epidemic control. A February 2021 study in Uganda suggested that public uptake would follow uptake among leaders. In May 2021, community dialogue meetings were held between Baylor Uganda and district leaders from Western Uganda to identify ways of promoting vaccine uptake among leaders. We assessed the effect of the meetings on interest in COVID-19 vaccine uptake. **Methods:** All departmental district leaders were invited to the meetings, which lasted approximately 4 hours. Scripts were used and the same topics were discussed in all meetings. Leaders completed self-administered questionnaires before and after the meetings. We used a 5-point Likert scale (1=strongly disagree; 5=strongly agree) to assess willingness to receive COVID-19 vaccines, interest in receiving the vaccine, COVID-19 risk perception, safety concerns, and COVID-19 vaccines attitudes and beliefs. We analyzed the findings using Wilcoxon's signed-rank test. **Results:** Among 268 attendees, 164 filled out the pre- and post-meeting assessment; 48 had already been vaccinated and 56 declined due to time constraints. Among the 164, median scores for willingness to receive vaccine changed from 3 (neutral) pre-meeting to 5 (strong willingness) post-meeting ($p<0.001$). Median scores for interest in receiving vaccine improved from 3 (neutral) pre-meeting to 5 (strong interest) post-meeting ($p<0.001$). Median personal COVID-19 risk perception scores changed from 3 (neutral) pre-meeting to 5 (highly at risk) post-meeting ($p<0.001$). There was a reduction in safety concerns with medians changing from 4 (worried about vaccine side effects) pre-meeting to 2 (not worried) post-meeting ($p<0.001$). Median scores regarding COVID-19 vaccines attitudes changed from 3 (neutral) pre-meeting to 5 (very positive) post-meeting ($p<0.001$). **Conclusion:** Dialogue meetings led to improvement in community leaders' willingness and intention to receive COVID-19 vaccines, and reduced fears. Broader use of such meetings with community leaders could reduce COVID-19 vaccine hesitancy and increase uptake.

### Poster 29. SARS-CoV-2 Transmission Potential and Disparities in Disease Burden in Rural and Urban Maine

**S.K. Ofori**[1], D. Babatunde[1], E.A. Akowuah[2], I.C.H. Fung[1]
[1]Jiann-Ping Hsu College of Public Health, Georgia Southern University, Statesboro, GA, USA, [2]Department of Public Health, Baylor University, Waco, TX, USA
**Background:** The study explores the transmission potential of SARS-CoV-2 in Maine, U.S., and quantifies the differences in burden among selected rural (Washington and Piscataquis) and urban (Cumberland, Androscoggin, and Penobscot) counties using the time-varying reproduction number ($R_t$). **Methods:** The R package "EpiEstim"

was used to determine the $R_t$ for Maine and the selected counties using the reported daily case counts obtained from the New York Times GitHub from March 12, 2020, to May 17, 2021. The impact of public health measures was quantified through changes in nonoverlapping time window $R_t$. The power-law relationship between the $\log_{10}$ transformed per capita cumulative case count and $\log_{10}$ population size at four-time points was assessed using linear regression. **Results:** The $R_t$ for Maine dropped from about 2 in March 2020, then increased in May, followed by fluctuations around 1 for five months. The $R_t$ dropped to <1 between January and February 2021. The rural counties experienced fluctuations in $R_t$ throughout the study period. Across the urban counties, there was a surge in $R_t$ (>1) in late mid-October 2020. $R_t$ dropped below 1 in January and February 2021. $R_t$ increased by 11.58% (95% CrI: 3.74%, 21.00%) despite the first mask mandate enacted on July 8, 2020, while the stricter mandate on November 5, 2020, was associated with 8.15% (95% CrI: 4.58%, 8.15%) decline in $R_t$ in Maine. Vaccination roll-out led to a significant reduction in transmission in Maine, and in Cumberland and Penobscot counties, while rural counties had insignificant results. Urban counties were found to have a higher per capita cumulative case count than rural counties on four selected dates in 2020-21. **Conclusion:** Our findings suggest a decline in SARS-CoV-2 transmission in Winter 2020-21 as $R_t$ was below 1. Vaccination and stricter mask mandates significantly reduced the $R_t$ in Maine and urban counties.

### Poster 30. COVID-19 Test Positivity among Travelers Seeking Pre-Departure Travel Certification at University Teaching Hospital, Lusaka, Zambia, October 2020 – March 2021

**O. Nzila**[1], A. Hamukale[2], N. Sinyange[3]
[1]Field Epidemiology Training Program (FETP), Lusaka, Zambia, [2]Zambia National Public Health Institute (ZNPHI), Lusaka, Zambia

**Background:** Pre-departure testing and certification for SARS-CoV-2 among travelers can help reduce the spread of SARS-CoV-2 across borders. Whether this screening identifies persons who are infected and may export infections to their destination is not known. We analyzed the test percent positivity among travelers seeking pre-departure SARS-CoV-2 testing at University Teaching Hospital (UTH) in Lusaka Zambia. **Methods:** We analyzed the dataset of travelers seeking SARS-CoV-2 pre-departure travel-certification from 1st October 2020 to 24th March 2021.The test positivity was calculated as the number of travelers with laboratory-confirmed SARS-CoV-2 divided by the total number of travelers tested. The compliance to valid negative certificates among travelers at Kenneth Kaunda International Airport was also compared during this period. We used spearman's correlation co-efficient to assess correlation between pre-departure travelers' positivity rate and the overall national test positivity rate in Stata v14 with $p<0.05$ considered significant. **Results:** A total of 15,125 travelers were tested at UTH for SARS-CoV-2 from October 1, 2020, to March 24, 2021. The median age for the travelers was 37years (interquartile range: 27-47). Overall, 1,071 (7.1%) travelers tested SARS-CoV-2 positive. The differences in the positivity rate among the different age categories were statistically significant ($P<0.001$). The test positivity rate of travelers correlated with increase in the national positivity rate (rho= 0.6, $p<0.001$). At Kenneth Kaunda international Airport, compliance to valid negative certificates among travelers was at 68% (38,627/56,547). Only travelers with negative test results were given travel certificates. **Conclusion:** Pre-travel testing identified a notable number of persons with SARS-CoV-2 prior to international travel. The study period encompassed the 2nd wave in Zambia, which could partially explain this finding. Routine pre-travel testing might help prevent exportation of SARS-CoV-2 infections during periods of community transmission.

### Poster 31. COVID-19 Vaccine Acceptability Assessment in Ghana

**G. Acheampong**[1], M. Owusu[1], B. Nkrumah[2], D. Sambian[1], P.O. Boadi[1], A.B. Amoasah[1], D.T. Barradas[2]
[1]Centre for Health System Strengthening, Kumasi, Ghana, [2]Division of Global Health Protection, US Centers for Disease Control and Prevention, Accra, Ghana

**Background:** Vaccines are effective pharmaceutical interventions that can reduce the burden of diseases globally. However, public attitude and response to vaccines are pressing problems for public health authorities. With the availability of COVID-19 vaccines, little information is known on public perceptions and attitudes towards the uptake of these vaccines in Ghana. We examined the willingness of Ghanaians to get vaccinated, if made available. **Methods:** From March 15 to April 26, 2021, a nationwide cross-sectional, self-administered internet-based survey was conducted. Targeted groups included churches, hospitals, and universities. The online data was extracted using Microsoft Excel and subsequently analyzed with STATA software version 14. Univariate analysis and multivariable logistic regression analysis were used to examine COVID-19 vaccine acceptability among the study population, and p-value < 0.05 was considered statistically significant. **Results:** A total of 896 participants completed the survey. Male participants (532/896; 59.38%) predominated the study and the majority (57.3%) of the respondents were within the 25-44 age group. Up to 75.9% of the participants agreed that vaccines play a vital role in the health and

wellbeing of populations. However, 43% had intentions to take the COVID-19 vaccines provided they become available. Females (Adj. OR = 1.770, 95 CI% = 1.236–2.536, $p < 0.005$), university students (Adj. OR = 1.245, 95 CI% = 0.798–1.944, $p = 0.334$) and Muslims (Adj. OR = 3.754, 95CI% = 1.513–9.312, $p < 0.005$) were seen to be more likely to have acceptance for COVID-19 vaccines. Participants were almost 10 times more likely to take the vaccines if they were made free of charge. **Conclusion:** This study identified relatively low (43%) acceptability of COVID-19 vaccines among Ghanaians. It is imperative for Ghana to intensify public educational campaigns on vaccine safety and efficacy. Data from this survey can serve as a guide for future projections of vaccine uptake.

### Poster 32. Ebola and COVID-19 Risk Perception and Vaccine Acceptance in North Kivu, Democratic Republic of the Congo

**B. Glenn**[1,2], M.K. Fleming[1], M.E. Ngole[3], A.B. Ombeni[3], R.F. Muhayangabo[3], R.M. Mutumwa[3], E. Song[4], J. Powell[4], S. Perera[5], S. Garbern[6], S.H.B. Mustafa[7], S. Kulkarni[1], M.F. Jalloh[8], N. Abad[1], D.D. Tchoualeu[1], D. Fitter[1], D. Prybylski[1], A.C. Levine[6], R.H. Doshi[1]
[1]Global Immunization Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]James A. Ferguson Infectious Disease Program, Atlanta, GA, USA, [3]International Medical Corps, Goma, Democratic Republic of the Congo, [4]Brown University, Providence, RI, USA, [5]International Medical Corps, Washington, DC, USA, [6]Department of Emergency Medicine, Brown University, Providence RI, USA, [7]Expanded Programme on Immunization, Goma, Democratic Republic of the Congo, [8]Division of Global HIV and TB, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The 2018-2020 North Kivu Ebola virus disease (EVD) outbreak in the Democratic Republic of the Congo (DRC) was the second largest Ebola outbreak globally. Vaccination with rVSV-ZEBOV was an integral component of the response. Institutional mistrust and widespread vaccine misinformation may have contributed to challenges in gaining the cooperation of communities, which may have led to low vaccine uptake. In March 2021, DRC introduced its first COVID-19 vaccine and the rollout was met with low acceptance. Understanding the perceived risk of disease and factors associated with acceptance is important to create targeted strategies to increase vaccine uptake. **Methods:** In March 2021, a cross-sectional survey was conducted among community members from three health zones with active Ebola transmission during the 2018-2020 EVD outbreak. Consenting individuals were eligible to participate if they were an EVD survivor, a household contact or neighbor of a survivor, and they lived or worked in the area during the outbreak, had heard of Ebola, and were 18 or older. In total, 631 out of 659 eligible community members consented and were asked about perceived risks of Ebola and COVID-19. All analyses were conducted in SAS 9.4. **Results:** Among the 631 survey participants 67% were female and the median age was 31 years (Interquartile Range: 22-42). Among all participants, 81.5% reported feeling at risk of Ebola, while only 53.6% felt at risk for COVID-19. Of the 494 individuals who were offered the Ebola vaccine, 80.4% accepted it. In contrast, only 27.6% of 631 individuals expressed intention to accept the COVID-19 vaccine. Of the 397 individuals vaccinated against Ebola, 32.7% intended to take the COVID-19 vaccine compared with 20.6% of the 97 participants who were not vaccinated against Ebola. **Conclusions:** Perceived risk of COVID-19 was much less in this population than to the perceived risk of Ebola. While most individuals who were offered the Ebola vaccine accepted it, fewer indicated they would accept a COVID-19 vaccine. Building vaccine confidence in this population will require targeted community engagement activities aimed at increasing disease awareness, severity, and prevention methods, including vaccination.

### Poster 33. Descriptive Epidemiology of Inbound International Passengers at Operational Airports across Pakistan (Point of Entry)

**N. Noreen**[1], I. Naveed[2]
[1]Directorate of Central Health Establishments, Islamabad, Pakistan, [2]Pakistan Institute of Medical Sciences (PIMS), Islamabad, Pakistan
**Background:** In lieu of emergence of Variants of concern In lieu of the increased cases and variants of concerns escaping immunity, the government of Pakistan as an immediate response to limit the strain's spread in Pakistan implemented a revised inbound passenger policy to filter the importation of virus as arrival Rapid antigen Testing (RAT) on all the operational Airports from May 5, 2021. This study was done to analyze the descriptive statistics of inbound international Passengers tested at the points of entry (airports) across Pakistan. **Methods:** It was a descriptive study conducted at the Directorate of Central Health Establishments (DOCHE), the focal point of all the points of entry of Pakistan from May 5, 2021, to October 5, 2021. The data were abstracted from the traveler's surveillance database maintained by DOCHE. Data analysis was done as descriptive statistics as percentages and frequencies using Epi info version 7 and Microsoft Excel 10 statistical components. **Results:** Of the total 4832 flights with 751,278 inbound passengers during the period from May 5, 2021, to September 5, 2021, 688,898

passengers were tested for SARS-COV-2 by Rapid antigen testing. Total confirmed positive were 1159.Majority of cases were reported from United Arab Emirates (UAE) (42.4%).Percentage positivity of testing was found to be 0.2%. The PCR positives samples were sent to NIH at Islamabad and Karachi stations for genomic sequencing. The data of positive cases were shared with relevant district health authorities for purpose of contact tracing. **Conclusion:** Measures to limit the spread of the variant strains are implemented in true letter and spirit at all the operational international airports. In addition to on-arrival testing, post-entry quarantine and health monitoring for travelers are essential to detect sufficient cases and to prevent local transmission. Points of entry are effective gateways to stop disease spread.

### Poster 262. Assessment of Anxiety and Psychological Distress among Pakistani People during COVID-19 Pandemic, 2020

**J. Alam**[1], S. Nadeem-ur-Rehman[2], T. Ghafoor[3], M. Amir Baig[3], A. Chaudhary[3], M. Zeeshan Iqbal Baig[3], Q. Ihtram ul Haq[4], S. Yasmin[4]
[1]Field Epidemiology and Laboratory training Program, Islamabad, Pakistan, [2]Directorate General Health, Muzaffarabad, Azad Jammu & Kashmir, Muzaffarabad, Pakistan, [3]Faculty Field Epidemiology and Laboratory training Program-Pakistan, National Institute of Health, Islamabad, Pakistan, [4]Department of Microbiology, University of Veterinary and Animal Sciences, Lahore, Pakistan
**Background:** The COVID-19 has created a very uncertain situation for the world. Lockdown and restricted movement had been imposed by countries to manage the spread of disease, however, quarantine and loss of freedom of movement are thought to affect the mental health of people. Therefore, this study aims to examine the level of anxiety and psychological distress among Pakistani people during the ongoing pandemic. **Method:** A cross-sectional study was conducted using an online questionnaire from May to June 2020. Adults with internet facilities and an understanding of English were recruited in this study using the snowball sampling technique. A consent form was attached, and confidentiality was maintained thoroughly. Information about demographical data, anxiety, and psychological distress was collected. Data were managed and analyzed using MS Excel. **Results:** Out of 358 respondents, 49.7% (n=178) were less than 25 years old and 53% were females. Approximately, 75% of the respondents felt anxious and 51% were experiencing a financial problem. A huge majority of the participants (95%) were worried about their safety and closed ones regarding the spread of disease. 32.4% of the participants were experiencing sleeping difficulty. Almost 48% of the people accepted that they feel there is a stigma attached to this disease. The majority (80%) of the participants had uncertainty about their future. 45.2% of the participants were found to be having severe psychological distress and among them, more women exhibited stress than males. **Conclusion:** The increasing prevalence of cases of COVID-19 and resulting lockdown to control the disease has resulted in an increased level of anxiety and distress among people, however, providing sufficient awareness to people and designing relevant psychological interventions can help in reducing anxiety and depression.

### Poster 177. Development of SARS-CoV-2 Serological Luminex Competition Assay for CDC's One Health

J. Lee
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The COVID-19 pandemic has presented a serious threat to global public health. Dozens of susceptible animal species are also impacted by SARS-CoV-2, highlighting the need to have validated diagnostic assays available for One Health investigations involving animals linked with people with COVID-19. **Methods:** In support of the One Health investigations and surveillance studies that address public health and animal health needs, we developed a SARS-CoV-2 serological Luminex competition assay to detect specific viral antibodies in multiple animal species. This bead-based assay measures total antibodies to the viral Spike protein independent of animal species and isotype. It is intended as an orthogonal test with existing serological assays to gain information about antibody binding outside the receptor binding domain (RBD) as well as low-titer neutralizing antibodies undetected by current assays. Antibody titers are measured in a competition platform where four discrete fluorescent magnetic beads are coupled to specific monoclonal antibodies recognizing unique spike protein epitopes. Animal sera antibodies compete for binding between beads and phycoerythrin (PE) labeled full-length Spike (trimeric stabilized ectodomain glycoprotein). Antibody levels are quantitated using titration of reference mAb standards. **Results:** We tested assay performance using a collection of Spike-immunized mice and confirmed cases among farmed mink outbreak investigations, aquarium river otters, Sumatran tigers from a zoo, and canine and felines from household transmission studies. Expected competition and quantitation for each antibody bead set was achieved for all species. Mouse sera with high titers measured by a spike protein ELISA were correlated with maximum signals in Luminex. To provide further Luminex assay confidence, samples were analyzed in the Total RBD Mix and Read Assay

developed as a surrogate viral neutralization test that measures antibody binding to the RBD via bridging of 2 luciferase RBD components in a complex. High correlation was observed between both assays. **Conclusions:** This SARS-CoV-2 serological Luminex competition assay is capable of multiplexing to detect neutralizing and non-neutralizing epitopes in the RBD and additional non-neutralizing epitopes within the S1 and S2 subunits of the spike protein. Furthermore, this assay is highly sensitive, species independent and can be used to profile anti-Spike epitopes among different animal species and individuals. The spread of SARS-CoV-2 between humans and animals can be controlled and prevented by early diagnostic detection of SARS-CoV-2 combined with a rapid One Health response. This SARS-CoV-2 serological Luminex competition assay can contribute to strengthening surveillance and laboratory diagnostic capacity in a One Health approach during the SARS-CoV-2 pandemic.

## Laboratory Studies and Diagnostics

### Poster 34. Evaluation of Stool Nucleic Acid Preservation Methods for Culture-Independent Pathogen Subtyping

**Y. Gao**[1,2], J.R. Hensley[1,2], E. Trees[1,3], H.A. Carleton[1], A.J. Williams-Newkirk[1], A.D. Huang[1]
[1]Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]ASRT, Inc., Atlanta, GA, USA, [3]Association of Public Health Laboratories, Silver Spring, MD, USA
**Background:** Culture-independent diagnostic tests can efficiently detect foodborne pathogens, but do not yield isolates critical for outbreak surveillance and investigation. Direct-from-stool subtyping assays are being developed using metagenomic sequencing techniques. Stabilization of nucleic acids is needed to prevent changes in the microbial community after stool collection. We tested two preservatives for stool DNA in conditions encountered in public health settings. **Methods:** A simulated disease-state stool was created by pooling 5 clinically healthy donor stools spiked with $10^6$ CFU/mL of Shiga toxin-producing *Escherichia coli* and *Salmonella enterica* strains and preserved in OMNIgene (DNA Genotek) or DNA/RNA Shield (Zymo Research). In one test, preserved stools were stored at 22°C and sampled over 112 days. In a second test, they were sampled after exposure to 55°C or 78°C for 2 days. Unpreserved frozen stools were used as positive controls, and stools in Cary-Blair (CB) were used as negative controls. Extracted DNA was analyzed using Qubit, Nanodrop, Fragment Analyzer, qPCR for pathogen level, and 16S rRNA V4 sequencing. All conditions were tested in triplicate. **Results:** Pathogen levels of stools in both preservatives at 22°C from all sampled days were similar to day 0 and positive controls, suggesting no cell growth or DNA degradation. Exposure to 55°C also did not affect the preserved samples in DNA quality or pathogen levels. 16S sequencing showed no changes in microbial composition in preserved stools over time. In contrast, pathogen levels in CB stools increased by 3 logs in the first 28 days and dropped 1 log by day 112. Unpreserved and CB stools experienced DNA degradation and microbial community shift over time and temperature exposures. Exposure to 78°C caused severe DNA degradation to all samples. **Conclusions:** Both preservatives were more effective than CB or no preservation in stabilizing pathogen levels and maintaining bacterial communities in conditions encountered in public health settings; however, cold packs would be needed for transport in higher temperatures. Additional consideration in choosing a preservative also include cost and versatility in collection kit form factors. An ongoing study focuses on how DNA/RNA Shield performs with clinical disease-state stool samples.

### Poster 35. Maintaining Whole Genome Sequencing during the COVID-19 Pandemic: Improving the Cost and Efficiency of WGS with High-Throughput Instrumentation

**M. Dickinson**, L. Mingle, K. Mitchell, D. Baker, A. Kidney, A. Sossei, K. Cummings, S. Gubbala, S. Morris, E. Nazarian, L. Thompson, S. Wirth, M. Shudt, W. Haas, K. Musser
Wadsworth Center, New York State Department of Health, Albany, New York, USA
**Background:** The Wadsworth Center Bacteriology Lab is a Regional Lab for the Antimicrobial Resistance Lab Network, PulseNet Area & GenomeTrakr Lab performing WGS on a large scale. Workload has increased by adopting new applications such as outbreak investigations for *Legionella pneumophila* and healthcare-associated infections. **Methods:** The MagNAPure 24, QIAcube HT, and QIAcube Classic were compared. Total costs were calculated including DNA extraction, library prep and WGS. Efficiency was measured by hands-on time and instrument run time. Sequence analysis was performed to compare pipeline results including genome assemblies, impact of sequencing diverse bacteria in one run, percentages of mapped reads, coverage, and number of Single Nucleotide Variants (SNV) detected. **Results:** The most cost-effective workflow was batching 80-90 samples, QIAcube HT extraction, Nextera DNA Flex library prep (using 1/4 of the suggested volume), and sequencing on Illumina NextSeq ($8.57/extraction + $68.00/prep & sequencing=$76.57/sample). DNA extraction cost/sample when using the QIAcube classic is ~$10.00, MagNA Pure24 cost/sample is ~$20.00. QIAcube HT requires the least amount of bench time (3.75 h/96 samples). To compare the XT and Flex Library prep kits, DNA was extracted from

various bacteria, libraries were prepared with either kit, and WGS was performed. In most cases, data from Flex libraries resulted in higher quality assemblies. Both library prep kits showed similar percentages of mapped reads and bases covered by reads when being mapped to appropriate reference genomes. The number of SNV's was similar for both methods. **Conclusions:** The combined use of the QIAcube HT, Nextera DNA Flex library prep kit and Illumina NextSeq platform streamlines sequencing requests across multiple laboratory units. The execution of this workflow maximizes cost-effectiveness and decreases turnaround time. The COVID-19 pandemic strained both our staffing and instrumentation resources as staff members were moved to pandemic response. This workflow allowed us to continue our sequencing responsibilities with less staff. High-volume public health laboratories should consider implementing these methods to aid in meeting testing requirements within budgetary restrictions in a timely manner while reducing staff burden.

### Poster 36. Tracking Low Frequency Variation within Intrahost Viral Populations Directly from Oxford Nanopore Sequencing Data with Variabel

**Y. Liu**[1], J. Kearney[1], M. Mahmoud[2], B. Kille[1], F.J. Sedlazeck[2], T.J. Treangen[1]
[1]Department of Computer Science, Rice University, Houston, TX, USA, [2]Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX, USA
**Background**: The COVID-19 pandemic forever underscored the necessity for monitoring systems tracking the emergence and spread of infectious disease. Infectious disease monitoring on Oxford Nanopore Technologies (ONT) platforms offers rapid turnaround times and low cost, exemplified by well over a half of million ONT SARS-CoV-2 datasets. Tracking low frequency intra-host variants has provided important insights with respect to elucidating within host viral population dynamics and transmission. However, given the high error rate of ONT, accurate identification of low frequency intra-host variants remains an open challenge. Here, we present Variabel, a novel variant call assessment tool that is able to recover intra-host variants with high precision from ONT data alone, for the first time, by exploiting the tendency of true variants to change in allele frequency across samples. **Methods**: Variabel is constructed as a series of filters that operate on the variant calls returned by an existing variant caller. It includes an allele frequency variation filter that identifies true variants that are shared across different samples based on the maximum difference of the allele frequencies, and an insertion/deletion (indel) filter that identifies false indel calls based on Shannon's entropy values of the region near indel sites. The aggregate set of filters are then applied on two or more ONT datasets. **Results**: We evaluated Variabel on both within patient and across patient paired Illumina and ONT datasets. Variant calls from the illumina sequences were used as a ground truth for evaluation. Our results show that Variabel can accurately identify low frequency variants from raw ONT data below 0.5 allele frequency, outperforming existing state-of-the-art ONT variant caller Clair3. Variabel exhibited a mean precision of 85% for the within patient dataset and 77.2% for the across patient dataset, compared to 48.3% and 64.1% for Clair3. **Conclusions**: In conclusion, we have shown that Variabel can be used to broadly identify low frequency variants in COVID-19 ONT data, which has been largely ignored to date due to within-host variation hidden within the ONT error rate. Variabel is open-source and available for download at: www.gitlab.com/treangenlab/variabel.

### Poster 37. A Human Papillomavirus (HPV) Whole Genome Plasmid Repository: A Resource for Validating and Monitoring HPV Typing Assays

**H.R. Thapa**, E.R. Unger, T.D. Querec
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Well characterized reference reagents are useful for assay validation, proficiency/competency assessment, daily run controls and to improve inter-laboratory comparisons. Synthetic human papillomavirus (HPV) DNA fragments or plasmid clones are available, however, as synthetic fragments include a limited region and many HPV plasmids have interrupted coding regions or contain partial genomes of HPV, they are not applicable to all typing assays. We aim to develop a standardized plasmid repository of all known HPV types in a standard vector, with each clone containing the whole genome without coding region interruptions. **Methods:** Whole genome HPV plasmids were constructed using same plasmid backbone to standardize quantitation and sequencing. DNA fragments for both HPV and vector backbone, with 20-50 bp overlapping ends, were generated using PCR and then assembled into a plasmid using Gibson assembly method. **Results:** To date, HPV plasmid clones for 16 HPV types (HPV6, 11, 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66 and 68) have been constructed. The whole genome of each HPV is present with no interruptions in coding regions. When compared to other 15 HPV types, construction of HPV31 whole genome plasmid was challenging and required Stbl2 *E. coli* strain suggesting unstable nature of HPV31. **Conclusions:** The Gibson assembly method is a feasible approach to develop whole genome HPV references universally applicable to DNA-based HPV typing assays. The newly constructed HPV whole genome

plasmids can serve as a resource of reference reagents for quality assurance of HPV typing assays. We plan to make these available for public health and research laboratories. The methods presented here can be applied to generate and improve DNA reference materials for other pathogens providing additional tools for quality improvements in laboratory detection of known and emerging pathogens.

### Poster 38. Comparison of Collection Sites for Successful Detection of *Acinetobacter baumannii* Colonization

**M.R. Lasure**[1], A. Valley[1], M. Mamerow[1], L. Patterson[1], M.J. Curran[2], C.C. Eldridge[2], B. Brennan[3], S. McNamara[3], H. Adil[4], S.E. Koske[5]
[1]Wisconsin State Laboratory of Hygiene, Madison, WI, USA, [2]Kentucky Department for Public Health, Frankfort, KY, USA, [3]Michigan Department of Health and Human Services, Lansing, MI, USA, [4]Chicago Department of Public Health, Chicago, IL, USA, [5]Wisconsin Department of Health Services, Madison, WI, USA
**Background:** Since 2019, the Wisconsin State Laboratory of Hygiene (WSLH) has provided colonization testing for carbapenem-resistant *Acinetobacter baumannii* (CRAB) in its role as the Midwest Regional Lab for the Antibiotic Resistance Lab Network. CRAB is known to colonize body sites such as skin, gastrointestinal tract, and tracheostomy secretions, especially in residents of long-term care facilities. Public health investigators should understand which body sites will be most likely to yield CRAB from culture if presented with limited screening options. **Methods:** For purposes of this analysis, all axilla/groin, axilla, or groin body sites collected were grouped together as axilla/groin swabs. WSLH performs CRAB colonization from swabs collected from axilla/groin, rectal, and tracheostomy body sites. Upon receipt of swabs, WSLH grows the organism in broth with meropenem before plating to chromogenic agar that selects for CRAB. A patient was considered CRAB-positive if CRAB was cultured from any of their sampled body sites. **Results:** From August 2020 through August 2021, 753 patients from Kentucky, Michigan, and Illinois had swabs collected simultaneously from more than one body site and submitted to WSLH. There were 705 patients swabbed at both rectal and axilla/groin body sites; 38 (5.4%) were CRAB positive, with 18 (47.4%) patients positive on both swabs. Fifteen (39.5%) were positive only on the rectal swab and 5 (13.2%) were positive only on the axilla/groin swab. Of the 48 patients were swabbed at both rectal and tracheostomy body sites, 27 (56.2%) were positive. Of those, 13 (48.1%) patients were positive on both swabs; 8 (29.6%) patients were positive only on the rectal swab, and 6 (22.2%) were positive only on the tracheostomy swab. **Conclusions:** CRAB was most frequently isolated from rectal swabs. If limited screening options are available, rectal swabs may be the most likely to detect CRAB.

### Poster 39. Designing Synthetic Positive Controls for Highly Multiplexed Amplicon Sequencing

**J.R. Hensley**[1], J.L. Rowell[2], S.T. Lucking[2], R. Jin[2], A. Khan[2], A.D. Huang[3], H.A. Carleton[3], A.J. Williams-Newkirk[3]
[1]ASRT, Inc., Atlanta, GA, USA, [2]WDS, Inc., Atlanta, GA, USA, [3]Bioinformatics and Metagenomics Team, Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Fast characterization of the resistome of complex metagenomic samples has broad applications for public health, environmental monitoring, and other fields. Highly multiplexed amplicon sequencing (HMAS) is a new tool that enables rapid detection of thousands of antimicrobial resistance determinants (ARDs) directly from clinical samples without requiring isolation of host microbes. However, validation of every primer pair on a HMAS panel is more challenging than single-plex or traditional multiplex assays. Additionally, creating positive controls for ARDs using traditional plasmid-based methods creates substantial biosafety concerns. Therefore, we designed a pool of synthetic positive controls to validate our ARD HMAS panel. **Methods:** The HMAS panel included 749 target amplicons covering 111 ARDs. Targets were selected from a published microarray for relevance to enteric bacteria. Primers were modified for compatibility with the Juno Targeted DNA Sequencing Library Preparation System (Fluidigm). Synthetic positive controls were designed based on public genome sequences for PhiX, *Streptomyces coelicolor*, and *Wolbachia pipientis* to match the length and GC content of the target amplicons in the ARD panel and were ordered as an oligo pool from Twist Bioscience. The Twist oligo pool was used as a template for panel amplification on the Juno. Amplicons (180-240 bp) were sequenced on the Illumina MiSeq using 2x250 bp chemistry. Mothur v.1.41.1 was used to perform sample demultiplexing, read assembly, quality filtering, and mapping. Mapping results were filtered using in-house R scripts. **Results:** Amplicons were successfully detected for all synthetic positive control sequences. However, amplification efficiencies varied across targets. **Conclusions:** The synthetic positive controls were an efficient way to validate a HMAS panel targeting sequences from many different genomes when using positive control plasmid constructs is unsafe. Furthermore, the synthetic control provides a commercially available custom positive control for use in production testing without fear of undetectable

contamination. Future studies will include expanding the primer panel to include additional targets and testing stool specimens to evaluate the use of this panel for public health surveillance.

### Poster 40. Validation of a BioNumerics wgMLST Database for Characterization and Subtyping Strains of *Clostridium botulinum*

**L. Gladney**[1], J. Halpin[1], G. Williams[1], H. Carleton[1], H. Pouseele[2], C. Lúquez[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Applied Maths, Sint-Martens-Latem, Belgium
**Introduction:** Development of tools that can rapidly subtype and characterize human pathogens such as *Clostridium botulinum* are needed for national surveillance. There is no standardized method for subtyping *C. botulinum* and sharing isolates might be difficult due to Tier 1 regulations; therefore, a central database is a necessary tool to compare whole genome sequences (WGS) among laboratories. A central, validated whole genome multi-locus sequence typing (wgMLST) database will allow public health laboratories to analyze their own sequencing data and also submit data to a national database for collaboration with CDC. **Methods:** We have validated a BioNumerics (v.7.6.3) wgMLST database for surveillance of Group I *C. botulinum* and detection of BoNT subtypes within serotypes A, B, E, and F from WGS. Five-hundred and forty-two strains associated with botulism cases were sequenced and included in the validation. An additional 134 isolates (including 60 technical replicates) were included in a verification study, to evaluate quality thresholds and clustering quality. WGS were generated using Illumina (2x250 bp MiSeq and 2x150 bp MiniSeq) and Ion Torrent (1x200 bp PGM and 1x400 bp S5) DNA sequencing. **Results:** We report the development and validation of a *C. botulinum* wgMLST database in BioNumerics 7.6.3 that supports Illumina technology. We evaluated two sequence technologies (Ion Torrent and Illumina) for use with our wgMLST schema and BoNT *in silico* typing. Only Illumina produced good quality sequence data - IonTorrent PGM data had quality issues that impacted clustering and so only the Illumina platform will be supported as part of our workflow. **Conclusions:** Our next step includes transition to a national PulseNet wgMLST database to use with our public health laboratory partners. The availability of a validated wgMLST database for *C. botulinum* will allow the use of standardized subtyping methods to assess the genetic relationship among isolates across the US and abroad.

### Poster 41. Nosocomial Amplification: Identifying Important Parameters in a Community-Hospital Model

K.C. Jackson, E.T. Lofgren
Washington State University, Pullman, WA, USA
**Background:** The phenomena of emerging infectious diseases accelerating once they reach healthcare facilities has been well documented. Outbreaks of MERS-CoV, SARS-CoV, and COVID-19 have led to the in-hospital transmission where the initial patient infects healthcare workers, patients, visitors, etc., with infection control policies unable to curtail the spread early on. We refer to this phenomenon as nosocomial amplification. Nosocomial amplification causes an undue burden on a hospital that's already strained from the pandemic. We aimed to understand which hospital-level parameters have the greatest impact on the community and vice versa.
**Methods:** We adapted an SEIR compartmental model to have three interconnected units: a community, a hospital-ER, and a hospital-ICU to determine the number of COVID-19 acquisitions in each of them over a hypothetical year. The model was stochastically simulated using Gillespie's Direct Method for 1000 iterations. A parameter sensitivity analysis assessed the effects each parameter had on the model. The original values of all parameters were allowed to vary +/- 50%. The number of acquisitions from the simulations was normalized as a percent change from the original model's mean acquisition. **Results:** Our analysis found that parameters impacting the shorter stay ER had a disproportionate impact as compared to the ICU, as did parameters governing the level of asymptomatic transmission. Transmission between healthcare workers facilitated within-hospital transmission even when strict patient-based cohorting and testing was in place. Extensive community-level transmission was also found to readily overwhelm hospital-level infection control at realistic levels of effectiveness and compliance. **Conclusion:** These findings illustrate that hospitals and the community are tightly linked systems. Hospitals may reintroduce infection into the community that might have contained or mitigated ongoing outbreaks or introduce the disease into a disease-free population; community transmission puts tremendous pressure on infection control. In the future, we can model policies to curb an existing COVID-19 outbreak or subsequent outbreaks to avoid or minimize nosocomial amplification, thus ameliorating the disproportionate burdens on the healthcare system.

### Poster 42. Splashes Generated during Device Decontamination Activities

**C.L. Ofstead**, K.M. Hopkins
Ofstead & Associates, Inc., Saint Paul, MN, USA

**Background:** Exposure of healthcare professionals to splashes and aerosols during medical procedures is well-documented and introduces a risk of infection or colonization, which has negative implications for occupational health and patient safety. Sterile processing personnel frequently report splashes of blood and contaminated fluids during manual cleaning of soiled instruments, but their risk of exposure has not been described in the literature. This pilot project sought to determine where and how far droplets were dispersed during manual cleaning of medical instruments. **Methods:** Splashes were detected by direct observation, photography, and the use of droplet-detection paper attached to personal protective equipment worn by technicians and surfaces around a decontamination sink during simulated cleaning activities performed with sterile instruments in a terminally disinfected decontamination area. **Results:** Droplets were observed at least three feet away during almost every activity, including filling a sink, placing an instrument in the sink, brushing an endoscope lumen, and rinsing a basin. Some activities generated droplets observed up to five feet away from the sink. Droplets were also observed on face shields, masks, gowns, gloves, and shoe covers. Even with proper use, face shields did not prevent exposure of masks or neck areas, and gloves did not prevent fluid intrusion from exposing hands and arms to cleaning solutions. **Conclusions:** This pilot project demonstrated that simulated manual cleaning activities in a sterile processing unit generated substantial splashes that landed on nearby surfaces and drenched personal protective equipment worn by technicians. Given the emergence of new pathogens and growing understanding of aerosols, these findings highlight the importance of frequent environmental disinfection and the provision of high-quality personal protective equipment for reprocessing personnel. More research is needed to determine the risk of colonization and infection transmission involving sterile processing personnel.

### Poster 43. Improved Detection and Characterization of *Clostridium* and *Clostridioides* Species from Fixed Tissues of Patients with Diverse Clinical Presentations by Using Multigene Targeted PCR and Sequencing

**E.L. Matthews**, M. DeLeon-Carnes, S. Reagan-Steiner, J.M. Ritter, R.B. Martines, S.R. Zaki, J. Bhatnagar
Infectious Diseases Pathology Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** *Clostridium* and *Clostridioides* genera comprise over 150 species combined that are generally ubiquitous. Conventional diagnostics include testing of stool or blood specimens by using bacterial culture, enzyme immunoassay and PCR. However, to establish a clear association with disease, it is important to detect *Clostridium* species directly in pathology tissues, particularly in sudden, fatal cases in which no premortem testing of clostridia was performed. Immunohistochemistry (IHC) can detect clostridial antigens in tissues, but for specific and accurate *Clostridium* species identification and characterization, tissue-based molecular analysis is critical. **Methods:** Formalin-fixed, paraffin-embedded (FFPE) autopsy or biopsy tissues from 120 cases (received during 2004-2020; 87% fatal) with clinical and histopathological suspicion of *Clostridium* spp. infection, and/or *Clostridium* spp. positive results by IHC, were evaluated by molecular assays. DNA was extracted from FFPE tissues and tested by multi-stage, multigene targeted Clostridium genus and species-specific PCR assays, followed by Sanger and/or pyrosequencing. **Results:** Molecular evaluation detected a *Clostridium* spp. in 109 of 120 (91%) cases. *Clostridium* IHC was also positive in 92 of 109 (84%) PCR-positive cases. Of 109 cases, specific *Clostridium* species were identified in 103 cases, including *C. perfringens* n=41, *C. sordellii* n=29, *C. septicum* n=8, *C. difficile* n=7, *C. novyi* n=3, and *C. sporogenes* n=2. Mixed infections of *C. perfringens* and *C. sordellii* was detected in 2 cases. Twenty of 41 (49%) *C. perfringens* cases had necrotizing enterocolitis/colitis, 9 had bronchopneumonia and 8 had pregnancy-associated necrotizing endometritis. Sixteen of 29 (55%) *C. sordellii* cases had necrotizing endometritis and/or septic-shock, including 14 pregnancy-associated cases, and 5 cases had pneumonia. A majority (86%) of *C. difficile* cases had pseudomembranous colitis/colitis. **Conclusions:** Tissue-based multigene targeted *Clostridium* PCR assays and sequencing enhance the ability for rapid, sensitive, and accurate species-specific diagnosis, may expand the known spectrum of disease caused by clostridia, and are particularly valuable for fatal cases in which conventional specimens are unavailable.

## Influenza

### Poster 44. Laboratory Evaluation of Two Point-of-care Detection Systems for Early and Accurate Detection of Influenza Viruses in the Lao People's Democratic Republic

**W. Kittikraisak**[1], B. Khamphaphongphane[2], S. Xayadethb[2], V. Som Oulay[2], V. Khanthamaly[3], O. Sengvilaipaseuth[2], C.T. Davis[4], G. Yang[4], N. Zanders[4], J.A. Mott[1,4], P. Xangsayarath[2]
[1]Influenza Program, Thailand Ministry of Public Health – U.S. Centers for Disease Control and Prevention Collaboration, Nonthaburi, Thailand, [2]National Center for Laboratory and Epidemiology, Vientiane, Lao People's

Democratic Republic, [3]U.S. Centers for Disease Control and Prevention, Vientiane, Lao People's Democratic Republic, [4]Influenza Division, U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** We evaluated molecular-based point-of-care influenza virus detection systems in a laboratory prior to a field evaluation of on-site specimen testing. **Methods:** The performance characteristics of 1) insulated isothermal polymerase chain reaction (PCR) on a POCKITTM device and 2) real-time reverse transcription-PCR (rRT-PCR) on a MyGo MiniTM device were evaluated using human clinical specimens, beta-propiolactone-inactivated influenza viruses, and RNA controls. The rRT-PCR carried out on a CXF-96$^{TM}$ real-time detection system was used as a gold standard for comparison. **Results:** Both systems demonstrated 100% sensitivity and specificity and test results were in 100% agreement with the gold standard. POCKIT$^{TM}$ only correctly identified influenza A (M gene) in clinical specimens due to the unavailability of typing and subtyping reagents for human influenza viruses, while MyGo Mini$^{TM}$ had either a one log higher or the same sensitivity in detecting influenza viruses in clinical specimens compared to the gold standard. For inactivated viruses and/or viral RNA, the analytic sensitivity of POCKIT$^{TM}$ was shown to be comparable to, or more sensitive, than the gold standard. The analytic sensitivity of MyGo Mini$^{TM}$ had mixed results depending on the types and subtypes of influenza viruses. **Conclusions:** The performance of the two systems in a laboratory is promising and supports further evaluation in field settings.

### Poster 45. Effect of Planned School Breaks on Absenteeism Due to Influenza-like Illness in School Aged Children - Oregon School District, Wisconsin, September 2014—June 2019

**C. He**[1], D. Norton[2], J.L. Temte[1], S. Barlow[1], M. Goss[1], E. Temte[1], C. Bell[1], A. Uzicanin[3]
[1]Department of Family Medicine and Community Health, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]Department of Biostatistics, UW School of Medicine and Public Health, Madison, WI, USA, [3]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Increased influenza-like illness (ILI) activity in communities coincides with increases in ILI-related absenteeism (a-ILI) in kindergarten through 12th grade (K-12) schools. Previous studies evaluated impacts of reactive K-12 school closures during seasonal and pandemic influenza outbreaks on medically attended influenza (MAI) in surrounding communities, but few assessed the impact of planned school breaks (i.e., school holidays) which coincide with influenza seasons while accounting for differences in seasonal peak timing. Breaks of 10 to 16 days correspond to 3 to 4 serial intervals for influenza. **Methods:** Between September 2014 and June 2019, we conducted a prospective observational study of a-ILI within the Oregon School District, Dane County, Wisconsin. Absenteeism was reported through the electronic student information system. MAI cases in the surrounding community for the first and second 7-day periods (week 1 and 2, respectively) before and after break were identified at 5 surveillance clinics using RT-PCR testing. We evaluated the association of planned school breaks (winter and spring; duration ranged from 10 to 16 days), on a-ILI counts during the 2-week period before and after the break using generalized linear regression models to account for the community's underlying influenza activity. To evaluate time effects, we also explored an annual 9-day "fake" break starting 5 weeks before the spring break using the same method. **Results:** The estimated proportional change in a-ILI counts following a planned break as compared to before the break was 0.483 (95% CI: 0.347-0.673; $p<0.001$) for winter break and 0.488 (95% CI: 0.327-0.730; $p<0.001$) for spring break. The weekly community MAI count was also strongly associated with a-ILI count ($p\leq0.001$). In contrast, there was consistently no statistically significant difference observed in a-ILI in the 2-week period before and after the "fake" break when school was in session. **Conclusions:** These findings suggest planned school breaks can reduce a-ILI in schools. Such an effect has biological plausibility as schools are important centers of influenza transmission and acceleration, and winter and spring breaks span 10-16 days. Additional research is needed to assess the role of planned school breaks to mitigate influenza in broader communities.

### Poster 46. Pandemic Influenza Preparedness (PIP) Framework: Building and Maintaining Sustainable Country Capacities for Longer-term Preparedness Against all Infectious Disease's Public Health Threats in the Eastern Mediterranean Region, 2018–2021

**H. Abou El Naja**, L. Al Ariqi, A. Abubakar, L. Al Ariqi, A. Aman, A. Barakat, A. Elkholy, R. Kawafha, W. Khan, S. Mohammed, E. Omran, S. Tempia
World Health Organization/Eastern Mediterranean Region, Nasr City, Egypt
Pandemic influenza is a threat that all WHO member states need to prepare for. Pandemic influenza viruses emerge periodically and influenza viruses with pandemic potential have been detected in the Eastern Mediterranean Region threatening public health. In this region, one third of the 12% world population live in 9 either high-medium intensity conflict or high institutional and social fragility countries. The Pandemic Influenza Preparedness (PIP) Framework aims to achieve more equitable access of developing countries to vaccines and therapeutics during a pandemic and improve pandemic preparedness and response to pandemic influenza. Ten priority high-medium

intensity conflict and high institutional and social fragility countries in the Eastern Mediterranean Region have been selected according to a criterium to benefit from PIP partnership contribution. Around 2.7 US$ was invested in Afghanistan, Egypt, Iraq, Jordan, Lebanon, Morocco, Yemen, Somalia, Sudan and Syria to strengthen influenza surveillance systems and influenza diagnostic capacities leading to improvement in detection and sharing of surveillance data and influenza viruses. We highlight the value of investing in long term influenza preparedness and response capacities. In addition, we provide an example of how building a strong surveillance system in countries in crises contributed to respond to Covid 19 pandemic. 19 out of 22 countries and territories in the Region have influenza surveillance systems, including the 10 PIP priority countries. Half of EMR PIP countries have capacity to conduct genomic sequencing surveillance. 16 countries with functioning influenza-like illness (ILI) and severe acute respiratory infections (SARI) sentinel surveillance sites report both epidemiological and virological data though FluNet and/or EMFLU. 16 National Influenza Laboratories and 4 Influenza Centres are operational with the ability to detect and confirm unusual influenza viruses with human pandemic potential. The increase in number of GISRS accredited institutions in EMR improves data representativeness and facilitates a timely and effective response to an influenza pandemic as countries became able to rapidly detect a novel influenza virus. In addition to that, 22 countries have national Rapid Response capacities, 15 of them enhanced their subnational RRT capacities. 16 of 22 countries reported having National Influenza Preparedness Plan. 70% of which used the plan as the basis of their COVID-19 response plan. The context in EMR is complex and unpredictable. Despite the emergency situation in the ten PIP countries; such as Covid 19 pandemic, high staff turnover, restriction in travel and movement and pollical instability, such countries were able to sustain timely virus and data sharing to inform influenza vaccine formulation and to monitor the start and severity of influenza virus circulation. Moreover, they were able to build on existing systems to response to newly emerged public health threats such as the COVID-19 pandemic.

### Poster 47. Characterizing the Countrywide Epidemic Spread of Influenza A(H1N1)pdm09 Virus in Kenya between 2009 and 2018

**D.C. Owuor**[1], Z.R. de Laurent[1], G.K. Kikwai[2], L.M. Mayieka[2], M. Ochieng[2], N.F. Müller[3], N.A. Otieno[2], G.O. Emukule[4], E.A. Hunsperger[5,6], R. Garten[7], J.R. Barnes[7], S.S. Chaves[4,7], D.J. Nokes[1,8], C.N. Agoti[1,9]
[1]Epidemiology and Demography Department, Kenya Medical Research Institute (KEMRI) - Wellcome Trust Research Programme, Kilifi, Kenya, [2]Kenya Medical Research Institute (KEMRI), Nairobi, Kenya, [3]Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center, Seattle, WA, USA, [4]Influenza Division, Centers for Disease Control and Prevention, Nairobi, Kenya, [5]Division of Global Health Protection, Centers for Disease Control and Prevention, Nairobi, Kenya, [6]Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, GA, USA, [7]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]School of Life Sciences and Zeeman Institute for Systems Biology and Infectious Disease Epidemiology Research (SBIDER), University of Warwick, Coventry, UK, [9]School of Public Health and Human Sciences, Pwani University, Kilifi, Kenya
**Background:** The spatiotemporal patterns of spread of influenza A(H1N1)pdm09 viruses on a countrywide scale are unclear in many tropical/subtropical regions mainly because spatiotemporally representative sequence data are lacking. **Methods:** We isolated, sequenced, and analyzed 383 A(H1N1)pdm09 viral genomes from hospitalized patients between 2009 and 2018 from seven locations across Kenya. Using these genomes and contemporaneously sampled global sequences, we characterized the spread of the virus in Kenya over several seasons using phylodynamic methods. **Results:** The transmission dynamics of A(H1N1)pdm09 virus in Kenya were characterized by: (i) multiple virus introductions into Kenya over the study period, although only a few of those introductions instigated local seasonal epidemics that then established local transmission clusters; (ii) persistence of transmission clusters over several epidemic seasons across the country; (iii) seasonal fluctuations in effective reproduction number ($R_e$) associated with lower number of infections and seasonal fluctuations in relative genetic diversity after an initial rapid increase during the early pandemic phase, which broadly corresponded to epidemic peaks in the northern and southern hemispheres; (iv) high virus genetic diversity with greater frequency of seasonal fluctuations in 2009-11 and 2018 and low virus genetic diversity with relatively weaker seasonal fluctuations in 2012-17; and (v) virus spread across Kenya. **Conclusion:** Considerable influenza virus diversity circulated within Kenya, including persistent viral lineages that were unique to the country, which may have been capable of dissemination to other continents through a globally migrating virus population. Further knowledge of the viral lineages that circulate within understudied low-to-middle income tropical and subtropical regions is required to understand the full diversity and global ecology of influenza viruses in humans and to inform vaccination strategies within these regions.

### Poster 48. Positivity and Risk Factors for Influenza Associated Severe Acute Respiratory Infection during 2018/2019 Season in Yemen

**M. Al Amad**[1], K. Almoayed[2]
[1]Field Epidemiology Training Program, Ministry of Public Health and Population, Sana'a, Yemen, [2]General Directorate for Diseases Control and Surveillance, Ministry of Public Health and Population, Sana'a, Yemen
**Background**: The burden of seasonal influenza in conflict countries such as Yemen is exacerbated due to limited resource and collapse of health system. During 2018 /2019 season, the incidence of influenza increased by two folds and the mortality among patients with severe acute respiratory infection (SARI) reached 22%. The aims are to determine positivity of influenza circulating viruses and risk factors for influenza associated-SARI. **Methods**: We used a retrospective analytical study based on surveillance data. All patients who meet WHO cases definition for SARI or influenza like illness (ILI) were included. Adjusted Odds ratio (AOR) with 95% confidence interval and P-value < 0.05 were used for statistically significant. **Results**; 768 of patients: 37% SARI and 63% ILI patients were reported. Of them 19% were children < 15 years, 15% ≥ 65 years, 69% males and 18% had chronic diseases. Influenza viruses were detected in 411 (53.5%), 68% influenza A subtype (H1N1)pdm09, 27% influenza B and 5% was influenza A not subtyped. The influenza positivity was significantly higher in SARI patients than ILI patients < 15 years (95% vs, 66%, P < 0.001), and ≥65 years (83% vs. 56%, p < 0.002), respectively. The highest positivity for *influenza type A* and type B was 44% and 33% among patients ≥ 65 years and <15 years, respectively. The risk factors for influenza-associated SARI were age < 5 [AOR 2.8] and ≥ 65 years old [AOR 3.1] compared to age 5-<25 years, diabetes [AOR 4.7], heart diseases [AOR 3.1] and chronic respiratory diseases [AOR 5.0]. **Conclusion**s: Influenza subtype A (H1N1) pdm09 was the predominant co circulated with influenza B during 2018 /2019 season in Yemen. Influenza positivity was varied by age distribution and severity. Influenza vaccination for risk group is crucial to reduce influenza-associated SARI and further prospective study is recommended for more comprehensive picture.

### Poster 49. Seroprevalence of Influenza A Viruses (H1N1 and H3N2) in Tunisia, 2017-2018

**R. Yazidi**[1], S. Abid[2], H. Bouguerra[3], L. Maazaoui[4], L. Charaa[2], I. Andolsi[2], I. Boutiba[2], J. Bettaieb[1], D. Laouini[5], J. Ben Khelil[6], A. Ben Salah[5,7]
[1]Service of Medical Epidemiology, Institut Pasteur de Tunis, Tunis-Belvédère, Tunisia, [2]Charles Nicolle Hospital, Laboratory of Microbiology, National Influenza Center, Tunis, Tunisia, [3]Observatoire National des Maladies Nouvelles et Emergentes de Tunis, Tunis, Tunisia, [4]Primary Health Care Directorate, Tunis, Tunisia, [5]Laboratory of Transmission, Control and Immunobiology of Infections, Institut Pasteur de Tunis, Tunis-Belvédère, Tunisia, [6]University of Tunis EI Manar Tunis, Faculty of Medicine, Medical Intensive Care Unit, Abderrahmen Mami Hospital, Ariana, Tunisia, [7]Department of Family and Community Medicine, College of Medicine and Medical Sciences (CMMS), Arabian Gulf University (AGU), Manama, Bahrain
**Background:** Seroprevalence studies remain an essential tool for estimating the extent of respiratory pathogens circulation. They can address shortcomings of reported incidence data by providing unbiased estimates of viruses' transmission to inform decisions towards scaled and targeted responses. We conducted a seroprevalence study in order to assess the prevalence of IgG anti-AH1N1 and - AH3N2 influenza virus antigens. **Methods:** A cross-sectional epidemiological survey enrolled 1200 individuals from the 5 main regions in Tunisia between November 2017 to April 2018. Samples were tested for the detection of antiAH1N1 and -AH3N2 antibodies using an indirect Enzyme-Linked Immuno-Assay (ELISA). Sociodemographic and exposure information was collected via questionnaires to analyze the patterns of the seropositives and related risk factors. $\chi$ 2 test permitted to compare seroprevalence levels and associations between categorical variables. **Results:** The prevalence of Influenza A (H3N2 and H1N1) was 12.8% (n=154), with a predominance of influenza AH1N1 serotype compared to the AH3N2 one (10.7% (n=128); 2.4% (n=29) respectively). Three cases showed a co-infection. The global prevalence of influenza A viruses was significantly different according to governorates (p< 10-3 ). The distribution by age showed that groups between 15-65 years were those who have the highest antibody levels (was 44.2% and 31.2% for 15-50 and 50-65 years respectively). On the other hand, the two extreme age groups (1-5 and ≥65 years) showed the lowest seroprevalence (7.1% and 11.7%; respectively) indicating a highest susceptibility for infection. Unsurprisingly, only 9.9% (n=119) of the study sample received anti-influenza vaccine during the study period. **Conclusion:** This study is the first assessing the sero-immunological status against natural infection by influenza A viruses in Tunisia, with a high infection levels by influenza AH1N1. Vaccination coverage remains low. These results would help to identify regions where increase of public awareness should be taken and to promote more effective preventive strategies.

### Poster 50. Detection of Influenza and Other Respiratory Viruses in a Community Cohort of Older Adults (≥60 years) in Pune, India

**V. Potdar**[1], S.D. Bhardwaj[1], R. Ghuge[1], V. Vipat[1], S. Jadhav[1], R. Amarchand[2], A.O. Prabhakaran[3], L. Dar[2], K.E. Lafond[4], E. Azziz-Baumgartner[4], S. Saha[3], A. Krishnan[2]
[1]Indian Council of Medical Research-National Institute of Virology, Pune, India, [2]All India Institute of Medical Sciences, Delhi, India, [3]Centers for Disease Control and Prevention, New Delhi, India, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: Burden estimates of respiratory viruses among older adults are critical for public health decision-making, but data about this vulnerable population are limited from lower- and middle-income tropical countries. **Methods:** During July 2018-March 2020, trained nurses weekly followed a cohort of community dwelling adults aged ≥60 years in an urban slum of Pune for acute respiratory infection (ARI). Nasal and throat swabs were collected from 20% of randomly selected ARI (defined as new onset/ worsening cough, or difficulty in breathing in the last 7 days) and all ALRI (defined as ARI with dyspnoea or chest pain, a respiratory rate of >20 breaths/minute, and either measured fever or a reported symptom complex of fever, sweating, headache and myalgia). All samples were tested for influenza, respiratory syncytial viruses (RSV), seasonal coronaviruses(hCoV), rhinoviruses (hRV), metapneumoviruses (HMPV), parainfluenza viruses (PIV) 1-4, enteroviruses (EV), EV-D68, bocaviruses and adenoviruses(Adev) by real-time reverse transcriptase polymerase chain reaction. **Results:** We followed 1178 older adults with median age 63 years (IQR 61-67), of whom 716 (61%) were female. We detected 3197 ARI episodes of which 624 (20%) were sampled and 155 ALRI episodes, of which 145 (94%) were sampled. Among these, 103 ARI samples (17%) and 35 ALRI (24%) were positive for ≥1 virus. The viruses detected among ARI were influenza (35, 6%)[A/H1N1pdm09 (16, 3%), A/H3N2 (9, 1%), B(10, 2%)], hCoV (31, 5%) [229E (8), HKU-1 (6), OC-43 (9), NL-63 (8)], RSV (8, 1%), hRV (14, 2%), HMPV (11, 2%), PIV (4, 1%), EV (2, 0.3%), and EV-D68 (1, 0.0%). Among ALRI cases, influenza (12, 4%)[ A/H1N1pdm09 (6, 4%), A/H3N2 (4, 3%), B(2, 1%)], hCoV (6, 4%) [229E (1), HKU-1 (2), OC-43 (2), NL-63 (1)], RSV (5, 3%), hRV (7, 5%), HMPV (3, 2%) and Adev (2, 1%) were detected. The incidence of ALRI cases due to influenza was 1.4/100person-years (py) (95% CI 0.8–2.4), hCoV 0.7/100py (0.3–1.4), hRV 0.8/100py (0.4–1.6), HMPVs 0.4/100py (0.1–1.0), RSV 0.6/100py (0.2–1.3) Adev 0.2/100py (0.04–0.8). **Conclusion:** Influenza was the most common viral pathogen identified among older adults with ARI and ALRI highlights the potential value of influenza vaccination and empiric antiviral treatment in this population during epidemic periods.

### Poster 51. Integrated Sentinel Surveillance System to Strengthen Laboratory Capacity for Infectious Disease Control, Lebanon

**M. Al Buaini**[1], H. Abou Naja[2,3], A. Zaghlout[2], N. Jammal[1], L. Mroueh[1], N. Ghosn[2]
[1]National Influenza Center at Rafik Hariri University Hospital, [2]Epidemiological Surveillance Program at Ministry of Public Health, [3]World Health Organization, Geneva, Switzerland
**Background:** In December 2014, the SARI surveillance system was established in Lebanon with the support of WHO. In November 2020, the integrated Influenza and COVID-Like Illness (ILI/CLI) sentinel surveillance in outpatient sites was established in the country. In December 2019, plans were set to include the RSV surveillance as recommended by WHO RSV initiative. **Objectives:** The main objectives are to estimate morbidity of RSV in the community for patients younger than 2 years, identify the beginning and trend of the RSV season, to participate in the RSV genomic surveillance, to enhance national laboratory capacity, and to contribute to the global RSV surveillance. **Methods:** Case definitions are based on WHO definitions for ILI and COVID like illness. The target age group was under 2 years. Cases were selected from sentinel network including 22 outpatient clinics: PHCs, MSF, UNRWA clinics, and ERs from various provinces. For cases meeting the case definitions, data on demographics and clinical presentation are collected, and nasopharyngeal swab is collected and preserved in viral transport media. Clinical specimens are referred to the National Influenza Center at Rafik Hariri University Hospital, where they are tested using Reverse Transcription Polymerase Chain Reaction. Samples are initially tested for both SARS-CoV-2 and Influenza by FluSC2 kit from CDC; negative specimens fitting ILI case definition and less than 2 years age are then to be tested for RSV for up to 400 patients. NIC shares results with MOPH within 24-48hrs, and MOPH feeds back to sentinel sites and partners within 24hrs. **Results:** The results of RSV testing will be presented. **Conclusion:** RSV surveillance is in the implementation phase with integration within existing ILI/CLI sentinel surveillance system. Although the system is still in its early implementation phases, the network provides valuable representative data for trend description, early detection, and timely response to any unusual virus circulation patterns and a good start on genomic surveillance in all of these respiratory pathogens and for any endangering pathogen of concern in future.

### Poster 52. Improvements in Influenza Surveillance, Specimen Testing, Sharing, and Reporting Globally, 2013–2019

Moved to Poster Session 3, Tuesday, August 9, 12:30 PM – 1:30 PM (in Respiratory Diseases and Influenza section, after poster 235)

### Poster 53. Detection of Reassortant Eurasian Avian-like H1N1 Clade 1C.2.3 Swine Influenza Virus by Real-Time RT-PCR

**B. Shu**, W.G. Davis, C. Warnes, M.K. Kirby, C.T. Davis, D.E. Wentworth, J.R. Barnes
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background**: Eurasian avian-like (EA) H1N1 viruses with multiple genotypes circulate in swine in China and new human cases of EA H1N1 variant viruses continue to emerge. Multiple reassortant genotypes co-circulate with most viruses encoding hemagglutinin (HA) genes from the progenitor EA H1N1 clade 1C.2.3. The clade 1C.2.3 viruses are capable of binding to human-like sialic acid α-2,6Gal receptors and replicating in human airway epithelial cells, have resulted in zoonosis and represent a pandemic threat. Given the pandemic potential of the clade 1C.2.3 viruses, we have developed a real-time RT-PCR assay (known as H1v_1C23) that targets the HA gene segment of this lineage. **Method**: The clade 1C.2.3 virus A/Hebei-haigang/SWL1572/2019 (G4) and A/Hunan/42443/2015 (G5), isolated in China, were initially tested with the CDC human influenza virus real-time RT-PCR diagnostic panel (CDC Flu rRT-PCR Dx Panel), and then used to evaluate the H1v_1C23 assay sensitivity compared to the Influenza A assay (InfA) targeting matrix gene within the CDC Flu rRT-PCR Dx Panel. H1v_1C23 assay specificity was evaluated by testing four seasonal and ten North American lineage swine influenza viruses. **Result**: When tested with the CDC Flu rRT-PCR Dx Panel, the clade 1C.2.3 viruses were positive for InfA assay and influenza A pdm09 assay (pdmInfA) targeting nucleoprotein gene but negative for the influenza A(H1)pdm09 assay (pdmH1) targeting HA gene, resulting in an inconclusive result interpretation. Analytical performance studies demonstrated the sensitivity of the H1v_1C23 assay is comparable to the InfA assay and had no cross-reactivity with H1N1pdm09 and H3N2 seasonal viruses or H1 or H3 variant viruses isolated in the USA. **Conclusion:** Implementation of the CDC H1v_1C23 assay described here with the CDC Flu rRT-PCR Dx Panel can serve as an effective method for rapid identification of EA H1N1 clade 1C.2.3 viruses that circulate in swine in China and cause sporadic human infection.

## Surveillance

### Poster 54. Implementation of an Acute Febrile Illness Surveillance Network in Belize, 2020-2021

**A. Maliga**[1], G.H. Morazan[2], S.M. Gunter[1,3], S.E. Ronca[1,3], E. Zielinski-Gutierrez[4], F. Morey[2], K. Bautista[2], A. Espinosa-Bode[4], M.B. López Castellanos[4], L. Cadena[4], R. Chacon-Fuentes[4], F.M. Munoz[1,5], J. Mackey[6], R. Manzanero[2], K.O. Murray[1,3] on behalf of the Belize Acute Febrile Illness Surveillance Team
[1]Department of Pediatrics and National School of Tropical Medicine, Baylor College of Medicine and Texas Children's Hospital, Houston, TX, USA, [2]Belize Ministry of Health and Wellness, Belmopan, Belize, [3]The William T. Shearer Center for Human Immunobiology, Texas Children's Hospital, Houston, TX, USA, [4]US Centers for Disease Control and Prevention—Central America Region, Division of Global Health Protection, Guatemala City, Guatemala, [5]Department of Pediatrics, Section of Infectious Diseases and Department of Molecular Virology and Microbiology, Baylor College of Medicine, Houston, TX, USA, [6]Henry JN Taub Department of Emergency Medicine, Baylor College of Medicine, Houston, TX, USA

**Background**: Belize is a low- to middle-income country with ~390,000 residents. Millions of tourists visit the country each year, increasing the risk of introduction of infectious pathogens. In January 2020, the Acute Febrile Illness (AFI) Surveillance Network was implemented country-wide in 11 hospitals and clinics with the purpose of collecting epidemiologic data and performing enhanced diagnostics for 51 different etiologic causes of AFI, including vector-borne (VBD), respiratory (RP), and gastrointestinal (GI) pathogens. **Methods**: Patients presenting with new onset fever (within 7 days) and/or ≥2 RP symptoms and/or ≥2 GI symptoms were invited to enroll. Demographic and epidemiologic data were collected along with a blood specimen; nasopharyngeal swabs, and/or stool samples were collected based on symptomatology. Whole blood was tested on a vector-borne PCR panel, and nasopharyngeal swabs and stool samples were tested on the BioFire platform (RP Panel 2.1 and GI Panel). Data were collated into a real time analytic dashboard for distribution to stakeholders. **Results**: From January 16, 2020, to September 15, 2021, 2238 patients were enrolled in AFI surveillance. Average age was 28 (range 2 months-97 years); 1166 (52%) were female. For the GI panel, 247 of 306 (81%) cases had at least one positive result, including pathogenic *E. coli*, norovirus, rotavirus, *Giardia*, *Campylobacter*, *Salmonella*, and cholera. For the RP panel, 762 of 1399 (54%) cases had at least one positive result, including human rhinovirus/enterovirus, SARS-CoV-2,

coronavirus OC43, adenovirus, influenza, and respiratory syncytial virus. VBDs included one acute Chagas case, 44 dengue cases, and 4 Zika virus cases. Since implementation, we have tracked the COVID-19 pandemic throughout the country, we confirmed the circulation of four dengue serotypes, and we identified the first case of acute Chagas disease in Belize and the first cases of Zika since 2017. **Conclusion**: AFI surveillance provides a valuable tool to understand the incidence of emerging pathogens and to identify epidemiologic trends. The data presented from our active surveillance of AFI patients addresses the critical need for active surveillance to inform public health measures to diminish the spread of pathogens and outbreaks, including SARS-CoV-2, in the region.

### Poster 55. The Role of Event-based Surveillance in the Successful Implementation of the 27th World Men's Handball Championship, Egypt 2021

**H. El Sood**, S. Afiffi, M. Fawzy Salem, H. Magdy, S. Samy
Ministry of Health and Population Egypt, FETP Egypt, Cairo, Egypt
**Introduction:** Event-based surveillance (EBS) system has been in operation in Egypt since 2015 with the aim of capturing information about events of potential risk to public health through formal and informal channels. Epidemic Intelligence from Open Sources (EIOS) developed by WHO is an important source of information for the EBS. A signal was captured through EIOS regarding an outbreak of COVID-19 among Cape-Verde handball team camping in Portugal in preparation to the World Men's Handball Championship hosted by Egypt from 13 to 31st January 2021. This study aims at describing the investigation and control measures implemented to prevent disease transmission among the tournament participants. **Methods:** Signal identified and filtered through risk assessment as infectious disease with very high risk. Event verified by Egypt Championship Medical Committee and International Handball Federation (IHF) as true. Egyptian Health authorities required that Cape-Verde delegation members travelling to Egypt must have negative PCR test certificate for COVID-19, within 48 hours before their arrival to Cairo airport. At the airport rapid-antigen test performed and team was kept under observation at special assigned hotel. PCR testing was performed on arrival at the hotel and every 48 hours. **Results:** The signal indicated that fifteen (53.6%) of the 28 Cape-Verde team members tested positive by Rapid-Antigen test during their stay in Portugal. Among 24 members with negative COVID-19 PCR certificates who travelled to Egypt, ten (41.7%) were positive by PCR on 14th-15th-17th of Jan 2021. Patients were immediately isolated according to the Egypt 2021 COVID-19 Medical Precaution Plan. As the number of Cape-Verde players available for participation in the games was less than allowed according to IHF regulation, hence Cape Verde team was excluded. Positive patients were kept under observation and released after two successive PCR negative tests 48 hours apart. **Conclusions:** Egypt EBS achieved its objective of capturing COVID-19 outbreak among Cape-Verde handball team prior to arrival to Egypt to participate in World Men's Handball Championship. EBS succeeded in preventing COVID-19 transmission among teams from 32 countries participated in the tournament. EBS and laboratory components are vital components of a multisectoral plan for COVID-19 -and other epidemic prone diseases- prevention and control when organizing similar international events.

### Poster 56. A Target Operating Model for Implementing Integrated Genomics-driven Public Health Surveillance Systems

**N.K. Lee**, M.A. Stewart, J.E. Dymond, S.L. Lewis
Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA
**Background:** There is a need to establish more effective genomic epidemiological public health workflows to better understand disease transmission and allow the implementation of rapid- response measures during disease outbreaks. An ongoing challenge for genomics-based surveillance efforts is effectively strategizing and executing sustainable programs capable of simultaneously generating data applicable for population-level disease monitoring and decision-making in clinical care settings. **Methods:** The method for implementing an integrated genomics-based public health surveillance workflow through execution of a target operating model includes six process steps. Step 1 defines regions of interest for sampling anticipated to have greatest relevance in early detection of infectious disease outbreaks based on historical trends and current understanding of risk. Step 2 determines optimal capacity needs based on these population dynamics through statistical analysis. Step 3 assesses current capabilities and resource requirements and formulates an optimal workflow execution plan. Step 4 defines and addresses procedural and workforce training needs. Step 5 determines the appropriate analytic and bioinformatic pipelines and initiates integration into established information systems. Step 6 creates digital visualization tools to provide risk assessment capabilities for end-users. **Results:** Together, these steps support the design of location-specific, indicator-based surveillance programs and allows for configuration of the workflow that prioritizes findings defined by the stakeholders while incorporating local context to ensure the right data is captured to support those decisions. This process also supports a framework that encourages construction of innovative solutions for systems development

through interdisciplinary engagement. **Conclusions:** Adopting a target operating model for the promotion of regional genomics-driven surveillance programs will ensure developed networks are agile, sustainable, and cohesive, which are crucial elements for mitigating future outbreaks. This data-driven framework will also help align priorities and resources across a diverse set of participants to better work together to implement relevant and sustainable surveillance strategies.

### Poster 57. Early Implementation of Standardized Healthcare-Associated Infection Surveillance in Vietnam, 2019-2020

**L.N. Khue**[1], N.T. Khoa[1], H.T.K. Phuong[1], T. Ninh[1], T.T.T. Ha[2], N.T. Nhu[2], N.T.P. Lan[3], B.T.T. Hien[3], P.A. Malpiedi[3], A.M. Vasquez[3]
[1]Medical Services Administration, Vietnam Ministry of Health, Hanoi, Vietnam, [2]PATH, Hanoi, Vietnam, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** In 2017, Vietnam established the first national standardized healthcare-associated infections (HAI) surveillance system for bloodstream infections (BSI), including central line-associated bloodstream infections (CLABSI), and urinary tract infections (UTI), including catheter-associated urinary tract infections (CAUTI), in a network of 6 hospitals. The system was expanded to 18 hospitals in 2019. We report data from the first two years of this expanded HAI surveillance network. **Methods:** From January 1, 2019 to December 31, 2020, surveillance was conducted in 31 adult, pediatric, and neonatal intensive care units (ICU). Cases were entered into a secure online portal via a standardized data collection form. Cases were identified among patients hospitalized in participating ICUs for at least two calendar days using case definitions adapted from the US National Healthcare Safety Network. BSI and UTI rates were calculated as number of infections per 1,000 patient-days; CLABSI and CAUTI as number of device-associated infections per 1,000 device-days. Pooled means were calculated by ICU type. Device utilization ratio (DUR) was calculated by dividing number of device days by number of patient days. **Results:** A total of 748 BSI were reported: 523 CLABSI, 121 primary BSI, and 104 secondary BSI. Neonatal ICU had the highest BSI (2.3) and CLABSI rate (3.9; DUR 0.39). A total of 345 UTI were reported: 304 CAUTI and 41 non-CAUTI. Adult medical ICU reported the highest mean UTI (0.7) and CAUTI rate (1.5; DUR 0.44). Of 770 pathogens reported from BSI, the most commonly identified was *Klebsiella spp.* (n=182; 24%) followed by *Acinetobacter baumannii* (n=130; 17%). Carbapenem resistance was 84% and 86%, respectively. Of 352 pathogens reported from UTI, most common was *Klebsiella spp.* (n=77; 22%) followed by *Enterococcus spp.* (n=62; 18%) and *Escherichia coli* (n=60; 17%). Carbapenem resistance was much higher in *Klebsiella spp.* (76%) than *E. coli* (14%). **Conclusions:** Vietnam successfully created its first national HAI surveillance network using standardized methodology and case definitions. Early data shows high rates of carbapenem-resistance among BSI and UTI. The system is preparing for further expansion, including focused efforts to improve HAI prevention.

### Poster 58. Evaluation of Whole Genome Sequencing for *Campylobacter* Surveillance and Outbreak Detection

**L.A. Joseph,** T. Griswold, E. Vidyaprakash, S. Im, G. Williams, K.B. Hise, H. Carleton
Enteric Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** *Campylobacter jejuni* is a leading cause of bacterial foodborne illnesses in the United States. Pulsed-field gel electrophoresis (PFGE) was the previous method used within PulseNet USA for *Campylobacter* surveillance and outbreak investigations. However, PulseNet USA has developed whole genome sequencing (WGS)-based methods for surveillance of all the pathogens it tracks, including *Campylobacter*. In this study, we evaluated the ability of whole genome multilocus sequence typing (wgMLST) and core genome (cg)MLST to cluster or differentiate outbreak-associated and sporadic *C. jejuni* and *C. coli* isolates indistinguishable by PFGE and/or 7-gene MLST in comparison to high quality single nucleotide polymorphism (hqSNP) analysis. **Methods:** 314 *C. jejun*i and 12 *C. coli* isolates (243 *C. jejuni* and 5 *C. coli* associated with outbreaks) were sequenced using an Illumina sequencer. Sequences were analyzed using wgMLST, cgMLST (Oxford scheme), and 7-gene MLST in BioNumerics 7.6.3 and hqSNP analysis using LYVE-SET v1.1.4f (github.com/lskatz/lyve-SET). The wgMLST database incorporating the cgMLST and 7-gene MLST subschemas was developed in collaboration with domestic and international partners for *Campylobacter* surveillance. PFGE was performed on a subset of isolates using the PulseNet *Campylobacter* protocol; patterns were compared and named in BioNumerics 6.6.10. **Results:** Outbreak-associated *C. jejuni* and *C. coli* isolates from 16 source confirmed outbreaks were differentiated from epidemiologically unrelated isolates (indistinguishable by *Sma*I/*Kpn*I PFGE or 7-gene MLST to outbreak isolates) by cgMLST, wgMLST, and hqSNP analysis which produced concordant results. **Conclusions:** In our study, wgMLST, cgMLST, and hqSNP provided greater concordance with epidemiologic data compared with PFGE and 7-gene MLST. However, hqSNP analysis is dependent on a priori knowledge of isolates to select the correct reference

genome before an analysis is run making wgMLST and cgMLST more user-friendly and requiring less specialized knowledge to perform. Furthermore, since cgMLST examines allele differences in genes that are common to all isolates being compared, it should be well suited to surveillance. If further resolution between potential outbreak isolates is needed, then wgMLST or hqSNP analysis can be used.

## Global Health Security and Preparedness

### Poster 59. "GLEWS+" -- the Joint Tripartite FAO–OIE–WHO Global Early Warning System for Emerging Health Threats Arising at the Human-Animal Ecosystems Interface

**D. Selenic**[1], E. Peron[1], E. Hamblion[1], P. Caceres[2], P. Tizzani[2], I. Gizo[2], R. Morales[2], M. Morini[2], F. Larfaoui[3], M. Dhingra[3], O. Rozov[3], A. Capobianco Dondona[3]
[1]World Health Organization (WHO), Geneva, Switzerland, [2]World Animal Health Information and Analysis Department, World Organisation for Animal Health (OIE), Paris, France, [3]Food and Agriculture Organization (FAO), Rome, Italy
**Background:** The Food and Agriculture Organization (FAO), the World Organization for Animal Health (OIE), and the World Health Organization (WHO) are responsible for minimizing the impact on health and livelihood from diseases arising at the human-animal-ecosystem interface. Since 2006, the Global Early Warning System (GLEWS+) for major animal diseases has been improving the timely exchange of information and assessment of risk to inform decisions and actions. This includes emerging zoonotic diseases with likely epidemic potential or undiagnosed diseases. This mechanism improves global early warning and response as well as transparency among countries. **Methods:** Information on animal disease threats are collected through event-based surveillance and networks. The information is disseminated to Members through the early warning mechanisms that each Organization has in place with the aim to inform countries to enhance preparedness and response. **Results:** From January 2020 to October 2021, 53 alerts were exchanged including: 24 events related to emerging zoonotic diseases with significant mortality or morbidity, 14 events associated with unknown causative pathogens, 5 associated with high morbidity or mortality in humans or animals, 5 with the first onset of a disease, and 5 with the recurrence of a disease. Two joint tripartite risk assessments were also disseminated (Rift Valley fever in the Republic of Sudan, 2019, SARS-CoV-2 in animals used for fur farming, 2021). **Conclusions:** Timely detection and monitoring of zoonotic pathogens will significantly reduce impacts on human and animal health and minimize socio-economic losses. To better address these challenges, it is crucial to improve the completeness, accessibility, quality and timeliness of information available from the human and animal sectors and to improve information sharing between One Heath sectors at all levels. This will enable appropriate response actions to prevent or reduce morbidity and mortality in humans and animals and avoid unnecessary interference with international traffic and trade. The Tripartite GLEWS+ has become a powerful One Health Intelligence mechanism to bring together information and expertise existing in the three Organizations and associated One Health networks.

### Poster 60. Public Health Bulletin Development in Seven Countries Reveals an Opportunity for Public Health Bulletins to Provide a Training Function for Staff

**K.M. Koporc**[1], N. Khurshid[2], M. Rahman[2], M.S. Uzzaman[2], H. Vandi[3], J.S. Moran[1], S. Bratton[3]
[1]CDC Foundation, Atlanta, GA, USA, [2]Institute of Epidemiology, Disease Control and Research, Dhaka, Bangladesh, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA
Public health bulletins are a useful tool in outbreak responses. They provide health professionals and the public with surveillance data and recommendations for actions to minimize public health threats. The Centers for Disease Control and Prevention and the CDC Foundation collaborated with seven ministries of health and national public health institutes in Bangladesh, Colombia, Ghana, Rwanda, Tanzania, Uganda, and Zambia between 2017-2021 to develop or strengthen national public health bulletins. Six new countries (Burkina Faso, Ethiopia, Mozambique, Pakistan, Thailand, and South Africa) were added in 2021. For the original seven countries, we reviewed project outcomes using issue quality (e.g., adherence to scope and policies, article content, figure and table quality, and article formatting and organization) and regular publication schedule as indicators. The review indicated the need to expand technical assistance to develop policies and standard operating procedures. It also revealed the need to support communication strategies that include developing dissemination channels, such as the media and email marketing campaigns. In addition, the review demonstrated the need to develop trainings in scientific writing, article review, and data analysis. Indicators measuring quality were revised to prioritize these activities. Policies and standard operating procedures need to be in place to guide and support a national public health bulletin's future. The public health bulletin can also serve as a training program to upskill staff in project management, communication,

and scientific writing. The presentation will feature the experiences of the Bangladesh's Institute of Epidemiology, Disease Control, and Research, which established the *National Bulletin of Public Health* in 2018.

### Poster 61. Status of the Implementation of National Action Plans—All Countries, 2020

**N.M. Mikanatha**[1], X. Yin[1,2], H. Tate[3]
[1]Pennsylvania Department of Health, Harrisburg, PA, USA, [2]Penn State Hershey College of Medicine, Hershey, PA, USA, [3]Food and Drug Administration, Silver Spring, MD, USA
**Background:** Antimicrobial resistance (AMR) threatens human and animal health and the economics and security of every country. At the 2015 World Health Assembly (WHA), members pledged to implement national AMR action plans (NAAPs) through a multi-sectoral One-Health approach. Whether NAAPs that address human, animal and the environment have been developed is unclear. Here we review progress in development and implementation of NAAPs including integrated One Health surveillance and AMR impact to the environment. **Methods:** Progress towards development and implementation of the NAAPs is monitored through a self-administered survey that since 2016 has been jointly conducted by the World Health Organization (WHO), World Organisation for Animal Health, and the Food and Agriculture Organization. We analyzed responses to the 2019/2020 survey (at www.amrcountryprogress.org) including AMR national plan, One Health surveillance, stewardship, and environmental monitoring. **Results:** Of 194 WHO member countries, 136 (70%) responded to the survey. Of respondents, 38 (28%) reported having AMR plans; 55 (40%) had approved NAAPs. Sixty-one (45%) indicated that they have nationwide AMR awareness campaigns targeting stakeholder groups. Prescribing practices and appropriate antibiotic use in human health are nationally monitored in 49 (36%). Sales of antimicrobials for veterinary use are tracked by 55 (40%) respondents. Fifty-five (40%) also reported that they monitor antimicrobials used in plants. A majority of respondents (101, 74%) reported that they have a national surveillance system for monitoring AMR in humans. Only 17 (13%) of respondents were conducting integrated surveillance and had One Health antimicrobial stewardship. Forty-nine (36%) respondents reported assessing the risk of AMR spread in the environment. **Conclusions:** Among the 70% of countries responding to the survey, many have made progress in the development and implementation of national action plans to address the threat of AMR. However, six years after the 2015 WHA resolution, few have the necessary infrastructure to conduct integrated surveillance in humans, animals, plants, and the environment. One Health approaches are needed in most countries to slow the emergence and spread of antimicrobial resistance.

### Poster 62. Global Health Security Preparedness and Response—An Analysis of the Relationship between Joint External Evaluation Scores and COVID-19 Response Performance

**L. Nguyen**, S.M. Brown, A. Couture, S. Krishnan, M. Shamout, L. Hernandez, J. Beaver, A. Gomez Lopez, C. Whitson, L. Dick, A.L. Greiner
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The coronavirus disease (COVID-19) pandemic has highlighted the importance and complexity of a country's ability to effectively respond. The Joint External Evaluation (JEE) assessment was launched in 2016 to assess a country's ability to prevent, detect, and respond to public health emergencies. We examined whether JEE indicators could be used to predict a country's COVID-19 response performance to tailor a country's support more effectively. **Methods:** From April–August 2020, we conducted interviews with Centers for Disease Control and Prevention (CDC) Country Offices that requested COVID-19 support and previously completed the JEE (version 1.0). We used an assessment tool, the "Emergency Response Capacity Tool" (ERCT), to assess COVID-19 response performance. We analyzed 28 ERCT indicators aligned with eight JEE indicators to assess concordance and discordance using strict agreement and weighted kappa statistics. Generalized estimating equation (GEE) models were used to generate predicted probabilities for ERCT scores using JEE scores as the independent model variable. **Results:** Twenty-three countries met inclusion criteria. Of the 163 indicators analyzed, 42.3% of JEE and ERCT scores were in agreement (p-value=0.02). The JEE indicator with the highest agreement (62%) was "Emergency Operations Center (EOC) operating procedures and plans" while the lowest (16%) was "capacity to activate emergency operations." Findings were consistent with weighted kappa statistics. In the GEE model, EOC operating procedures and plans had the highest predicted probability (0.86) while indicators concerning response strategy and coordination had the lowest (≤0.5). **Conclusions:** Overall, there was low agreement between JEE scores and COVID-19 response performance, with JEE scores often trending higher. JEE indicators concerning coordination and operations were least predictive of COVID-19 response performance, underscoring the importance of not inferring country response readiness from JEE scores alone. More in-depth country-specific investigations are likely needed to accurately estimate response capacity and tailor countries' global health security activities.

### Poster 63. Establishing a National Infection Prevention and Control Program to Improve Preparedness and Response to Infectious Disease Emergencies in the Democratic Republic of Congo (DRC)

**A.N.H. Bulabula**[1], F. Malele[1], J. Safstrom[2], E. Bancroft[2], M. Lahuerta[1]
[1]ICAP at Columbia, Columbia University, Kinshasa, Democratic Republic of Congo, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** The Democratic Republic of Congo (DRC) has experienced a record number of infectious disease (ID) outbreaks including Ebola, meningitis, COVID-19 and monkey pox with noticeable recurrence. The lack of national programs for infection prevention and control (IPC) has been a considerable challenge in executing preparedness and response initiatives in the context of ID emergencies in the DRC. **Methods:** In March 2021, a week-long workshop was held by the DRC National Directorate of Hygiene (DOH) in Matadi. Different thematic areas were covered, including IPC. At the workshop, data on IPC capacity and practices from healthcare facilities in Mbandaka were presented to the 26 provincial heads of the DOH to illustrate the need for a robust IPC program. The provincial heads participated in individual interviews aimed at identifying specific gaps in IPC at provincial level. **Results:** We identified specific and common IPC gaps across the 26 provinces. The major gap reported by all participants was the lack of an IPC program at all levels of the DRC health system. Areas of great concern in all 26 provinces included: lack of IPC training among healthcare workers (100%), scarcity of IPC guiding documents (100%), insufficient IPC resources (funds and supplies, 100%), and lack of a surveillance system for healthcare-associated infections (100%). Recommendations from the workshop included the creation of the Division of Public Health and Infection Prevention and Control. The latter has been assigned the mandate to develop and implement activities of a national IPC program with its core components. **Conclusions:** The workshop recommendations were informed by data from the 26 provinces and major emphasis was placed on the creation of a functional national IPC Program. A national IPC program can address the identified gaps, by activities such as the development of IPC guiding documents, IPC training materials and coordination of funding.

### Poster 64. The Abbott Pandemic Defense Coalition: A Global Network Addressing a Gap in Response to Emerging Infectious Disease Threats

**F. Averhoff**[1], M.G. Berg[1], M.A. Rodgers[1], M.A. Anderson[1], S. Osmanov[1], X. Luo[1], A.L. Landay[2], E. Kallas[3], J. Manasa[4], T. de Oliveira[5], M. Alkhazashvili[6], A. Gamkrelidze[6], Y. Suputtamongkol[7], J. Lindo[8], S. Solomon[9], S. Mboup[10], J. Osorio[11], G.A. Cloherty[1]
[1]Infectious Diseases Research, Abbott Diagnostics, Abbott Park IL USA, [2]Rush University Medical Center, Chicago, IL, USA, [3]University of Sao Paulo, Sao Paulo, Brazil, [4]University of Zimbabwe, Harare, Zimbabwe, [5]Center for Epidemic Response and Innovation, Stellenbosch University, South Africa, [6]National Center for Disease Control, Tbilisi, Georgia, [7]Mahidol University, Bangkok, Thailand, [8]University of the West Indies, Kingston, Jamaica, [9]Johns Hopkins University School of Medicine, USA, and YRG CARE, Chennai, India, [10]Institute for Health Research, Epidemiologic Surveillance and Training (IRESSEF), Dakar, Senegal, [11]Colombia Wisconsin One Health, University of Wisconsin and National University of Colombia, Medellin, Colombia

**Background:** Early detection and epidemiological characterization of infectious diseases of pandemic potential are critical elements for containment and mitigation of the threat. The COVID-19 pandemic has demonstrated that coordinated multi-sector partnerships are needed for an effective response. **Methods:** Abbott, a global leader in healthcare technology, launched the Abbott Pandemic Defense Coalition (APDC) in early 2021 as a scientific and public health partnership consisting of a network of international partners whose primary purpose is the early detection, characterization, and mitigation of infectious disease threats of pandemic potential. A novel element of the APDC is Abbott's capacity for early development and rapid deployment of scalable, quality diagnostics targeting newly identified pathogens. **Results:** As of September 2021, the APDC has recruited 11 partners on 5 continents including academic institutions, and governmental and non-governmental organizations. The APDC is building on existing capacity of member institutions to conduct surveillance for emerging pathogens by improving epidemiologic and laboratory capacity, including instituting next generation sequencing and bioinformatics for virus discovery. Methods and data collection will be harmonized across the network, allowing for high quality analysis and interpretation. Upon detection of a pathogen of concern, diagnostic tools for molecular and serological tests will be developed and distributed across the network to track its spread and inform public health decision-making. Abbott provides technical and financial support for the APDC. **Conclusions:** The APDC is an extension of Abbott's work over the last 26 years in diagnostics, virus discovery, and virus surveillance and aims to complement global efforts in pandemic preparedness and response. The APDC can improve the response to a pathogen of pandemic potential by reducing the time between detection and development and deployment of diagnostics at scale. The APDC will enhance and supplement current international pandemic preparedness efforts.

### Poster 65. Implementation of an Integrated Specimen Referral System in Burkina Faso Using the National Courier Services

**E. Dama**[1], I. Yameogo[2], S. Porgho[2], F. Tarbangdo[3], M. Kamaté[3], S. Ouattara[2], H. Flavien Aké[3]
[1]Division of Global Health Protection, Country Office Burkina Faso, US Centers for Disease Control and Prevention Ouagadougou, Burkina Faso, [2]Direction de la Protection de la Santé de la Population, Ministère de la Santé, Ouagadougou, Burkina Faso, [3]Davycas International, Ouagadougou, Burkina Faso
**Background:** In 2017, the Ministry of Health (MoH) of Burkina Faso designed and piloted a specimen transport system using the national courier services (La Poste-BF) in 4 districts. Monitoring and evaluation performance indicators showed satisfactory results. Based on this success, the MoH developed a national guide aiming at expanding and implementing an integrated biological specimen referral system using La Poste-BF's services to transport all specimens type from districts to reference laboratories across the country. **Methods:** A stepwise and participatory approach was used in the view to gain buy-in of all the stakeholders. This includes the creation of a technical working group, the development of an action plan and its implementation. A web-based system, leveraging on an existing electronic platform for tracking epidemiological data and laboratory specimens was used to collect data. Cooler's departure/arrival date and time as well as the samples temperature and cooler status at arrival were collected. The delivery timeline requested was 24h. **Results:** 866 laboratory staff from 70 health districts and La Poste-BF were trained in triple packaging, transport and biosecurity. From January 2020 to June 2021, 11,598 packages containing 91,629 specimens of which 18,329 COVID-19 samples were transported, and 99,3% (11,514/11,598) were delivered within 24h of pick-up. Packages delivered after 24h were due to incorrect addresses, extending the time for delivery. Sample compliancy at the reception was 99,6% (91,247/91,629). No packages were lost. Data collected through the electronical tracking system allowed the production of monthly bulletin that progressively addressed gaps. **Conclusion:** Stakeholders' engagement throughout the process, standardized procedures, and resources are the key elements for a robust and sustainable integrated system of specimen transport in Burkina Faso. Furthermore, the good national coverage of La Poste-BF is an important factor for its performance. From multiple vertical specimen transport systems for specific diseases, the country now has a unique, maximized and more effective system.

### Poster 66. WHO Public Health Research Agenda for Managing Infodemics

**T.D. Purnat**[1], E. Wilhelm[2], S. Burzo[3], D. Prybylski[2], S. Briand[4], C. Czerniak[4], J. Lamichhane[4], T. Nguyen[4]
[1] European Centre for Disease Prevention and Control, Stockholm, Sweden, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]University of British Columbia, Vancouver, BC, Canada, [4]World Health Organization, Geneva, Switzerland
**Background:** An infodemic is an overflow of information of varying quality that surges across digital and physical environments during an acute public health event. It leads to confusion, risk-taking and behaviors that can harm health and lead to erosion of trust in health authorities and public health responses. The global scale and high stakes of the emergency have made responding to the infodemic related to the COVID-19 pandemic particularly urgent. Building on diverse research disciplines and expanding the discipline of infodemiology, more evidence-based interventions are needed to design infodemic management interventions and tools and implement them by health emergency responders. **Methods:** WHO organised the first global infodemiology conference, entirely online during June-July 2020, and a follow up August-October 2020, to review current multidisciplinary evidence, interventions and practices that can be applied to the COVID-19 infodemic response. This resulted in a public health research agenda for managing infodemics. **Results:** The public health research agenda for infodemic management has five work-streams: (i) measuring and continuously monitoring the impact of infodemics during health emergencies; (ii) detecting signals and understanding the spread and risk of infodemics; (iii) responding and deploying interventions that mitigate and protect against infodemics and their harmful effects; (iv) evaluating infodemic interventions and strengthening the resilience of individuals and communities to infodemics; and (v) promoting the development, adaptation and application of interventions and toolkits for infodemic management. Each work-stream identified research questions and highlights 49 high priority research questions. **Conclusions:** Public health authorities need to develop, validate, implement and adapt tools and interventions for managing infodemics in acute public health events in ways that are appropriate for their countries and contexts. For that to be possible, infodemiology provides a scientific foundation. This research agenda proposes a structured framework for targeted investment for the scientific community, policymakers, implementing organizations and other stakeholders to consider.

## Vaccines and Vaccine-preventable Diseases

### Poster 67. Circulating Vaccine Derived Polio Virus Type 1 Outbreak, Saadah Governorate, Yemen, 2020

**M. Al-Qassimi**[1], M. Al Amad[2], L. Anam[2], K. Almoayed[3], A. Al-Dar[1], F. Ezzadeen[1]
[1]National Polio Surveillance, Ministry of Public Health and Population, Sana'a, Yemen, [2]Field Epidemiology Training Program, Ministry of Public Health and Population, Sana'a, Yemen, [3]General Directorate for Diseases Control and Surveillance, Ministry of Public Health and Population, Sana'a, Yemen
**Background**: In 2020, 30 Vaccine Derived Polio Virus type 1 (VDPV1) isolates were detected in Saadah governorate. The aims are to characterize the outbreak and address the gaps predisposing the emergence and circulation of VDPV1 in Saadah governorate, Yemen. **Methods**: A retrospective descriptive study of confirmed cases of VDPV1 between January and December 2020 was performed. Surveillance staff collected data from patient cases, contacts, as well as stool specimens that tested in WHO accredited polio labs. The average of lab confirmation delayed days form sample collection was calculated **Results**: From January to December 2020, a total of 114 cases of acute flaccid paralysis (AFP) were reported. VDPV1 was confirmed in 26% (30) of them; 75% (21) were < 5 years and 73% (20) had zero dose of Oral Polio Vaccine (OPV). The first confirmed case (3%) was from Saadah city, with onset of paralysis at the end of January 2020 followed by 5 cases (17%) in March from another four districts, 8 cases (27%) in April and 13 (43%) up to December 2020 were from the same five districts. The lab confirmation was received after an average of 126 days (71 to 196) from sample collection. The isolates differ from the Sabin 1 type by 17- 30 VP1 nucleotides (nt) and were linked to VDPV1 with 13 (nt) divergence that isolated in July 2020 from stool specimens collected before one year from contacts of inadequate AFP case reported from Sahar district. **Conclusions**: The new emerging VDPV1 was in Sahar district and retrospectively confirmed after one year. Delayed lab confirmation as well as response and low immunization profile of children against polio were the main predisposing factors for cVDPV1 outbreak. Establishing national polio lab is crucial for early lab confirmation and response to VDPV in Yemen.

### Poster 68. Response to Vaccine-derived Polio Viruses Detected through Environmental Surveillance in Guatemala in 2019: Results from an International Evaluation

**R. Rodríguez**[1], C. Cajas[2], A. Ramírez[1], J.C. Rodríguez[1], C.F. Estívariz[3], M.C Freire[4], A.-E. Chévez[1], G. Rey[1], E. Cain[1], E. Juárez[5], M.O.B. Amézquita[5], L. Gobern[5], A. Paredes[5], L. Mendoza[5], L. Castillo[5], C.A. Ovando[5], J. Cifuentes[5], H. de Jesús Barillas Mayorga[5], M. Rondy[2]
[1]Pan American Health Organization, Washington, DC, USA, [2]Pan American Health Organization, Guatemala City, Guatemala, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Laboratorio Regional de Referencia para Poliovirus, Instituto Malbrán, Buenos Aires, Argentina, [5]Ministry of Public Health and Social Assistance of Guatemala, Guatemala City, Guatemala
**Background:** Guatemala is considered a high-risk country for polio reintroduction by the Technical Advisory Group in the Region of the Americas. During January–December 2019, wastewater samples collected in two cities contained three genetically unrelated vaccine-derived polioviruses (VDPVs). An international team conducted a poliovirus outbreak response assessment (OBRA) in July–August 2021. **Methods:** The OBRA team reviewed surveillance and vaccination activities implemented by the Guatemalan Ministry of Health (MoH) following June 2019 notification of VDPV types 1 and 3 isolated from samples collected in January and March 2019, and May 2020 notification of VDPV type 1 isolated from a sample collected in December 2019. **Results:** The MoH response team conducted a polio vaccination coverage survey and a stool survey in several communities within the catchment area of the environmental site within 7 days of each notification and a national retrospective search in healthcare facilities for unreported cases of Acute Flaccid Paralysis (AFP). In 2019, the MoH conducted a bivalent oral poliovirus vaccine (bOPV; types 1 and 3) vaccination campaign. No additional VDPV was isolated from stool surveys, subsequent wastewater samples, or specimens from routine AFP surveillance. Retrospective searches found 33% and 51% of potential AFP cases unreported in each year. During the September–October 2019 national campaign, 93% of children <7 years of age received bOPV. In 2020, 79% of children <1 year of age received three bOPV doses in routine immunization; no campaign was conducted. **Conclusions:** The detection of three unrelated VDPVs in Guatemala highlights the persistent risk of reemergence of poliomyelitis in low-coverage settings. An action plan is needed to address the OBRA recommendations to achieve higher vaccination coverage in routine immunization, to strengthen AFP surveillance and to test wastewater samples promptly for timely detection of potential VDPV outbreaks.

### Poster 69. Responding to Outbreaks of Type 2 Circulating Vaccine-Derived Poliovirus, Using the Novel Oral Poliovirus Vaccine under Emergency Use Listing during COVID-19 Pandemic–Sierra Leone, 2021

**V.A. Eboh**[1,2], C.K. Korir[3], T.U. Igbu[4], T. Sesay[5], A. Nunie[5], A.K. Kemoh[5], B. Boye[6], C.O. Wuraola[6], B. Abebe[6], D.S. Bangura[7], R.S. Dankoli[7], F. Nsubuga[7], G.N. Gebru[7], C.M. Peak[8], F. Abebe[1,2], E. Dagoe[2], M. McKinlay[1], T. Singh[9], E. Wiesen[2], F.V. Diomande[1], M. Ndoutabe[3], E. Durry[1,2]
[1]Task Force for Global Health Atlanta, Decatur, GA, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]World Health Organization African Regional Office, Brazzaville, Republic of the Congo, [4]World Health Organization, Freetown, Sierra Leone, [5]Ministry of Health and Sanitation, Freetown, Sierra Leone, [6]United Nations International Children's Emergency Fund, Freetown, Sierra Leone, [7]African Field Epidemiology Network, Field Epidemiology Training Program, Freetown, Sierra Leone, [8]Bill and Melinda Gates Foundation, Seattle, WA, USA, [9]Centers for Disease Control and Prevention, Freetown, Sierra Leone

**Background:** Vaccine-derived polioviruses (VDPVs) emerge following mutations of Sabin strains comprising the oral poliovirus vaccine (OPV) during prolonged circulation in under-immunized populations. Genetically-stabilized, novel type 2 OPV (nOPV2) was recently introduced under Emergency Use Listing for cVDPV2 outbreak response, with a lower potential for seeding new cVDPV2 emergence. In Sierra Leone, an outbreak of type 2 circulating VDPV (cVDPV2) was confirmed in December 2020. Two nationwide nOPV2 supplementary immunization activities (SIAs) and a mop-up SIA in three under-performing districts were conducted in May, June and August 2021, concurrent with ongoing COVID-19 and Ebola virus vaccination efforts. **Methods:** Supervisors, healthcare workers and community volunteers were trained for house-to-house vaccination under modified COVID-19 guidelines. Vaccination teams and supervisors were monitored using open data kit (ODK) tools on mobile devices. District Rapid Refusal Resolution Teams (RRRTs) and Adverse Events Following Immunization (AEFI) committees were constituted to promptly resolve vaccine hesitancy and refusals and to report all cases of AEFIs. **Results:** Over 1.6 million children were vaccinated in the two national SIAs and >600,000 children in the mop-up, representing 96%, 99% and 115% of the targeted population, respectively. Lot quality assurance sampling surveys demonstrated limitations in SIA quality at the 90% threshold, but improvement from 55% (5/9) districts passing for the first SIA to 63% (10/16) districts for the second. A cumulative 98% of vaccine refusals were resolved by RRRTs. As of 5 October 2021, 15 cVDPV2 cases were reported, and 21 isolates were identified in specimens from healthy children or sewage, most recently on 1 June 2021. **Conclusions:** In one of the first large-scale uses of nOPV2, in a challenging setting, our findings suggest that high coverage can be achieved and outbreaks of cVDPV2 can be interrupted with nOPV2 SIAs, utilizing RRRTs and efficient monitoring of supervisors and vaccination teams.

### Poster 70. A Country Classification System to Inform Travelers' Health Prevention Recommendations for Rabies

**J.D. Blanton**, K.M. Angelo, J. Allen, M. Glynn, C.R. Friedman, E. Pieracci, R. Wallace, A. Walker
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Assessing the global risk of rabies exposure is a complicated task requiring individual risk assessments and knowledge of rabies epidemiology, surveillance capacity, and accessibility of rabies biologics, on a national and regional scale. In many parts of the world, availability of information is limited and, when available, is often dispersed across multiple sources. This complicates the tasks of clinicians and policy makers when making recommendations. **Methods:** CDC conducted a country-by-country qualitative assessment of risk and protective factors for rabies to develop an open-access database of metrics consisting of the presence of lyssaviruses (specifically canine or wildlife rabies virus variants and bat lyssaviruses), access to rabies immunoglobulin and vaccines, rabies surveillance capacity, and canine rabies control capacity. Using these metrics, we developed a risk scoring system to inform rabies prevention guidance for travelers and regulations for dog importation. Higher risk was assigned to countries with enzootic rabies (particularly canine rabies). The risk scoring system for travelers also considered protective factors such as the accessibility of rabies biologics for post-exposure prophylaxis (PEP). Cumulative scores were calculated across the assessed metrics to assign a risk value of low, moderate, or high. **Results:** In 2021, we assessed 240 destinations. For the travelers' health assessment 31 destinations had no risk, 90 were low risk, 47 were high/moderate risk with access to PEP, and 72 were high/moderate risk with limited access to PEP. The risk of canine rabies importation was assessed as high from 111 destinations. Guidance for clinicians assessing travel risk for their patients was developed for each risk level. **Conclusions:** We developed a comprehensive and accessible source of information for assessing the classification of rabies risk by country. This database provides a link to the evidence base used for current CDC clinical guidance for pretravel rabies prevention recommendations and for canine importation regulations.

### Poster 71. Human Rabies Infection with Suspected Host-mediated Failure of Post-exposure Prophylaxis following a Recognized Bat Exposure—Minnesota, 2021

**S.M. Holzbauer**[1,2], C.A. Schrodt[3,4], R.M. Prabhu[5], R.J. Asch-Kendrick[6], M. Ireland[1], C. Klumb [1], M. Firestone[1,3], G. Liu[1], K. Harry[1], J.M. Ritter[4], M.Z. Levine[7], L.A. Orciari[4], K. Wilkins[4], P. Yager[4], C.M. Gigante[4], J.A. Ellison[4], H. Zhao[4], M. Niezgoda[4], Y. Li[4], P.S. Satheshkumar[4], B.W. Petersen[4], A.K. Rao[4], W.R. Bell[8], S. Bjerk[5], S. Forrest[5], W. Gao[9], R. Dasheiff[5], K Russell[5], M. Pappas[5], J. Kiefer[5], W. Bickler[5], A.C. Wiseman[5], K.E. Smith[1], R. Lynfield[1], J. Scheftel[1], R.M. Wallace[4], J. Bonwitt[4]
[1]Minnesota Department of Health, St. Paul, MN, USA, [2]Career Epidemiology Field Officer Program, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Division of High-Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta GA, USA, [5]Essentia Health, Duluth, MN, USA, [6]Midwest Medical Examiners Office, Ramsey, MN, USA, [7]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]University of Minnesota, Minneapolis, MN, USA, [9]Allina Health, Minneapolis, MN, USA

**Background:** In January 2021, an 84-year-old male with no known immunodeficiency died 6 months after being bitten by a rabid bat, despite starting rabies post-exposure prophylaxis (PEP) 3 days after exposure. Pre- and post-mortem testing confirmed the rabies diagnosis. Serum collected 7 days before death did not contain rabies neutralizing antibodies, revealing unexpected failure of PEP. We investigated to determine the reason for the breakthrough rabies infection. **Methods:** We performed whole genome sequencing (WGS) to compare rabies virus isolates from the patient and bat and reviewed medical records, laboratory results, and autopsy findings to ascertain potential undiagnosed immunocompromising conditions. Human rabies immunoglobulin (HRIG) administered to the patient was evaluated for potency by Rapid Fluorescent Focus Inhibition Test; hospital protocols and logs were reviewed for appropriate PEP storage and administration; and manufacturer records were reviewed to assess HRIG and vaccine integrity. We performed risk assessments for persons potentially exposed to the bat and close contacts and healthcare personnel (HCP) who interacted with the patient during his infectious period. **Results:** Rabies virus sequences obtained from the patient and bat were identical by WGS. Absence of rabies neutralizing antibodies 179 days from exposure, 162 days from vaccination completion and 7 days from death indicated impaired immunity and premortem testing demonstrated a Monoclonal Gammopathy of Unknown Significance. Autopsy findings revealed rabies meningoencephalitis and prostate adenocarcinoma metastatic to bone marrow. There were no deviations identified in potency, quality control, administration, or storage of administered PEP. Of 332 persons assessed for rabies exposure, three (0.9%) received PEP, one close contact and two HCP. **Conclusion:** Secondary impaired immunity likely prevented response to PEP, enabling fatal progression of rabies infection. The need for assessment of unrecognized immunocompromising conditions and potential additional rabies vaccine doses should be considered by clinicians administering rabies PEP. This case report highlights the need to better understand and reduce the risk of PEP failure but does not challenge the efficacy or safety of rabies vaccination.

### Poster 72. A Knowledge, Attitudes, and Practices (KAP) Survey on Dog-mediated Rabies Prevention and Elimination in Battambang Province, Cambodia, 2020

**B. Um**[1], M. Chao[2], B. Ung[3], S. Sorn[3], D. Holl[3], K. Kuy[3], S. Sao[4], P. Yourk[5], J. Rainey[6]
[1]Defense Threat Reduction Agency-Biological Threat Reduction Program, Phnom Penh, Cambodia, [2]Office of Animal Health and Production, Battambang Province, Cambodia, [3]General Directorate of Animal Health and Production, Phnom Penh, Cambodia, [4]Cambodia Communicable Disease Control (CDC) Department, Phnom Penh, Cambodia, [5]Kampong Cham National Institute of Agriculture, Kampong Cham Province, Cambodia, [5]Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Dog-mediated rabies is a fatal zoonotic disease and remains endemic in Cambodia. Dog rabies vaccination coverage remains low, particularly in rural areas where free-roaming dogs are common. Assessing the knowledge, attitudes, and practices (KAP) of villagers could help inform approaches to reduce dog-mediated rabies in these areas. **Methods:** We conducted a rabies KAP survey in Battambang province from July to December 2020. Using a purposeful multi-stage sampling approach at district and sub-district levels, we selected 10 villages, including five that had recently conducted a mass rabies vaccination campaign. In each village, we interviewed a sample of 9 to 37 villagers, proportional to each village's population size of the 10 villages. The survey captured socio-demographics, dog ownership, and knowledge about rabies. Scores, for 19 total possible points, were assigned to responses to five knowledge questions: severity of rabies, availability of effective dog rabies vaccination, mode of rabies transmission, clinical signs in dogs and animal species susceptible to rabies. Knowledge scores were compared between respondents from vaccinated (VV) and unvaccinated villages (UVV). Two rabies vaccinators were interviewed on barriers to dog vaccination. **Results:** Of the 187 villagers interviewed, the mean age was 45 years (range: 15-68), 106 (57%) were female, 149 (79%) were literate. Most respondents (n=149, 80%) owned a

dog. The overall knowledge score was 7.0 in VV and 5.8 in UVV ($p<0.001$). Respondents in VV had statistically higher scores for four of the five knowledge questions. Scores on the severity of rabies were similar ($p=0.09$). Vaccinators reported that about half of dog owners usually agree to vaccinate their dogs, a third agree to vaccination after learning more about rabies, and the remaining villagers refuse vaccination due to challenges in capturing their dog. **Conclusions:** Knowledge on rabies was low in all villages and issues with free-roaming dogs creates barriers to rabies vaccination. Educational activities implemented prior to and during dog rabies vaccination campaigns can be helpful to increase knowledge about rabies. Innovative approaches for delivering the rabies vaccine may be needed in areas where free-roaming dogs are common.

### Poster 73. Risk Factors and Outcome associated with Chickenpox Cases in a Tertiary Care Hospital, Faisalabad, Dec. 2018-Dec. 2019

**N. Ashraf**, Z. Iqbal, M.W. Malik, A. Qamar, M. Ali Khan, J.A. Ansari, A. Ikram
National Institute of Health, Islamabad, Pakistan

**Introduction:** Chickenpox is highly contagious viral disease caused by varicella zoster. Infection can be observed in all age groups but most common in children <10 years. Globally 140 million cases are reported annually. Multiple small outbreaks have been reported in Pakistan, a major outbreak in Pakistan was reported in 2017 in Punjab province. This study aimed to assess the risk factors and outcome associated with chickenpox. **Methods:** An analytical cross-sectional study conducted from Dec 2018 to Dec 2019. Hospital records were reviewed, a pretested structured questionnaire was adopted to collect the information. Any patient admitted to hospital with Vesiculo-Papular rash, fever with/without history of contact during the study period enrolled as a case. Descriptive analysis followed by inferential statistics was done. **Results:** Among 173 admitted cases, median age was 20 years (range: 1-65 ), male to female ratio 2:1 while 45% cases were reported during May to July and 78% cases were reported from Faisalabad district. Most affected age group was 11-31 years with an AR of 6/100,000. Clinical presentation revealed that 100% had Vesiculo-Papular rash followed by fever (88%) and cough (85%) whilst 4% developed severe illness and shifted to ICU. Duration of stay at hospital ranges from1-23 days. Overall CFR was 3.4%, the highest CFR (28%) was observed for 51-60 years. Majority of the cases (95%) had low socio-economic status (LSE), 55% had contact history and all were unvaccinated. Cases with LSE status ($X^2$: 20.5), comorbidities ($X^2$:18.1) and contact history ($X^2$:18.6) found statistically significant at p-value <0.05. **Conclusion:** Old age group and immuno-compromised patients due to other chronic ailment had high risk of disease severity. People with LSE status had close contact and very low vaccine uptake. Prolong hospital stay may have financial implications. There is a dire need to increase vaccine uptake and aware community about hygiene practices.

### Poster 74. Expression of High-Yield Monoclonal Antibodies to Rabies Virus in ExpiCHO-S Cells

**X. Tang**[1], L. Orciari[2], P.A. Yager[2], S.S. Panayampalli[2], J. Lee[1], A. Chida[1], D. Petway Jr.[1], D.A. Bagarozzi Jr.[1], J.M. Goldstein[1]
[1]Reagent and Diagnostic Services Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2] Poxvirus and Rabies Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background**: Rabies is estimated to cause 59,000 human deaths annually, with 95% cases occurring in Africa and Asia. In the United States, rabies is mostly found in wild animals. The direct rapid immunohistochemical test (DRIT) is an OIE (World Organization for Animal Health) approved test and been widely used for surveillance and laboratorial diagnosis of rabies. The DRIT uses highly concentrated and biotinylated monoclonal antibodies (mAbs) to rabies virus as primary reagents. However, the low yield of these antibodies in hybridoma culture represents a limitation to its wider use in testing. **Methods:** A new expression system using ExpiCHO-S mammalian cells was developed for a high yield production of recombinant mAbs to rabies virus. Briefly, hybridoma cells expressing anti-rabies mAb1 and mAb2 were harvested for RNA extraction and applied to RT-PCR and sequencing. Then variable domain of heavy chain and light chain were optimized and synthesized before subcloning into pCDNA3.4 vector and integrated with constant domain of mouse IgG. After transfection into ExpiCHO-S cells and incubation for 13 days, the recombinant mAbs were harvested and purified by Protein G column and applied for quality analysis. **Results:** Both purified recombinant anti-Rabies mAb1 and mAb2 demonstrated high purity (>90%) on size exclusion chromatography and SDS-PAGE gel. Compared to purified mAbs from hybridoma culture, the yield of recombinant mAbs from ExpiCHO-S cells was increased more than 10 times. By estimation, both mAbs could reach to a yield of about 300 mg from one liter of transfection. **Conclusions:** Compared to mAbs purified from hybridoma culture, recombinant anti-rabies mAb1 and mAb2 demonstrated a much higher yield and retained original antigen specificity and affinity. These recombinant mAbs have potential to be used in the DRIT which contributes to rabies control.

### Poster 75. Phylogenetic Analysis of Raccoon Rabies Virus Variant in Florida, USA

**C.M. Gigante**[1], RE. Condori[1], V. Mock[2], G. Scilabro[3], E. Quaye[4], R. Davis[5], A. Kunkel[1], R. Wallace[1], Y. Li[1], D. Stanek[6]

[1]Poxvirus and Rabies Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Florida Department of Health, Bureau of Public Health Laboratories – Jacksonville, Jacksonville, FL, USA, [3]Florida Department of Health, Bureau of Public Health Laboratories – Tampa, Tampa, FL, USA, [4]Florida Department of Health, Bureau of Public Health Laboratories – Miami, Miami, FL, USA, [6]Kansas State University Rabies Laboratory, Manhattan, KS, USA, [5]Florida Department of Health, Bureau of Epidemiology, Tallahassee, FL, USA

**Background:** The first outbreak of raccoon rabies was identified in Florida (FL) in the 1950s, and the enzootic range of raccoon rabies virus variant currently extends along eastern North America from Florida to Canada. Detailed genetic studies of raccoon rabies virus variant have often focused on the epizootic that led to expansion of the variant's geographic range and associated outbreaks in the northeastern United States and US-Canadian border; however, similar analysis of raccoon rabies variant in the southern United States is lacking. **Methods:** The Florida Department of Health and U.S. Centers for Disease Control and Prevention collaborated on several rabies virus investigations from 2018 – 2021 that led to sequencing of over 150 rabies virus samples from rabid raccoons, cats, and foxes from FL. **Results:** Sequencing revealed an astonishing diversity of raccoon rabies virus variant in FL, with differences in nucleoprotein gene sequences as large as 4.3%. In comparison, the differences among raccoon variant examined from the Northeast and Mid-Atlantic US was <1.5%. Phylogenetic analysis revealed clustering by geographic region in FL, and not by host species, suggesting the raccoon as the reservoir species with regular spillover events to domestic animals and other wildlife. Geographic and oral rabies vaccination barriers separated sub-variants in several cases. **Conclusion:** Analysis of raccoon rabies virus variant in Florida revealed insight into rabies within the state and into the diversity and history of raccoon rabies virus variant.

### Poster 76. Establishment of a Canine Rabies Burden in Phu Tho Province, Vietnam, through the Implementation of a Novel Surveillance Program from 2016 to 2019

**D.T. Nguyen**[1], C.D. Vo[1], M.Q. Phan[1], Y. Ross[2], S. Bonaparte[2], L.V. Nguyen[1], T.D. Nguyen[3], G. Veytsel[2], O.K.T. Nguyen[3], T.X. Nguyen[4], H.H.T. Nguyen[4], T.T. Nguyen[4], R.M. Wallace[2], T.T. Do[5], A.P. Dao[5], A. Gibson[6], P.T.T. Tran[1], B.V. Ngo[3], D.V. Pham[1]

[1]Department of Animal Health, Ministry of Agriculture and Rural Development of Vietnam, Hanoi, Vietnam, [2]Rabies Epidemiology Unit, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]National Center for Veterinary Diagnostics, Department of Animal Health, Hanoi, Vietnam, [4]Phu Tho Sub Department of Animal Health, Phu Tho, Vietnam, [5]Office of the US Centers for Disease Control and Prevention, Hanoi, Vietnam, [6]Mission Rabies, Dorset, UK

**Background:** Dog-mediated rabies resulted in 351 human deaths and almost two million human rabies exposures in Vietnam between 2016 and 2019. An integrated bite cases management (IBCM) surveillance program has been introduced to improve knowledge of the canine rabies burden in Phu Tho province of Vietnam since 2016. **Methods:** The Vietnam Animal Rabies Surveillance Program (VARSP) was developed with four stages: Strengthening Laboratory capacity, Training of Rabies surveillance officers, Introduction of paper-based-reporting (VARSP version 1.0) and Introduction of electronic case reporting (VARSP 2.0). Investigation and data collected from March 2016 to December 2019 were analyzed and compared with historical records of animal rabies cases from 2012 to 2015. A probabilistic risk assessment was conducted to evaluate the risk of exposure to rabies based on data collected at the time of IBCM investigations. **Results:** Totally, 1048 IBCM investigations were conducted in Phu Tho province where identified 79 (8%) confirmed rabies cases and 233 (22%) probable cases from 2016 to 2019, significantly increased in comparison with the recorded investigations (on average one investigation conducted per year, with two confirmed and two probable animal cases in total) between 2012 and 2015. VARSP identified a 6.5-fold increase in the annual number of detected animal rabies cases (four cases compared with 26 cases identified per year before and after introduction of VARSP, respectively). The risk people died of rabies was 0.02% when they were bitten by apparently healthy dogs managed at the in-home quarantine for 10 days and assessed by VARSP. **Conclusions:** The IBCM investigations in Phu Tho province identified a 6.5-fold increase in the annual number of detected animal rabies cases using the VARSP. The risk people died of rabies without post-exposure prophylaxis (PEP) was relatively low when they were bitten by apparently healthy dogs managed at the in-home quarantine for 10 days and assessed by VARSP. This supports a protocol to delay PEP for this category of bite victims and the VARSP should be further carried out in all high-risk rabies provinces of Vietnam.

### Poster 77. Risk Factors for Measles Outbreak in Ataq and Habban Districts, Shabwah Governorate, Yemen, February to May 2018

**A.A. Nassar**[1], M.A. Al-Amad[2], M. Qasim[3]
[1]Ministry of Public Health and Population, Sana'a City's Public Health and Population Office, Sana'a, Yemen, [2]Ministry of Public Health and Population, Field Epidemiology Training Program, Sana'a, Yemen, [3]World Health Organization, Sana'a, Yemen

**Background:** Recent conflict and war in Yemen lead to collapse of the health system, decrease of immunization coverage and spread of many outbreaks. On May 22, 2018, the surveillance officer in Shabwah governorate reported an increased number of suspected measles. On May 24, 2018, a team from Yemen-Field Epidemiology Training Program was sent to investigate. The aims were to describe the outbreak, determine the risk factors for measles infection and recommend control measures. **Methods:** A case-control study design (1:2 ratio) were performed. National Measles Surveillance Program case definition and predesigned questionnaire were used to collect data from 73 cases and 146 controls. Crude and adjusted odds ratios (aOR) and 95% confidence intervals (95%CI) were calculated. P value < 0.05 was considered as the cut point for significant. Epi info version 7.2 was used. **Results:** A total of 73 suspected cases were found. In multivariate analysis, malnourished children aged 6–60 months (aOR = 24.9, 95% CI:1.9–329.6), unvaccinated children (aOR = 17.2, 95% CI:2.9–100.7) and contacted patient with measles (aOR = 27.3, 95% CI:1.3–551.7) remained significantly associated risk factors with being a measles case. **Conclusions:** In conclusion, contact with measles cases, malnutrition and un-vaccination were the potential contributing factors of measles outbreak in Shabwah governorate. An urgent vaccination campaign with health education interventions are highly recommended. Reactivation of the outreach immunization services and strengthening surveillance and response systems are top priority to take place at district and governorate levels.

### Poster 78. Factors associated with Measles in Côte d'Ivoire, 2009-2019

**A.J. Bonzou**[1,2], N. Meda[1], O.J.B. Otshudiandjeka[1], L.B.N. Aka[2], V.J. Benie Bi[3]
[1]Burkina Field Epidemiology and Laboratory Training Program, Université Joseph Ki-Zerbo, Ougadougou, Burkina Faso, [2]Direction de coordination du programme Elargi de Vaccination (DCPEV), Ministère de la santé et de l'hygiène publique, Abidjan, Côte d'Ivoire, [3]Institut national d'hygiène publique (INHP), Abidjan, Côte d'Ivoire

**Background:** Measles remain a challenge for most West African countries with more than 522 884 cases in 2019.In Cote d'Ivoire, this disease affected more than 312 people in 2019 with 95% of children under 5 years. A way to control the spread of measles was based on surveillance and vaccination. The aim of this study is to determine factors associated to measles occurrence in Cote d'Ivoire. **Methods:** Case control study design was used to conduct this study using secondary data from immunization national program database. Vaccine data from 2009 to 2019 were extracted and analyzed using R.0.2. univariate analysis was done to describe collected variables; continuous variables were summarized and categorical variables were tabulated in term of frequency and proportion. Logistic regression was used to evaluate factors associated to measles occurrence with $\alpha \leq 0.05$. **Results:** Results from this study shown a decrease of incidence in the trend of measles from 2011 to 2016 due to an average of 97% of vaccination coverage. But from 2017 to 2019 we observed an increase in the trend. Indeed, we noticed high incidence in the northern and eastern part of the country. Regarding factors associated to measles occurrence, vaccination reduce the risk of getting measles to 72% (OR=0.28, CI: 0.24-0.32) and living in rural also reduce this risk to 21% (OR=0.79, CI: 0.69-0.91). We also found that delay in notification and laboratory result increase the risk of getting measles to 55% (OR= 1.55; CI: 1.35-1.83) and 48% (OR= 1.48; CI:1.24-1.77) respectively. Inadequate specimen condition was detected as factor that increase the risk to multiply it by 6.75 (OR= 6.75; CI:5.21-8.66). **Conclusions:** Study founding demonstrated that most factors are related to the measles detection and vaccination. Indeed, most factors that increase the risk can be controlled by putting in place a protocol that combine vaccination program and sample laboratory management.

### Poster 79. Factors Affecting the Uptake and Administration of the Routine Second Dose of the Measles Containing Vaccine for Young Children, Oromia Regional State, Ethiopia

**A.B. Woyessa**[1], M. Shah[2], S. Teshome[3], B. Moges[4], X. Pan[5], P. Samuel[1], B. Tolera[1], B. Kenate[1], L. Lisanwork[4], G. Wako[6], A. Shiferaw[6], H. Teklie[7], A. Bekele[1], G. Yimer[4], S.H. Wang[5], A. Wallace[2], C. Sugerman[3]
[1]Oromia Regional Health Bureau, Addis Ababa, Ethiopia, [2]Global Immunization Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Global Immunization Division, CDC-Ethiopia, Addis Ababa, Ethiopia, [4]Global One Health Initiative, Ohio State University, Addis Ababa, Ethiopia, [5]Ohio State University, Columbus, OH, USA, [6]United Nations International Children's Emergency Fund (UNICEF), Addis Ababa, Ethiopia, [7]Ethiopian Public Health Institute, Addis Ababa, Ethiopia

**Background:** Measles-containing vaccine (MCV) is a part of the routine immunization program since 1980 in Ethiopia, but coverage remains low at 59%. Oromia Region, the largest, most populous regional-state accounts for half of all unvaccinated children at 49%. In February 2019, Ethiopia added a second dose of MCV (MCV2) to the routine immunization program for children 2 years and older. We evaluated the measles vaccination coverage two years after MCV2 introduction among selected districts in Oromia Region and described barriers to its uptake. **Methods:** A stratified random sample of 18 woredas (districts) was selected based on high/low first dose of MCV1 coverage, urban/rural classification, and recent measles outbreak status. A total of 36 kebeles (wards) within the selected woredas were randomly sampled. A cross-sectional household survey was conducted among caregivers of children aged 12-35 months between February - March 2021. Caregivers were interviewed about their knowledge, attitudes, and behaviors related to immunizations and immunization coverage was measured from vaccination card validation and/or caregiver recall. **Results:** Caregivers of 602 children aged 12-23 months and 502 children aged 24-35 months were interviewed: MCV1 coverage was 72%; and MCV2 coverage was 33%. The difference in vaccination rate of the routine childhood pentavalent vaccine to MCV1 was 20%. For children aged 24-35 months, the dropout vaccination rate from MCV1 to MCV2 was 48%. Although 87% of caregivers had heard of the measles vaccine, only 29% were aware of the need for a second dose. Most common reasons mentioned for not receiving MCV2 were that the mother was too busy and that two doses of MCV are not needed. **Conclusion:** Two years post-introduction, MCV2 coverage remains low in Oromia Region. The high dropout-rates indicated gaps in vaccine knowledge, utilization and services. As MCV2 is the first vaccine to be administered in the second year of life in Ethiopia, increased awareness creation and innovative social mobilization are required to improve coverage. Additional analyses to explore the association between barriers and facilitators and MCV2 coverage are also needed to overcome challenges and increase vaccine uptake.

### Poster 80. Estimating Global Demand for Measles and Rubella Microarray Patches

**L.K. Kayembe**, L.S. Fischer, B.B. Adhikari, B.R. Greening, E.B. Kahn, J.K. Knapp, M. Papania, M.I. Meltzer
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Compared with needle-and-syringe delivery, a measles and rubella microarray patch (MR-MAP) technology offers solutions for problems of cold chain, waste management, and workforce capacity associated with measles and rubella immunization programs. However, potential demand for MR-MAP technology is unknown. **Methods:** We produced a spreadsheet-based tool to estimate the potential global demand for MR-MAP. The tool includes five population-level immunization scenarios for Routine Immunization (RI) and Supplementary Immunization Activities (SIAs): **Scenario 1:** Preventive SIAs in (A) GAVI Vaccine Alliance-eligible countries and (B) WHO member states that routinely hold large-scale SIAs. **Scenario 2:** Preventive & outbreak response SIAs in WHO member states that routinely hold large-scale SIAs. **Scenario 3:** Preventive SIAs & RI in Measles & Rubella Initiative (M&RI) priority countries (Democratic Republic of the Congo, Ethiopia, India, Indonesia, Nigeria, Pakistan). **Scenario 4:** Preventive SIAs & RI in GAVI-eligible countries and M&RI priority countries. **Scenario 5:** Reaching the chronically unreached during RI in 180 WHO member states. The tool is pre-populated with vaccination program data for 180 countries (e.g., country-specific annual coverage data for the first and second dose of measles and rubella vaccine, SIA coverage, population by age, and wastage factor). We estimated potential demand for the period 2030-2039, assuming 100% conversion from current MR needle-and-syringe vaccine administration to MR-MAP-administered vaccination. For sensitivity analysis (SA), we assumed changes of 70%, 80% and 90% from needle-and-syringe to MR-MAP. **Results:** If MR-MAP were adopted as the MR vaccine delivery technology of choice, estimates of MR-MAP demand for the period 2030-2039 varied from 137 million (M) doses (SA: 96-123M) in Scenario 5 to 1,912 M (SA: 1,338-1,721M) in Scenario 4. MR-MAP demand for remaining scenarios was 434M (SA: 304-390M) in Scenario 1A, 710M (SA: 497-639M) in Scenario 1B, 810M (SA: 567-729M) in Scenario 2 and 1,083M (SA: 758-975M) in Scenario 3. **Conclusions:** There is potentially a large global demand for MR-MAPs however, their minimum demand which would guarantee financial viability to vaccine manufacturers is not known; forecasts for some scenarios might not be viable.

### Poster 81. Gender Disparities in Mortality Outcomes from Non-cancerous HPV infection

S. Banerjee, U. Usua
Walden University College of Health Sciences, Minneapolis, MN, USA

**Background:** Non-cancerous HPV strains are often neglected and yet can cause genital warts and respiratory papillomatosis. The mistaken over-identification of HPV as a female-specific disease has resulted in the feminization of HPV and HPV vaccines. However, there is a paucity of studies assessing long-term outcomes of infection. In this study, we wanted to determine if the non-cancerous HPV is associated with mortality in both males and females. **Methods:** All respondents from the National Health and Nutrition Examination Survey (NHANES)

survey in a non-institutionalized population, who were 20 years or older between the years 2003-2010 were included in the analysis with mortality follow-up through 2015. This method uses the competitive Luminex immunoassay of antibodies to neutralizing epitopes on HPV 6, 11, 16, and 18 L1-Virus-Like Particles (VLPs). Analysis was performed using complex samples Cox regression to determine how gender influences HPV-related outcomes. **Results:** Percent mortality among individuals with HPV-6 was 2.1% (CI: 1.6%-2.9%) among males and 1.6% (CI: 1.1%-2.3%) among females with mean follow-up of 10.8 years. For all-cause mortality, the overall hazard ratio (HR) for HPV-6 infection to no HPV-6 infection among males was 2.39 (95% confidence interval [CI], 1.05-1.96, p = 0.02). The adjusted HR was elevated, 2.19 (CI 1.38-3.48, p = 0.001) among males who had HPV-6 but close to 1.0 (1.40 CI 0.66-2.95, p = 0.38) among females who had HPV-6 after adjusting for medical (diabetes) and demographic (age, education, poverty-income-ratio, and ethnicity) risk factors. Similar patterns did not persist with HPV-11, 16, or 18. **Conclusions:** In a multiethnic population, males with HPV-6 demonstrated 119% increased mortality even after controlling for medical risk factors. As male vaccination rates continue to lag behind female rates, improved education and literacy efforts need to be tailored towards counseling about the benefits of the vaccine. Additionally, surveillance efforts need to better focus around non-cancerous HPV strains as well.

## HIV and Sexually Transmitted Infections

### Poster 82. HIV Seroprevalence and Risk Factors among Incarcerated Women in Brazil: Results from a National Survey

**D.G. Smith**[1], L.R.S. Kerr[2], C.D. Smith[1], R.M.S. Mota[2], R.H.M. Macena[2], V.F. Gonçalves[3], M.A.N. Bhuiyan[1], C. Kendall[4]
[1]Louisiana State University Health Shreveport, Shreveport, LA, USA, [2]Federal University of Ceara, Fortaleza, CE, Brazil, [3]Fortaleza University, Fortaleza, CE, Brazil, [4]Tulane University, New Orleans, LA, USA
**Background:** HIV prevalence among incarcerated people is higher than in the general population worldwide, and it is necessary to identify risk factors associated with HIV prevalence among incarcerated people in order to design more effective HIV prevention programs for the future. This study aimed to identify the seroprevalence and factors associated with HIV among incarcerated women in Brazil. This was the first national survey conducted on female health in Brazilian penitentiaries. **Methods:** A cross-sectional study was conducted among 1,327 women in fifteen female prisons across nine states in Brazil. The participants were selected through multi-stage sampling. Each participant's HIV serostatus was determined by rapid HIV testing at the time the survey was administered. Participant sociodemographic information and potential risk factors were obtained through a structured questionnaire and analyzed using STATA 12. Odds ratios (ORs) were calculated to determine risk factors associated with HIV infection. **Results:** The HIV seroprevalence among female prisoners was 2.3%, which is higher than women in the general population of Brazil (0.4%). Higher prevalence rates were associated with self-identifying as black or mulatto, being 41 years old or older, being single or divorced, having no education or lower levels of education, and having difficult access to healthcare. Multivariate analysis showed risk factors associated with HIV infection: no condom use at first intercourse (OR=2.5), not completing elementary school (OR=1.9), prior experience living on the streets (OR=6.6), not knowing where to get tested for HIV (OR=3.2), having a sexual partner (OR=3.9), and being arrested three or more times (OR=1.9). **Conclusions:** Prevention and promotion efforts are necessary to help reduce the circulation of HIV inside prisons. While the prison environment can contribute to an increase in HIV prevalence, incarceration can be an opportunity to implement prevention strategies, diagnosis, and treatment of HIV among vulnerable populations who would otherwise have poor access to health services.

### Poster 83. Minimally Invasive Tissue Sampling to Compare the Cause of Death Among HIV Exposed Uninfected and HIV Unexposed Uninfected Children in South Africa

**S. Mahtab**, R. Chawana, B.N. Thwala, P.C. Mutevedzi, C. Ntuli, V.L. Baillie, F. Solomon, M. Hale, P. Swart, S.A. Madhi
South African Medical Research Council Vaccines and Infectious Diseases Analytics Research Unit, University of the Witwatersrand, Johannesburg, South Africa
**Background:** HIV-exposed uninfected children (HEU) are at greater risk of death compared to HIV-unexposed children in the first six months of life. We investigated the causes of death (CoD) between HEU and HIV-unexposed children using postmortem minimally invasive tissue sampling (MITS). **Methods:** This prospective, observational study enrolled children under 60 months of age at Chris Hani Baragwanath Academic Hospital in Soweto, South Africa. The MITS included needle core-biopsy sampling for histopathology of brain, lung, and liver tissue. Microbiological culture and/or molecular tests were performed on lung, liver, blood, and cerebrospinal fluid. Underlying, immediate and antecedent CoD were determined by an international multidisciplinary team of medical

experts. **Result:** Overall, 205 (0-6-month-old) child deaths were enrolled. After excluding children living with HIV or unknown HIV-exposure status, analysis included 48 HEU and 93 HIV-unexposed neonates (0-27 days), and 17 HEU and 26 HIV-unexposed young infants (28-182 days) age group. Prematurity as underlying CoD were higher among HEU (68.8%) than HIV-unexposed neonates (46.2%), and respiratory and cardiovascular disorders 6.3% vs 2.1%, than HIV-unexposed neonates, respectively. For young infants, congenital anomalies were the common underlying CoD among HEU (41.2%) vs HIV-unexposed (34.6%). Regarding infectious diseases, community-acquired pneumonia was more dominant among HEU compared to HIV-unexposed neonates (8.3% vs 2.2%) and young infants (47.1% vs. 38.5%). Furthermore, sepsis in the causal pathway was more common among HEU compared with HIV-unexposed neonates (45.8% vs 38.7% [for hospital acquired 35.4% vs 31.2% and community acquired 10.4% vs 7.5%]) and young infants (47.1% vs 38.5% [for hospital acquired 35.3% vs 26.9% and community acquired 11.8% vs 11.5%]). *Acinetobacter baumannii* (22.9% vs 10.8%), *Staphylococcus aureus* (8.3% vs 5.4%), and *Escherichia coli* (6.3% vs 2.2%) were the common pathogens for sepsis among HEU vs HIV-unexposed neonates. HEU young infants had higher prevalence of *Klebsiella pneumoniae* (17.6% vs 3.8%) and Respiratory syncytial virus (17.6% vs 11.5%) for community acquired pneumonia compared to HIV-unexposed infants. **Conclusion:** HEU neonatal deaths were mainly attributable to complications of prematurity/low birth weight. HEU children who died within 0-182 days from birth were more likely to get sepsis (hospital and community-acquired) compared to HIV-unexposed, furthermore, community-acquired pneumonia was found to be more prevalent among HEU than HIV-unexposed.

### Poster 84. Social Network Strategy to Reach Persons Who Inject Drugs With Harm-Reduction Services During an HIV Outbreak in Cabell County, West Virginia, 2019

**S. Handanagic**[1], T. Surtees[1], S. Cha[1], D. Broz[1], C. Agnew Brune[1], C. Wright[1], S.B. Lyss[1], S. Balleydier[2], M. Kilkenny[3], A.M. Oster[1], R.P. McClung[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]West Virginia Bureau for Public Health, Charleston, WV, USA, [3]Cabell-Huntington Health Department, Huntington, WV, USA
**Background:** In January 2019, the West Virginia Bureau for Public Health (BPH) identified an increase in HIV diagnoses among persons who inject drugs (PWID) in Cabell County, WV. BPH, Cabell-Huntington Health Department (CHHD), and CDC collaborated on a comprehensive response to this outbreak. We describe the implementation of a social network strategy using peer recruitment to recruit PWID and link them to HIV testing and essential prevention services, including a syringe services program (SSP) at CHHD. **Methods:** Initial participants ("seeds") who inject drugs were identified by CHHD staff and other community partners and were asked to recruit up to five peers from their social network ("recruits"). All participants were offered anonymous HIV testing and were asked to complete a questionnaire about demographic information, history of injection drug use, HIV testing, HIV status, and current enrollment in treatment and prevention services. Participants received a package of food and toiletries for their participation and an additional package for the successful recruitment of peers. **Results:** During May–August 2019, 194 participants were recruited, 108 (56%) of whom were seeds. The median age of participants was 37 (IQR: 31-44); 63% were male and 91% were non-Hispanic White persons. In total, 183 (94%) were tested for HIV, and 21 (11%) of participants either tested positive for HIV or self-reported having HIV. Among 161 (83%) participants who reported injecting drugs in the past 12 months, 102 (63%) reported not being enrolled in the SSP; of these, 94 (92%) were referred to the SSP and 90 (96%) of these were successfully enrolled. At the time of recruitment, lower percentages of recruits were using the SSP (25% vs. 44%) and had tested for HIV in the past 12 months (58% vs. 78%) compared to seeds. **Conclusions:** In a response to this HIV outbreak, a social network strategy was rapidly implemented to recruit almost 200 PWID and to link them to essential prevention services. Participants who were recruited by their peers were less likely to have used the SSP or tested for HIV, indicating that peer recruitment was successful in reaching PWID with lower utilization of prevention services. Social network strategies are useful tools for public health response to HIV outbreaks among PWID.

### Poster 85. Prevalence, Risk Factors, and Association with Delivery Outcome of Curable Sexually Transmitted Infections among Pregnant Women in Southern Ethiopia

**M. Hailemariam**[1,2 3], Z. Mekonnen[2], E. Loha[4], E. Padalko[3,5]
[1]School of Medical Laboratory Sciences, Hawassa University College of Medicine and Health Sceinces, Hawassa, Ethiopia, [2]School of Medical Laboratory Sciences, Jimma University Institute of Health Jimma University, Jimma, Ethiopia, [3]Department of Diagnostic Sciences, Ghent University, Ghent, Belgium, [4]Centre for International Health, University of Bergen, Bergen, Norway, [5] Laboratory of Medical Microbiology, Ghent University Hospital, Ghent, Belgium

**Background**: Curable sexually transmitted infections (STIs) such as infection with *Chlamydia trachomatis* (*C. trachomatis*), *Neisseria gonorrhoeae* (*N. gonorrhoeae*), and *Trichomonas vaginalis* (*T. vaginalis*) can lead to adverse pregnancy. There are limited data on the prevalence and correlate of STI in Ethiopia, yet pregnant women are not screened for curable STI. Hence in this study, the prevalence of STIs and associated risk factors were assessed. **Methods**: A cross-sectional study was conducted on consecutive women attending the delivery ward at the Hawassa comprehensive and specialized hospital. Vaginal swabs collected at the time of labor and delivery were tested for *C. trachomatis*, *N. gonorrhoeae* and *T. vaginalis* using GeneXpert. Study participants responded to a questionnaire about their previous and currentobstetric history and socio-demographic characteristics. Possible independent factors for curable STIs were assessed by chi-square, bivariable, and multivariable logistic regression. **Results:** Of the 350 vaginal swabs tested, 51 (14.6%, 95% CI: 10.9-18.3) were positive for one or more curable STIs. The prevalence of *C. trachomatis*, *N. gonorrhoeae* and *T. vaginalis*were 8.3%, 4.3%, and 3.1%, respectively. STIs was associated ($p<0.005$) with the birth weight and gestational age. A 3-fold increase in odds of acquisition STIs was documented in currently unmarried women (AOR, 3.5; 95% CI: 1.2-10.6; $p =0.028$), and in younger pregnant women (AOR, 3.2; 95% CI 1.3-7.9; $p=0.01$). Moreover, women reporting for presence of vaginal discharge (AOR, 8.3; 95% CI: 3.4- 20.5; $p < 0.001$) and reporting pain during urination (AOR, 6.4; 95% CI: 2.5-16.4; $p <0.001$) found significant associate with curable STIs. **Conclusion:** The higher magnitude of STIs found in this population, and the absence of symptoms in many illustrate the need for systematic follow-up during routine antenatal care primarily history taking and asking for signs and symptoms to provide early management and avoid long term sequelae.

## Late-breakers

### Poster LB-1. Determinants of COVID-19 Vaccine 2nd Dose Dropout among Residents of Islamabad from May 2021 to June 2021

**S. ur-Rehman**[1], W. Waqar[1], M. Iqbal[2], M.A. Khan[3], Z. Iqbal[4], A. Ikram[5]
National Institutes of Health, Islamabad, Pakistan

**Background:** In response COVID-19 pandemic, many vaccines are being produced against and approved by WHO till date. Possible side effects are mild to moderate and short-lasting. Pakistan started mass vaccination for COVID-19 on 22nd February 2021 in community. Islamabad with highest literacy rate in country, faces challenges to vaccinate community at a maximum level. A list of about 1000 local residents of Islamabad was provided by concerned authority who received first dose of Sinopharm vaccine in the month of April 2021 and did not complete 2nd dose after 3 weeks. Main objectives of this study was to determine various factors/reasons of dropout for second dose and to recommend actions for enhancing vaccine uptake. **Methods:** This study was investigated as a descriptive cross-sectional study, carried out in the Islamabad among 1000 people who have completed 1st dose of Sinopharm vaccine and their second dose is due but did not follow. It was carried out from May 2021 to June 2021. Concerned authority was taken in confidence for use of data. **Results:** In this study male: female ratio was 1.5:1 with 65.5 mean age while 66 median age was observed (age range: 30-95y). Most participants were from 60-69 years (n.363). 24% of people (n.235) were reluctant due to fear of developing adverse reaction of vaccine. About 17% of people reported that they carried COVID-19 infection after getting 1st dose of vaccine. Moreover, high proportion of males showed un-responsive attitude as compared to females. **Conclusion:** It is clear that infodemics about COVID-19 vaccine in the community create gap against COVID-19 response. There is a perception in community that vaccine causes COVID-19 infection and severe side effects can be seen after COVID-19 vaccination. People should be encouraged for positive effects of COVID-19 vaccines in order to curb this pandemic. Furthermore, community awareness campaigns are necessary to address reservations of peoples regarding vaccine.

### Poster LB-2. A “Drop-in” Surveillance Tool to Identify and Prioritize Clusters of COVID-19 Cases for Investigation By Local Epidemiology Staff

**D. Drociuk**, O. Babatunde, A. Diedhiou
South Carolina Department of Health and Environmental Control, Columbia, SC, USA

**Background:** During the early phase of the COVID-19 pandemic in South Carolina, the need to rapidly identify clusters of cases based upon common address/venue was determined to be critical, to address high priority clusters in congregate settings and single-family dwellings. Due to limitations in data reports available from the South Carolina Nationally Notifiable Disease Surveillance System (NNDSS) a mechanism to quickly identify newly clusters was needed to assist with initiating disease prevention and control measures in a timely manner. **Methods:** Newly received COVID-19 positive lab reports from the previous day were extracted from the data feed into NNDSS and provided for analysis. Criteria were established to identify, by County, three or more positive lab

reports with common addresses. Analysis was performed to identify clusters and an online address matching service was used to identify venue names to provide information regarding congregate living venues or single-family dwellings. Identified clusters were compiled by county containing case identifying information (Case ID, Address, phone number, etc.) to allow local response staff to contact the cases within the cluster and reach out to venues identified. A summary report entitled the "Daily Cluster Report" was also provided, displaying identified clusters to provide situational awareness for both local and Central Office Leadership. Reports were made available for use by local staff daily by 8:00am. **Results:** Since June 2020, the Snapshot Cluster Report has been used by Local Epi Response staff to prioritize their daily case investigation and contact tracing and monitoring activities. The daily compiled data along with summaries of actions taken for disease control and prevention were also provided to staff in the Agency-level Incident Command for awareness. **Conclusions:** To address surges in COVID-19 cases and the effective use of disease control and mitigation measures, the "Cluster Report" became a useful tool to identify clusters among household contacts and people living and working in congregate living facilities, rather than waiting for individual investigations to identify common venues from routine investigation processes. This simple tool allowed for targeted and rapid initiation of case investigations beginning the next business day.

### Poster LB-3. Airborne Transmission between Hamsters via Fine Aerosols is Blocked Using UV-C Light

**R.J. Fischer**[1], J.R. Port[1], M.G. Holbrook[1], K.C. Yinda[1], M. Creusen[2], J. ter Stege[3], M. de Samber[2], V.J. Munster[1]
[1]Laboratory of Virology, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT, USA, [2]Signify, High Tech Campus 48, Eindhoven, The Netherlands, [3]UVConsult BV, Hoofdstraat 249, Bovenkarspel, The Netherlands

**Background:** Airborne transmission is the major contributor to the spread of SARS-CoV-2. It has been extensively shown that UV-C light is effective at inactivating SARS-CoV-2 deposited on surfaces. We will present data showing that UV-C light can prevent airborne transmission using a hamster model. **Methods:** A ducted air system between infected and naïve hamster cages was designed and constructed. The size distribution of particles that traversed distances of 16 cm, 1 m and 2 m between cages were measured with an aerodynamic particle sizer. The physical breathing parameters of infected and naïve hamsters were measured using whole body plethmography and aerodynamic particle sizing. Finally, a UV-C light source was used to treat the air passing between infected and naïve hamsters separated by 1 m over 4 hours of exposure. **Results:** Of a broad range of particle sizes generated with a 20% glycerol mist, 98% were ≤ 5µm and 2% 5 – 10 µm after traversing 1m. Greater than 90% of expired hamster breath consisted of <10 µm particles with the highest percentage consisting of particles <0.53 µm. UV-C treatment of air ducted from infected hamsters prevented infection in naïve hamsters while 100% of control hamsters were infected with SARS-CoV-2. **Conclusions:** In efforts to introduce additional transmission control measures to combat the current pandemic, we demonstrate that transmission occurs via fine aerosols, the size distribution of aerosol exhaled by infected hamsters falls within fine aerosols and that direct aerosol transmission between hamsters can be blocked by treating environmental air with UV-C light. This work was funded by the NIH Division of Intramural Research.

### Poster LB-4. Antiviral Activities of Homoharringtonine against Japanese Encephalitis Virus

**J.E. Kim**, Y.J. Song, S.H. Gu, H.S. Yun, S.H. Lee, G.H. Hur, Y.H. Lee, C.H. Yu
Agency For Defense Development, Daejeon, Republic of Korea

**Background:** Japanese encephalitis virus (JEV) is an emerging mosquito-borne flavivirus in the Asia-Pacific region that causes Japanese encephalitis with an average mortality rate of 30%. While the JEV vaccine is well developed, there are no approved antiviral drugs against JEV yet. Homoharringtonine (HHT) is a natural compound, alkaloid ester isolated from the genus *Cephalotaxus*, that is reported to exhibit antitumor activities as well as antiviral effects. Here, we investigated the potential antiviral efficacy of HHT for JEV in vitro and verified using a lethal mouse model by JEV infection. **Methods:** BHK-21 or vero cells were inoculated at an 0.1 or 1 multiplicity of infection (m.o.i.) of JEV KUMC-27, 99% identity with HE861351.1 strain, with post-treatment of HHT, then harvested for virus titration using plaque assay and RNA extraction using QIAamp viral RNA mini kit. For *in vivo* efficacy test, 14-days-old mice were infected i.c. with ~20 lethal dose (LD)50 of JEV, followed by i.c. or i.p. with HHT treatment. We identified the anti-viral effect of HHT *in vitro* or *in vivo* using quantitative reverse-transcription PCR, immunofluorescence assay, or histopathological analysis. **Results:** We demonstrated novel antiviral effects of HHT against JEV. HHT significantly inhibited the growth of JEV by plaque titration. JEV RNA load was reduced by HHT treatment. A JEV lethal mouse model was constructed by age-dependent ICR mice and used for anti-viral effect and toxicity testing of HHT. As a result of evaluating the anti-JEV efficacy of HHT *in vivo*, mouse mortality due to JEV infection was inhibited by HHT treatment. It was intended to determine the final administration

concentration of HHT, which is non-toxic and exhibits optimal antiviral efficacy. **Conclusions:** In this study, HHT exhibited an anti-viral activity against JEV infection *in vitro* and *in vivo*. HHT seems to be applicable as a potential therapeutic agent for the treatment of JEV. To address the mechanism of action of HHT, a better understanding of JEV will help develop effective anti-JEV treatments.

### Poster LB-5. Assessment of Preparedness and Vulnerability of Countries from Emerging and Re-emerging Public Health Threats

**Y. Jinnai**, J. Mendoza-Alonzo, A. Bennici, S. Young, C. Blanton, M. Mahar, C.H. Cassell
Division of Global Health Protection, Center for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Building and measuring global health security is critical for preparing countries for public health threats. The World Health Organization (WHO)'s Joint External Evaluation (JEE) provides a standardized tool to identify strengths and weaknesses in countries' preparedness in various technical areas. We examined the relationship between JEE indicators and the Research and Development (RAND) Infectious Disease Vulnerability Index to analyze a country's susceptibility and preparedness against public health threats. **Methods:** We examined eight technical areas and 26 JEE indicators from the 2015 JEE edition using data available on 79 countries whose JEE scores were published and completed in the WHO Mission Reports between January 2016 and July 2019. Using exploratory factor analysis, we determined the weights for each of the 26 JEE indicators to develop a composite indicator that defines a country's capacity in a compounded score based on their individual JEE indicator scores. We used a graphical representation to examine the RAND Infectious Disease Vulnerability Index and the JEE composite indicator scores for 16 U.S. Centers for Disease Control and Prevention partner countries. **Results:** The JEE composite indicator scores showed Mali, followed by Guinea and Burkina Faso (all in West Africa), was the least prepared for public health threats, and Uganda, followed by Vietnam and Indonesia, were the most prepared. The relationship between the JEE composite indicator scores and the RAND Infectious Disease Vulnerability Index measured Vietnam and Indonesia as less vulnerable and better-prepared countries. **Conclusions**: Our findings underscore the regional risk to public health threats in West Africa and the strengths and weaknesses within each technical area. This analysis may help inform countries in their efforts to strengthen capacities within some technical areas to improve global health security.

### Poster LB-6. Daily Rapid Antigen Testing To Inform University COVID-19 Isolation Policy: Findings and Lessons from the SARS-Cov-2 Omicron Variant

**R. Earnest**[1], C. Chen[2], C Chaguza[1], N.D. Grubaugh[1,3], M.S. Wilson[2], the Yale COVID-19 Resulting and Isolation Team
[1]Department of Epidemiology of Microbial Diseases, Yale School of Public Health, New Haven, CT, USA, [2]Yale Health Center, Yale University, New Haven, CT, USA, [3]Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA

**Background**: The suitability of the currently recommended 5-day COVID-19 isolation period is unclear as emerging SARS-CoV-2 variants rise to dominance, each with potentially differing infection dynamics. As the Omicron variant emerged, evidence gaps remained regarding appropriate isolation durations in high-density university settings, the best use of limited rapid antigen tests to exit isolation, and factors associated with isolation duration. **Methods**: We evaluated daily rapid antigen test case series data from 324 university students in a managed isolation program who initially tested positive between January 1 and February 11, 2022, an Omicron-dominant period. Arrival tests and twice-weekly screening were mandated. Positive persons isolated and began mandatory daily self-testing on day 5 until testing negative. Trained staff proctored exit testing. We report the percentage of persons remaining positive on isolation day 5+. We also conducted a survival analysis to assess the association between possible prognostic factors and isolation duration as measured by event-time-ratios (ETR). **Results**: We found 47% twice-weekly screeners and 26-28% less frequent screeners remained positive on day 5, with the percentage approximately halving each additional day. Having a negative test ≥ 10 days before diagnosis (ETR 0.85 (95% CI 0.75-0.96)) and prior infection > 90 days (ETR 0.50 (95% CI 0.33-0.76)) were significantly associated with shorter isolation. Symptoms before or at diagnosis (ETR 1.13 (95% CI 1.02-1.25)) and receipt of 3 vaccine doses (ETR 1.20 (95% CI 1.04-1.39)) were significantly associated with prolonged isolation. **Conclusions**: We present a review of the literature on COVID-19 isolation policy, discuss the possible onward transmission risk posed by different isolation periods, and examine our finding that receipt of 3 vaccine doses was associated with a longer isolation duration. We conclude with a discussion of how to continually assess isolation period policies in light of emerging variants.

### Poster LB-7. Detection of SARS-COV-2 Armored RNA in Global Interlaboratory Harmonization Study

D. Eveleigh
Asuragen, Austin, TX, USA

**Background:** Towards the beginning of 2020 a global effort began to effectively respond to the COVID-19 pandemic by developing molecular tests that could accurately and rapidly diagnose this emerging disease. A critical component lacking was a control to harmonize the results of the myriad of tests being developed. In order to address this urgent need, a Coronavirus Standards Working Group was formed in March of 2020 to provide recommended infrastructure for COVID-19 testing and ensure reliability of test results. This international consortium was convened by the Joint Initiative for Metrology in Biology at Stanford University and included a variety of represented disciplines. The group systematically considered different aspects of the measurement process, including standards and controls, and how they impacted various stages of the testing process. **Methods:** Part of this effort was a study planned by the consortium and executed globally by independent laboratories to assess multiple sources and types of molecular controls. The study involved fourteen laboratories running digital and real-time RT-qPCR worldwide that were provided SARS-CoV-2 RNA control material from eight vendors, one of which was Asuragen. Additionally, World Health Organization International Standards (WHO-IS) were prepared for each laboratory to use as calibrators. **Results:** Measurements of the Asuragen Armored RNA Quant SARS-CoV-2 (RUO) control were reported by each institution and plotted. In general, replicates within each institution were very tight as reported. **Conclusion:** Despite the differences in quantitation methods of starting material, dilution schema, assays used, detection chemistry involved, platform used, and laboratory location, all controls submitted to this interlaboratory global study demonstrated linearity, accuracy, and precision acceptable for clinical testing. The data summary highlights that bacteriophage-like RNA controls like Armored RNA Quant® perform as well as inactivated virus in the hands of laboratorians. These types of commutable, surrogate controls can be rapidly and widely deployed as an important part of future response planning. Another advantage of Armored RNA controls is that once agreement on a consensus sequence is achieved, sufficient flexibility remains to allow quick updates when new variants emerge. Regardless of which control format is utilized, agreement between control suppliers and assay developers should be made to ensure that the supply of controls and standards does not become a limiting factor when faced with an aggressive timeline for assay development and validation during emerging pandemics.

### Poster LB-8. Develop a Series of Maps To Predict the Special Distribution of Emerging Infectious Diseases in South Caucasus

**N. Bolashvili**[1], T. Chichinadze[1], I. Burjanadze[2], L. Malania[2]
[1]Vakhushti Bagrationi Institute of Geography at I.Javakhishvili Tbilisi State University, Georgia, [2]National Center for Disease Control and Public Health, Tbilisi, Georgia

**Background**: Zoonotic diseases are an important cause of human morbidity and mortality; around 75% of recently emerging human infectious diseases are zoonoses (Taylor et al., 2001). The movement of people, goods, and animals, globally, as facilitated by free trade and tourism may allow emerging diseases to spread quickly. Animal movement caused by natural migration, trading and marketing livestock represents an especially critical aspect in dissemination of zoonotic and vector-borne diseases. To protect human and animal health, it is essential to have efficient, robust surveillance systems for infectious diseases. Previous data collected on the occurrence of infections provides health networks the opportunity for early detection and the ability to respond through national and international means. Otherwise, serious tolls can occur on the economy and social structure of local and national communities. **Methods**: In order to predict the spatial distribution for selected pathogens (*F. tularensis, B. anthracis, B. melitensis*), we developed models linking geo-referenced covariate information on geographical, ecological, anthropological, and social factors with geo-referenced samples of the selected pathogens. Depending on the type and coverage of sampling available for each of the selected pathogens, the best modeling methodology for characterizing the covariate relationship and prediction will be determined. **Results**: The proposed work will modernize national surveillance and identify areas at risk for diverse zoonotic pathogens in the South Caucasus. Zoonotic pathogens, their arthropod vectors, and vertebrate reservoirs are an integrated system in the natural environment and various ecological and social factors determine the distribution of these pathogens. Quantitative disease ecology provides useful tools to analyze spatially referenced data on distributions of animal hosts, arthropod vectors, and infectious agents, and their spatial concordance with environmental and social parameters. Animal movement caused by trading and marketing livestock represents an especially critical aspect in dissemination of zoonotic diseases. The Atlas will identify areas where zoonotic diseases might occur, but human cases have not been recognized, but where further surveillance should be targeted. **Conclusions**: Effective surveillance systems rely on local and national participants' ability and willingness to accurately report disease outbreaks, and their capability to

implement local and national responses. Early identification of zoonotic disease emergence is essential to rapidly contain outbreaks, yet many local and national authorities lack the human and technical capability, capacity, and supporting financial resources to do so. By developing the Atlas, we will acquire information on the specifics of where and how the pathogen emerged, in what populations, in the past and, by extension, identify other similar regions where their circulation has gone undetected. The analysis and interpretation of data will be supported through information on demography, socioeconomic conditions, and environmental factors. In so doing, the Atlas specifically acknowledges the broad range of determinants that impact patterns of infectious disease transmission.

### Poster LB-9. Emerging and Re-emerging Diseases – Challenges for Health Security

**C.U. Anyanwu,** S.C. Enemuor
Department of Microbiology, University of Nigeria, Nsukka, Nigeria
**Background:** Emerging and re-emerging diseases pose considerable public health problems and challenges worldwide, including Nigeria. The dynamic relationships between the pathogens, hosts and the environment contribute immensely to the emergence or re-emergence of these diseases. The progressive evolution of viral and microbial variants coupled with the issue of drug resistance is known to facilitate the emergence and perhaps increase of infections. These diseases include Lassa fever, Ebola virus disease, yellow fever, monkeypox and the ongoing coronavirus which have been listed among priority diseases for reporting under the National Integrated Disease Surveillance and Response Strategy. **Methods:** Extensive literature search of the publications by the Centre for Disease Control and Prevention (CDC), World Health Organization (WHO) and other Health Institutions were used for the situation analysis of emerging and re-emerging disease infections in Nigeria. Efforts were made to situate possible strategies of managing these diseases including integrated disease surveillance and response. **Results:** Increasing evidence of outbreak of emerging and re-emerging infectious diseases were linked to social and demographic factors such as rapid urbanization, increased population growth and movement, globalization, political will of the Governments with particular reference to integrated disease surveillance and response. Other studies emphasized the link with such critical factors as technological limitations, insecurity, poor healthcare funding, development of new pathogens occasioned by microbial resistance to antibiotics and increased human–animal interaction. **Conclusion:** Emerging and re-emerging diseases outbreaks remain a public health threat and challenge to vulnerable populations in Africa and Nigeria in particular. These call for strong public health organization and preparedness and disease outbreak response to prevent public health crises in order to secure the health of the people.

### Poster LB-10. Enhancement of In-country Laboratory Capacity for Detection, Identification, and Characterization of Acute Febrile Illnesses in the Country of Georgia

**E. Khmaladze,** N. Chitadze, T. Chikviladze, M. Chubinidze, S. Avdalova, T. Tevdoradze, M. Zakalashvili, D.Tsaguria, E.Zhgenti, G. Chanturia, K.Sidamonidze, P. Imnadze
National Center for Disease Control and Public Health of Georgia, Tbilisi, Georgia
**Background:** Acute febrile illness (AFI) represents a broad spectrum of infectious disease etiologies which frequently share common symptoms complicating an accurate diagnosis based solely on clinical symptomology. Understanding the etiology of AFI in a population or region can act as a guide for empiric therapies and case management; as well as identifying gaps in surveillance systems that need to be strengthened. In our study we focus on a selected number of AFI etiologies, which are endemic or have a potential to be introduced in Georgia. **Methods:** Samples were collected as part of AFI sentinel surveillance from the first pilot AFI sentinel site in Georgia from August 2021. A total of 153 whole blood (WB) samples were received for molecular and serological testing respectively. In addition, 72 nasopharyngeal swab samples were submitted for COVID-19 PCR testing since February 2022. Multiplex real-time PCR (Tropical Fever Core-FTD) and ELISA assays were conducted for the following etiologies: *Leptospira* spp.; West Nile virus; Chikungunya virus; Dengue virus; *Plasmodium* spp.; *Rickettsia* spp., *Salmonella* spp. and SARS-CoV-2. **Results:** Overall, 123 patients screened serology positive, among them 66 (54%) were positive by more than one ELISA assay. Of those 109 patients were positive for IgM antibodies and 52 patients were IgG antibodies positive. Sample positivity rate assessment by each ELISA assay is in currently in progress. Only one WB sample was positive for *Plasmodium* spp. by multiplex PCR. Five nasopharyngeal swab samples tested positive for SARS-CoV-2. **Conclusion:** Samples screened positive by ELISA assays will require further interpretation based on the collected epidemiologic and clinical data coupled with the results of the confirmatory assays. Validated novel techniques will become routine in Georgia, thus, will enhance in-country laboratory capacity for rapid detection, identification and characterization of infectious diseases causing AFI clinical manifestations.

### Poster LB-11. Gonococci Microparticulate Microneedle Vaccine Induces Immune Correlates of Protection and Resistance to Infection in Mice

**P. Bagwe**[1], L. Bajaj[1], R. Gala[1], S.M. Zughaier[2], M.J. D'Souza[1]
[1]Vaccine Nanotechnology Laboratory, Center for Drug Delivery Research, College of Pharmacy, Mercer University, Atlanta, GA, USA, [2]College of Medicine, QU Health, Qatar University, Doha, Qatar
**Background:** *Neisseria gonorrhoeae* is the bacteria that causes gonorrhea infection and has gradually developed antimicrobial resistance. There is an urgent need for alternative therapy for gonorrhea. However, there is no vaccine for gonorrhea. This study investigates the *in vivo* immunogenicity of an inactivated gonococci microparticle vaccine along with adjuvant microparticles delivered intradermally using dissolving microneedles. **Methods:** Female mice were immunized using microneedles containing adjuvanted gonococci microparticles (Gc-MP+ Alum MP+ AddaVax™ MP). The mice received one prime and two booster doses at two weeks intervals. Enzyme-linked immunosorbent assay was used to measure total IgG, IgG sub-types, and IgM levels in mice sera and IgA in vaginal washes. The bactericidal antibodies were also assessed. At week 8, mice were challenged intravaginally using an established murine female genital tract infection model with live bacteria. At end of week 10, the mice were sacrificed, and their secondary immune organs were isolated to determine cellular immunity. The induction of T-cell immune response was assessed by analyzing CD4 and CD8 T-cell surface markers using flow cytometry. **Results:** The data shows that after immunization, gonorrhea-specific serum total IgG, IgG1, IgG2a and vaginal IgA antibodies were generated in groups receiving the adjuvanted and non-adjuvanted gonococci vaccine MP. The antibodies generated in mice after immunization were bactericidal towards live *Neisseria gonorrhoeae* as observed in serum bactericidal assay. The immunized mice cleared infection in 6 to 9 days, whereas the control groups were starting to clear the infection beginning on day 10. Thus, significant resistance to infection manifested as faster clearance was seen in immunized mice. In addition, mice receiving adjuvanted vaccine showed enhanced expression of cellular immunity markers CD4 and CD8 on surface of T cells in spleen and lymph nodes. **Conclusion:** Microneedle immunization with an inactivated gonococci MP in mice induced humoral and cellular immunity to gonococcal infection.

### Poster LB-12. Harnessing Clinical Trial Capacity To Mitigate Zoonotic Diseases: The Role of Expert Scientists in Ethiopia

**S.B. Adugna,** M. Giday, T. Manyazewal
Center for Innovative Drug Development and Therapeutic Trials for Africa (CDT-Africa), College of Health Sciences, Addis Ababa University, Addis Ababa, Ethiopia, Faculty of Veterinary Medicine, Hawassa University, Hawassa, Ethiopia
**Background**: The emergence and resurgence of zoonotic diseases have continued to be a major threat to global health and the economy. Scientifically sound clinical trials are important to find better ways to prevent, diagnose, and treat zoonotic diseases. This study aimed to investigate expert scientists' perceptions and experiences in conducting clinical trials toward zoonotic diseases in Ethiopia. **Method**: This study employed a descriptive, qualitative study design. It included major academic and research institutions in Ethiopia that had active engagements in veterinary and public health research. It included the National Veterinary Institute, the National Animal Health Diagnostic and Investigation Center, the College of Veterinary Medicine at Addis Ababa University, the Ethiopian Public Health Institute, the Armauer Hansen Research Institute, and the College of Health Sciences at Addis Ababa University. In-depth interviews were conducted with expert scientists. Data were collected from October 2019 to April 2020. Data analysis was undertaken using open code 4.03 for qualitative data analysis. **Results**: Five major themes, with 18 sub-themes, emerged from the in-depth interviews. These were: challenges in the prevention, control, and treatment of zoonotic diseases; One Health approach to mitigate zoonotic diseases; personal and institutional experiences in conducting clinical trials on zoonotic diseases; barriers in conducting clinical trials toward zoonotic diseases; and strategies that promote conducting clinical trials on zoonotic diseases. Conducting clinical trials on zoonotic diseases in Ethiopia is hampered by a lack of clearly articulated ethics and regulatory frameworks, trial experts, financial resources, and good governance. **Conclusion**: In Ethiopia, conducting clinical trials on zoonotic diseases deserves due attention. Strengthening institutional and human resources capacity is a pre-condition to harness effective implementation of clinical trials on zoonotic diseases in the country. One Health approach has the potential to form multidisciplinary teams to systematically improve clinical trials capacity and outcomes in the country.

### Poster LB-13. Knowledge, Attitudes, and Practices Regarding Human Papillomavirus Vaccination among Physicians in Qatar

**S. Albayat**[1], J. Mundadan[1], K. Elmardi[1], R. Baaboura[1], S. Hasnain[1], H. Khogali[1], H. Al-Romaihi[1], N.J. AlKubaisi[2], M. Iheb Bougmiza[2]
[1]Vaccination section, HP-CDC, Ministry of Public Health, Doha, Qatar, [2]Community Medicine Consultants, Primary Health Care Corporation, Doha, Qatar
**Background:** Human papilloma virus (HPV) is a global problem that affects sexually active women and men, with cervical cancer being the most serious associated disease. Most of cervical cancer cases can be prevented by vaccination against HPV early in life. The objective was to identify the knowledge, attitudes and practices among physicians working in Qatar regarding HPV infection and HPV vaccines. **Methods**: A cross-sectional study targeting physicians working in various health facilities in Qatar was conducted, using a web-based questionnaire. Knowledge was assessed and those with a score more than the median score were considered to have good knowledge; association between knowledge and attitude/practices/independent variables were looked for using bivariate analysis and logistic regression. **Results**: 557 physicians participated in the study. 83.7% have good knowledge, though many did not know of its availability in Qatar. The perceived barriers to community acceptance of HPV vaccination include lack of awareness regarding relationship between HPV and cancer, regarding availability of HPV vaccine, concerns of the community regarding vaccine efficacy and safety, HPV vaccination may encourage risky sexual behavior, and community's self-perceived low-risk. Three-fourths of the physicians were willing to provide HPV vaccine for their adolescent daughter and they were very likely to recommend to their clients. **Conclusion**: Most of the physicians have good knowledge regarding HPV. Physicians who were willing to give their daughters HPV vaccine and who were willing to recommend to their clients were not very high. This issue may affect the intended HPV vaccination program implementation if not well addressed.

### Poster LB-14. Low Levels of Knowledge, Attitudes, and Practices towards Vaccination and COVID-19 Vaccines among Healthcare Providers—Kazakhstan, 2021

**A. Bayashova**[1], A. Shtabaeva[1,2], L. Kassabekova[2], S. Alaverdyan[3], R. Horth[4], D. Nabirova[4]
[1]Central Asia Region Field Epidemiology Training Program, Almaty, Kazakhstan, [2]Scientific and Practical Center for Sanitary and Epidemiological Expertise and Monitoring, Almaty, Kazakhstan, [3]American University of Armenia, Yerevan, Armenia, [4]US Centers for Disease Control and Prevention, Central Asia Regional Office, Almaty, Kazakhstan
**Introduction:** Annually in Kazakhstan ~5,000 newborns are not vaccinated because of parental hesitancy. Hesitancy has resulted in resurgence of diseases with 16,967 measles cases registered nationally in 2019. Poor knowledge, attitudes, and practices (KAP) among healthcare providers contributes to vaccine hesitancy, and additional data was needed for developing interventions. **Method:** We conducted a cross-sectional study which included all healthcare providers directly involved in vaccine administration at 54 facilities in Shymkent, Turkestan, and Aktobe from March–May 2021. We used logistic regression to test association with good KAP; cut-off for good KAP was 70%. Odds ratios (OR) and 95% confidence intervals (CI) are reported. **Results:** We interviewed 1,461 providers, 951 (65%) nurses, 360 (25%) general practitioner (GP), and 150 (10%) pediatricians. Of these providers 93% were females. Their mean age was 36 years old. Among the providers, 622 (43%) had good knowledge, 237 (16%) had good attitudes, and 473 (32%) had good practices. Additionally, 75% agreed that measles vaccines were effective, <49% thought COVID-19 vaccines were effective, and 59% said they would not get the COVID-19 vaccine. Good knowledge was associated with being female (OR: 3.1, CI: 1.7–6.1), being a GP (1.7, 1.1–2.5), 11–20 years' work experience (1.5, 1.1–2.4), and >21 years' work experience (2.5, 1.5–2.0). Good attitude was associated with >21 years' work experience (2.7, 1.5–4.9). Good practice was associated with not living with people >65 years old (1.5, 1.1–2.0), >21 years' work experience (1.5, 1.1–2.0). Good knowledge and good practice were associated with good practice (OR: 4.2 [3.2–5.6] and 2.3 [1.8–3.0], respectively). **Conclusion:** Our study revealed markedly low levels of KAP among healthcare providers. Results can be used to improve knowledge and attitudes towards vaccination, with focused effort on providers with less work experience, nurses, and pediatricians.

### Poster LB-15. Prevalence and Hospital Outcome of Bacterial Co-infection in Respiratory Tract Specimen among COVID 19 Patients with SARS-CoV-2 Pneumonia in a Tertiary Hospital: A Cross-sectional Study

D.J. Soliman
Amang Rodriguez Memorial Medical Center, Marikina City, MM, the Philippines
**Introduction**: COVID-19, a zoonotic disease caused by the novel coronavirus SARS-CoV-2, is a highly transmittable pathogenic viral infection, infecting millions of people globally. Guidelines recommend the use of

empiric antimicrobials based on clinical judgment, patient host factors and local epidemiology in patients suspected or confirmed severe COVID-19. However, current evidence does not support a high rate of bacterial respiratory co-infections in patients with SARS-CoV-2 infection. At present, there is no known study regarding the prevalence of bacterial co-infection in COVID-19 patients in the Philippines. **Methods**: This research is a cross-sectional hospital-based study that utilized hospital electronic and printed medical records, chest radiograph and microbiologic results. All respiratory specimen bacteriologic results for the year 2020 and 2021 were collected from the hospital's laboratory unit followed by review of the hospital electronic records, printed medical records and chest radiograph results. Data were analyzed using Two-tailed Z-test for significance test for proportions and Chi-square test. **Results**: Among 100 subjects, only 22% (n=22) of the subjects were found to have bacterial isolates. the only demographic that is dependent with presence of bacterial infection is gender. The three most common bacterial isolate among COVID confirmed patients are *Klebsiella pneumoniae* (n=9), *Pseudomonas aeruginosa* (n=5), and *Acinetobacter baumannii* (n=3). Although the most common bacterial isolate is *Klebsiella pneumoniae*, the most common bacterial co-infection in patients who died are *Acinetobacter baumannii* (n=2, 29%) and *Pseudomonas aeruginosa* (n=2, 29%). **Conclusion**: The prevalence of bacterial co-infection among COVID confirmed patients is relatively low, hence appropriate guidelines regarding antibiotic use should be formed taking into consideration local data on antimicrobial resistance.

### Poster LB-16. Rapid Multiplexed Detection of Arboviruses using Surface Plasmon Resonance Imaging

**J.M. Obliosca**, K. Johnson, O. Vest, T. Ferguson, Y. Xu, C.K. Tison
Luna Labs USA, LLC., Charlottesville, VA, USA

**Background:** A multiplexed assay platform, MultiNanoSPRi™, has been developed to provide a versatile diagnostic tool for clinicians in ruling out and confirming infection status. Here, simultaneous analysis of infectious indicators in both protein and nucleic acid forms from Zika, Dengue, and Chikungunya arboviruses in sera from infected patients is demonstrated. **Methods:** The development of MultiNanoSPRi is based on nanoenhanced surface plasmon resonance imaging technique to monitor target pathogen indicators IgM, IgG, and RNA on a single sensing chip. Specific capture arrays (antibodies and aptamers) were immobilized onto a chip which was then surface blocked and run using a benchtop SPRi instrument equipped with a charge coupled device to monitor reflectivity changes of the flow as indicators bound onto specific capture probes in real-time. Detection was achieved using specific biotinylated detection probes followed by a streptavidin-coated nanoenhancer for signal amplification. **Results:** The sensing arrays were first constructed for parallel detection of three indicators for each arbovirus using spiked and clinical sera samples. We also selected the surface activation reagent parameters for clinical use, developed SPRi disposable chips, developed quality control for the overall MultiNanoSPRi operation, conducted stability tests of assay reagents, and developed an algorithm for SPRi signal readout. Ongoing clinical performance studies for ZIKV indicators IgM and IgG were conducted. Preliminary results demonstrated multiplexed detection sensitivity and specificity of 86% and 67% for ZIKV IgM, and 100% and 83% for ZIKV IgG, respectively in an hour of analysis time. Multiplexed indicator detection for three arboviruses, and tests for assay cutoff, reproducibility, and cross-reactivity will next be conducted. **Conclusions:** The MultiNanoSPRi platform is a promising multiplexed assay for detecting various serum pathogen indicators. It can be reconfigured for the study of various pathologies such as Ebola and COVID-19 and extended to analyses of other matrices such as urine and semen.

### Poster LB-17. Safety, Pharmacokinetics, and Predicted Lung Concentration of a Novel SARS-CoV-2 $M^{pro}$ Inhibitor in Healthy Volunteers

**M. Hu**[1], F. Lee[2], S. Reddy[2], Y. Liu[3], J.Y. Jia[3], L. Xu[4], X.M. Tao[5], X. Liu[1], D. Xie[1], C. Yao[1]
[1]Frontier Biotechnologies Inc., Nanjing, Jiangsu, China, [2]Frontage Clinical Services Inc., Secaucus, NJ, USA, [3]Shanghai Xuhui Central Hospital, Shanghai, China, [4]Shanghai University of Traditional Chinese Medicine, Shanghai, China, [5]Beijing BioVoice Technology Co. Ltd., Beijing, China

**Background:** During the delta and omicron variants-predominant period, COVID 19-caused hospitalization and death remained high. Remdesivir is the only approved antiviral for hospitalized patients. We aim to develop an intravenously administered formulation of FB2001, one of the earliest reported small molecule inhibitors of coronavirus main protease ($M^{pro}$), for this vulnerable population. **Methods:** Two randomized, double-blind, placebo-controlled phase 1 studies were conducted in the US and China, to evaluate the safety, tolerability and pharmacokinetics of FB2001 in healthy subjects. Eighty subjects in US and 40 subjects in China were enrolled with 6 active and 2 placebo in each cohort. Subjects were administered by intravenous infusion of FB2001 at single doses from 5 mg to 400 mg, and at multiple doses of 30 mg to 400 mg daily for 5 days, respectively. For selection of an

effective dose, a physiologically based pharmacokinetic (PBPK) model was established and validated by using blood and tissue FB2001 concentration in rat and canine, and blood concentration in human respectively. Using this model, we predicted FB2001 concentration in human lung tissue. **Results:** No dose limiting toxicities (DLTs) were observed. A total of 24 adverse events were reported with grade 1 or 2 in severity. The half-life was about 5 hours. The plasma exposure was dose-dependent, consistent with linear kinetic characteristics, with no drug accumulation. The plasma $C_{trough,\ ss}$ of FB2001 was 33.9 ng/mL at 300 mg daily for 5 days. Based on the PBPK model, the predicted $C_{trough\ ss}$ in lung at 300 mg daily was 1.7μg/mL, 50-fold higher than that in plasma. No significant safety and pharmacokinetics difference was found between US and Chinese population. **Conclusions:** FB2001 were generally safe and well tolerated. A PBPK model showed significantly higher lung drug concentration than in plasma. Without using a pharmacokinetic enhancer at a dose of 300 mg to 400 mg daily, FB2001 exhibited plasma and lung drug concentration above the *in vitro* antiviral $EC_{50}$ value. The results warrant further development of FB2001 for treatment of *SARS-CoV-2* infection.

### Poster LB-18. SARS-CoV-2 Virus Seroprevalence in the Population of the Kyrgyz Republic

**Z.S. Nurmatov**[1], T.E. Kuchuk[1], K.T. Kasymbekov[2], Z.N. Nuridinova[1], A. Vaughan[3]
[1]"Preventive Medicine" Research and Production Association of the Kyrgyz Republic Ministry of Health, Bishkek, Kyrgyzstan, [2]WHO Country Office in Kyrgyzstan, Bishkek, Kyrgyzstan, [3]WHO Regional Office for Europe, Copenhagen, Denmark
**Introduction:** To measure the population immunity of the Kyrgyz Republic population, two rounds of seroepidemiological study for the presence of SARS - CoV -2 virus antibodies were carried out. **Methods:** Cross–section population-based study stratified by age and geographical region during the periods of 26 June – 25 July 2020 and February 1–April 15, 2021. Sampling was conducted based on the computer statistical formula. Total of 4816 people, consented to participation in the study, were sampled and tested during the I round and 4735 people during the II one. Blood samples and epidemiological data were collected in the territorial Family Medicine Centers, and testing was performed in Reference laboratories, using «SARS-CoV-2-Ab ELISA WANTAI» test systems to measure cumulative SARS-CoV-2 virus antibodies. **Results**: In the I-st study round antibodies were detected in 30,8% of the population (95% CI 29,5 - 32), and in the II-nd round – in 71,2% of the population studied (95% CI 69,9 - 72,5). In the I-st study round, are-wise seroprevalence ranged from 16,5% in children of 0-9 years of age up to 36,1% in persons aged 45-64 years. In the II-nd study tour seroprevalence ranged from 51,4% in children of 0-9 years old up to 79,4% in people aged 45-64 years. From regional geography perspective, seroprevalence in the I-st round ranged from 13,0 (95% CI 9,7–16,3) to 62,7% (95% CI 59,2–69,2), and in the II-nd - from 63,9% (95% CI 62,5–65,3) to 77,8% (95% CI 76,6-79,0). In the I-st study round, out of 1446 seropositive individuals, 925 (64,0%) had COVID-19 symptoms, and in the II-nd one - out of 3372 seropositives symptoms were noted in 1696 (50,3%). Out of 1446 seroprositives - 21,8% (315/1446) were seeking for health care in the I-st round and out of 3372 positives 25,3% (855/3372) in the II-nd round of the study. 80 people (5,5%) out of the seroprositive people were hospitalized (95% CI 4,3 - 6,7) in the I-st round and 342 (10,1%) (95% CI 9,1 - 11,1) in the second round of the study. **Conclusions:** According to the results of the II-nd round of the study the seroprevalence indicator of the population increased by 2,3 times compared to the previous round results and amounted to 71,2% versus 30,8%. 28,8% of the population remained susceptible to Coronavirus infection. It was noted in both study rounds that seropositivity, as well as COVID-19 symptoms presence, seeking health care and hospitalization patterns were statistically ($p<0,001$) increasing with age. Seropositivity rates in many regions were not statistically different from the republican level. The indicated statistically reliable differences ($p<0,05$) in some regions were attributed to the fact that blood samples were collected from people at earlier stages of epidemiological peak.

### Poster LB-19. Upamostat, a Serine Protease Inhibitor, for Outpatient Treatment of COVID-19: A Placebo-controlled, Randomized Pilot Study

**T. Plasse**[1], B. Delgado[2], J. Potts[3], D. Abramson[1], C. Fehrmann[1], G. McComsey[4]
[1]RedHill Biopharma, Ltd, Tel Aviv, Israel, [2]South Florida Research, Miami, FL, USA, [3]Great Lakes Research Group, Bay City, MI, USA, [4]University Hospitals of Cleveland and Case Western Reserve University, Cleveland, OH, USA
**Background:** SARS-CoV-2 requires processing by cell surface proteases to infect host cells. Upamostat is a serine protease inhibitor which blocks SARS-CoV-2 in vitro. Prior to a pivotal study, we performed a pilot study in outpatients with symptomatic COVID-19. **Methods:** SARS-CoV-2 patients (pts) with ≥2 moderate to severe symptoms, onset ≤5 days prior to study were eligible. Pts could be of any risk level, have received prior COVID-19 vaccination and receive anti-SARS-CoV-2 monoclonal. Pts were randomized to oral upamostat 200 or 400 mg or matching placebo daily x14 and followed for 6 more weeks. Pts completed a COVID-19 symptom questionnaire

daily x28 then thrice weekly x4 weeks and were examined with nasal swabbing for virology and safety and disease marker blood sampling periodically. **Results:** 20 pts each received placebo or upamostat 200 mg daily; 21 received upamostat 400 mg daily. Median age was 49; 44% male, 59% had ≥1 factor associated with high risk for progression; 48% had ≥1 severe baseline symptom. Treatment was well tolerated; one patient (upamostat 400) reported an adverse event related to study medication: mild, transient skin rash. Median (interquartile) time to sustained recovery considering all symptoms was 38 (15.5-57) days for placebo, 29.5 (18.5-57) days for upamostat 200 and 38 (16-57) days for upamostat 400. Median (interquartile) time to sustained recovery from severe symptoms was 8 (4-26), 4 (2-6) and 3 (2-6) days for the 3 treatment groups, respectively. New severe symptoms developed in 20% of placebo versus 5% and 0% of upamostat 200 and 400 groups respectively (p=0.036 comparison between placebo and combined upamostat group). Three placebo pts (15%) versus no pts in either upamostat group were hospitalized for worsening COVID (p=0.03). Mean D-dimer level remained constant in placebo patients but decreased by 38% and 48% over the study in upamostat 200 and 400 patients. **Conclusions:** Upamostat was well tolerated. Entering patients based on symptomatology selected an outpatient population with a higher probability of hospitalization than studies not requiring minimal symptomatology. Oral upamostat was safe and effective in shortening time to recovery from and decreasing incidence of new severe symptoms and hospitalization for COVID, and decreased D-dimer levels.

### Poster LB-20. Use of Mobile Applications/mHealth Solutions during the COVID-19 Pandemic in Lao PDR: A Commentary of Technology Used and Its Impact on Healthcare Delivery during the Pandemic

V. Phompanya
Department of Communicable Diseases Control, Ministry of Health, Vientiane, Lao, PDR
**Introduction:** The Covid-19 pandemic has increased the attention of the Lao government to digital health solutions, particularly mobile health (mHealth), to support COVID-19 mitigation efforts and outbreak response across the health sector. This paper describes the mHealth landscape prior to the COVID-19 pandemic and the technological solutions implemented during the pandemic response. It discusses the strengths and limitations of the digital technologies used, their impact, and future directions for mHealth in Lao PDR. **Methods:** A commentary report using observational data and stakeholder views on the usage of mobile applications before and during the COVID-19 pandemic. Quantitative data relating to downloads of applications, trends of usage, and feedback from users supplement the commentary. Data and published literature are used to identify strengths and limitations in the applications implemented in Lao PDR and discuss the generalizability of the results to other low-income settings. **Results:** Prior to the COVID-19 pandemic, mHealth applications used in Lao PDR were limited and not widely utilized by either healthcare professionals or Lao citizens. During the pandemic, there was an attempt to shift toward using mobile applications for disseminating credible health information, recording vaccine history, registering for COVID vaccination certificates, reporting symptoms, and making appointments for COVID-19 vaccination and testing. However, the application which was developed received poor reviews, mostly relating to useability and application infrastructure, which limited the use of the application and hampered the successful implementation of these innovative technologies in the Health sector. **Conclusions:** the use of mHealth technologies during the COVID-19 pandemic has indicated the utility of mHealth solutions and potential opportunities to accelerate long-term digital health transformation for Lao PDR and other low-income countries. Increasing the investment and uptake of mHealth will have a greater impact on healthcare delivery for Lao citizens as the country enters the endemic phase of the COVID-19 pandemic.

### Poster LB-21. Using Historically Black Colleges and Universities (HBCUs) as an Educational Bridge to Address Vaccine Hesitancy within the African-American Community

**C. Gillard**, S. Al-Dahir, M. Earls, B. Singleton, B. Turner
Xavier University of Louisiana, New Orleans, LA, USA
**Background:** Historically Black Colleges and Universities were established to allow more opportunities to higher education for African-Americans. Many of these institutions are located in the Southern United States and have a legacy of service that fosters longstanding community partnerships. The COVID-19 pandemic significantly impacted Southeastern Louisiana and New Orleans, particularly among African-Americans. Before the release of the COVID-19 vaccine, United States polls estimated low vaccine acceptance, notably among African-Americans. Xavier University of Louisiana College of Pharmacy, an HBCU has engaged partnerships with the goal to reduce health disparities among the African-American community. The researchers aim to leverage the University's existing position as a trusted educational institution in the community, to address ongoing disparities compounded by the COVID-19 pandemic, and to increase vaccine uptake in a culturally competent healthcare model. The study

objective is to describe how faculty at an HBCU created a forum for engagement to obtain the perspectives of local communities of color, disproportionately impacted by COVID-19. **Methods:** In a nationwide initiative sponsored by the Robert Wood Johnson Foundation, African-American community members participated in a series of focus groups to understand concerns surrounding COVID-19 vaccination. These focus groups included facilitator led dialogue and poll response questions. The focus groups were led by a Xavier University faculty research team and foundation facilitators. During these conversations, the community members discussed their individual perspectives and attitudes towards COVID-19 vaccination. **Results:** Among African-American participants, historical mistrust of government and safety concerns were cited as an impediment to COVID-19 vaccination. A desire to return to normal life and protection from COVID illness for themselves and family members were positive influences of vaccine uptake. **Conclusion:** The faculty at this HBCU aim to use the information obtained from this project to provide ongoing education about COVID-19, address vaccine hesitancy, and serve the local community based on their experiences and perspectives.

### Poster LB-22. Virus-virus Interactions in the Temporal Patterns of Co-circulating Acute Respiratory Infections in China over an 11-year Period

**Z.J. Madewell**[1], L. Fang[2], N.E. Dean[1], I.M. Longini[1], Y. Yang[1]
[1]Department of Biostatistics, University of Florida, Gainesville, FL, USA, [2]State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology, Beijing, China
**Background**: Immune responses to a viral infection can modify immune responses to subsequent unrelated viral infections via protective immunity or increased immunopathology. There is limited long-term population-level data on virus-virus interactions or change in the course of one viral infection from concomitant or prior infection of another virus. We use a Bayesian framework to evaluate interactions between acute respiratory viruses in China. **Methods**: Our study included passive surveillance data of ten acute respiratory viruses from Beijing, Chongqing, Guangzhou, and Shanghai from 2009-2019: influenza A (IAV) and B (IBV); respiratory syncytial virus A (RSV-A) and B (RSV-B); and human parainfluenza virus (HPIV), adenovirus (HAdV), metapneumovirus (HMPV), coronavirus (HCoV), bocavirus (HBoV), and rhinovirus (HRV). We used a multivariate Bayesian hierarchical model to evaluate correlations in monthly infection prevalence between virus pairs, adjusting for potential confounders. **Results**: There were 101,643 patients of whom 33,650 tested positive for any acute respiratory virus and 4,113 were co-infected with more than one virus. Bayesian multivariate modeling revealed 11 significant correlations in at least two cities: ten positive (HPIV/HRV, RSV-B/HCoV, RSV-B/HPIV, RSV-B/HRV, IBV/RSV-A, HCoV/HPIV, HCoV/HMPV, HPIV/HMPV, HMPV/HBoV, HAdV/HBoV) and one negative (IAV/RSV-A). **Conclusions**: Virus-virus interactions may influence disease severity, transmissibility, immune response, and vaccine effectiveness. Our research provides evidence of virus-virus interactions among four large cities over 11 years. Negative interactions may indicate viral interference via non-specific immunity or competition for resources. Conversely, positive interactions were observed in virus pairs known to typically infect children and may suggest that one virus increases risk for co-infection.

## Oral Presentation Abstracts

## E1. Preparedness and Emergency Response

### 3:15 PM – 4:45 PM

### Centennial Ballroom I

### The Role of the Environment: How Mask Wearing Varies Across Different Settings

**C. Nestor**, G. Earle-Richardson, C. Prue
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** As the COVID-19 pandemic continues into its second year, mask wearing remains an important infection control measure. Most research on mask wearing simply asks respondents how frequently they wear a mask in public. However, mask wearing may vary across settings. Understanding where people are more or less likely to wear masks and why, may help to inform public health messaging around mask wearing. This analysis aims to understand: 1) the variability in mask wearing frequency in different settings and 2) the demographic and psychosocial factors associated with observed variability. **Method:** Online, opt-in, cross-sectional surveys were conducted every 2 months from November 2020 to May 2021 (n = 2508), with quota sampling and weights applied to make the sample representative of the U.S. population. Respondents were asked how frequently they wore masks in public and in 12 specific settings including on public transportation, while shopping, and attending social

gatherings indoors and outdoors. Respondents were also asked about attitudes and perceptions related to mask wearing, including the efficacy of masks, risk of becoming infected and expectations from others to wear a mask. Simple frequencies and correlations were calculated. In the next analytic step, patterns of mask wearing across various settings will be identified using latent class analysis. Psychosocial and demographic factors will then be used to predict class membership. **Results:** For those who completed the activity in the previous week, always wearing a mask was most common when shopping (62%) and going to a medical appointment (57%) and least common when visiting family or friends indoors (25%) and outdoors (25%). Correlations between frequency of mask wearing in various environments were all significant ($p < .05$) and ranged from weak ($r$ =0.26, shopping and visiting family indoors) to strong ($r$ = 0.76, attending indoor and outdoor gatherings). Frequency of mask wearing in public, a general measure, was weakly correlated with mask wearing across the 12 specific settings ($r$ = 0.14 to 0.27). Masking frequency remained stable across the survey samples at each month, with a 0.29% ($SD$ = 0.05) average increase in "always" wearing a mask across all settings from November 2020 to May 2021. **Conclusion:** The wide variability in mask wearing frequency suggests that setting-specific questions are more useful than a single, general question. The fact that mask wearing in social settings, indoors or outdoors, is more consistent than either is with other settings suggests that people are responding to other considerations besides the inherent greater risks of indoor exposure. The key distinction in mask wearing across these environments may be whether someone will be encountering people they know personally or mostly strangers and the types of requirements that exist for entering public spaces (such as mask mandates).

### Process Evaluation in Emergency Response: Evaluating COVID-19 Screening Testing Programs in K-12 Schools

**B. Carter**[1], M. Williams[1], M. LaBelle[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Global Government Solutions, Atlanta, GA, USA
**Background**: The pervasiveness of the COVID-19 pandemic has created unparalleled challenges for K-12 schools in the U.S. In response, schools have had to mount an enormous effort to meet students' needs while ensuring a safe space for in-person learning. One prevention strategy for keeping schools safely open is implementing school-based screening testing programs. Such programs help to isolate cases early and reduce transmission. This study evaluated school-based screening testing programs in spring and summer 2021 to determine what facilitates implementation and to inform screening testing programs in schools for the current school year. **Methods**: CDC carried out two assessments. One examined community perspectives along with building-level testing logistics and data management. For this CDC conducted field observation of one district's pilot program, surveyed staff and parents to gauge attitudes toward screening testing and interviewed school and public health leaders about their experiences. The second focused on barriers and facilitators to program implementation. CDC conducted semi-structured group interviews with officials from seven state and local school screening testing programs. **Results**: Field observation demonstrated the importance of testing model design for attenuating staff burden and minimizing disruption of classroom time. Across assessments, increasing community confidence and reassuring safe and healthy environments emerged as the most salient reasons for implementing testing programs. COVID-19 fatigue, lack of buy-in from officials and parents, and staff burden surfaced as common barriers to implementation. Robust communications strategies, established community partnerships, and program scalability were facilitators to implementing screening testing. **Conclusions:** Strategies that attend to safety, confidence, and staff workload, and involve robust communications and strong partnerships promote sustained, successful screening testing in schools.

### COVID-19 DART (During Action Review and Tabletop): One Health Approach for Assessing Readiness and Preparing for Future Crises in Bangladesh

**M.S. Uzzaman**, A.S.M. Alamgir, M. Rahman, M. Husain, T. Shirin
Institute of Epidemiology Disease Control & Research, Dhaka, Bangladesh
**Background**: To ensure readiness and resiliency, the Institute of Epidemiology, Disease Control and Research (IECDR) in Bangladesh conducted a During Action Review & Tabletop exercise (DART) with technical support from Sandia National Laboratories and Ending Pandemics from November 2020–January 2021. DART allowed for both retrospective evaluation of strengths and gaps in the response to COVID-19 and prospective testing of potential scenarios that might complicate future resiliency. DART is designed to enable engagement from multiple sectors using a One Health lens. Bangladesh engaged both animal and public health sectors in laboratory, epidemiology, and communication to evaluate its response to COVID-19. **Methods**: Twenty-five experts representing Public Health, Animal Health, Wildlife, Case Management & Countermeasures, Point of Entry, Emergency Response and Communication, Epidemiology & Laboratory, and Overall Coordination participated in retrospective, participant-led analysis guided by a role-based questionnaire. Participants subsequently conducted a remote, multirole, multisector

Tabletop looking at scenarios three months, six months and three years out to explore readiness for situations such as concurrent outbreaks, internet outages, variants, and public compliance. A participant-led After Action Review identified key priorities and recommendations for future preparedness. **Results**: Using DART, IEDCR identified One Health coordination as a key strength for integrating human and animal health along with other sectors to address surge capacity needs. Flexibility and leveraging current systems were also identified as strengths. Thirteen response planning recommendations included developing surge capacity rosters, backup communication systems, waste management protocols, and dedicated wards for COVID-19 patients. All recommendations were completed or in progress as of July 2021. **Conclusions**: DART allowed relevant Bangladesh experts to efficiently identify planning priorities to improve readiness and resiliency for the COVID-19 response and future challenges using a One Health approach.

### Keeping Pace: How to Evolve Training Development and Delivery in an Ever-changing Response

K. Singler, **E. Davenport**, V. Terrell, S. Robinson, M. Hoppe
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** The COVID-19 pandemic changed most facets of our lives, including how we train our public health workforce. Staff from CDC's Quarantine and Border Health Services Branch (QBHSB) were the first to respond to COVID-19 at US ports of entry. Within months, QBHSB's mission *and* size expanded—from approximately 150 to 700 staff. However, its training team remained small (n=3-5), requiring shifts in training methods to meet these increased needs. **Methods:** To match the urgency of the pandemic response, QBHSB's training team transformed staff trainings from eLearning modules—each taking months to create—to multi-modality instruction that could be developed in days. New trainings included a live webinar (which was recorded), job aids, practice scenarios, and a required quiz. Training team members rotated development, clearance, delivery, and evaluation roles. Live remote trainings reached staff across seven time zones and three shifts. Targeted trainings and Q&A sessions boosted staff confidence. As processes changed—sometimes multiple times a day—training kept pace. In-training knowledge checks gauged staff's understanding of changes, and a "Bottom Line Up Front" daily newsletter reiterated current guidance. All training materials were emailed to staff and posted to an internal site for quick reference on phones or laptops. **Results:** From January 2020-September 2021, QBHSB's training team delivered approximately 150 live response trainings and sent 185 editions of their newsletter to over 1000 branch staff and deployers. While the pace of the early response impeded the team's ability to conduct adequate needs assessments and evaluations, later trainings embraced each of CDC's Quality Training Standards. Trainings were well attended (>80% targeted staff participation) and understood (>85% in-training and post-training scores), and the new multi-modality format is now the QBHSB training standard. **Conclusions:** Large-scale workforces who must juggle attending essential trainings with the urgent demands of emergency response need guidance that is as dynamic as their jobs. By choosing modalities that can be quickly developed, altered, delivered, and evaluated, small training teams can keep pace with constantly shifting response protocols while not sacrificing training quality.

### Learning from the Field for Better Emergency Preparedness: The WHO Compilation of Innovative Science Communication Concepts

**R. Ludolph,** S. Rahmatullah, J. Van Holten, T. Nguyen, S. Briand
Global Infectious Hazard Preparedness Department, World Health Organization, Geneva, Switzerland

**Background:** Translating science into messages, recommendations and actions that are easily comprehensible, accessible, and relevant to different audiences is a vital element of health emergency preparedness. In April 2021, WHO launched a global call for innovative science communication solutions to develop a good practice compilation fostering international exchange and scale up of initiatives. The analysis of existing field initiatives further contributes to the qualitative evidence base for an upcoming science translation manual. **Methods:** Cases were analyzed using a semi-structured online questionnaire. Besides evaluating formal information on initiator, funding and country of implementation, the assessment focused on (i) innovation factor, (ii) accuracy of scientific information, (iii) impact on knowledge, attitude, and behavior of the target audience, and the (iv) promotion of gender equality, equity and human rights through the initiative. Each category was operationalized through several indicators and rated independently by two reviewers. Besides, thematic analysis was applied. **Results:** The call received 78 submissions from 21 countries, mostly the USA, UK, Germany, and Brazil. 18 submissions described initiatives led by researchers, 22 by media and 38 by civil society representatives. 23 cases were excluded due to poor-quality scoring. Thematic analysis showed that the COVID-19 pandemic has motivated an unprecedented number of individuals and small groups to actively engage as science communicators on social media. While many of these actors produced creative and accurate content, they often struggled to reach a larger audience due to limited resources. Science communication concepts initiated in a more

institutionalized setting such as a university or non-governmental organization had a larger reach and focused on concepts including train-the-trainers, serious games, and artistic science communication. Most grass-root initiatives had a strong equity lens, specifically targeting minority groups. **Discussion:** Learning from grass-root initiatives through a systematic analysis as opposed to peer-reviewed evidence only will allow for a better understanding of what works and why in science translation across different contexts and inform future pandemic preparedness activities.

### Enabling Factors and Barriers to the Success and Sustainability of National Public Health Institutes in Seven Countries

M.A. Woldetsadik[1], **S. Bratton**[1], K. Fitzpatrick[1], F. Ravat[1], L.D. Castillo[2], K. McIntosh[1], D. Jarvis[1], C.R. Carnevale[1], C.H. Cassell[1], C. Chhea[3], F. Prieto[4], J. MaCauley[5], I. Jani[6], E. Ilori[7], S. Nsanzimana[8], V. Mukonka[9], H.C. Baggett[1]
[1]Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]RTI International, Durham, NC, USA, [3]Cambodia National Institute of Public Health, Phnom Penh, Cambodia, [4]Instituto Nacional de Salud, Bogotá, Colombia, [5]National Public Health Institute of Liberia, Monrovia, Liberia, [6]Instituto Nacional de Saúde, Maputo, Mozambique, [7]Nigeria Center for Disease Control, Abuja, Nigeria, [8]Rwanda Biomedical Center, Kigali, Rwanda, [9]Zambia National Public Health Institute, Lusaka, Zambia
**Background:** The success of national public health institutes (NPHIs) in low- and middle-income countries is critical to countries' ability to deliver public health services to their populations and effectively respond to public health emergencies. However, empirical data are limited on factors that promote or are barriers to the sustainability of NPHIs. **Methods:** This qualitative evaluation explores stakeholders' perceptions about enabling factors and barriers to the success and sustainability of NPHIs in seven countries where the US Centers for Disease Control and Prevention (CDC) has supported NPHI development and strengthening. We interviewed a total of 96 stakeholders, including NPHI staff (N=43), non-NPHI government staff (N=29), and non-governmental and international organization staff (N=24) in Cambodia, Colombia, Liberia, Mozambique, Nigeria, Rwanda, and Zambia. **Results:** Participants identified five enabling factors critical to the success and sustainability of NPHIs: (1) strong leadership, (2) financial autonomy, (3) political commitment and country ownership, (4) strengthening capacity of NPHI staff and (5) forming strategic partnerships. Three themes emerged related to major barriers or threats to the sustainability of NPHIs: 1) reliance on partner funding to maintain key activities, 2) changes in NPHI leadership and 3) staff attrition and turnover. **Conclusions:** Our findings contribute to the scant literature on sustainability of NPHIs by identifying essential components of sustainability and types of support needed from various stakeholders. Integrating these components into each step of NPHI development and ensuring sufficient support will be critical to strengthening public health systems and safeguarding their continuity. As next steps, countries' leadership might consider the potential implications of our findings and determine what may work best for their situation.

## E2. Laboratory Diagnostics and Systems

### 3:15 PM – 4:45 PM

### Centennial Ballroom II

### Phylogenetic Characterization of Hantavirus Pulmonary Syndrome Cases in Bolivia, 2018-2019

R.L. Mafayle[1], C. Romero[2], S. Whitmer[3], M. Morales-Betoulle[3], C.M. Cossaboom[3], J. Dyal[3], J.C.A. Ardaya[1], J.R. Guzmán[1], **N.M. Loayza**[1], J. Mendez-Rico[4], J. Graziano[3], E. Talundzic[3], K. Patel[3], M. Choi[3], S.T. Nichol[3], C.F. Spiropoulou[3], T. Shoemaker[3], J. Klena[3], J.M. Montgomery[3]
[1]Centro Nacional de Enfermedades Tropicales, Santa Cruz de la Sierra, Bolivia, [2]Unidad de Epidemiología, Ministerio de Salud, La Paz, Bolivia, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Pan American Health Organization, Washington, DC, USA
**Background:** Hantavirus pulmonary syndrome (HPS) has been reported in Bolivia since 1997, primarily among high-risk groups including agricultural workers and soldiers. However, it is likely underdiagnosed due to lack of awareness and testing in endemic agricultural areas. Although the primary transmission route is inhalation of infected rodent excreta, human-to-human transmission of one hantavirus, Andes virus, is documented. We report clinical and phylogenetic characteristics of 2018 – 2019 HPS cases in Bolivia. **Methods:** Serum specimens from January 2018 – June 2019 were submitted to the Bolivian National Center for Tropical Diseases via the national hantavirus surveillance system. Specimens were tested by commercial enzyme-linked immunosorbent assay (ELISA). Positive samples from 24 patients were shipped to CDC for confirmation using CDC's ELISA, reverse-transcriptase polymerase chain reaction (RT-PCR), next generation sequencing, and phylogenetic analysis. **Results:**

Hantavirus RNA was identified by RT-PCR. Of 14 patients with available clinical data, 10 (71%) presented between January and April 2019. Median age was 36 years (range 17-71); 13 (93%) were male; 9 (64%) were from Chapare or Aniceto Arce Provinces; and 6 (43%) were agricultural workers. Symptoms included fever (14/14), gastrointestinal (12/14), and respiratory complaints (11/14). IgM and IgG antibodies were identified in 12 (86%) and 7 (15%) of the 14 patients, respectively. Sequencing provided preliminary identification of hantaviruses from 17 patients as Oran (7/17), Tunari-like (6/17), Alto Paraguay-like (2/17), Laguna Negra (2/17), and Lechiguanas-like (1/17) from various geographic locations in Bolivia. **Conclusions:** Despite clinical severity and wide geographic distribution, HPS in Bolivia is likely underreported. We report 24 confirmed cases between 2018-2019. Sequencing revealed at least 5 unique species of hantavirus. Of note, Oran, Tunari, Laguna Negra and Lechinguanas viruses are closely related to Andes virus and may have human-to-human transmission potential; however, we cannot confirm this in the cases reported herein due to a lack of epidemiologic data. Continuing reinforcement of surveillance and diagnostic capacity is critical for rapid case identification, isolation, and investigation.

### Quantitative Measurement of Antibiotic Resistance in *Mycobacterium tuberculosis* Reveals Genetic Determinants of Resistance and Susceptibility in a Target Gene Approach

**JJ Carter**, The CRyPTIC Consortium
Stanford University, Stanford, CA, USA
**Background:** The World Health Organization has a goal of universal drug susceptibility testing for patients with tuberculosis; however, molecular diagnostics to date have focused largely on first-line drugs and always on predicting binary susceptibilities. **Methods:** We used a multivariable linear mixed model alongside whole genome sequencing and a quantitative microtiter plate assay to relate genomic mutations in a target gene panel to minimum inhibitory concentration in 15,211 *Mycobacterium tuberculosis* patient isolates from 27 countries across five continents. Where possible, we calculate homoplasy and map mutations to available protein structures to verify our results. **Results:** We identified 449 unique MIC-elevating variants across thirteen drugs after correction for multiple testing, as well as 91 mutations resulting in hypersensitivity. Our results also reveal differential effects of mutations between drugs of the same class such as rifampicin and rifabutin or the fluoroquinolones. Finally, we also identify genetic signatures of epistasis for the aminoglycosides, clofazimine and bedaquiline that cause reversion of resistant isolates to a susceptible state. **Conclusions:** Our results advance genetics-based diagnostics for tuberculosis and serve as a training set for drug resistance prediction algorithms. In addition, they can serve as a guide for further development of trials for use of high-dose drug regimens to treat tuberculosis.

### Inflammatory Biomarkers of Chronic Disease associated with Chronic Viruses: Evidence from the NHANES Study

S. Banerjee, R. Panas
Walden University; Minneapolis, MN, USA
**Background:** Chronic viruses are known to be associated with cardiovascular disease (CVD) due to medication side effects and pathophysiological burden of the virus. However, in this retrospective cross-sectional analysis the hypothesis was tested if inflammatory biomarkers are associated with cardiovascular disease (CVD) in those with chronic viral infections. High sensitivity C-reactive protein (hs-CRP) is a tangible and under-recognized biomarker that can signal health care practitioners about the eminent risk of CVD. **Methods:** The National Health and Nutrition Examination Survey (NHANES) is a cross sectional survey done on the non-institutionalized population of the United States by the Center for Disease Control and Prevention and National Center for Health Statistics. All patients from the nationally representative NHANES study, 20 years and older with HIV, Hepatitis B, or Hepatitis C between the years 1999-2010 were included in the analysis. Due to the complex sampling design, sample weights were utilized in order to analyze the data. Comparisons were analyzed using Pearson's Chi Square, simple, and multivariable logistic regression to determine the relationship of hs-CRP and chronic viruses. All missing variables were excluded. **Results:** Data on at least one viral infection was available for 470 individuals (64.7% males & 35.3% females) who met the criteria of having chronic viruses and was representative of 2,737,489 individuals. Out of those with known viral status, 19.3% had HIV mono-infection, 23.6% had hepatitis B mono-infection, 55.3% had Hepatitis C mono-infection, and 1.9% had co-infection. Elevated hs-CRP (>2 mg/dL vs. <1 mg/dL) was associated with CVD in unadjusted analyses (OR = 7.44, 95% CI: 2.42, 22.87, $p < .001$) among individuals with chronic virus; the association remained strong (OR = 9.04, 95% CI: 2.50, 32.66, $p < .001$) after the results were controlled for current infection and CVD risk factors (e.g., diabetes status and hypertension). **Conclusions:** We found a consistent and significant relationship between high hs-CRP levels and patients with CVD, among patients with chronic viruses. Consequently, hs-CRP may be used as an effective prognostic biomarker to predict the occurrence of CVD

before it proves fatal for the patient, in this subpopulation. More longitudinal studies need to be done to understand the role of other inflammatory markers and how anti-inflammatory agents may prevent CVD.

### Unprecedented Approach in Unprecedented Times

C. Rothenbacher, **L. Liu**
Indiana Department of Health, Indianapolis, IN, USA
**Background:** In mid-March 2020, the Indiana Department of Health (IDOH) Laboratory (IDOHL) had limited capacity for SARS-CoV-2 testing due to lack of a high throughput nucleic acid extraction platform and reagents/supplies. Despite a sophisticated web-based electronic ordering and reporting system, LimsNet, IDOHL couldn't keep up with the testing demand in Indiana. **Methods:** IDOHL collaborated with a private partner that had high testing capacity but no ordering and reporting capability to form a hybrid system: All test orders were submitted through LimsNet via a rapidly developed Application Programming Interface. The partner laboratory received orders and transmitted results to submitters through LimsNet. This same model was soon expanded to nine other laboratories that joined IDOH's laboratory testing network (LTN). IDOHL served as the orders/reports datahub and created a program that allocated testing orders in real time based on each LTN Laboratory's capacity and locations of specimen collection sites. The model was further enhanced via integration of a third-party system that provided test scheduling, ordering, and reporting directly to patients. **Results:** The hybrid system went live three days after conception of the idea. The data network expanded to 11 laboratories total, allowed IDOH to rapidly expand testing capacity from 30 specimens to a peak of more than 10,000 per day. The LTN laboratories have tested 757,870 specimens in the pandemic response. The integration of the third-party system eliminated the data entry burden by staff at collection sites and shortened the time taken to receive results by patients. **Conclusions:** An innovative approach that combined a nimble IT infrastructure and laboratory testing capacity from private partners eliminated the need for a potential army of data entry staff and enabled IDOH to scale up and meet the state's pandemic testing needs months earlier than otherwise could have been achieved.

### Modeling Interactive Effects of the World Health Organization Joint External Evaluation Laboratory Specimen Referral and Transport Indicator in 17 Countries

**J. Barker**[1,2], C.H. Cassell[1], S. Shah[3,4], C. Blanton[1]
[1]Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Associated Universities, Oak Ridge, TN, USA, [3]Department of Epidemiology, Rollins School of Public Health, Emory University, Atlanta, GA, USA, [4]Hubert Department of Global Health, Rollins School of Public Health, Emory University, Atlanta, GA, USA
**Background:** Strengthening a country's public health system, including surveillance and national laboratory systems, is pivotal to creating a healthier and safer environment by detecting infectious disease threats at their source and preventing them from spreading to other countries and becoming pandemics. Within a nation's laboratory system, the presence of a specimen referral and transport system plays a principal role in the rapid detection and diagnosis of diseases. The study explores the extent to which this laboratory indicator interacts with other World Health Organization (WHO) Joint External Evaluation (JEE) indicators. **Methods:** This study examined the relationship between the laboratory specimen referral and transport JEE indicator (outcome variable) and other JEE indicators across seven technical areas of the WHO JEE Tool version 1.0 in 17 countries between October 2016 and September 2019. These technical areas included biosafety and biosecurity, national laboratory systems, real-time surveillance, reporting, emergency response operations, and workforce development. Countries included were Bangladesh, Burkina Faso, Cameroon, Cote d'Ivoire, Ethiopia, Guinea, India, Indonesia, Kenya, Liberia, Mali, Pakistan, Senegal, Sierra Leone, Tanzania, Uganda, and Vietnam. Data were collected from US Government interagency progress reports that are used to assess a country's capacity in several technical areas. Descriptive and multivariate models were assessed using linear regression. After obtaining a final multivariate model, collinearity and interaction assessments also were analyzed. **Results:** Our results showed that two indicators, (1) effective modern point of care and (2) laboratory-based diagnostics and reporting network and protocols in a country, were significantly associated with the laboratory specimen referral and transport indicator, p=0.05 and 0.04, respectively. The interaction assessments yielded non-statistically significant results (p-value=0.19). **Conclusions:** Our findings can help countries make better informed decisions on resource allocation by understanding the interactive effects and relationships between JEE indicators within various technical areas.

### Creating a Network of Global Laboratory Leaders: A Multisectoral Collaboration to Build Laboratory Capacity and Advance Global Health Security

**A. Albetkova**[1], V. Kumar[1], T. Puente[1], J. Isadore[2], S. Musumeci[2], S. Emery[2], V. Dolmazon[3], P. Gomez[3], J. Lasley[4], A. Jasir[5], L. Wiersma[6]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Association of Public Health Laboratories, Silver Spring, MD, USA, [3]World Health Organization, Lyon, France, [4]World Organisation for Animal Health, Paris, France, [5]European Centre for Disease Prevention and Control, Solna, Sweden, [6]Food and Agriculture Organization of the United Nations, Rome, Italy
**Background:** Effective and sustainable national laboratory systems, governed by well-trained laboratory leaders, are needed to safely, accurately, and quickly identify and respond to public health emergencies. Staff working in health laboratories are essential to ensure national and global health security. Disease outbreaks, such as the COVID-19 pandemic, have exposed the need for specialized training to strengthen laboratory leaders. **Methods:** Recognizing this need, six global partners – the Association of Public Health Laboratories (APHL), the Centers for Disease Control and Prevention (CDC), the European Centre for Disease Control and Prevention (ECDC), the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (OIE), and the World Health Organization (WHO) – collaborated to develop the Global Laboratory Leadership Programme (GLLP). The GLLP partners mobilized over 140 international subject matter experts to develop and review the program's Learning Package, which is rooted in the nine competencies outlined in the Laboratory Leadership Competency Framework. The Learning Package provides the materials needed to implement GLLP in any country around the world. It covers 43 subject areas and includes guides for mentors, instructors, and participants. **Results:** GLLP combines didactic learning, hands-on experience supported by mentorship, and a community of practice to facilitate continued peer-to-peer learning and to support laboratory systems strengthening. GLLP can be implemented virtually or in-person and can be adapted to the needs of each individual country. In-country validations began in Pakistan and Liberia in 2019, and there are currently 17 GLLP country programs in progress at various stages utilizing the Learning Package materials. **Conclusion:** The completion of the Learning Package allows for program implementation, creating a network of trained laboratory leaders across the globe, sharing common standards and strengthening collaboration across health sectors. Implementing GLLP furthers the program's mission of providing tools to develop laboratory leadership competencies and advance national laboratory systems for improved health security, using a One Health approach.

## E3. COVID-19 and SARS-CoV-2

### 3:15 PM – 4:45 PM

### Centennial Ballroom III

### Investigation of a COVID-19 Cluster in Achwa Hydroelectric Power Plant, Pader District, Uganda -- October 2020

**J. Namayanja**, I. Wadunde, E. Katana, L. Bulage
Uganda Ministry of Health, Kampala, Uganda
**Background:** Achwa Hydroelectric Power Plant (AHPP) in Pader District, Uganda introduced multiple measures starting in April 2020 to reduce the risk of COVID-19 introduction and spread. These included testing of visitors and returnees to the plant for COVID-19 on arrival, enforcement of regular hand washing, face mask use and social distancing. Despite these measures, on October 3, 2020, a cluster of COVID-19 cases was reported at AHPP. We investigated to identify factors facilitating spread of COVID-19 and recommend control measures. **Methods:** A confirmed case was a positive RT-PCR for SARS-CoV-2 in a person who lived, worked at, or visited AHPP from August 1-October 5, 2020. We reviewed routine COVID-19 test results from medical records at AHPP and actively searched for cases to develop the line list. We performed environmental assessment and conducted a retrospective cohort study to identify risk factors for transmission. **Results:** We identified 105 case-persons residing in 6 work camps at AHPP (overall attack rate (AR)=20%); mean age was 32 years (range, 18-60 years). The index case-person delivered supplies to the plant from Kampala and left after his sample had been taken on August 10; his positive test result was returned on August 17. The second case-patient was a plant employee who had travelled to Gulu City 10 days before his sample was collected on August 18 and tested positive on August 25. One camp, Alnour camp, was both the most congested, with all workers sharing a single dining area, and the most affected (AR=61%) of the 6 camps. Risk was higher among persons sleeping >2 per room (aRR=2.4, 95%CI=1.5-4.1) than those who slept ≤2 per room. **Conclusion:** Long test turnaround time for the index case and crowded employee sleeping and living conditions facilitated the spread of COVID-19 at AHPP. We recommended decongesting sleeping areas at the station and continued surveillance for early detection and management of infections.

### Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Transmission in Georgia, USA, February 1–July 13, 2020

**Y. Wang**[1], C. Siesel[1], Y. Chen[1], B. Lopman[1], C. Adams[1], M. Lau[1], P.F.M. Teunis[1], L. Edison[2,3], M. Thomas[3]
[1]Rollins School of Public Health at Emory University, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Georgia Department of Public Health, Atlanta, GA, USA
**Background:** Beginning in early February 2020, coronavirus disease (COVID-19), caused by transmission of SARS-CoV-2, spread across the state of Georgia, United States, leading to 118,225 cumulative cases as of July 13, 2020. To better understand the COVID-19 transmission patterns in Georgia, we examined key measures for COVID-19 transmission: serial interval (time between symptom onsets in a primary and secondary case-patient pair) and effective reproduction number (average number of secondary cases per primary case at specific time) by region and period. **Method:** During February 1–July 13, 2020, we identified 4,080 pairs of primary case-patient (index case-patient) and secondary case-patient (infected by the primary case-patient) in Georgia, by using contact tracing data from COVID-19 cases reported to the Georgia Department of Public Health. We examined how transmission characteristics were affected by age and period (during shelter-in-place in April 2020 and after subsequent reopening in May–July 2020) and estimated the time course of reproduction numbers for all 159 Georgia counties. Temporal and spatial patterns of COVID-19 transmission were examined. **Results:** The mean serial interval decreased from 5.97 days in February–April to 4.40 days in June–July. Adults aged 20–50 years were involved in most transmission events occurring since reopening on April 30th, 2020. During February–mid-July 2020, two waves of COVID-19 transmission were apparent, separated by the shelter-in-place period in April in Georgia. Counties around major cities and along interstate highways had decreasing but consistent spreading during the shelter-in-place period. **Conclusions:** COVID-19 transmission in Georgia varied by area and time period. The increase after reopening indicated that the shelter-in-place period may not have been long enough to prevent sustained virus transmission in densely populated urban areas. Studying local transmission patterns may help in predicting and guiding states in preventing and controlling COVID-19 according to population and region.

### SARS-CoV-2 Infection, Severity, and Reinfection within a Prospective Pediatric Cohort in Managua, Nicaragua

**J.T. Kubale**[1], A. Balmaseda[2,3], N. Sanchez[3,4], M. Plazaola[3], A.M. Frutos[1], S. Ojeda[3,4], S. Saborio[2,3], R. Lopez[2,3], C.C. Cruz[2,3], M. Chowdhury[1], E. Harris[5], G .Kuan[3,4], A. Gordon[1]
[1]Department of Epidemiology, University of Michigan School of Public Health, Ann Arbor, MI, USA, [2]Centro Nacional de Diagnóstico y Referencia, Ministry of Health, Managua, Nicaragua, [3]Sustainable Sciences Institute, Managua, Nicaragua, [4]Centro de Salud Sócrates Flores Vivas, Ministry of Health, Managua, Nicaragua, [5]Division of Infectious Diseases and Vaccinology, School of Public Health, University of California, Berkeley, Berkeley, CA, USA
**Background**: The SARS-CoV-2 pandemic has led to substantial morbidity and mortality worldwide; however, its impact on children remains less clear. We assessed the incidence, severity, and protection from symptomatic re-infection with SARS-CoV-2 among children aged 0-14 years in the Nicaraguan Pediatric Influenza Cohort Study. **Methods**: Respiratory samples were collected from participants at the study clinic and tested for SARS-CoV-2 via RT-PCR. Blood samples were collected in March 2020 and February/March 2021 and tested for antibodies against SARS-CoV-2 receptor binding domain (RBD) by ELISA. RT-PCR positive samples collected >59 days apart from the same individual were considered distinct episodes, and PCR positives occurring in ELISA positive participants were considered re-infections. Incidence rates were calculated using a Poisson distribution, and protection from re-infection was calculated using a Binomial model. **Results**: Between March 1, 2020, and October 1, 2021, 1942 children participated in the study. Transmission occurred in Nicaragua throughout the study period, but largely during two waves occurring from April-July 2020 and April-September 2021. Overall, 52.7% of children tested were seropositive by April 2021, early in the second wave. There were 188 PCR-confirmed episodes of SARS-CoV-2, 12 (6.4%) of which were severe enough to require hospitalization. Incidence of PCR-positive SARS-CoV-2 was highest among children aged <2 years—15.4 (95% Confidence Interval [CI]: 12.0, 19.8) per 100 person-years. This was approximately three times that of children in any other age group assessed (2-4, 5-9, and 10-14 years). Additionally, 46 (24.5%) SARS-CoV-2 episodes were re-infections, with younger children appearing to have the lowest protection from symptomatic reinfection. Among children aged <5 years, protection (beyond April 2021) was 39% (Odds Ratio [OR]: 0.61, 95% CI: 0.3-1.1), while protection among children aged 5-9 and 10-14 years was 59% (OR: 0.4, 0.2-0.8) and 60% (OR: 0.4, 0.2-0.7), respectively. **Conclusions**: Rates of symptomatic and severe SARS-CoV-2 were highest among the youngest participants, with rates stabilizing at age 5. Reinfections were also relatively common, particularly among children aged <5 years, representing nearly a quarter of all PCR-confirmed infections.

### Regional Differences in COVID-19 Population Testing Rates in Ethiopia

**S.A. Abayneh**[1], D. Habte[1], B.E. Seid[1], E.B. Tadesse[2], G. Teka[2], D. Sugerman[1]
[1]US Centers for Disease Control and Prevention, Addis Ababa, Ethiopia, [2]Ethiopian Public Health Institute, Addis Ababa, Ethiopia

**Background: F**rom March 2020, Ethiopia continuously reported COVID-19 cases from 10 regions and 2 city administrations. We present the country -wide temporal and spatial patterns of COVID-19 testing and confirmed cases from March 13-September 7, 2021. **Methods:** We calculate testing patterns and disease burden from COVID-19 surveillance data reported from all regions. Population testing rates per 100,000 people over 28 days per region were continuously calculated to assess the adequacy of testing for surveillance. As per WHO guidelines, A test-to-case ratio of less than 10 tests per case might indicate restrictive testing. The regional testing rate were used in interpreting the epidemiologic curve. **Result:** A total of 3,284,610 COVID-19 tests were performed. The COVID -19 testing per 100,000 population was higher for urban regions: 45,575 for Addis Ababa; 20,455 for Harari and 6,698 for Dire Dawa. The testing rate in these three regions was adequate to estimate incidence, however, these regions cover only 4.5% of the country's 103,005,158 population. The testing rate for other regions was generally low and could be characterized as inadequate for calculating incidence: 833 for Oromia, 1,147 for Amhara, and 1182 for South Region. Of note, these three regions account for 76% of the population in the country. The national COVID-19 epi-curve shows three waves: Sept-Oct 2020; April-May 2021; August 2021. 316,177 COVID-19 cases were reported with an average positivity rate of 9.6%. Introduction of new SARS-CoV2 were attributed for the two of three waves in Ethiopia: alpha and beta for the second wave , and Delta variant for the third wave. **Conclusions:** Most of the COVID-19 testing and cases were reported from the three most urbanized regions in Ethiopia. The low level of testing rate in other regions may hide localized epidemics. Strategic population testing is needed to estimate the disease burden.

### Strategies To Maximize COVID-19 Immunization Coverage among the General Population

**D.G. Smith**[1], J.A. Vanchiere[1], M. Whyte[2], K. Murnane[1], A.D. Yurochko[1], M.A.N. Bhuiyan[1], J. Kamil[1], J. Rush[1], R. Scott[1], M. Barclay[1], C. Kevil[1]
[1]Louisiana State University Health Shreveport, Shreveport, LA, USA, [2]Louisiana Department of Health, Shreveport, LA, USA

Vaccination is key to ending the COVID-19 pandemic worldwide. However, specific strategies are needed to increase the acceptance of the vaccine in the general population in the United States. In September of 2021, the Centers for Diseases Control and Prevention (CDC) reported that 54% of the United States population were fully vaccinated. As of that date, 50.6% of the population had received at least one dose of the vaccine in Louisiana. Our study aims to describe how Louisiana State University Health Shreveport (LSUHS) distributed and administered vaccines during the COVID-19 pandemic and make recommendations to increase the public's response to vaccinations now and in the future. In March of 2020, LSUHS established the Center of Excellence for Emerging Viral Threats (CEEVT) to address the COVID-19 pandemic needs in Northwest Louisiana. As of September of 2021, the LSUHS vaccine team administered 90,655 vaccines among the general population in urban and rural areas of Northwest Louisiana. Among the population who received at least the first dose of the vaccine, 57% were female and 43% male. The majority, 46%, were over 60 years of age. Regarding race, 56% were Caucasian, and 39% were African American. Although vaccine hesitancy nationally is much higher among black than white Americans, our results suggest that the LSUHS conducted a targeted outreach effort that yielded greater African American COVID-19 vaccine uptake. Our study showed that the Center of Excellence for Emerging Viral Threats had a considerable impact on vaccinating the community in Northwest Louisiana. Dissemination of the policies and procedures shown from our experiences for mass vaccination can assist other states and public health institutions in developing their respective strategies to maximize immunization coverage and improve vaccination efforts in future pandemics. We also believe that sharing best practices in vaccination delivery is essential to achieve population health during health emergencies.

### Non-Physician Medical Worker Stress and SARS CoV-2 Infection Prevention

**W.L. Mahony**[1], L.J. Hirth[1,2], R. Rupp[1], S. Gonzalez[2], R. Zoorob[2]
[1]University of Texas Medical Branch, Galveston, TX, USA, [2]Baylor College of Medicine, Houston, TX, USA

**Background:** The impact of the COVID-19 pandemic on physician mental health is well understood. However, less is known about the pandemic-related stress for other types of healthcare workers, such as medical assistants. Training related to prevention of SARS CoV-2 infection may play a role in stress levels, but it may not have been as rigorous for other health professionals as for physicians. The aim of this study was to examine associations of infection prevention training with perceived stress and examine COVID vaccination rates. **Methods:** A 91-item

online survey was advertised January 2, 2021-September 1, 2021, to US healthcare workers, including physician assistants, nurses, and medical assistants (MAs) through social media. It consisted of demographics, questions about employment and perceived stress (Perceived Stress Scale, PSS). PSS items were combined for a total, continuous score which was then categorized according to stress severity (score ≥27=high perceived stress). Unpaired t-tests were performed for statistical analyses of quantitative variables. **Results:** Of 300 participants who consented to take the survey, 230 participants completed it. Seventy-nine percent of the sample were MAs and 15% were nurses. In this sample, 92% had high perceived stress. Those who highly rated their understanding of protocols related to preventing transmission of the SARS-CoV-2 virus were less likely to have high perceived stress compared to those who reported lower understanding (XX% vs. XX%, respectively, $p < .01$). Of 219 participants who reported their vaccination status, 82% were vaccinated and 2% planned to get vaccinated. Six percent of unvaccinated workers would consider vaccination with employer mandates and 2% would consider it if additional information about the vaccine was provided to them. **Conclusions:** Non-physician healthcare workers reported a high level of stress, overall. Increasing information on how to prevent the transmission of the SARS-CoV-2 virus may improve healthcare worker mental health by reducing stress. Employer mandates combined with providing additional information about the vaccine could increase healthcare worker vaccination rates from 84% to 92%. Further infection safety training is needed among MAs, which could potentially reduce stress and increase retention.

## E4. Late-breakers I: Vaccine-preventable Diseases, Vaccines, and Therapeutics

**3:15 PM – 4:45 PM**

**Centennial Ballroom IV**

### Public Health Actions to Address Measles in Recently Evacuated Afghans through Operation Allies Welcome: September–October 2021

**N.B. Masters**, A. Mathis, K. Raines, S. Crooke, B. Bankamp, P. Rota, D. Sugerman, F. Alvarado-Ramy, L. Rotz, M. Bell, L. Talley, P. Gastanaduy
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** From August 29–November 1, 2021, 70,256 evacuees from Afghanistan were brought to the United States via Operation Allies Welcome (OAW). Evacuees were transported from seven overseas locations to eight U.S. military bases and two hotels. Following identification of measles among several evacuees and given ~64% coverage with one dose measles-containing vaccine and an ongoing measles outbreak in Afghanistan, CDC recommended a pause of incoming flights, mass vaccination of evacuees aged ≥6 months without a known contraindication at domestic and overseas locations, and a 21-day quarantine after vaccination. We characterized cases, identified transmission patterns, and assessed outbreak control measures. **Methods:** We conducted measles case and contact investigations. A case was defined as acute febrile rash illness and laboratory confirmation of measles or epidemiologic link to a laboratory-confirmed case. Measles genotyping was performed at vaccine-preventable disease reference centers and CDC. **Results:** Forty-seven measles cases (attack rate: 0.67/1,000 evacuees) were reported across five bases and one hotel in four jurisdictions (22 in Virginia, 22 in Wisconsin, 2 in New Mexico, 1 in New Jersey); rash onsets ranged from September 2–October 15. The median case-patient age was 1 year (range 0–26 years); all case-patients were unvaccinated or had unknown vaccination status. Thirty-seven sequenced specimens were genotype B3, consistent with genotypes detected in Afghanistan. Six separate transmission chains were identified (size: 1–22 cases, duration: 0–2 generations). Vaccination campaigns reached 99% coverage among eligible evacuees; before and after completion of mass vaccination, 0% (0/25) and 22.7% (5/22) of case-patients were aged <6 months, respectively. Twenty vaccinees developed measles after vaccination, with rash onsets 0–15 days following vaccination (median: 8 days). No community spread or fatalities were identified, and there were no additional measles importations following resumption of flights on October 5 from overseas locations. **Conclusions:** During OAW, rapid containment, a high-coverage vaccination campaign, and a 21-day post-vaccination quarantine reduced measles importation and spread among evacuees and prevented introduction into U.S. communities.

### Progress of Clinical Development of a Live-Attenuated Single Shot Chikungunya Vaccine Candidate

**M. Schneider,** R. McMahon, S. Hadl, M. Narciso, S. Toepfer, U. Fuchs, R. Hochreiter, A. Bitzer, K. Kosulin, R. Mader, O. Zoihsl, K. Dubischar, N. Wressnigg, S. Eder-Lingelbach, J.C. Jaramillo, V. Buerger
Valneva Austria GmbH, Vienna, Austria

VLA1553 is a live-attenuated chikungunya virus (CHIKV) vaccine candidate designed for active immunization as a prophylactic measure. Due to the sporadic epidemic occurrence of chikungunya, an immunological surrogate to assess clinical efficacy was accepted by regulators. A blinded, randomized phase 1 clinical trial evaluated the safety and immunogenicity of three dose levels of VLA1553, administered as a single intramuscular immunization in 120 participants (NCT03382964). This was followed by a pivotal phase 3 double-blinded, multicentre randomized trial that enrolled 4,115 adults to receive the selected final VLA1553 dose or placebo (NCT04546724). A further phase 3 trial evaluated bioequivalence between three lots of VLA1553 in 408 healthy adults randomized to each lot 1:1:1 (NCT04786444). Safety and immunogenicity data was collected for 29 days post vaccination in both trials. In phase 1 clinical trial a single-shot of VLA1553 was well tolerated and highly immunogenic in an adult population. Participants were protected from vaccine-induced viremia upon re-vaccination. The first pivotal trial met its primary endpoint with 98.9% of subjects achieving seroprotection (263 of 266 participants in the per-protocol immunogenicity subgroup, 95% CI: 96.7-99.8). The bioequivalence study showed no significant differences between lots with regard antibody titres. VLA1553 was also highly immunogenic as seroprotection was achieved in 97.5% of participants. VLA1553 was also well tolerated with a favourable safety profile across phase 3 trials. The generation of protective titers in nearly 100% of vaccinated participants analyzed indicates VLA1553 is an effective candidate for the prevention of disease caused by the CHIKV.

### Behavioral and Social Drivers of COVID-19 Vaccine Demand and Uptake in Kampala and Wakiso Districts, Uganda: A Mixed-methods Assessment

N. Ryan[1], S. Miller[2], S. Biraro[3], M. Lahuerta[2,4], M. Farahani[2], P. Bakkabulindi[3], T. Tindyebwa[3], D. Prybylski[1], L. Nelson[5], A. Boore[5], F. Banage[5], **S. Kulkarni**[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]ICAP at Columbia University, New York, NY, USA,[3]ICAP, Kampala, Uganda, [4]Department of Epidemiology, Mailman School of Public Health, Columbia University, New York, NY, USA, [5]U.S. Centers for Disease Control and Prevention, Kampala, Uganda
**Background:** A persistent challenge of the COVID-19 vaccine rollout in many contexts has been its low acceptance among the public. Understanding the behavioral and social drivers of vaccine demand is important to inform targeted strategies to increase vaccine uptake. As part of a broader assessment to understand the effect of the pandemic on childhood, we examined social, behavioral, and access-related issues of COVID-19 vaccine demand and uptake among health care workers (HCW) and caregivers of young children in Kampala and Wakiso districts with high COVID-19 burden in Uganda. **Methods:** This mixed-methods study consisted of a cross-sectional household survey, with two-stage stratified cluster sampling of 456 caregivers of children aged 6-35 months; 18 key informant interviews (KII) with HCW and health managers; and six focus groups discussions (FGD) with caregivers of young children in November-December 2021. Survey data were analyzed to obtain weighted descriptive statistics, and key themes were identified from the qualitative data. Results from the survey and qualitative inquiry were reviewed to identify common findings across data sources. **Results:** One third of caregivers received at least one dose of a COVID-19 vaccine, with significantly greater uptake in Kampala (44%) than Wakiso (27%). Among unvaccinated caregivers (67%), 77% were willing and 23% were unwilling to get vaccinated or unsure about vaccination in the future. Among those unwilling or unsure, 69% reported lack of trust in the vaccine and 52% had concerns about vaccine side effects. Among vaccinated caregivers, 80% reported getting vaccinated to protect their health, and 31% reported issues such as long distances to and waiting times at vaccination sites. Among all caregivers, friends or family (79%) and social media (29%) were major sources of misinformation but most caregivers were likely to follow vaccine information from HCW (82%). Themes from KII and FGD — fear of vaccine side effects, misconceptions, and access issues — aligned with the survey findings. **Conclusions:** Our results showed that the majority of caregivers were willing to get vaccinated. Strategies to increase vaccine confidence and uptake could include working with trusted messengers such as HCW to reach communities.

### Case Rates by Vaccination Status and Waning among Children and Adolescents Ages 5-17 in California

**N.M. Linton**, C.M. Hoover, L. Nelson, R. Zhao, J. Myers, S. Jain, T.M. Leon
Division of Communicable Diseases, California Department of Public Health, Sacramento, CA, USA
**Background:** We assessed weekly vaccine effectiveness (VE) of BNT162b2 for children and adolescents 5– 17 years of age in California beginning in December 2021, during the SARS-CoV-2 Omicron wave, to gauge levels of vaccine waning in this population. From a policy and planning perspective, insight into VE is needed to inform our understanding of immunity among this age group, determine whether there are differences in VE based on dose type (adult or pediatric), and assess implications for vaccination strategy and K-12 school transmission trends in fall 2022 and beyond. **Methods:** The incident rate ratio (IRR) of unvaccinated to vaccinated cases reported in California was

calculated over time and used to obtain VE, calculated as 1-IRR. We also estimated IRR stratified by time since completion of primary series (PS), defined as 14 days following receipt of a second dose of BNT162b2. Additional subgroup analyses include sex, recent infection, and a geographically-based equity metric. **Results**: VE against detection as a case measured on a weekly basis waned more rapidly for the 5–11-year-old age group compared with the older age groups (12–15 and 16–17-year-olds, who were also eligible for a booster dose starting in December). VE against hospitalization was relatively robust across all age groups, ranging between 50–90% with no clear waning trend. VE was higher in the most advantaged areas of California during the height of the Omicron wave. There was no significant difference in VE between sexes for any age and accounting for recent infection did not affect the overall findings. **Conclusions:** Faster waning of case-based VE for 5–11-year-olds in California who have received two doses of BNT162b2 compared with 12–15-year-olds was observed. Vaccine dosage, timing of vaccination, and Omicron all likely played a role in the observed trends. The evidence suggests that a different vaccination strategy for younger age groups may be necessary to maintain protection against SARS-CoV-2 infection.

### Oral Sabizabulin Reduces Mortality in Hospitalized COVID-19 Patients at High Risk for ARDS

**M. Gordon**[1], A. Skolnick[2], K.G. Barnette[3], D. Rodriguez[3], S. Dasgupta[4]; M. Steiner[3]
[1]Honor Health, Scottsdale, AZ, USA, [2]HD Research, Houston, TX, USA, [3]Veru Inc, Miami, FL, USA, [4]Inspira Health, Vineland, NJ, USA

**Background:** Sabizabulin is an oral, novel microtubule disruptor that has dual antiviral and anti-inflammatory activity being developed for the treatment of hospitalized COVID-19 patients at high risk for acute respiratory distress syndrome (ARDS). **Methods:** A double-blind randomized (1:1) Phase 2 study (NCT04388826) of sabizabulin or placebo (up to 21 days or discharge) was conducted in 39 COVID-19 patients with WHO score of ≥4 (required $O_2$) and comorbidities for ARDS. Standard of care (SOC) was allowed. The key efficacy endpoints were the proportion that died by day 60, days in ICU and on mechanical ventilation. **Results:** There was an 82% relative reduction in mortality in the sabizabulin group (5.3%) compared to placebo (30%) (p=0.04). Days in ICU decreased a mean of 7 days and days on ventilation reduced a mean of 4.2 days in the sabizabulin group compared to placebo group. Sabizabulin was well tolerated. **Conclusions: In this Phase 2 study,** sabizabulin had clinically meaningful reductions in mortality, days in the ICU and days on mechanical ventilation. Veru initiated and has completed a double-blind, multicenter, and placebo-controlled Phase 3 clinical study evaluating sabizabulin 9 mg versus placebo (randomized 2:1) in 204 hospitalized moderate-severe COVID-19 patients (requiring oxygen) who were at high risk for ARDS (NCT04842747). At a planned interim analysis in the first 150 patients randomized, the study was halted by the Independent Data Monitoring Committee for clear demonstration of efficacy. A statistically significant (p=0.0041) 55% relative reduction in deaths was observed in the intent-to-treat population. Additionally, in mortality through Day 29 sabizabulin treatment resulted in 17% mortality rate compared to placebo rate of 35%, a relative reduction in deaths of 52%. Sabizabulin treatment also resulted in a 43% relative reduction in days in ICU (p=0.0013), 49% relative reduction in days on mechanical ventilation (p=0.0013), and 26% relative reduction in days in hospital (p=0.0277) vs placebo (patients that died on study were set to the maximum days of 60 in each of these secondary endpoints). The proportion of patients with an adverse event or a serious adverse event was lower in the sabizabulin compared to the placebo group.

### ABC-201: Opaganib, a Sphingosine Kinase-2 (SK2) Inhibitor in COVID-19 Pneumonia: A Randomized, Double-blind, Placebo-Controlled Phase 2/3 Study, in Adult Subjects Hospitalized with Severe SARS-CoV-2 Positive Pneumonia

**M.L. Levitt**[1], F. Neuenschwander[2], S. Piconi[3], Y. Maor[4], E. Sprinz[5], N. Assy[6], O. Khmelnitskiy[7], N. Lomakin[8], B. Goloshchekin[9], R.L. Gerlach[1], E. Campbell[1], A. Bibliowicz[1], R. Fathi[1], P. Anderson[1], G. Raday[1], M. Klein[10], C. Fehrmann[11], G. Eagle[12], O. Barnett-Griness[10], V. Katz Ben-Yair[1] on behalf of the ABC-201 Investigator Team
[1]RedHill Biopharma Ltd., Tel-Aviv, Israel, [2]Núcleo de Pesquisa Clínica - Hospital Vera Cruz, Belo Horizonte, Brazil, [3]ASST di Lecco - Presidio Ospedaliero A. Manzoni di Lecco, Trapianto, Italy, [4]Wolfson Medical Center, Holon, Israel, [5]Hospital de Clínicas de Porto Alegre, Brazil, [6]Galilee Medical Center, Nahariya, Israel, [7]Saint-Petersburg State Budget Healthcare Institution City Pokrovskaya Hospital, Russian Federation, [8]Federal State Budgetary Institution Central Clinical Hospital of the Management Affair of President Russian Federation, Moscow, Russian Federation, [9]Saint-Petersburg SBHI City Hospital 15, Russian Federation, [10]Bioforum Ltd., Ness Ziona, Israel, [11]CEEF Solutions, Pointe-Claire, QC, Canada, [12]G.E.T Pharma Consulting LLC, Lambertville, NJ, USA

**Background:** Vaccinations have been effective in mitigating the severity of SARS-CoV-2 infection however, few therapeutics have been proven consistently effective for the treatment of SARS-CoV-2 infection, particularly in hospitalized patients. Opaganib is a novel, orally available SK2 inhibitor with potent antiviral and anti-inflammatory

properties currently investigated in hospitalized patients with COVID-19 pneumonia. **Methods:** Study ABC-201 was a randomized, double-blind, placebo-controlled Phase 2/3 trial evaluating the primary objective of 'no longer requiring supplemental oxygen by Day 14', in hospitalized patients with COVID-19 pneumonia meeting WHO Ordinal Scale 5. Key secondary endpoints included clinical improvement based on the WHO scale, time to hospital discharge, proportion of patients intubated for mechanical ventilation and mortality over the 42 days of the study. In addition to the prespecified analyses, a number of post-hoc analyses were performed. **Results:** In the prespecified primary and secondary endpoints, opaganib was numerically but not statistically superior to placebo. In a post-hoc analysis using the median baseline fraction of inspired oxygen (FiO2 of 60%), a subpopulation was identified that required ≤FiO2 60% at baseline (54% of the mITT) and for which clinically relevant endpoints such as 'no longer requiring supplemental oxygen', WHO scale measurements, time to discharge, intubation and mortality showed clinically meaningful and nominally significant improvement in favor of opaganib vs. placebo. Extensive evaluation of potential confounding variables did not reveal any confounders that may have potentially altered these outcomes for this subpopulation. Overall, TEAEs were balanced between the two arms with no new safety signals identified. **Conclusion:** While the trial did not meet statistical significance in prespecified analyses, a large subpopulation was identified post hoc, for whom there may be a potential benefit, identified by FiO2 requirement at baseline. Baseline FiO2 may provide further refinement for the parameters used to evaluate disease severity in COVID-19 pneumonia.

## Poster Session 2 Abstracts

**5:00 PM – 6:00 PM**

**Grand Hall**

## COVID-19 and SARS-CoV-2

### Poster 86. Performance of Rapid Antigen Testing for SARS-CoV-2 Compared to RT-PCR at an On-Site School Setting in San Mateo County, California

**J. Altamirano**[1], G.K.-Y. Tam[1], I.G. Robinson[1], M. Lopez[1], L.X. Chun[1], N.J. Shaikh[1], E.G. Hoyte[1], Y.J. Carrington[1], S.G. Jani[2], E.Y. Toomarian[3], J.C. Hsing[2,4], J. Ma[2], U. Pulendran[2], A.P. Aguirre[1], P. Govindarajan[5], A.L. Blomkalns[5], C.J. Wang[1,2,6], Y. Maldonado[1]

[1]Department of Pediatrics, Stanford University School of Medicine, Stanford, CA, USA, [2]Center for Policy, Outcomes, and Prevention, Department of Pediatrics, Stanford University School of Medicine, Stanford, CA, USA, [3]Graduate School of Education, Stanford University, Stanford, CA, USA, [4]Department of Epidemiology and Population Health, Stanford University School of Medicine, Stanford, CA, USA, [5]Department of Emergency Medicine, Stanford University School of Medicine, Stanford, CA, USA, [6]Department of Health Policy, Stanford University, Stanford, CA, USA

**Background:** Over 200 million SARS-CoV-2 cases have been reported globally as of August 2021. As communities reopen, there is an urgent need to provide scalable, accurate, and time-sensitive COVID-19 testing, particularly in schools. Rapid antigen tests are a fast and economical way to monitor the spread of SARS-CoV-2. We evaluated the efficacy of rapid antigen tests in comparison to RT-PCR tests in detecting SARS-CoV-2 within a typical commuter school environment. **Methods:** Participants from a San Mateo County, CA K-8 school were tested weekly for SARS-CoV-2 from April-July 2021. Participants provided two anterior nares swabs, with one swab submitted for RT-PCR testing and the other tested using Abbot BinaxNOW rapid antigen kits. Paired testing was conducted to compare the two methods. **Results:** 2013 paired samples were collected from 265 participants. Of the 1996 negative antigen tests, all were RT-PCR negative, showing a 100% concordance with molecular tests. 17 false positives were detected by rapid antigen testing, providing a specificity of 99.16%. Per isolation protocols in schools, were rapid kits the only test available, these false positives would have led to 310 individuals being isolated for 2 days each, totaling 3720 missed school hours. **Conclusions:** Our study confirmed that the Abbott BinaxNOW rapid antigen tests are an effective tool for surveillance due to their high specificity and may be useful in mitigating transmission for the safe reopening of schools. Rapid antigen testing is an efficient way to provide scalable surveillance testing to larger populations. Taking 15 minutes to run BinaxNOW vs. an estimated 72 hours for RT-PCR turnaround, rapid antigen tests can enable schools to quickly identify and isolate infected individuals while minimizing school time lost. Mitigating loss of school time as a result of false positives will be critical as testing is further expanded.

### Poster 87. Establishing COVID-19 Dashboards – Enhanced Data Access and Use in Ethiopia

**B. Eskinder**[1], S.A. Abayneh[1], M. Abate[2], M. Robi[2], A. Selamsew[3], B. Kanate[4], D. Habte[1]
[1]Division of Global HIV and Tuberculosis, US Centers for Disease Control and Prevention (CDC), Addis Ababa, Ethiopia, [2]ICAP at Columbia University (CU/ICAP), Addis Ababa, Ethiopia, [3]Addis Ababa City Administration Health Bureau (AACAHB), Addis Ababa, Ethiopia, [4]Oromia Regional Health Bureau (ORHB), Ethiopia
**Background:** The first case of COVID-19 was reported on March 13, 2020, and the country has been managing the surveillance and response using the existing public health emergency management (PHEM) system. Health facilities use different mechanisms (phone, paper, DHIS2) to submit COVID 19 reports to the next higher level. Data is received at regional PHEMs on daily basis and compiled into Excel and other data management tools. The recording, reporting and data management for COVID-19 in the early phase of the outbreak was not standardized. To support this challenge CDC supported the development of a dashboard as a show case for two regional PHEM partners Addis Ababa and Oromia. **Methods:** The two regional PHEMs and their partners worked on a regional dashboard using Google Sheets and Google Data Studio summarizing critical COVID-19 indicators: laboratory tests, new cases, recovering cases, admission, and deaths. The senior leaders at respective regional PHEM as well as relevant technical teams (surveillance, response, laboratory, logistics, data managers) were granted access to the dashboard. **Results:** We present the process and implementation of the regional dashboard in Addis Ababa and Oromia used for COVID-19 management in Ethiopia. As of Sept 9, 2021, 1,966,098 and 363,107 of the total national 3,301,802 tests were reported in the dashboard from Addis Ababa and Oromia regions respectively (212,227 and 42,095 of the total national 319,101 COVID-19 cases). The two regions reported 3833 of the total national 4830 deaths. Daily COVID-19 tests, positive cases, positivity rate, recovery and deaths are displayed with easy to understand and interpretable charts. The dashboard also displays the seven- and fourteen-days moving average. The dashboard is interactive whereby viewers can select lower administrative structures or time-periods to be visualized. The Senior Leaders are using the dashboard for reporting and disease monitoring. Implementing partners found the dashboard to be efficient and timely. **Conclusions:** Ethiopia has established an important regional platform for a standardized COVID-19 reporting and data-driven decision making. The regional dashboards are user friendly for high level leaders and technical team which significantly addressed the information gap seen during the initial months of COVID-19.

### Poster 88. Identification of a Novel SARS-CoV-2 Strain with Truncated Protein in ORF8 Gene by Next Generation Sequencing

**S. DeRonde**[1,2], H. Deuling[1], J. Parker[2], J. Chen[1,2]
[1]Department of Biology and Wildlife, Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK, USA, [2]Alaska State Virology Laboratory, Alaska State Public Health Laboratories, Fairbanks, AK, USA
**Background:** SARS-CoV-2 ORF8 gene encodes for an immunoglobulin-like protein that is believed to inhibit presentation of viral antigens by major histocompatibility complex (MHC) class I, suppress the type I interferon antiviral response and interact with host factors involved in pulmonary inflammation and fibrogenesis. The ORF8 is a hypervariable gene rapidly evolving among SARS-related coronaviruses, with a tendency to recombine and undergo deletions that are deemed to facilitate the virus adaptation to the human host. The deleted variant resulted in a less severe infection and lower concentrations of proinflammatory cytokines, chemokines and growth factors that are strongly associated with severe COVID-19. **Methods:** Positive COVID-19 samples were collected in Alaska State Virology Laboratory from testing centers around the state. Construction of next generation sequencing library for Illumina Sequencer were performed using NEBNext Ultra II RNA Library Prep Kit for Illumina. Sequencing runs were performed on Illumina MiSeq System using 2x250 bp MiSeq Reagent Kit v2. Bioinformatic analysis was performed using Sequencher software and QIAGEN CLC Genomics Workbench for genome assembly. CoViZu, an open source COVID-19 genome analysis tool provided by the GISAID Initiative was used for sequencing and phylogenetic analysis. **Results:** We identified a truncated protein mutation located in the ORF8 gene which is near the end of the genome from nucleotides 27,878 to 27,958. The mutation in this novel strain created a stop codon and translates to the novel truncated ORF8 protein, creating a much smaller protein than most other strains of SARS-CoV-2. The novel truncated mutation is most closely related to nine SARS-CoV-2 strains found in Washington state. The full genomic sequencing data of this SARS-CoV-2 isolate has been submitted to GISAID (virus name: hCoV-19/USA/AK-PHL676/2020; Accession ID: EPI_ISL_586254) and NCBI (GenBank: MW264435.1). **Conclusions:** Our results show a novel strain of SARS-CoV-2 with a truncated ORF8 gene resulting in a much short version of the ORF8 protein. The effects of this truncated ORF8 protein and its functions are still uncertain but a truncated ORF8 protein could affect antibody response, severity of infection and inflammatory response.

### Poster 89. Early Epidemiological Investigations: World Health Organisation UNITY Protocols Provide a Standardized and Timely International Investigation Framework during the COVID-19 Pandemic

**I. Bergeri**[1], H.C. Lewis[1], L. Subissi[1], A. Nardone[1,2], M. Valenciano[1,2], B. Cheng[1], K. Glonti[1], B. Williams[1], I.O.O. Abejirinde[1], A. Simniceanu[1], A. Cassini [1], R. Grant[1], A. Rodriguez[3], A. Vicari[3], L. Al Ariqi[4], T. Azim[5], P. Wijesinghe[5], S. Rajatonirina[6], J. Okeibunor[6], L.V. Le[7], M. Katz[8], A. Vaughan[8], P. Jorgensen[8], G. Freidl[8], R. Pebody[8], WHO Unity Initiative Collaborators, M.D. Van Kerkhove[1]

[1]World Health Organization Headquarters, Geneva, Switzerland, [2]Epiconcept, Paris, France, [3]Pan American Health Organization, Washington, DC, USA, [4]World Health Organization for the Eastern Mediterranean, Cairo, Egypt, [5]World Health Organization, Regional Office for South-East Asia, New Delhi, India, [6]World Health Organization, Regional Office for Africa, Brazzaville, Republic of the Congo, [7]World Health Organization, Regional Office for the Western Pacific, Manila, Philippines, [8]World Health Organization Regional Office for Europe, Copenhagen, Denmark

**Background:** The declaration of Coronavirus disease 2019 (COVID-19) as a public health emergency of international concern (PHEIC) on 30 January 2020 required rapid implementation of early robust investigations to inform appropriate national and global public health actions. **Methods:** The suite of existing pandemic preparedness generic epidemiological early investigation protocols was rapidly adapted for COVID-19, branded the 'UNITY studies' and promoted globally for the implementation of standardized and quality studies. Ten protocols were developed investigating: household (HH) transmission; the first few cases (FFX); population seroprevalence (SEROPREV); health facilities transmission (n=2); vaccine effectiveness (n=2); pregnancy outcomes and transmission; school transmission; and surface contamination. Implementation was supported by WHO and its partners globally, with emphasis to support building surveillance and research capacities in low- and middle-income countries (LMIC). **Results:** WHO generic protocols were rapidly developed and published on the WHO website, 5/10 protocols within the first three months of the response. As of 30 June 2021, 172 investigations were implemented by 97 countries, of which 62 (64%) were LMIC. The majority of countries implemented population seroprevalence (71 countries) and first few cases/household transmission (37 countries) studies. **Conclusion**: The widespread adoption of the WHO Unity Studies, especially in LMICs, helped generate much-needed robust and comparable data to inform national, regional, and global public health actions. This global sero-epidemiological initiative gives countries the tools they need to enhance routine surveillance and strengthen research by providing a standardized framework. Moreover, because the tools can be adapted to any resource setting, it was an invaluable tool for research equity. Finally, it promotes the international comparability of enhanced surveillance and applied research increasing the evidence-based knowledge for action. It could serve as a field-tested foundation of future global pandemic preparedness and readiness efforts.

### Poster 90. Demographic and Clinical Characteristics of COVID-19-related Deaths in Eswatini, 2020–2021

**Z. Zikalala**[1,2], C. Ngcamphalala[3], N. Nhlabatsi[4], L. Dlamini[4], M. Mbuli[4], N. Mkhonta[4], B. Tsabedze[4], S. Simelane[3], P. Mokgolane[4], N. Nxumalo[4], M. Li[5], S. Ruben[3], K. Ravhuhali[1] ,H. Mdose[1], H. Nuwagaba-Biribonwoha[1,2], V. Lokotfwako[4]

[1]South African Field Epidemiology Training Program, Johannesburg, South Africa, [2]University of Pretoria, School of Health System and Public Health, Pretoria, South Africa, [3]ICAP, Columbia University, Mailman School of Public Health, Mbabane, Eswatini, [4]Department of Epidemiology, Mailman School of Public Health, New York, New York, [4]Epidemiology and Disease Control Unit, Ministry of Health, Mbabane, Eswatini, [5]Centers for Disease Control and Prevention (CDC)/PEPFAR, Mbabane, Eswatini

**Background:** Since the first reported COVID-19 related death in Eswatini in April 2020, there has been a steady increase in the number of deaths. We describe demographic and clinical characteristics of COVID-19 related deaths in Eswatini. **Methods:** We analyzed COVID-19 related deaths nationally between April 2020 and August 2021. We extracted demographic, clinical, epidemiological and laboratory data from the Ministry of Health COVID-19-line list. Descriptive statistics were used and STATA 16 was used to calculate the case fatality rate (CFR). **Results:** A total of 28 535 COVID-19 cases with 818 related deaths(CFR 2.9%) were recorded in the period under review. Deaths were equally distributed by gender: 51% (n=418) males and 49% (n=400) females. The mean age among those who died was 62 years (SD14.7), the highest proportion of deaths was among the 60-69year age-group (28% n=228, CFR 2.9%), and lowest proportion of deaths was among children 0-9 years (0.2%, n=2, CFR 0.2%). More deaths were from the Manzini region (41.3%, n=338), Lubombo had the least proportion of deaths (10%, n=84). Over half the COVID-19 deaths occurred within 3 days of hospitalization (57%, n=467), and 1.3%(n=11) occurred outside health facilities. The most common underlying health conditions among the COVID-19 related deaths were

hypertension (55%, n=447), diabetes mellitus (44%, n=360), obesity (13%, n=110), and HIV (10%, n=85). One third of deaths had both diabetes mellitus and hypertension (34%, n=279). Less common comorbidities were renal diseases (3%, n=22) central nervous system diseases (3%, n=26), asthma (1% ,n=11), tuberculosis (2%, n=12). A quarter of COVID-19 related deaths had no comorbidities (24%, n=197). The COVID-19 related deaths included 5 pregnant women (0.6%). **Conclusion:** Our findings show that most COVID-19 deaths occurred among the elderly, younger individuals without comorbidities and those with hypertension, diabetes, and HIV comorbidities. Mitigation interventions should extend to these priority populations.

### Poster 91. Salivary Immune Responses after COVID-19 Vaccination

**K. Nguyen**[1], B. Relja[2], V. Costantini[3], J. Vinjé[3]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Cherokee Nation Assurance, Arlington, VA, USA, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** mRNA-based COVID-19 vaccines have played a critical role in reducing severe outcomes of COVID-19. Humoral immune responses against SARS-CoV-2 after vaccination have been extensively studied in blood; however, limited information is currently available on the presence and duration of SARS-CoV-2 specific antibodies in saliva and other mucosal fluids. Saliva offers a non-invasive sampling method which may also provide a better understanding of mucosal immunity at sites where the virus enters the body. Our objective was to evaluate the salivary immune response after vaccination with the COVID-19 Moderna mRNA-1273 vaccine. **Methods:** Two hundred employees of the Centers for Disease Control and Prevention (CDC) were enrolled prior to receiving their first dose of the mRNA-1273 vaccine after providing informed consent. Demographic data included age (range: 23-68 years), sex (64% female, 36% male), and race (total distribution: 66% White, 18% Black or African American, 16% Asian, 3% Other). The participants were asked to self-collect 6 saliva specimens at days 0 (prior to first dose), 14, 28 (prior to second dose), 42, and 56 using a SalivaBio saliva collection device. Saliva samples were tested for anti-spike protein SARS-CoV-2 specific IgA and IgG using CDC-developed and validated enzyme immunoassays. The results were validated by normalizing against total antibody for each isotype. **Results:** Overall, SARS-CoV-2-specific salivary IgA titers peak 2 weeks after each vaccine dose, followed by a sharp decrease the following weeks. The IgG results showed a slightly different pattern with a titer showing first approximately 2 weeks after the first dose and peaked 2 weeks after the second dose. In contrast to the IgA levels, IgG titers showed no significant decrease after the second dose and persisted at least until 8 weeks after the first vaccine dose. Additionally, no significant differences in IgA/IgG titers were observed based on age, sex, or race/ethnicity. **Conclusions:** All participants mounted salivary IgA and IgG immune responses against SARS-CoV-2 after receiving the mRNA-1273 COVID-19 vaccine but more studies are needed to assess the antibody levels beyond 2 months after the first dose. Salivary antibody testing can provide further insights into mucosal antibody response after COVID-19 vaccination.

### Poster 92. Development and Validation of a Versatile, PCR-Based Assay for SARS-CoV-2 Variant Monitoring

**O. Pernet**[1], M. Weisenhaus[1],C. Stafylis[2], J.F. Emerson[3], P.M. Ward[3], S. van Orman[4], F.D. Gilliland[2], D. Conti[2], A. Ghanem-Uzqueda[4], C. Hernandez-Tamayo[2], S. Stellar[2], A. Tadanki[2], J. Kravitz[2], T. Chu[2], H. Hu[2], A.A.Z. Kovacs[1], J.D. Klausner[2]
[1]Maternal, Child and Adolescent Center for Infectious Diseases, University of Southern California, Los Angeles, CA, USA, [2]Department of Population and Public Health Sciences, University of Southern California, Los Angeles, CA, USA, [3]Department of Clinical Pathology, University of Southern California, Los Angeles, CA, USA, [4]Department of Family Medicine, University of Southern California, Los Angeles, CA, USA
**Background:** As the pandemic progresses, new SARS-CoV-2 variants continue to emerge. Several have achieved increased transmissibility, immune evasion, or both, making it critical to monitor their dynamics. Current variant surveillance methods have relied mostly on whole genome sequencing (WGS), which is costly and time-consuming. Although WGS is important for understanding the pandemic evolution at the global scale, a more targeted and less expensive approach could be adopted for routine variant monitoring. Therefore, we developed and validated a versatile, high-throughput digital-droplet(dd) PCR protocol to identify SARS-CoV-2 variants. **Method:** We designed 7 primers-probe sets targeting specific mutations allowing discrimination between the variants α, β, γ, δ, δ+ (or δ417N), ε, η, λ, and the original Washington SARS-CoV-2 sequence. Optimal concentration, temperature, and cycle protocols were established on the BioRad QX200 system using previously whole genome sequenced samples. Total RNA from saliva samples were purified with magnetic beads on a semi automatized Kingfisher Apex system. Finally, WGS on selected samples was used to confirm our assay results. **Results:** We successfully defined 2 panels of seven total primers/probe combinations to identify a variant with only 2 PCR reactions. We validated the assay using 200 remnant saliva samples that previously tested positive by SARS-CoV-2 RT-qPCR Amplitude EUA

assay. As expected, original sequences were initially detected in Fall 2020 and were later displaced by α variants and finally the more dominant δ variants. The assay also showed higher copy number in samples with the δ variant. **Conclusions:** We created a novel multiplex ddPCR assay to rapidly discriminate SARS-CoV-2 variants using only 2 PCR reactions. This study demonstrated that a ddPCR based approach is an efficient alternative to WGS for variant monitoring. As new variants emerge, the assay can be updated with new primers/probe sets.

### Poster 93. SARS-CoV-2 Surveillance on Mink Farms in British Columbia, Canada: Design, Implementation, and Findings

**Y.L.E. Chan**[1,2], M. Coombe[3], C. Himsworth[3,4], A. Paiero[5], I. Sekirov[1,4], N. Prystajecky[1,4], E. Newhouse[5], J. Tyson[1], J. Zlosnik[1,4], Y. Chang[1], E. Fraser[1,4], B. Radke[3], V. Clair[1,4]
[1]BC Centre for Disease Control, Vancouver, BC, Canada, [2]Public Health Agency of Canada, Ottawa, ON, Canada, [3]Ministry of Agriculture, Food and Fisheries, Abbotsford, BC, Canada, [4]University of British Columbia, Vancouver, BC, Canada, [5]Fraser Health Authority, Surrey, BC, Canada
**Background:** Mink farms are susceptible to SARS-CoV-2 outbreaks, providing opportunity for viral mutation in a non-human host and potential for spillback leading to new variants. SARS-CoV-2 outbreaks on two mink farms in British Columbia (BC), Canada in Dec 2020 highlighted the rapid need for mink farm worker and animal surveillance. We describe the design and implementation of COVID-19 surveillance for BC mink farms using a One Health approach and summarize the findings to date. **Methods:** In Jan/Feb 2021, mink farm workers began COVID-19 testing using self-collected saline gargles on a weekly to triweekly basis; samples were delivered via same-day medical courier to the BC Centre for Disease Control's Public Health Laboratory (BCCDC PHL) for testing and whole genome sequencing (WGS) if positive. Any indeterminate results were followed up with nasopharyngeal (NP) swab. Natural mink mortalities were collected from every farm on a weekly basis, NP swabs tested at the BC Animal Health Centre, and non-negative results confirmed by the National Centre for Foreign Animal Disease (NCFAD). Positive samples from mink mortalities underwent WGS at BCCDC PHL, with some also sequenced at NCFAD. An ongoing multidisciplinary One Health working group facilitated timely data sharing, enabling coordinated investigation and linkage of epidemiological, laboratory, and genomic information. **Results:** From Jan to Sep 2021, enhanced passive human surveillance detected eight COVID-19 positive workers (7 via gargle, 1 via follow-up NP swab) from three mink farms, out of 125 workers on six farms. A positive NP swab (1 of 13 mink) from the active surveillance of mink mortalities was detected on one farm in May 2021, leading to the declaration of a third mink farm outbreak and quarantine of the affected premise. WGS found genetic relatedness amongst samples from the affected premise, all identified as SARS-CoV-2 lineage B.1.618. **Conclusions:** Targeted surveillance at mink farms allowed for timely detection of SARS-CoV-2 infection, isolation/quarantine to minimize spread, and implementation of increased testing and control measures as required. Together with enhanced biosecurity measures and mandated vaccination of workers, coordinated human and animal surveillance decreases the public health risk from COVID-19 associated with mink farms.

### Poster 94. Utilizing the Terra.Bio Platform to Rapidly Develop and Distribute Resources for SARS-CoV-2 Sample Characterization and Genomic Epidemiology to Public Health Laboratories

**K.G. Libuit**, F. Ambrosio, R. Petit, C. Kapsak, J. Sevinsky
Theiagen Genomics, Highland Ranch, CO, USA
**Background:** SARS-CoV-2 (SC2) sample characterization and genomic epidemiological analysis has become an increasingly critical function for public health laboratories. Integration of these practices, however, has been a major challenge due to the technical workforce and compute infrastructure development required to access many SC2 bioinformatics solutions. **Methods:** Best-practice approaches for SC2 sample characterization and genomic epidemiology were captured into a series of workflow description language (WDL) workflows deemed the Titan workflow series. The Titan workflow series was made accessible through the Terra.Bio platform, a bioinformatics web application that connects non-technical users to bioinformatics WDL workflows and dynamic cloud compute resources through a clean and intuitive graphical user interface. Public health scientists were introduced and trained on the Titan workflows to enable routine SC2 sample characterization and genomic epidemiological analysis in laboratories with otherwise limited bioinformatics capabilities. **Results:** The Titan workflow series has been adopted in over 20 public health laboratories across the United States and over 15 countries internationally. To date, the US laboratories have analyzed an estimated 200,000 SC2 samples using the Titan workflows on the Terra platform. **Conclusions:** Use of WDL workflows and the Terra.Bio platform has allowed various public health laboratories to overcome the major barriers to accessing advanced bioinformatics solutions for SC2 genomic analysis. Continued use of the Terra.Bio platform may also provide value in developing and distributing bioinformatics solutions for other pathogens of concern.

### Poster 95. Persistence of SARS-CoV-2 Antibody among RT-PCR Positive Cases after 6 Months of Infection

**R. Raihan**[1], S.A.H. Abdullah[2], S. Islam[3], M. Murshed[4], G.D. Harun[5], M. Ul Anwar[6]
[1]US Bangla Medical College and Hospital, South Rupshi, Bangladesh, [2]South Asia Field Epidemiology & Technology Network (SAFETYNET), Dhaka, Bangladesh, [3]American Society of Microbiology (ASM) Bangladesh, [4]Holy Family Red Crescent Medical College, [5]Icddrb, Dhaka, Bangladesh, [6]Dhaka University, Dhaka, Bangladesh
**Background:** Antibody response to severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) remains controversial and needs to be addressed carefully. Studies have shown that the peak antibody responses appear after the second week of infection thus could never be used in early diagnosis of cases. In addition, the knowledge of SARS-CoV-2 antibody persistence after natural infection is poorly studied in Bangladeshi SARS-CoV-2 patients, which could help us to develop insights of an effective vaccine strategy. **Methods:** 77 PCR confirmed patient's serum were tested with two different RDT kits (Instant View, USA and Diagret, China) after 6 months of their PCR positivity to check the persistence of antibody against SARS-CoV-2. These patients have no history of reinfection during this period. **Results:** Among the 77 cases, 57.1% were male; majority of them (42%) were between 26-45 years of age; and 68.8% were symptomatic. Anti-SARS-CoV-2 antibody (IgM/IgG) was found among 93.5% and 70.1% cases after six months, detected by Instant view and Diagret kit respectively. Symptomatic cases had antibody present in blood among 96% and 75.5% cases, while it was 87.5% and 58.3%, for asymptomatic cases accordingly. **Conclusion:** Results documented a high number of cases has antibody persistence due to the natural SARS-CoV-2 exposure, which is more among the symptomatic cases. The results imply that more than half of the cases has natural protection against SARS-CoV-2 even after six months of exposure, which can be utilized for vaccination policies for resource constrained countries.

### Poster 96. One Health Investigations of SARS-CoV-2 Outbreaks in People and Multiple Animal Species on Eight Mink Farms in the United States-Utah, Wisconsin, & Michigan, 2020-2021

**N.M. Wendling**[1], C.M. Cossaboom[1], S.A. Shriner[2], D.J. Taylor[3], D. Konkle[4], N. Wineland[5], H. Rettler[6], R. Klos[7], M.G. Stobierski[8], S. Gibbons-Burgener[7], A. Carpenter[1], C. Tansey[1], A. Straily[1], R. Harvey[1], B. Amman[1], J.S. Towner[1], K. Varela[1], E. Curren[1], Y. Torres-Mendoza[1], M. Waltenburg [1], J.R. Spengler[1], J.A. Condrey[1], R.R. Ghai[1], K. Poulsen[9], K.F. Oakson[10], E. Young[10], A. Lim[9], D.K. Riner[8], H. Blankenship[8], S. Tong[1], A. Uehara[1], C.R. Paden[1], K. Queen[1], M.H. Kainulainen[1], O. Herzegh[1], M.L. Killian[2], T.J. DeLiberto[2], J.M. Ritter[1], L. Murrell[1], J.A. Rooney[2], J.A. Korslund [2], C. Barton Behravesh[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]United States Department of Agriculture, Animal and Plant Health Inspection Service, Riverdale, MD, USA,[3]Utah Department of Agriculture and Food, Taylorsville, UT, USA, [4]Wisconsin Department of Agriculture, Trade and Consumer Protection, Madison, WI, USA, [5]Michigan Department of Agriculture and Rural Development, Lansing, MI, USA, [6]Utah Department of Health, Salt Lake City, UT, USA, [7]Wisconsin Department of Health Services, Madison, WI, USA, [8]Michigan Department of Health and Human Services, Lansing, MI, USA, [9]Wisconsin Veterinary Diagnostic Laboratory, University of Wisconsin, Madison, WI, USA, **[10]**Utah Public Health Laboratory, Taylorsville, UT, USA
**Background:** Mink are highly susceptible to SARS-CoV-2; 437 outbreaks were reported from 12 countries as of 10/14/2021. The U.S. confirmed 17 mink farms with SARS-CoV-2 infections in five states between August 2020-July 2021. A One Health approach was used to investigate SARS-CoV-2 infection in people and multiple animal species associated with U.S. mink farms. **Methods:** From August-December 2020, CDC and USDA-Wildlife Services were invited by state health and agricultural officials to deploy field teams to conduct investigations of SARS-CoV-2-positive mink farms identified through passive surveillance. On-farm investigation and epidemiologic interviews with representatives from eight farms were conducted. Diagnostic specimens were collected from humans, farmed mink, on-farm domestic animals, and on- and off-farm peridomestic wildlife. Multiple laboratories performed rRT-PCR, serology, genomic sequencing, and histopathological analyses for SARS-CoV-2 on human and animal specimens. Comparative analyses of animal and human sequences were performed. **Results:** At least one human epidemiologic link was identified on all eight farms as a likely source of SARS-CoV-2 introduction to mink. Mink with respiratory signs and mortality rates from 20% to 50% were documented on all eight farms. SARS-Cov-2 RNA was detected in specimens from farmed mink, on-farm domestic cats and dogs, and one wild mink. SARS-CoV-2 neutralizing antibodies were detected in farmed mink, including escaped mink from two farms, and on-farm domestic cats and dogs. Genomic analyses suggested possible mink to human transmission (2 cases) on one farm. **Conclusions:** Widespread morbidity and mortality from SARS-CoV-2 infection were documented on most affected mink farms in the United States. Comprehensive biosecurity and enhanced worker safety practices including use of personal protective equipment combined with human COVID-19 vaccinations, were recommended to prevent the spread of SARS-CoV-2 between people and animals. A One Health approach that includes collaboration across

sectors and industry partners is critical for successful investigation and implementation of recommendations to prevent SARS-CoV-2 introduction, spread between people and animals on mink farms, and subsequent spillover to wildlife.

### Poster 97. Nonpharmaceutical Interventions (NPIs) Implemented by Institutions of Higher Education (IHEs) in Response to the COVID-19 Pandemic, United States, Academic Year 2020-21

**S. Moreland**[1,2], N. Zviedrite[1], F. Ahmed[1], A. Uzicanin[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA

**Background:** In response to the coronavirus disease 2019 (COVID-19) pandemic, nonpharmaceutical interventions (NPIs) were implemented across the United States, including an unprecedented pivot to online learning for Institutions of Higher Education (IHEs) beginning in March 2020. **Methods:** From January to June 2021, we collected data from official webpages of 847 four-year institutions, including all public (n=547) and a stratified random sample of private IHEs (n=300). Abstracted data included NPIs deployed during the academic year such as COVID-19 testing, face mask protocols, and changes to the calendar, classroom, housing, and common areas. We assessed congruence with the October 5, 2020, US Centers for Disease Control and Prevention (CDC) guidance for IHEs. Focusing on IHEs that offered ≥50% courses with in-person learning, we used multivariable linear regression to explore the association between IHE characteristics and the summated number of implemented NPIs. **Results:** Among the 847 IHEs, 182 (21%) implemented all CDC-recommended NPIs. The most frequently utilized NPI was changes to the classroom (94%), practiced as one or more of the following three modalities: 6-feet spacing (55%), reduced class sizes (49%), or ≥75% online course delivery (20%) were implemented. Additionally, 784 (93%) IHEs specified facemask protocols, 691 (82%) physically changed common areas, and 641 (76%) offered COVID-19 testing. Among the subset of 227 (33%) IHEs that reported offering ≥50% courses in person, having <1,000 students enrolled was associated with having implemented fewer NPIs (adjusted coefficient, $\beta = -0.81$, $p < 0.01$) compared to IHEs with ≥1,000 students. Additionally, IHEs located in in the Midwestern ($\beta = -0.70$, $p < 0.01$), Southern ($\beta = -0.61$, $p = 0.01$), and Western ($\beta = -0.97$, $p < 0.01$) Census regions implemented fewer NPIs than those located in the Northeastern region. **Conclusions:** Only 1 in 5 IHEs implemented all CDC recommendations, while a majority implemented a subset, most commonly changes to the classroom, facemask protocols, and COVID-19 testing. Choice and number of NPIs implemented varied by student enrolment size and IHE location. Additional research is needed to assess NPI implementation and effectiveness in IHE settings.

### Poster 98. Characterization of Structural Epitopes and Binding Affinities of SARS-CoV-2 anti-Spike Receptor Binding Domain Monoclonal Antibodies to Variants of Concern

**A.S. Chida**[1], M.H. Kainulainen[2], B. Zhou[3], J. Lee[1], X. Tang[1], A. Chapman[4], D.A. Bagarozzi Jr[1], M.G. Finn[4], J.M. Goldstein[1]
[1]Immunodiagnostic Development Team/Reagent Diagnostic Services Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Vaccine Preparedness Team/Virology Surveillance and Diagnosis Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA, USA

**Background**: The COVID-19 pandemic caused by Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) presents a global health crisis and has rapidly spread worldwide causing more than 4.7 million deaths globally as of Sept 22, 2021. Emerging Variants of Concern (VOC) with amino-acid substitutions and deletions in spike protein (S) are a public health concern for unvaccinated individuals and in individuals with waning immunity post-vaccination. **Methods**: We previously generated mouse monoclonal antibodies (mAbs) against the wild-type Spike receptor-binding domain (RBD) of SARS-CoV-2 and classified them based on functional characterization. To determine the effects of VOCs on antibody binding, we selected 7 representative mAbs and evaluated them against Alpha (B.1.1.7), Beta (B.1.351), Gamma (P.1) and Delta (B.1.617.2) recombinant (r) spike proteins in vitro. We performed an ELISA to compare the binding affinities between mAb clones (1-3H2, 1-3D2, 1-3H6,1-3A2, 1-3G7, 1-3F2, 1-3D7) against the following r-proteins: RBD wt; RBD (N501Y); (Y453F); (E484K); (K417N); (L452R); (E484Q); (L452R+E484Q); (L452R+T478K); Spike S1 wt and S1(K417N+E484K+N501Y+D614G). **Results**: We obtained EC50 using nonlinear regression binding curve-fitting. Neutralizing mAb 1-3H2 showed complete loss of binding to the RBD (E484K; L452R+E484Q; K417+E484K+ N501Y), S1 (4- mutations) suggesting the role of glutamic acid in neutralization epitope. Related clone 1-3H6 showed a reduction in binding to these 4 r-proteins. Yet 1-3F2 bound all variants except Delta (L452R+T478K) where binding was significantly reduced. The remaining mAb bound all 11 r-proteins suggesting the mutations have negligible effect on their binding. We also examined the

epitope properties after protein denaturation and reduction. We found that 1-3H2 and 1-3H6 recognized primarily conformational epitopes. 1-3F2 bound to all variants except Delta suggesting an epitope comprised of residues at L452 and/or T478K. The remaining mAbs were capable of binding linear epitopes. mAbs were assayed by a Focus Reduction Neutralization Test and Plaque Reduction Neutralization Test. 1-3H2 and 1-3H6 were sensitive to E484K and E484Q indicating Glu484 as a critical epitope. 1-3F2 was not sensitive to E484K yet susceptible to Delta. **Conclusions**: A subset of mAbs are sensitive to defined mutations found in the VOCs. and have provided insight into the loss of antibody function. This translates to decreased efficacy in serum titers seen in breakthrough infections as well as a decrease in neutralization from vaccine immunity and therapeutic mAbs treatment. This data will be invaluable in our understanding of spike protein structural determinants for antibody recognition through natural-and vaccine-induced immunity. Also, this study will have a huge impact on developing improved diagnostics identifying SARS-CoV-2 VOCs and for therapeutic applications.

### Poster 99. A Retrospective Analysis of the Relative Risk of SARS-CoV-2 Infection among Asymptomatic vs. Symptomatic Patients in a Population of At-Home Test Takers

**D.P. Humphreys**[1], K.M. Olds[1], K.M. Gavin[1,3], M.P. Bonaca[2,3], T.A. Bauer[1,3]
[1]Everly Health, Inc., Austin, TX, USA, [2]CPC Clinical Research, Aurora, CO, USA, [3]University of Colorado Anschutz Medical Campus, Aurora, CO, USA
**Background:** At-home sample collection for PCR testing has been highlighted as a key tool in controlling the spread of SARS-CoV-2 among symptomatic and asymptomatic patients. A strong understanding of the relative risk of infection among asymptomatic patients compared to those with symptoms and estimates of the percentage of patients positive for COVID-19 who are asymptomatic, is key to determining the value of at-home sample collection and asymptomatic screening in curbing transmission of SARS-CoV-2. **Methods:** Subjects were included in the study by retrospectively querying the Everlywell user database for those who had used the Everlywell COVID-19 Test Home Collection Kit. Collection dates ranged from May 17, 2020 to September 21, 2021. Samples were self-collected at home and shipped to a partner lab for RT-PCR testing under the FDA EUA framework. Patients self-reported symptoms at the time of kit registration and were categorized as symptomatic (mild to moderate symptoms) or asymptomatic (no symptoms). Individuals with severe symptoms were redirected to acute care centers. Relative risk of infection was calculated as the positivity rate among asymptomatic patients over that among symptomatic patients. The percentage of all patients who tested positive for SARS-CoV-2 and reported no symptoms at the time of kit registration was also calculated. **Results:** A total of 282,831 eligible subjects were included in the study, from which 634,791 unique results were analyzed. Estimates of the relative risk of infection given no symptoms to the risk given symptoms was 0.080 (95% CI - 0.078 to 0.082). Of all participants who tested positive for SARS-CoV-2, 48.75% reported no symptoms at the time of kit registration. **Conclusions:** Nearly half of the identified positive cases were asymptomatic at the time of kit registration. Although the relative risk of infection among patients without symptoms was low, the high percentage of positive cases showing no symptoms suggests that regularly screening patients with and without symptoms may be an important strategy in controlling the pandemic. At-home sample collection can facilitate such screening.

### Poster 100. Results of Early SARS-CoV-2 Sero-Epidemiological Surveys in the WHO Eastern Mediterranean Region in 2020-21

**E. Aly**, L. Al Ariqi, A. Barakat, A. Abubakar, A. Rashidian
World Health Organization Eastern Mediterranean Regional Office, Cairo, Egypt
**Background:** The emergence of a novel virus in human populations raises multiple questions on its epidemiology, distribution, clinical features and risk factors for infection. These unknowns challenge the control of this virus's spread in communities. The emergence of SARS-CoV-2 and its rapid spread worldwide has urged international cooperation and collaboration in research to fill key knowledge gaps needed to drive the response. The WHO has spearheaded these efforts through 'Unity Studies', which included developing a master population-based sero-epidemiological protocol and supporting its adaptation and implementation in countries. **Methods:** Between January 2020 and September 2021, the WHO Eastern Mediterranean Office and Country Offices supported 11 low- and middle-income countries (Afghanistan, Egypt, Jordan, Lebanon, occupied Palestinian territory, Pakistan, Somalia, Sudan, Syria, Tunisia, Yemen) to conduct cross-sectional household sero-epidemiology surveys for population aged one year and above. The main objectives of the surveys were to identify levels of immunoglobulin (IGs) prevalence among the studied populations, monitor their trends over time to understand disease spread, advance understanding of their association to clinical presentation of the disease and identify risk groups. Several teleconferences were held with countries' Ministries of Health and Principal Investigators to provide technical support and document experiences. **Results**: Between June 2020 to August 2021, 15 rounds of data collection were completed in the 11

countries. During the last 6 months of 2020, the levels of IGs ranged between 0.3% and 39%. In the first 4 months of 2021, the levels were reported up to 42% in some countries. This prevalence almost doubled in the second four months of 2021 to reach up to 74%. Several studies were conducted in convenient manner due to security issues and limitations of sample transportation systems. **Conclusions:** Results of the SARS-CoV-2 sero-epidemiological surveys early in the pandemic has complemented the epidemiological surveillance efforts of countries and supported their decision making on public health measures. These efforts have also supported building countries capacities in designing and conducting household surveys.

### Poster 101. Automated Classification of COVID-19 Illness Severity among Pregnant People

**S. Newton**[1], L. Gosdin[1,2], R. Boyd[3], C. Hilton[3], K. Woodworth[1], V. Tong[1]
[1]Centers for Disease Control and Prevention COVID-19 Response, Atlanta, GA, USA; [2]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, USA; [3]Georgia Tech Research Institute, Atlanta, GA, USA

**Background:** Pregnant people are at increased risk for severe COVID-19 illness compared to non-pregnant people. CDC receives data from health departments on laboratory-confirmed SARS-CoV-2 infections in pregnant people (cases). An automated approach to classifying illness severity was implemented to identify risk factors for severe disease, but it lacks validation. **Methods:** CDC's Surveillance for Emerging Threats to Mothers and Babies Network identifies cases through case reports, laboratory reporting, and vital records; data are abstracted from existing data sources (e.g., medical records) into electronic forms with indicator variables and free-text fields. Using data reported as of August 6, 2021, illness was classified into severity categories (asymptomatic, mild, moderate-to-severe, or critical) or insufficient information to classify severity. Classification was based on a hierarchy prioritizing indications of more severe disease (intensive care unit (ICU) admission, invasive ventilation, COVID-19 therapies, complications, and death) compared to mildly symptomatic or asymptomatic. The primary approach used indicator variables and keyword searches of free text and was developed to maximize agreement with a clinician's categorization of >600 cases. The secondary approach used indicator variables and natural language processing (NLP) of free text. We applied both approaches to a subset of data to assess concordance. A clinician reviewed discordant and unclassified cases. **Results:** Of 4378 cases, 4350 were concordantly categorized by severity or as having insufficient information (99.4% agreement, kappa= 0.99). The primary and NLP approaches classified severity for 76.9% and 77.2%, respectively, and only 1 of 999 unclassified cases was classifiable by a clinician. Of 28 discordant cases, 15 with clinical notes that mentioned ICU admission were improperly classified by both approaches. The NLP approach correctly classified 7 remaining discordant cases, the primary approach correctly classified 3, and 3 could not be classified. **Conclusions:** Concordance between approaches was high, validating that automated approaches could reduce the need for clinical review to classify COVID-19 severity. Surveillance of illness severity is important to direct clinical and prevention strategies.

### Poster 102. High Throughput Ion Semiconductor Sequencing of SARS-CoV2 Viral Genomes from Patient Samples

**R. Razzaque**, E. Yeboah, L. Boyed, L.J. Tsaknaridis, V. Makris, L. Grenz, S.A. Sevey, J.L. Fontana
Oregon State Public Health Laboratory, Hillsboro, OR, USA

**Background:** In this study, we describe a comprehensive and CLIA-validated set of working protocols for generating high quality SARS-CoV-2 genome sequences from clinical specimens by using the Ion AmpliSeq SARS-CoV-2 Insight Research Panel on the Ion GeneStudio S5 Plus platform by Thermofisher Scientific, which is the only known whole genome sequencing tool using semiconductor technology. The panel allows for targeted sequencing by overlapping amplicons. The understanding of the genetic features of SARS-CoV-2 is essential to track the ongoing pandemic through evolutions of newer viral lineages and their amino acid substitutions and to continuously reevaluate the existing diagnostic procedures, vaccines, and other therapeutic strategies as well as public health interventions. **Methods:** The two major specimen types used in this study were nasal and nasopharyngeal swab from patients infected with SARS-CoV2 with a positive PCR test using the CDC developed multiplex assay having a CT value <30 using the Ion AmpliSeq SARS-CoV-2 Insight Research Panel assay kit (Cat. A51305) following manufacturer's procedure. The Torrent Suite 5.10.1 was used for sequence data analysis using plugins, such as, variantCaller, generateConsensus, SARS_CoV_2_coverageAnalysis and COVID19AnnotateSnpEff. The FASTA files of different viral isolates were then further evaluated using various bioinformatic tools such as GISAID Epicov app, Pango web app, NCBI Nucleotide blast and Geneious Prime Software. The sequence data that passed the QC threshold were submitted to GISAID and GenBank. **Results:** Since April 2021 we have sequenced SARS-CoV-2 genome from about 3000 patients in Oregon with >90% genome coverage from different specimen types which are publicly shared through GISAID and GenBank databases. We identified specific lineages and accompanying amino

acid substitutions that confers increased transmissibility for the variants of concern as described by the US government SARS-CoV-2 Interagency Group Variant classification scheme. Using this CLIA validated approach, our results were reported to state and local health departments and submitting facilities. **Conclusions:** This workflow and accompanying supplemental protocols of sequence data analysis provide a reliable starting point and a complete reference for those seeking to generate SAR-CoV-2 genome sequences using semiconductor technology. Phylogenetic analysis with 3000 SARS-CoV-2 genomes in the GISAID database identified origins and transmission events as well as community spread.

### Poster 103. Timing of Implementation of Global Non-pharmaceutical Interventions for COVID-19 Mitigation — January–June 2020

**L. Kazazian**, E. Sikare, D. Weikum, D. Martin, A. J. Hakim
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Countries across the world initially responded to the COVID-19 pandemic by implementing various non-pharmaceutical interventions (NPI) to slow the spread of disease. Timely and effective NPI implementation is crucial to limit disease transmission, avoid overwhelming health systems, and prevent new variants and the introduction of disease into new locations. While early warnings alerted the world of the pandemic potential of COVID-19, the global and local context that motivated governments to implement NPI remains unexplored. **Methods:** We conducted a content analysis to characterize the use and timing of NPI against COVID-19 during the first six months of the pandemic (January–June 2020). Information was abstracted on implemented NPI from media reports and official government and United Nations webpages for 200 countries and territories. Timing of NPI implementation was assessed relative to the first reported case in a country or territory as well as the World Health Organization (WHO) Public Health Emergency of International Concern declaration on January 30, 2020, and pandemic declaration on March 11, 2020. **Results:** Nearly all countries and territories (98.5%) enacted international travel restrictions by June 30, 2020, while face mask wearing requirements were implemented least frequently (57.0%). Travel-related NPI were applied a median of 14 days before other NPI, and most countries and territories implemented international travel restrictions (56.7%) and passenger screenings (65.0%) on or before the date of their first COVID-19 case. The week following the WHO pandemic declaration coincided with a large uptick in application of domestically oriented NPI, particularly business closures (5.5% to 40.0%), academic closures (12.5% to 61.0%), and mass gathering restrictions (16.0% to 55.5%). **Conclusions:** This analysis highlights common patterns in the first wave of COVID-19 NPI and suggests an important role for WHO declarations in prompting action by governments. Results can inform revisions of pandemic alert mechanisms and provide context for future assessments of NPI impact on morbidity and mortality.

### Poster 104. Cost Effectiveness and Decision Analysis for Evaluation of the National Airport Screening Options in COVID-19 Surveillance in Uganda, 2020

**G. Amanya**[1], M.L. Washington[2], J. Harris[3]
[1]Uganda Public Health Fellowship Program, Uganda Ministry of Health, Kampala, Uganda, [2]US Centers for Disease Control and Prevention, Kampala, Uganda, [3]Division of Global Health Protection, US Centers for Disease Control and Prevention, Kampala, Uganda
**Background:** Early during the COVID-19 outbreak, various approaches were utilized to prevent COVID-19 introductions from incoming airport travelers. However, the costs and effectiveness of airport-specific interventions have not been evaluated at Entebbe International Airport to inform future decision-making. **Methods:** We compared three different airport interventions for costs and impact on case counts over a two-week time horizon, the primary outcome was cost per case averted. We took the government perspective. Policy options included(1) no screening, testing, or mandatory quarantine for any incoming traveler; (2)mandatory symptom screening for all incoming travelers with RT-PCR testing only for the symptomatic and isolation of positives; and (3) mandatory quarantine and one-time testing for all, with isolation of persons testing positive. We assumed a 5% prevalence of SARS-CoV-2 infection among incoming travelers, 92% test sensitivity and 98% specificity, and a reproductive number of 2.6(symptomatic) or 1.4 (asymptomatic). We included direct costs and indirect costs. We calculated expected cost per person entering through the airport for each option, and incremental cost effectiveness ratios (ICERs) in US$ per additional COVID-19 case averted. **Results:** Expected costs per incoming traveler were $0 (Option 1), $6 (Option 2), and $502 (Option 3). ICERs per case averted were $156 for Option 2(which averted 2,761 cases compared with Option I), and $4,143 for Option 3 (which averted 8,175 cases). Two-week costs were $0 for Option 1, $430,442 for Option 2, and $33,867,033 for Option 3. The cost-effectiveness of our interventions was modestly sensitive to the prevalence of COVID-19, diagnostic test sensitivity, and testing costs. **Conclusion:** Screening all incoming travelers for symptoms, testing symptomatic persons, and isolating positives (Option 2) was the most cost-effective option for

airport interventions against COVID-19. Higher prevalence of infection among incoming travelers increased cost-effectiveness of airport-specific interventions. This model may be used to evaluate prevention options even to other diseases with similar requirements for control.

### Poster 105. The Development of a Medical Countermeasures Plan and its Implementation During the COVID-19 Pandemic in Nigeria

**A. Aminu-Alhaji**[1], C. Ihekweazu[2], C. Eneh[2], G.S. Joseph[2], M.M. Saleh[1], L. Damisah[3], F. Abba[4], E. Agogo[5], O.B. Ipadeola[1], J. Oladejo[2], F. Husain[1]
[1]Centers for Disease Control and Prevention, Abuja, FCT, Nigeria, [2]Nigeria Center for Disease Control, Abuja, FCT, Nigeria, [3]Office of the National Security Adviser, Abuja, FCT, Nigeria, [4]Public Health England, London, UK, [5]Resolve to Save Lives, Abuja, FCT, Nigeria
**Background:** Medical countermeasures (MCMs) are life-saving interventions used to diagnose, prevent, and treat conditions associated with public health threats. During Nigeria's Joint External Evaluation (JEE) in July 2017, the absence of a national MCM plan highlighted a significant gap in management and insufficient manpower during large scale emergencies. Consequently, an MCM plan was drafted by the Nigeria Centre for Disease Control (NCDC). **Methods:** Nigeria's MCM capacity during public health emergencies was externally assessed following the 2017 JEE assessment. Based on the findings, multi-sector working partners drafted an MCM plan, and a table-top exercise was conducted in December 2018 to review and validate it. The MCM plan was tested during the COVID-19 pandemic, from January 2021 to date. **Results:** The MCM plan highlighted the effectiveness of cross-sector coordination. The plan was activated as part of the COVID-19 response. Government and regulatory authorities waived customary approval steps and import duties for response materials thereby reducing the processing time from an average of 21 days to an average of 7 days. Federal, state, and local governments, development partners and the military provided resources such as personnel and storage space for supply chain coordination. Storage capacity increased from approximately 400 sqm to approximately 8,000 sqm. Government agencies, with established logistics infrastructure, facilitated the transportation of commodities and safe passage at security checkpoints especially during lockdown. **Conclusion:** The development of the MCM plan has been critical to facilitate Nigeria's COVID-19 response. Through established and new partnerships, commodities were received, stored, and deployed in a more coordinated and efficient manner, highlighting the importance of strengthening systems and partnerships in responding specially to COVID-19 pandemic and public health events in general. While response efforts are still ongoing, successes and lessons learned continue to be documented by NCDC to modify the MCM plan and guide future public health emergencies.

### Poster 106. Exploration of Laboratory Capacity to Support SARS-CoV-2 Variant Surveillance in New York City

**A. Geevarughese**, L. Malec, J. Sullivan Meissner, E. Jacobs, R. Burns, K.A. Alroy, E.H. Lee, R. Paneth-Pollak, J.A. Ackelsberg, A. Fine
New York City Department of Health and Mental Hygiene, Long Island City, NY, USA
**Background:** To enhance SARS-CoV-2 variant surveillance, the New York City (NYC) Department of Health and Mental Hygiene (Health Department) conducted outreach to clinical laboratories to determine their capacity to store and transfer specimens with positive SARS-CoV-2 molecular test results and adequate cycle threshold (Ct) values (≤32) to the NYC Public Health Laboratory (PHL) for whole genome sequencing (WGS). **Methods:** Telephone and email outreach was conducted with laboratories electronically reporting ≥ 80 positive polymerase chain reaction (PCR) test results from NYC residents to the Health Department between January 10–March 10, 2021. Laboratories already coordinating with the Health Department to conduct WGS and those that store specimens off-site or at room temperature were excluded. Eligible laboratories completed a survey regarding reporting of Ct values and specimen storage. Results were analyzed along with PCR reporting volumes from the COVID-19 surveillance system to inform further outreach and capacity-building efforts. **Results:** Of 104 eligible laboratories, 80 (77%) responded to the survey. Fifty-four (68%) reported the ability to retrieve Ct values for individual specimens, with 21 (26%) able to report these electronically. Forty (50%) laboratories reported the ability to store all positive specimens for later retrieval, including 28 (35%) that could store specimens at ≤-70 C°. Barriers to storage included lack of staff and physical space. Sixteen laboratories (20%) stored specimens at ≤-70 C° for at least two weeks. An additional 7 (8.7%) laboratories stored specimens at ≤-70 C° for less than two weeks but had capacity to store for longer periods; 7 (8.7%) other laboratories reported conducting WGS or sending specimens to other laboratories for WGS. These latter 30 laboratories accounted for 17.5% of all PCR tests reported. **Conclusions:** The surveyed laboratories had variable capacity for Ct value reporting and specimen storage. These data enhanced access to SARS-CoV-2 specimens for WGS by identifying laboratories that can store and transfer to PHL specimens appropriate for WGS.

Jurisdictions may employ similar methods to assess local laboratory capacity and identify opportunities for enhancing laboratory processes to support WGS in the event of future public health emergencies.

### Poster 107. How to Support Acute Care Hospitals During a Global Pandemic: Findings from the Maryland COVID-19 Statewide Prevention and Reduction Collaborative (SPARC)

**L.L. Smith**[1], S. Leekha[2], C. Rock[1], P.J. Desai[3], D. Leaphart[3], A.B. Chiao[3], J. Rubin[4], H. Saunders[5], P. Dullabh[3], R. Perlmutter[4]
[1]Johns Hopkins University School of Medicine, Baltimore, MD, USA, [2]University of Maryland School of Medicine, Baltimore, MD, USA, [3]NORC at the University of Chicago, Bethesda, MD, USA, [4]Maryland Department of Health, Baltimore, MD, USA, [5]Johns Hopkins Office of Population Health, Baltimore, MD, USA
**Background:** The Statewide Prevention and Reduction Collaborative (SPARC) is a quality improvement infrastructure formed by the Maryland Department of Health (MDH), Johns Hopkins University, and the University of Maryland. During 2018-2020, SPARC successfully reduced statewide hospital-onset *Clostridioides difficile* infection rates by 33%. In September 2020, SPARC pivoted focus to COVID-19; facilitating weekly webinars with expert-led discussion and peer-to-peer learning of evolving guidance and science related to SARS-CoV-2 transmission and infection prevention in the healthcare setting. This assessment evaluates SPARC's responsiveness to Maryland hospitals' needs and its impact on hospitals' pandemic response. **Methods**: We invited webinar attendees to provide feedback from March to June 2021 using: 1) a survey; 2) interviews; and 3) a group feedback session. The RE-AIM framework (reach, effectiveness, adoption, implementation, and maintenance) guided assessment questions. We reviewed webinar chat box content and participant lists to understand reach. We summarized survey results and used content analysis methods for interviews and feedback sessions. **Results**: Thirty-one participants completed the survey, five participants were interviewed, 53 attended a feedback session. From September 2020-March 2021, SPARC participated in 21 MDH webinars, each with 120-185 attendees, who shared the information with > 480 additional people (Reach). Over 76% of survey respondents indicated that SPARC was very responsive to their information needs (Effectiveness). All participants found SPARC to be a trustworthy information source. Participants shared that discussion on SPARC webinars informed changes in hospital COVID-19 policies e.g., personal protective equipment use, care partner visitation and screening (Adoption, Implementation). Participants emphasized the benefit of a regular forum for discussions of evolving COVID-19 related policies and practices (Maintenance). **Conclusions**: SPARC for COVID-19 successfully addressed the needs of Maryland hospitals. SPARC highlights the importance of collaboration between public health and academia and the role of peer-to-peer learning during public health emergencies. SPARC may inform quality improvement collaboratives in other states.

### Poster 108. Household Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV2) in a Prospective Community-Based Study – Dane County, Wisconsin (WI), March 2020—April 2021

**J.L. Temte**[1], S. Barlow[1], M. Goss[1], E. Temte[1], C. Bell[1], C. He[1], A. Bateman[2], A. Uzicanin[3]
[1]Department of Family Medicine and Community Health, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]Wisconsin State Laboratory of Hygiene, Madison, WI, USA, [3]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Assessments of SARS-CoV-2 (SC2) household (HH) transmission clusters most often follow identification of a HH index case in a medical setting. We utilized an ongoing, prospective laboratory-supported community-based influenza study that enrolled school-aged children and family members to evaluate SC2 transmission in HHs where ≥1 member had laboratory-confirmed SC2. **Methods:** The ORegon CHild Absenteeism due to Respiratory Disease Study (ORCHARDS) prospectively enrolls children aged 4—18 years who have ≥2 symptoms consistent with an acute respiratory infection with onset ≤7days prior to enrolment. All consenting HH members are recruited to participate in a HH transmission sub-study. Participants self-collect anterior nasal swab specimens on day 0 (date of home visit) and 7 and 14 days later. Respiratory specimens were evaluated for SC2 using RT-PCR. **Results:** During March 2020—April 2021, 16 of 136 participating HHs (12%) had ≥1 case of SC2. Of 56 cases, 35 (63%) occurred in November 2020, coinciding with peaks of reported SC2 in Dane County and WI. Of 71 individuals residing in HHs with SC2, 56 (77%) were SC2(+) within the 14-day specimen collection window. In 7 (44%) of affected HHs, all individuals were SC2 (+); 5 HHs (31%) had 1 SC2(-) member; 2 HHs (13%) had 2 SC2(-) members; 2 HHs (13%) had 3 SC2(-) members. In 13 HH (81%) with possible transmission events, initial cases—based on timing of RT-PCR positivity and/or symptom onset—occurred equally among children of any age (5: 38%), mothers (5: 38%) and fathers (5: 38%) [sum >100% due to coincident symptom onset in 2 HHs]. **Conclusions:** The first known case of SC2 in Wisconsin occurred in a traveler returning from China in January

2020 and the first HH cluster was documented by ORCHARDS in mid-March 2020. This prospective community-based study identified additional HH cases occurring within 14 days of a HH index SC2 case with acute respiratory symptoms. The data are consistent with high levels of HH transmission, with all members becoming SC2(+) in 44% of affected HHs. The first symptomatic cases of SC2 in HHs appeared to be balanced between children, mothers, and fathers. Peak occurrence of HH cases and clusters reflected community trends in laboratory-confirmed SC2 cases. Person-to-person transmission within HHs may contribute to SC2 spread in communities.

### Poster 109. "*Public health is all about the last adopters*": COVID-19 Vaccine Uptake in San Francisco According to the Diffusion of Innovation Theory

**L. Gutierrez-Mock**[1], A. Nickerson[1], L. Buback[1], S. Welty[1], L. Anciete[1], W. Enanoria[2,3], M. Reid[1,4,5]
[1]Institute for Global Health Sciences, University of California, San Francisco, CA, USA, [2]Department of Epidemiology and Biostatistics, University of California, San Francisco, CA, USA, [3]San Francisco Department of Public Health, San Francisco, CA, USA, [4]Division of HIV, Infectious Diseases and Global Medicine, University of California, San Francisco, CA, USA, [5]School of Medicine, University of California, San Francisco, CA, USA
**Background:** Increasing the COVID-19 vaccination rate is an urgent public health issue. However, the reasons for vaccine hesitancy and decline are varied. This study sought to better understand vaccine uptake and hesitancy among San Francisco residents. **Methods:** Semi-structured qualitative telephone interviews were conducted from July 20 - August 31, 2021, with key informants from the SF Department of Public Health (SFDPH) vaccine call center (N=14) and with San Francisco residents (ages 13+) who tested for COVID-19 within the prior two weeks from the SFDPH COVID testing database (N=83). Adult parents/guardians responded for their minor children. Interviews were conducted in English and Spanish and ranged in length from 20 - 35 minutes. Interviews were audio recorded, transcribed, translated into English, and rapidly analyzed using matrix analysis methodology. Participant responses were categorized by vaccination timing according to the Diffusion of Innovation Theory. **Results:** The vast majority of vaccine innovators, early adopters, and early majority participants reported negative views about unvaccinated individuals, including labeling them as annoying, selfish, ignorant, and anti-vaxxers. In contrast, late adopters and last adopters/decliners reported feeling scared, confused, overwhelmed, and discussed vaccine concerns. The social pressure and judgmental attitudes from those who vaccinated earlier were unhelpful and unlikely to change the minds of unvaccinated participants. The group with the best understanding of how to change the minds of unvaccinated individuals were the late majority, who discussed specific recommendations based on their own experiences with recent vaccination. Furthermore, key informants discussed their approach to vaccine hesitancy, including heavy employment of motivational interviewing and health coaching skills. **Conclusion**: Many negative perceptions of unvaccinated individuals by those who vaccinated earlier are unwarranted and lead to feelings of frustration among the unvaccinated. Those who have been recently vaccinated may provide the best insight into specific interventions to increase vaccine uptake among unvaccinated people.

### Poster 110. In Vitro Accessibility of Novel Anti-COVID-19 Treatment Strategy by FANA-conjugated Antisense-Oligonucleotides

**Y. Tan**[1], N. Lai[1,2]
[1]R&D Division, US Medigene. Inc., Rockville, MD, USA, [2]R&D Division, Vast Sea Biotechnology, Inc., Rockville, MD, USA
**Background:** Coronavirus disease (COVID-19) is a new contagious disease outbroke in Wuhan, China, 2019 and spread widely around the world which caused by SARS-CoV-2. In 2020, WHO has announced pandemic and still ongoing. Millions of people are suffering respiratory related symptoms, including pneumonia, dyspnea, hypoxia and respiratory failure in worse cases. There is no a specific anti-COVID-19 drug available in the market yet. Therefore, anti-COVID-19 drug development is huge demand in scientific research field. **Purpose:** To develop and evaluate accessibility of FANA-conjugated Antisense-Oligonucleotides (FANA-ASO) treatment as anti-COVID-19 drug candidate. To develop a novel cell-based platform to evaluate binding affinity against ACE2 for drug/molecule screening, which design to target ACE2. **Methods:** human primary small airway epithermal cells (HSAEC) were cultured and transduced with SARS-CoV-2 N-protein to generate Nprotein-HSAEC. Nprotein-HSAEC were treated with FANA-ASO (FITC conjugated) or vehicle for 48hrs. Nprotein-HSAEC were harvested and detected FITC signal via confocal microscope (FITC channel) and FACS. SARS-CoV-2 N protein expression were confirmed by western blot. **Results:** Nprotein-HSAEC were detected high intensity of FITC signal in significant cell population (FITC-: 44.9%, FITC+: 55.1%) via FACS (Fig 1A-C). Live cell images in microscope were observed FITC signal in Nprotein-HSAEC (Fig. 1D). Both FACS and live cell images indicate naked FANA-ASO-FITC internalized Nprotein-HSAEC successfully without additional molecular assistant (such as lipofectamine). Western blot confirmed SARS-CoV-2 N protein expression was significantly suppressed under FANA-ASO-FITC treatment (Fig

1E). **Conclusion:** FANA-ASO is a novel anti-COVID-19 treatment strategy and showed significant therapeutic efficiency (in vitro) against SARS-CoV-2 N protein.

### Poster 111. Estimation of SARS-CoV-2 Global and Regional Seroprevalence over Time

**H. Ware**[1], I. Bergeri[2], M. Whelan[1], L. Subissi[2], A. Nardone[2,3], M. Valenciano[2,3], HC Lewis[2], N. Bobrovitz[4], M.D. van Kerkhove[2], D. Buckeridge[5], R. Arora1[6]
[1]Centre for Health Informatics, Cumming School of Medicine, University of Calgary, Canada, [2]World Health Organization, Geneva, Switzerland, [3]Epiconcept, Paris, France, [4]Temerty School of Medicine, University of Toronto, Canada, [5]Department of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, Canada, [6]Institute of Biomedical Engineering, University of Oxford, England, UK
**Background:** As the COVID-19 pandemic continues, it is challenging to pinpoint the true extent of SARS-CoV-2 infections and immunity. Serosurveys are crucial data for understanding humoral immunity and hence the extent of past infection and vaccination. However, serosurveys vary in quality, omit some geographic regions, and are sparsely distributed over time. Pooling results from high quality serosurveys allows estimation of global and regional seroprevalence and ascertainment over time. **Methods:** We conducted a living systematic review of national or subnational SARS-CoV-2 serosurveys in the general population published to May 2022. We included data from yet unpublished serosurveys from low and middle-income countries (LMIC) aligned with the WHO Unity protocol. We stratified the Americas and Europe regions by high-income countries (HIC) vs. LMIC. For each WHO region with available data, we produced pooled estimates of seroprevalence from Jan 2020 to Mar 2022. We did so by meta-analyzing serosurveys in each country within 3-month rolling windows to generate seroprevalence time series. We estimated seroprevalence for each WHO region as the population-weighted average of seroprevalence in each country with available data, and global seroprevalence as the population-weighted average of regional estimates. We fit a generalized additive model to regional and global estimates to visualize the trend of seroprevalence over time. **Results:** We identified data from over 700 serosurveys across 86 countries. Combined infection and vaccine-induced seroprevalence increased to 63.8% globally in Oct 2021. There was considerable variation in dynamics and data robustness across WHO regions. Seroprevalence ranged from 30.4% seropositive in the Americas (LMIC) in Apr 2021 to over 95% seropositive in Africa, Europe (HIC) and the Americas (HIC) in Mar 2022. The ratio of infection-induced seroprevalence to confirmed cases in Mar 2022 varied across WHO regions from 2:1 in Europe (HIC) to 117:1 in Africa. **Conclusion:** This research provides insight into SARS-CoV-2 infection and ascertainment over time, particularly in data-scarce geographical regions. Our results show substantial case under-ascertainment globally, emphasizing the importance of serosurveys to complement case data for global COVID-19 surveillance.

### Poster 112. SARS-Cov2 Case Detection Using Event-Based Surveillance System: Lessons Learn from Senegal, February 2 to September 30, 2020

**O. Seck**[1], L. Roka[2], J. Coraldine[3], S. Abdoulaye[1], A. Mangane[1], N.L. Dieye[1], M.M. Ndiaye[1], B. Ndoye[2], B. Diop[1], J. Ting[3], M. Ndiaye[1,2], O. Pasi[3]
[1]Ministry of Health Senegal/MSAS, Dakar, Senegal, [2]FETP-Senegal, Dakar, Senegal, [3]U.S. Centers for Diseases Control and Prevention-Senegal Office, Dakar, Senegal
**Background:** Over 10 months, a SARS-Cov2 outbreak resulted in over 15,000 positive cases and 500 deaths in Senegal. The country response benefited from an event-based surveillance (EBS) system put in place a few months before the pandemic. We evaluated this system's contribution and sustainability to SARS-Cov2 case detection in Senegal. **Methodology:** A digitalized EBS platform was setup to collect information on triggers coming from the community. The platform functioned 7 days a week and 24 hours per day, supported by a team composed of data clerks, surveillance technicians, and doctors. 20 officers rotated to ensure the system was always functional. 9 hotlines were available including one free of charge to callers. At the beginning of the outbreak, SARS-Cov2 data collection and analysis were conducted manually. In the end, all data were uploaded into the digitalized-EBS framework. We analyzed the data using Excel and Stata.15. **Results:** Overall, 10,760 calls were received between February 2nd to September 30th, 2020 (Average: 320 calls per week), coming from all 14 regions. Calls were mostly from the Dakar Region 9,134 (85%), likely due to a more aggressive communication strategy. Through identification using the name, surname, and cellphone number, 400 calls were noted to be the same callers calling multiple times. A total of 2,817 (26% of all calls) were made by callers who were later laboratory-confirmed cases of SARS-Cov2. Investigation of these callers (cases and their contacts) contributed to 19% (14,768) of all lab-confirmed cases, in which 6,140 lab-confirmed cases were asymptomatic contacts. The cost of setting the system was estimated to be 46,278 USD, partially supported by partners. Sixteen of 20 (80%) of those working on EBS

were salaried permanent staff. **Conclusion:** EBS, made significant contributions to SARS-Cov2 detection. Our results suggest including the EBS system into routine surveillance even though sustainability challenges remain.

### Poster 113. Combating Further COVID-19 Waves: Significance of Crisis Communication for Vaccination Compliance

S. Omidoyin
American University of St. Vincent School of Medicine, Kingstown, St. Vincent & Grenadines
**Background:** The outbreak and global spread of COVID-19 in November 2019 took the world by surprise. Policy makers have worked and still working with theoreticians, scientists, and public health experts, as there were and still are many unknowns, especially regarding mutation properties of virus variants. A lot of viral evolution comes down to statistics. A particular mutation may confer the increased ability of SARS-CoV-2 to evade antibodies or increase transmissibility. There are growing concerns whether these variants will dampen the effectiveness of available vaccines and escape recognition by vaccine-induced immunity. **Methods:** One-to-one interviews (using semi structured questionnaire) with male and female respondents of various ages in Kingstown, Saint Vincent and the Grenadines, April 2021. Two hundred and sixteen (216) respondents (132 males, 84 females) were interviewed. Archival study/secondary data analysis of relevant literatures completed the mixed methods approach. **Results:** 37.0% of participants responded that they have received at least a dose of the COVID-19 vaccines. 63.0% have not being vaccinated. When asked a probing question to state reasons for not receiving COVID-19 vaccines; 44.0% stated mistrust of the health institutions, 26.5% stated concern for vaccines' side effects, 26.5% stated concern for breakthrough infections despite vaccination, 3.0% stated other concern. **Conclusions:** Many individuals are still hesitant about receiving COVID-19 vaccines. Effective public health measures, such as social distancing, limiting the size of gatherings, and wearing masks, will be needed for at least several more months, and potentially longer. While variants do pose a real threat to vaccines effectiveness, the available vaccines remain potent tools in fighting the pandemic. And this underscores the importance of a global approach to surveillance, tracking, and vaccines deployment. Frontline workers have a key role in helping patients/clients make decisions about vaccination. Providing evidence-based information will be particularly important in an environment of polarization and mistrust.

### Poster 114. Participatory Surveillance Improves COVID-19 Forecasting of Case Trends: Brasil Sem Corona

**O.B. Leal-Neto**[1], S. Wittwer[1], N. Divi[2], D. Paolotti[3], G. Lichand[1]
[1]Department of Economics, University of Zurich, Zurich, Switzerland, [2]Ending Pandemics, San Francisco, CA, USA [3]ISI Foundation, Torino, Italy
**Background:** Participatory surveillance (PS) has shown several applications in public health settings by detecting disease outbreaks early. With the occurrence of the COVID-19 pandemic, there is a demand for complementary sources of up-to-date information to complement the traditional surveillance systems (TS). This study compared forecasting models using PS and TS data to predict cases trends in Brazilian cities. **Methods:** We complemented traditional COVID-19 data from three Brazilian cities with PS data collected through the Brazil Sem Corona platform from March to October 2020. Using linear auto-regressive forecasting models we compared forecasts from a univariate baseline model with forecasts from a bivariate combination model which integrates PS and TS data to assess the value added from the PS data inclusion. For each city, we estimate a 1-day, 7-day, and 14-day ahead forecast. **Results:** While we find ambiguous results in the models for the 1- and 7-day forecasts across the cities, the root mean square error (RMSE) shows slightly higher forecasting accuracy in the combination model for the 14-day horizon. The RMSE decreased by 3% concerning the baseline model. This indicates that PS data can improve forecasting accuracy under more significant uncertainty, usually found in longer forecast horizons. Even though most participants did not receive a test, the system captured a complementary signal, creating a hybrid model combining TS and PS information and providing accurate results up to 14 days in advance compared to a baseline model. Additionally, since PS can include subsets of the population missed by TS systems, this complementary data allows for inclusion of information from a broader population. **Conclusion:** The PS network can capture patients that are overlooked by traditional sources. This includes individuals who do not seek medical attention in clinics or hospitals, leading to underreporting cases. The inclusion of PS data is essential as it captures data at the community levels, generating near real-time data and supporting public health departments to have an additional data layer in their disease surveillance systems.

### Poster 115. Measuring COVID-19 Vaccine Impact on Confirmed Cases in Virologically Changing Settings

**M. Rondy**[1], L. Gobern[2], L.F. Quezada[1], D.A. Campos[1], L. Parra[1], E. Balsells[1,3], M. Ghiselli[4], C. Jarquin[1]

[1]Pan American Health Organization, Guatemala City, Guatemala, [2]Ministry of Public Health and Social Assistance of Guatemala, Guatemala City, Guatemala, [3]University of Edinburgh, Edinburgh, Scotland, [4]Pan American Health Organization, Washington, DC, USA
**Background:** In 2021, COVID-19 vaccination was implemented gradually in the Americas. In most countries, phased introduction prioritized healthcare workers and older adults. Non-pharmaceutical public health measures continued as a tool to reduce COVID-19 cases. As vaccination activities were deployed, variants of concern were detected and COVID-19 cases increased significantly. To control for changing virological patterns over time, we measured the impact of COVID-19 vaccine introduction by age groups, using non-eligible population group as a reference population in four countries of the Americas. **Methods:** Using national databases of confirmed COVID-19 cases between July 1, 2020, and July 31, 2021, we measured the impact of COVID-19 vaccination in adults eligible for vaccination during different phases of vaccine implementation (groups of 50-59, 60-69, and ≥70 years) using the age group of 0-49 years as reference in the United States (US), Mexico (MX), Guatemala (GTM), and Colombia (COL). We compared ratios (as a percent change) of eligible groups over the reference group for confirmed COVID-19 cases before and after vaccine introduction in eligible groups. **Results:** Between pre- and post-vaccination periods, reductions in the ratio of confirmed COVID-19 cases among adults aged ≥50 years versus those <50, were 23.5% (±0.6) in the United States, 38.1% (±1.4) in Mexico, 19.4% (±0.3) in Guatemala and 23.3% (±0.6) in Colombia. Specific reductions in the ratio of COVID-19 cases by age groups (50-59, 60-69, and ≥70 over those aged 0-49 years) ranged from 18.2% (±0.4) to 35.7% (±1.2) in the United States, 31.8% (±1.1) to 50.0% (±2.5) in Mexico, 13.3% (±0.2) to 28.6% (±1.2) in Guatemala and 10.0% (±0.5) to 40.0% (±1.7) in Colombia. **Conclusions:** Ratio analysis is a practical approach to measure the impact of phased vaccine introductions in evolving virological and epidemiological settings. Validating this approach using multi-country data contributes to vaccine impact data that can support vaccination programs and policies.

### Poster 116. A Vision for Integrated Surveillance and Response Based on Lessons Learned from the COVID-19 Pandemic

**P.J. Nicholas**, J.D. Freeman
Johns Hopkins Applied Physics Laboratory, Laurel, MD, USA
**Background:** During the national response to COVID-19, many government agencies came together with the common goal of curbing the spread and lessening the impact of infection. However, it became evident early on that critical data for understanding the state of the pandemic did not exist or was not collected; public health surveillance systems were not sufficiently robust or were inaccessible to broader audiences; methods for analyzing available data were not standardized or transparent; and the existing models for forecasting were not sufficiently developed or validated. The data and analytics capabilities that did exist were not sufficiently integrated and provided disparate and sometimes contradictory outputs to their users. **Methods:** A national Integrated Surveillance and Response (ISR) capability would provide an end-to-end system for collecting and processing critical public health information, provide a robust analytic platform for analysis, support transparent and validated forecasting, and leverage analytic techniques to plan, schedule, and allocate resources. Neither a silver bullet nor an autonomous system, an ISR capability rather provides critical information to support the government and its partners make better and more defensible decisions faster. This increases the likelihood of maximizing positive health outcomes during a public health emergency, while minimizing social and economic disruptions. **Results:** Critical to success are sufficient data pedigrees, thorough model verification and validation, and the use of transparent methodologies to ensure outputs are trusted and defensible. Without trust and defensibility, a system simply won't be used. The Johns Hopkins Applied Physics Laboratory has provided analytic support across the National Response since March 2020. This unique opportunity has provided us a deep understanding of the most important capabilities required to overcome the data and analytic shortfalls experienced during the pandemic, and to chart a path forward to achieving a national ISR vision. **Conclusions:** We will discuss the components, design characteristics, and functional requirements necessary to engineer, deploy, and sustain an ISR system, and describe a scenario to provide concrete examples of the benefits such a framework would provide to the nation.

### Poster 117. Translating Theory into Action: Strengthening ESAVI and Vaccine Safety Surveillance during COVID-19 Vaccine Implementation in Guatemala

**S. Santamarina**[1], J. Hernández[2], F. Velásquez[1], L. Gobern[2], I.L. Contreras-Roldán[1], E. Balsells[1,3], M. Rondy[1], C. Jarquin[1], E. Gaitán[2]
[1]Pan American Health Organization, Guatemala, Guatemala, [2]Ministerio de Salud Pública y Asistencia Social, Guatemala, Guatemala, [3]University of Edinburgh, Edinburgh, UK

**Background:** Roll-out of COVID-19 vaccines in Guatemala began in February 2021. As with other vaccines, their use may be associated with undesirable effects that require rapid identification, response, and documentation to ensure safety is monitored. We describe the impact of activities and initiatives carried out to support and strengthen ESAVI surveillance of COVID-19 vaccines by the Ministry of Health. **Methods:** Using WHO guidelines, national ESAVI surveillance protocols were updated by the Ministry's Department of Epidemiology, National Regulatory Agency and key health sector stakeholders. An intersectoral committee of national experts was established in February 2021 to evaluate serious adverse events (CERASV) and determine their association with vaccination. Ten two-day regional workshops were conducted to train clinic and hospital Ministry, Social Security and Military health services personnel on adequate implementation of updated protocols. Workshops were replicated at the local level, assisted by regional liaisons who support ESAVI surveillance activities and COVID-19 vaccination. Participants completed pre-and post-workshop assessments. We compared ESAVI notifications received by the Department of Epidemiology from epidemiological week 23 to epidemiological week 37 to assess improvements in surveillance. **Results:** Pre- and post-workshop evaluations of 160 participants in 10 workshops in 9 departments of the country revealed 4.5%-point improvement in knowledge about ESAVI concepts, 31.4%- and 35.8%-point improvements in knowledge about national notification and investigation protocols, respectively. 18/29 health areas have increased ESAVI notification by more than 50%, ten of which have increased surveillance notifications by more than 70% since COVID-19 vaccination began in Guatemala. Five health areas which were previously non-reporting, have increased notification rates by 100%. **Conclusions:** Increases in ESAVI notifications in Guatemala after training and capacity building activities are essential for the development of ESAVI surveillance systems and public health action. Continued attention to ESAVI surveillance is required to strengthen vaccination efforts in Guatemala.

## Epidemiologic Tools

### Poster 118. Crowdsourcing Epidemic Intelligence through EpiCore, 2017-2021

**J.Mantero**, N. Divi, M. Libel, M. Smolinski
Ending Pandemics, San Francisco, CA, USA
**Background**: Early detection through automated processes such as web- and media-based surveillance has become a critical part of epidemic intelligence. These approaches have improved early detection capacities but have also led to an increased volume of signals to be managed. EpiCore is a crowdsourced network of over 3,200 health professionals from 159 countries providing 'ground truths' to improve the specificity of signals used for epidemic intelligence. Requests for information (RFI) are sent to members on a secure platform and findings are compiled online. EpiCore data also feeds into WHO's Epidemic Intelligence from Open Sources (EIOS) Initiative. **Methods**: EpiCore traffic over the past 4 years (Oct 2017-Sep 2021) was analyzed to document utilization. To capture the impact of COVID-19 on system utilization, we also divided the data analysis pre-COVID-19 and during the COVID-19 period using the date of the first COVID-19 RFI (January 1, 2020). **Results**: During the entire observed period, 616 RFIs were sent out globally (76% human health, 24% animal health) with a 64% response rate by members; 58% of RFIs with a response contributed to the epidemic intelligence of the reported events. In the divided data analysis, 426 RFIs were sent through the system pre-COVID-19, with a 64% response rate; 52% of RFIs with a response contributed epidemic intelligence insights. In the COVID-19 period, 190 RFIs were sent through the system with a response rate of 66%; 71% of RFIs with a response contributed epidemic intelligence insights. Of all RFIs with a response, 82% were responded to in under 24 hours. **Conclusion**: EpiCore continues to strengthen epidemic intelligence by providing timely information useful for enhancing risk assessments. The ongoing COVID-19 pandemic has not reduced the response rate or reaction time of EpiCore members.

### Poster 119. Aspen: A Free, No-Code Tool for Genomic Epidemiology in Public Health

**A. Black**[1], S.M. Bell[1], D. Lu[1], P. Ayscue[2], T.J. Chen[1], S. Axelrod[1]
[1]Chan Zuckerberg Initiative, San Francisco, CA, USA, [2]Chan Zuckerberg Biohub, San Francisco, CA, USA
**Background**: The SARS-CoV-2 pandemic response has substantially expanded the application of pathogen genomic data to inform public health decision making. Unprecedented volumes of pathogen genomic data pose new challenges for public health departments learning to manage, analyze, interpret, and take action from genomic data. We aim to lower these barriers through development of a no-code, free software tool for supporting applied genomic epidemiology. **Methods**: We developed an open-source, cloud-based, GUI platform where public health users can manage, track, analyze, and interpret their genomic data without needing to code. Users upload consensus genomes and non-identifiable metadata. The tool provides automatic Pango lineage assignment, linkage to UShER for phylogenetic placement, and point-and-click creation of phylogenetic trees with Nextstrain Augur. To facilitate

accurate epidemiologic interpretation of these trees, Aspen integrates publicly-available sequence data alongside user-selected samples of interest, ensuring stable estimates of molecular clocks and tree structure. We released Aspen to California-based departments of public health in May 2021 in conjunction with wet lab, bioinformatics, and genomic epidemiology training and user support. User feedback was collected through interviews and surveys. **Results**: Aspen has been successfully integrated into SARS-CoV-2 response, helping users manage and analyze over 14,500 genomes and supporting over 30 outbreak investigations as of Oct 15, 2021. Users report that they can more easily manage the data and generate phylogenetic trees, even without familiarity with the command-line, enabling use cases that would not otherwise be accessible to them. **Conclusions**: The proliferation of sequencing capacity and data have highlighted bottlenecks in genomic data management, analysis, and interpretation by public health agencies. Aspen enables public health practitioners to access and analyze these data easily and is available at no-cost.

### Poster 120. Use of a Toll-free Call Center for COVID-19 Response and Continuity of Essential Services During Lockdown, Greater Kampala, Uganda, 2020

**E. Katana**[1,2], A. Ndyabakira[1,2], D.N. Gonahasa[1], R. Migisha[1], G. Amanya[1], A. Byaruhanga[1], I. Chebrot[2], C. Oundo[2], D. Kadobera[1], L. Bulage[1], A.R. Ario[1,3], D.A. Okello[2], J.R. Harris[4]
[1]Uganda Public Health Fellowship Program, Ministry of Health, Kampala, Uganda, [2]Directorate of Public Health and Environment, Kampala Capital City Authority, Kampala, Uganda, [3]Uganda National Institute of Public Health, Ministry of Health, Kampala, Uganda, [4]Division of Global Health Protection, US Centers for Disease Control and Prevention, Kampala, Uganda
**Background**: Establishment of a call center during public health emergencies is essential in reducing unnecessary calls to emergency telephone systems and providing relevant information to the public. Following the introduction of COVID-19 in Uganda on March 21, 2020, a total lockdown was initiated on March 30, 2020, and lifted in stages through June 30, 2020. On March 25, 2020, a toll-free call center with two hotlines was set up at Kampala Capital City Authority to respond to public concerns about COVID-19 and the lockdown. Call-related data were entered into a database. We documented the set-up and use of the call center and key concerns raised by the public during COVID-19 lockdown. **Methods:** We abstracted data on incoming calls between March 25-June 30, 2020, from the database. We summarized the call data into categories and conducted descriptive analysis of public concerns raised during different phases of the lockdown. **Results:** Of 10,167 calls made, 6,578 (65%) were about health services access, 1,565 (15.4%) about other social services access, and 1,375 (14%) about COVID-19 concerns. Among the 6,578 calls about access to health services, 2,152 (33%) were requests for ambulances for non-COVID-19 emergencies, 1,155 (18%) were about persons stranded at health facilities, and 1,004 (15%) were about mothers in labor. Among the 1,565 calls about other social services, 1,184 (76%) were requests for food and relief items and 158 (13%) were about price hikes for basic goods. Fifty-three percent of the 1,375 calls about COVID-19 response were seeking disease-related information and 360 (26%) were reporting suspected cases. There were no calls about COVID-19 emergencies. **Conclusion:** The toll-free call center was used by the public during the COVID-19 response. Calls indicated gaps in health and social services delivery during the COVID 19 lockdown. Continuity of essential services amidst a public health emergency-related lockdown should be planned accordingly.

### Poster 121. Universal Epidemic Rapid Qualitative Text Coding App: Prototype Demonstration

**G. Earle-Richardson,** C. Nestor, H. Bulambo, C. Prue
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Effective community engagement during epidemics requires quickly collecting and interpreting community feedback about how epidemic response efforts are being received. To gather this type of information, during the 2018-2020 outbreak in the Democratic Republic of Congo (DRC), social scientists collected, coded, and analyzed more than 300,000 unstructured community comments, using a coding framework created during the outbreak. This work highlighted the need for an “off-the-shelf” text coding application specifically designed to capture critical information needs common to epidemics. Coding specialists have designed and tested a universal text coding tool that can be used in a wide range of epidemic emergencies. **Methods:** Starting with the coding scheme used in DRC, developers reviewed peer-reviewed publications identifying common areas of public discussion during Ebola, Zika, COVID-19, influenza (H1N1) and HIV to confirm and expand coding categories. Next, they consulted with coding experts to review the coding architecture and to consider alternatives that would meet a wider range of analytical needs. Next steps will be to assess interrater reliability and to have experienced text coders beta test using existing text data. **Results:** The main coding scheme includes 6 key areas, (each with 10-20 specific codes): 1) disease characteristics; 2) epidemic status; 3) community reactions (how people feel, what they are doing); 4) efforts to control the spread (by government or others); 5) medical care for the ill; and 6) other

community issues. Two additional optional coding schemes: emotions reflected in text strings, and syntax (e.g., question, suggestion, belief, etc.), allow for more in-depth thematic analysis. Lastly, a set of optional special issue "flags" make it possible to identify text segments that can alert coders to operational problems with response activities, rumors/misinformation, or security issues. **Conclusions:** A universal text coding application tailored to epidemics streamlines qualitative data collection and simplifies data triangulation.

### Poster 122. ChainChecker 2.0 – Evaluating Epidemiological and Genomic Evidence for Chains of Transmission

**M.A. Stewart**[1], M. Choi[2], J.C. Eng[1], A. Siva[1], S. Whitmer[2], A. Joyce[2], J. Safstrom[2], J. Klena[2], J. Freeman[1], J. Montgomery[2]
[1]Johns Hopkins Applied Physics Laboratory, Laurel, MD, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The ability to determine epidemiological links between confirmed cases of infection is an integral part of outbreak control. The vast quantity of data available from varying sources coupled with the risk of data entry errors and input irregularities make it challenging to discern epidemiological links. Increasing availability of genomic sequencing information has further complicated outbreak investigations with conflicting data points. The Centers for Disease Control and Prevention (CDC) and the Johns Hopkins Applied Physics Laboratory (APL) recently developed a new version of the ChainChecker application to integrate both epidemiological and genomic Ebola Virus Disease (EVD) data to enhance this process. **Methods:** ChainChecker is an offline application that can import and map fields from existing contact tracing and genetic distance files. Visualizations render the chains of transmission, display longitudinal case information, and enable overlay of genetic distances relative to selected cases. Users can toggle available algorithms to calculate and show estimated exposure windows, suspected Hospital-Associated EVD (HA-EVD) cases, and windows for expected nucleotide changes. Chains of transmission can be viewed in aggregate and filtered on specific underlying case values at the healthcare facility level or in a longitudinal case view. **Results:** Users of the ChainChecker tool were able to visualize existing EVD 2018 – 2020 outbreak data to perform a more detailed analysis focused around the validation of alignment of epidemiological and genomic information for a case or transmission, revealing cases that required further investigation due to genomic evidence. The process of visualizing the transmissions, which can take days to weeks by hand, can now be done in a matter of minutes. **Conclusions:** Based on existing utility, the CDC and APL are collaborating to expand the functionality of ChainChecker to aid in active and retrospective analysis of other disease outbreaks such as COVID-19 and foodborne disease. Future work includes integrating a data anomaly and quality component to help target cases for analysis.

### Poster 123. SeroTracker-ROB: An Approach to Expediting Risk of Bias Assessments for Seroprevalence Studies

**K.C. Noel**[1], N. Bobrovitz[2], C. Cao[3], Z. Li[4], A. Selemon[3], M. Yanes Lane[5], T. Yan[2], R. Arora[6,7]
[1]Faculty of Medicine and Health Sciences, McGill University, Montreal, Quebec, Canada, [2]Temerty Faculty of Medicine, University of Toronto, Toronto, Ontario, Canada, [3]Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada, [4]Faculty of Engineering, University of Waterloo, Waterloo, Ontario, Canada, [5]COVID-19 Immunity Task Force, McGill University, Montreal, Quebec, Canada, [6]Centre for Health Informatics, University of Calgary, Calgary, Alberta, Canada, [7]Institute of Biomedical Engineering, University of Oxford, Oxford, UK
**Background:** SARS-CoV-2 seroprevalence studies provide key epidemiological information but are of varying quality. While quality appraisal is an important part of evidence synthesis, it can be time-consuming and subjective. We aimed to evaluate the efficiency and reliability of an approach to partially automate the risk of bias assessment for seroprevalence studies. **Methods:** We developed the SeroTracker-ROB approach, which applies a decision rule to data routinely extracted in a systematic review on prevalence to determine a risk of bias assessment (low, moderate, high). Nine key data points mapping to the items of the Joanna Briggs Institute (JBI) Checklist for Prevalence Studies are extracted. The decision rules consider different permutations of these data points to compute a risk of bias assessment. The decision rules were informed by published guidance on estimating disease prevalence, opinions of experts in evidence synthesis and epidemiology, and our experience reviewing thousands of seroprevalence studies. As part of a living systematic review on SARS-CoV-2 seroprevalence we evaluated as feasibility (proportion of studies for which the approach yielded an assessment), efficiency (paired t-test comparing time per SeroTracker-ROB versus manual assessment within reviewers), and reliability (intraclass correlation measuring consistency of the SeroTracker-ROB approach compared to the final manual assessment for ROB) of the SeroTracker-ROB approach. **Results:** The SeroTracker-ROB approach yielded a ROB for 100% (n=2,472) of articles in the SeroTracker database and was significantly faster at deriving assessments compared to the manual

approach in a 50-study pilot with nine reviewers (0.61 vs. 2.88 minutes/article, p<0.001). ROB assessments generated using the SeroTracker-ROB approach showed good reliability with manual assessments conducted by two independent reviewers 0.77 (95% 0.75-0.79). **Conclusions:** The SeroTracker-ROB approach was feasible to implement, significantly reduced the time to assess risk of bias, and was reliable. This approach may support efficient and reliable evidence synthesis of infection prevalence data with particular value during infectious disease outbreaks and pandemics.

### Poster 124. Contact Tracing Knowledge, Attitudes, and Behaviors: A Cross Sectional Study of Adults in the Maryland General Population

**P. Carroll**, S. Linden, H. Sim, A. Rakochi, A. Allnutt, B. Blouse, M. Pearlowitz, K. Feldman
Maryland Department of Health, Baltimore, MD, USA
**Background**: Contact tracing is a widely used tool to mitigate the spread of COVID-19, which functions by isolating those who have tested positive for COVID-19 and quarantining those who were exposed. To be effective, contact tracing relies on individuals' consent to participate and provide information. We aimed to assess Maryland residents' knowledge, attitudes, and behaviors towards contact tracing. **Methods**: This study was cross-sectional, and study participants consisted of a convenience sample of Maryland residents, 18 years or older, who completed a web-based survey from June to September 2021. Participants were recruited through community partners and the Maryland Department of Health and local health department social media platforms. **Results**: We received 1,537 responses, 1,118 of which were complete. The majority of survey respondents identified as female (78%) and white (77%), with over half (53%) being 51 years or older. All Maryland jurisdictions were represented, with 64% of respondents from largely populated jurisdictions in central Maryland. Respondents overwhelmingly (92%) indicated they are likely to speak with a contact tracer about an illness or exposure. More than half of those unlikely to speak to a contact tracer cited, "I don't want the government in my business" as the reason for not participating. Additionally, 97% said they know how to safely isolate or quarantine, which was substantiated in that only 8% incorrectly selected, "if you are not feeling sick, attend work or school" as a quarantine/isolation recommendation. **Conclusions**: In this survey population, we saw a high understanding and likelihood to participate in contact tracing. While the respondents are not representative of Maryland's general population, the results indicate that trust can be built and the population educated about public health recommendations. Efforts should be taken to better understand other populations in Maryland and engage with communities with low contact tracing participation.

## Influenza

### Poster 125. Leveraging International Influenza Surveillance Systems and Programs during the COVID-19 Pandemic

**P. Marcenac**, M. McCarron, W. Davis, L.S. Igboh, J.A. Mott, K.E. Lafond, W. Zhou, M. Sorrells, M.D. Charles, P. Gould, C.S. Arriola, V. Veguilla, E. Guthrie, V.G. Dugan, R. Kondor, E. Gogstad, T.M. Uyeki, S.J. Olsen, G.O. Emukule, S. Saha, C. Greene, J.S. Bresee, J. Barnes, D. Wentworth, A.M. Fry, D.B. Jernigan, E. Azziz-Baumgartner
Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** A network of global respiratory disease surveillance systems and partnerships has been built over decades in response to the persistent threat of seasonal, zoonotic, and pandemic influenza. These efforts have been spearheaded by the World Health Organization (WHO), Ministries of Health (MoHs), the U.S. Centers for Disease Control and Prevention (CDC), non-profit organizations, academic groups, and others. We describe how global influenza surveillance systems, programs, and partnerships were leveraged to support the international response to the COVID-19 pandemic, with a particular focus on the work of countries partnered with the CDC Influenza Division (hereafter Influenza Division). **Methods:** We reviewed published literature, organizational webpages, and internal Influenza Division and COVID-19 response records to describe and assess influenza surveillance platforms, activities, and partnerships that were used for SARS-CoV-2 surveillance and evaluations. **Results:** The Influenza Division worked closely with MoHs and WHO to leverage influenza surveillance systems and programs to respond to SARS-CoV-2 transmission. WHO adapted their Global Influenza Surveillance and Response System (GISRS) to allow countries to monitor and report SARS-CoV-2 transmission and strains with technical support from the Influenza Division. Countries used their severe acute respiratory infection and influenza-like illness surveillance systems, respiratory disease laboratory resources, pandemic preparedness plans, and existing population-based studies to track, study, and respond to SARS-CoV-2. The Influenza Division developed a multiplex assay capable of detecting both influenza viruses and SARS-CoV-2 in respiratory specimens. CDC and the non-profit Task Force for Global Health supported countries in their COVID-19 vaccine roll-out plans. **Conclusions:** Despite delays in accessing guidance and testing resources, countries and programs supported by the Influenza Division utilized

influenza surveillance systems and programs for their response to COVID-19. The incorporation of COVID-19 surveillance into existing influenza sentinel surveillance systems and GISRS can facilitate continued global surveillance for respiratory viruses with pandemic potential.

### Poster 126. Naturally Occurring HA Stabilizing Mutations in Low Pathogenic H7 and H9 Influenza Viruses that Impact Viral Replication and Airborne Transmission

**X. Sun**, J.A. Belser, J.A. Pulit-Penaloza, N. Brock, H. Zeng, T.R. Maines
Influenza Division, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Airborne transmissibility is a prerequisite for a pandemic influenza virus, and a better understanding of how zoonotic influenza viruses evolve to acquire a transmissible phenotype is important for pandemic preparedness. Previous studies with recombinant H5N1 mutant viruses demonstrated that a mutation in the HA, resulting in a lowered threshold pH for fusion activation, was indispensable for airborne transmission in the ferret model. In recent years, human and avian H7 and H9 isolates with lower pH thresholds for fusion have emerged and it is important to understand whether such H7 and H9 viruses present an increased pandemic risk. **Methods:** Two H7 and H9 low pathogenic avian influenza (LPAI) viruses associated with human infection, and their isogenic counterparts bearing an HA mutation (H9 HA1-Y17H, H7 HA2-E64K) that emerged in natural isolates and modulates the threshold pH for HA fusion, were rescued. All viruses were evaluated for fitness in both in vitro and vivo ferret models. **Results:** Regardless of subtype, both pairs of wildtype and mutant viruses exhibited comparable replicative capacities in a human bronchial epithelial cell line (Calu-3) and in ferret primary nasal and tracheal cell cultures. The recombinant viruses with lower pH thresholds for fusion exhibited a modest enhancement in transmission in a respiratory droplet ferret transmission model, which was not strongly associated with virus shedding in nasal washes. However, significantly higher levels of acid stable recombinant viruses were detected in airborne particles (>4μm) exhaled from infected animals compared with viruses displaying a higher pH threshold for HA fusion. **Conclusions:** Collectively, these data support the capacity for low pathogenic avian influenza viruses to maintain a high degree of infectivity and replication in mammals while possessing a range of fusion pH thresholds (pH 5.3-5.9). The transmission phenotypes of the H7 and H9 viruses with lower pH thresholds for fusion and the detection of elevated levels of airborne virus in exhaled breath of donor animals offers a plausible link between HA acid stability and airborne transmissibility in mammalian hosts and warrants further investigation.

### Poster 127. Influenza Transmission during the COVID-19 Pandemic in Nine Tropical Asian Countries

**W.W. Davis**[1,2], J.A. Mott[1,2], S.J. Olsen[1]
[1]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Thai-US CDC Collaboration, Nonthaburi, Thailand

**Background:** Low global influenza circulation was reported during the coronavirus-19 (COVID-19) pandemic; nonpharmaceutical interventions (NPIs) for COVID-19 may have contributed to this. We explored relationships between NPIs and influenza circulation in tropical Asian countries. **Methods:** We identified countries that reported influenza surveillance to WHO (> 50% of weeks) since 2015 and had data on the implementation timing of 10 different NPIs categorized in the Oxford Stringency Index (ordinal data combining geographic scope of implementation and degree of restrictiveness). Using data from 2015-2019, we constructed expected seasonal influenza epidemic curves for each country from March 2020 to June 2021 and compared the timing, duration, and intensity with observed data. We used multivariate regression to test associations between the ordinal NPI data four weeks before the expected 2020/21 seasons and presence of an epidemic, peak intensity, and average percent positivity across the epidemic. **Results:** Data from nine countries (Bangladesh, Indonesia, India, Cambodia, Lao PDR, Malaysia, Singapore, Thailand, Vietnam) predicted 18 seasonal epidemics from March 2020 to June 2021; 7 epidemics were observed. Of these, 5 started 6-24 weeks later, and all were 4-21 weeks shorter than expected. Five epidemics had lower peak intensity than expected, and all but one had lower average percent positivity across the epidemic. All countries implemented all NPIs to some degree. Each increased level of school closure reduced risk of a seasonal epidemic by 43% (incidence rate ratio 0.57, 95% confidence interval [CI]: 0.34, 0.95). Each increased level of cancelling public events reduced the average percent positivity across the season by 44% (95% CI: 0.39, 0.82) and each increased level in restricting domestic travel reduced the average seasonal percent positivity by 41% (95% CI: 0.36, 0.96). Mask mandates, border closures, and stay at home orders were not associated with changes. **Conclusions:** Among the countries assessed, the 2020/21 seasonal epidemics tended to be delayed, shorter, and less intense than previous epidemics. Although layered NPIs are difficult to tease apart, school closings, canceling public events and restricting domestic travel before influenza circulation reduced seasonal influenza transmission.

### Poster 128. The Changing Pattern of Influenza Viral Infections amid COVID-19 Pandemic: Results from Egypt Integrated Sentinel Surveillance for Acute Respiratory Infections, Egypt 2020-2021

**M. Fahim**[1], H. Abu ElSood[1], B. AbdElGawad[1], A. Naguib[1], W.M. Roshdy[1], S. Afifi[2], M. Abdel Fatah[1], A. Eid[1], A. Mohsen[3]

[1]Ministry of Health and Population, Cairo, Egypt, [2]Consultant for Ministry of Health and Population, Cairo, Egypt, [3]National Research Center, Cairo, Egypt

**Background:** WHO called for integrating COVID-19 and influenza surveillance to monitor epidemiological trends of the viruses and characterize virologic features for guiding interventions. Studies indicated that cocirculation of multiple acute respiratory viruses (ARVs) can lead to competitive or cooperative forms of pathogen–pathogen interactions resulting in interlinked epidemiological patterns of infection. A change in influenza viral infection pattern noticed in 2021 compared to 2020 through Egypt Integrated Acute respiratory infections (ARI) surveillance. This study aims at describing the virological and epidemiological characteristics of influenza infections pattern amid COVID-19 pandemic. **Methods:** Egypt ARI System involves 16 ILI and SARI sentinel sites distributed all over the country for monitoring ARV infections. Patients enrolled are swabbed to be tested for influenza type and subtype, and SARS-CoV-2 by PCR. Data from March 2020 to August 2021 were obtained, descriptive analysis was performed, and rates of influenza and SARS-CoV-2 infections were calculated by time. Influenza viruses were characterized by type and subtype. **Results:** Overall 9,049 patients were enrolled, their mean age was 50.9±17 years, 48.0% were males, 5,539 (56.9%) admitted to hospitals and 3680 (40.7%) were positive for viral cause. Overall, 3,424 (37.8%) infections caused by SARS-CoV-2, 225 (2.5%) by Influenza and 31 (0.3%) co-infection. Most SARS-CoV-2 infections 64.8% reported in 2020, while most of influenza 70.7% reported in 2021. Rate of influenza positivity increased from 0.2% in winter 20-21 to 6.7% in spring and 6.6% in summer 2021. While SARS-CoV-2 rates decreased compared to spring and summer 2020 (36.0 vs 37.4% and 23.1 vs 47.4% respectively). A/H1pdm caused 50.8% of influenza infections in 2020, 31.3% H3 and 17.5% FLU-B, while A/H3 dominated in 2021 representing 89.2% and Flu-B caused 10.8% of influenza infections. **Conclusions:** Egypt succeeded to integrate COVID-19 in its ARI surveillance. System identified unusual peak of influenza in spring and summer 2021 and described the pattern of influenza infections in relation to SARS-CoV-2. Additional studies are required to describe dynamics and predict rates of infection with ARVs in relation to each other to guide vaccination and intervention policies.

### Poster 129. Influenza Detected through Routine Medical Care Reported from Selected Hospitals – Vietnam, 2020

**L.T.P. Nguyen**[1], T.T.M. Nguyen[1], P.T. Truong[2], P.T. Truong[3], T.V. Mai[4], L.P.H. Nguyen[5], S.T. Bui[6], N.T. Le[7], T.Q. Le[8], T.T.T. Le[9], T.P. Vu[10], N.T.B. Hoang[11], Q.T. Lai[12], T.H. Bui[13]; P. Gould[1]

[1]U.S. Centers for Disease Control and Prevention, Hanoi, Vietnam, [2]Bach Mai Hospital, Hanoi, Vietnam, [3]Cho Ray Hospital, Ho Chi Minh City, Vietnam, [4]Hue Central Hospital, Hue, Vietnam, [5]Hospital of Tropical Diseases, Ho Chi Minh City, Vietnam, [6]108 Military Central Hospital, Hanoi, Vietnam, [7]National Lung Hospital, Hanoi, Vietnam, [8]Pediatric Hospital # 1, Ho Chi Minh City, Vietnam, [9]Pediatric Hospital #2, Ho Chi Minh City, Vietnam, [10]Saint Paul Hospital, Hanoi, Vietnam, [11]Vietnam National Children Hospital, Hanoi, Vietnam, [12]Viet Tiep Hospital, Hai Phong, Vietnam, [13]Vietnam-Sweden Hospital, Quangninh, Vietnam

**Background**: Influenza was infrequently reported worldwide to the WHO's Global Influenza Surveillance and Response System during 2020, including from the two National Influenza Centers in Vietnam. Specimens collected as part of sentinel outpatient influenza-like illness (ILI) surveillance in Vietnam have also declined in part due to the COVID-19 pandemic but also because the national ILI guideline has not been updated. **Methods**: To explore development of a new hospital-based influenza surveillance project, a questionnaire was sent to a convenience sample of 16 hospitals within Vietnam include both large national referral hospitals as well as smaller provincial ones, and not currently part of the ILI surveillance. The survey collected information about routine testing for influenza, including number of specimens collected and tested from patients at the hospitals, type of influenza testing performed (e.g., rapid test, reverse transcription polymerase chain reaction [RT-PCR]), and number of influenza positive results in 2020. **Results**: Twelve hospitals (75%) responded to the questionnaire, seven (58%) provided both the number of specimens tested and number positive for influenza and had tested >50 specimens per month. Four (57%) of 12 hospitals performed only rapid tests, two performed only RT-PCR testing, and one performed both but >95% were rapid tests. The total number of specimens tested by hospital during 2020 ranged from 61 to 9,951; two hospitals tested fewer than 200, two tested 200-700, and three tested >1,700. The percent of samples positive for influenza ranged from 3–28%, with a mean of 15% (3,493/22,791). Laboratory information system (LIS) is available at all 12 hospitals and seven of those have data interface to connect LIS to hospital information system, including clinical data. **Conclusions**: While Vietnam's National Influenza Centres did not

detect much ambulatory influenza during the last six months of 2020, hospitals where influenza tests were routinely performed in medical care continued to detect influenza activity during the whole of 2020. A national hospital-based surveillance would help describe a broader picture of influenza activity and could be linked to clinical data.

### Poster 130. Leveraging Sentinel Surveillance for Influenza to Monitor Community Transmission of SARS-CoV2 in the Kingdom of Cambodia, 2021

**B. Sar**[1], S. Chin[2], H. Seng[3], S. Um[3], D. Chau[2], J. Rainey[1], J. Mott[4], S. Ly[3]
[1]CDC Cambodia Country Office, [2]National Institute of Public Health Laboratory, NPHL, [3]Cambodia Communicable Disease Control Department, CCDC, [4]CDC Influenza Program Thailand
**Background:** Cambodia detected its first case of COVID-19 on January 27, 2020. Additional cases were detected until February 20th, 2021, when a large COVID-19 outbreak linked to international travelers occurred in Phnom Penh. Routine testing capacity to detect community transmission was limited. Here, we describe data from influenza-like-illness (ILI) and severe acute respiratory infections (SARI) sentinel surveillance systems also monitored SARS-CoV2 circulation from December 2019 to August 2021. **Methods:** Surveillance for ILI and SARI was conducted at 15 sentinel hospitals located in Phnom Penh and six provinces. At each sentinel site, staff collected one nasal and one oropharyngeal swab combined into viral transport medium, from persons meeting the case definitions. From April through November 2020, swabs were tested for influenza A and B viruses and subtyped, and for SARS-CoV2 using singleplex RT-PCR. Multiplex RT-PCR testing was initiated in December 2020. Specimens collected from December 2019 to March 2020 were tested retrospectively. **Results:** From December 2019 to August 2021, 1,799 ILI and 3,663 SARI patients were tested for influenza viruses and SARS-CoV2, including 644 specimens tested retrospectively. Among hospitalized SARI patients, test positivity for SARS-CoV2 increased monthly in 2021 from 2.0% (4/197) in March to 13.2% (33/250) in July, then decreased to 10.2% (27/266) in August. The test positivity for SARS-CoV2 among outpatient ILI patients increased from 3.5% (3/85) to 23.5% (12/51) from April to July 2021 then decreased to 17.0% (8/47) in August 2021. Influenza A(H1N1)pdm09 (18) and A(H3N2) viruses (326) were detected among 2,916 ILI and SARI patients identified in 2020. None of the specimens tested positive for influenza in 2021. **Conclusions:** Cambodia successfully demonstrated the efficient use of existing influenza surveillance systems to detect community transmission of SARS-CoV2. The positivity rate varied over time, providing an indicator of community transmission for decision makers.

### Poster 131. Early Start of the Lebanon Flu Season 2021-2022 with InfA H3 Dominance after Complete Absence of Influenza Virus Circulation in the Flu Season 2020-2021

**M. Al Buaini**[1], H. Abou Naja[2], A. Zaghlout[2], N. Jammal[1], M. Roueh[1], N. Ghosn[2]
[1]National Influenza Center at Rafik Hariri University Hospital, Beirut, Lebanon, [2]Epidemiological Surveillance Program at Ministry of Public Health, Beirut, Lebanon
**Background:** Lebanon SARI surveillance system, was established in the country in 2014, and later on with the support of WHO, MOPH the integrated influenza and covid-like illness (ILI/CLI) sentinel surveillance in outpatient sites in November 2020 was established. During the Flu season 2020-2021 there was complete absence of Influenza virus circulation. It appeared earlier in first week of September 2021 with InfA H3 dominance. **Methods:** The SARI was established in Lebanon in 2014 and was based on network of 8 hospitals from both public and private sectors. Cases are detected using the WHO SARI case definition targeting all inpatients. The ILI/CLI was established in Nov 2021, including sentinel sites selected from different outpatient clinics: PHCs, MSF, UNRWA clinics, and ERs to represent all residents of the country, and cases meeting the ILI/CLI case definition were included one day per week. For detected and selected cases, epidemiological and virological data are collected every week from each sentinel site. Data is collected and entered in DHIS2 platform. Samples are are sent to the National Influenza Center (NIC) at Rafik Hariri University Hospital and tested using Reverse Transcription Polymerase Chain Reaction. Samples are initially tested for both SARS-CoV-2 and Influenza by FluSC2 kit from CDC; NIC shares results with MOPH and by turn gives feedback to sentinel sites and partners. **Results:** Since November to December 2020, 284/585 were tested for Influenza, and from 1st January 2021, 2024/6072 were tested for Influenza. Only 13 were positive in September 2021 and mainly InfA H3, announcing the early starting of the Flu season 2021-2022 r. **Conclusion:** After abstinence of circulating Influenza virus in Lebanon due to the dominance of SARS-CoV-2, we have started to get positive influenza testing. Thus is showing early start in the Flu season 2021-2022 with respect to previous years.

### Poster 132. Childhood Influenza Vaccine Effectiveness for Symptomatic Infection in a Community-based Setting: Wisconsin (2015-2020)

**K.M. Schmit**[1], M. Arnold[2], J. Temte[3], S. Barlow[3], C. Bell[3], M. Goss[3], E. Temte[3], E. Reisdorf[4], P. Shult[4], M. Wedig[4], J. Birstler[5], G. Chen[5], D. Sill[6], A. Uzicanin[7]

[1]Department of Pediatrics, Division of Infectious Diseases, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]Medical College of Wisconsin, Milwaukee, WI, USA, [3]Department of Family Medicine and Community Health, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA,[4]Wisconsin State Laboratory of Hygiene, Madison, WI, USA,[5]Department of Biostatistics, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [6]Wisconsin Immunization Registry, Wisconsin Department of Health and Human Services, Madison, WI, USA, [7]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: Influenza infections have a tremendous impact on communities and the healthcare system within the US. Seasonal influenza immunizations reduce hospitalizations and deaths, especially in high-risk individuals, although vaccine effectiveness (VE) for symptomatic infections varies by season. Most of influenza VE studies are conducted in medical settings even though most individuals with influenza-like-illness (ILI) do not seek medical care for their illness. Community-based settings allow the opportunity to include those with various healthcare seeking behaviors providing an alternative estimate of VE. **Methods**: The ORegon CHild Absenteeism due to Respiratory Disease Study (ORCHARDS) is an observational study of ILI and school absenteeism in children 5 to 18 years of age that attend the Oregon School District in Wisconsin. Eligible participants had at least two acute respiratory symptoms within the previous seven days. Home study visits were conducted from January 5, 2015 to March 13, 2020 to collect demographics, symptom data, and a nasopharyngeal (NP) or oropharyngeal (OP) specimen. NP/OP swabs were analyzed by RT-PCR for multiple respiratory pathogens including influenza A and B. Influenza VE was estimated using a test-negative design with influenza PCR(+) participants as cases and influenza PCR(-) participants as controls. **Results**: There were 2375 children included in the analysis with 711 (30%) having laboratory-confirmed influenza and 1221 (51%) being vaccinated for influenza based on ACIP criteria. Most participants (87%) did not have prior healthcare visits nor were planning on being seen for their illness. Overall VE was -25% (95% CI: -51 to -4, p=0.02) when adjusting for influenza season, healthcare use, and age. Comparing PCR-positive cases that were and were not vaccinated, there were no statistically significant differences in school absenteeism or ILI symptoms except for a slightly lower mean Jackson score in vaccinated cases. **Conclusion**: Influenza vaccination in school-aged children did not provide a significant risk reduction in symptomatic influenza infections in a predominantly non-healthcare seeking study population. Community-based settings that include individuals that do and do not seek healthcare provide an alternative estimate of VE in children.

## Parasitic Diseases

### Poster 133. Knowledge and Practices of Health Care Workers of Human African Trypanosomiasis in an Endemic Area – Nyimba and Mambwe Districts of the Luangwa Valley, Zambia, 2020

**J.E. Zulu**[1,2], J. Banda[2], S. Ngalande[3], C. Simukoko[4], M. Mbewe[4], L. Soko[4], E. Bulaya[4], J. Mulambya[2], G. Zulu[2], N. Sinyange[5]
[1]Zambia Field Epidemiology Training Program, Lusaka, Zambia, [2]Eastern Provincial Health Office, Chipata, Eastern Province, Zambia, [3]Eastern Provincial Livestock and Fisheries Office, Chipata, Zambia, [4]Nyimba District Health Office, Nyimba, Eastern Province, Zambia, [5]Zambia National Public Health Institute, Lusaka, Zambia
**Background:** Human African Trypanosomiasis (HAT) caused by *Trypanosoma brucei Rhodesiense* is a neglected tropical disease (NTD) transmitted by a bite of an infected tsetse fly. This disease is still endemic at very low scale in North-Eastern and Southern Zambia. In 2019 seven cases of HAT were reported in the valley areas of Mambwe and Nyimba districts, and four (57%) of them died. Health care workers play a pivotal role in the identification and early treatment of this disease. We sought to describe the knowledge and practices of the health care workers (HCWs) in the affected areas in order to institute control measures. **Methods:** We did a cross sectional survey of HCWs from the 13th to the 22nd of March 2020. Health facilities (HFs) reporting cases of HAT and those in the tsetse fly-infested belt in Nyimba and Mambwe districts, were purposively selected. All HCWs working in outpatient department and laboratory were interviewed with a pre-tested structured questionnaire about HAT transmission, symptoms, signs, diagnosis, treatment, prevention and control. **Results:** A total of 10 HCWs were interviewed from four affected HFs. Of those, five (50%) were females and the mean age was 31 years. All knew about HAT and that it's transmitted by a bite from an infected tsetse fly. Fever was mentioned by 80% of them as an early-stage symptom. All said fever patients are first tested for malaria, and for a negative malaria test, only 20% mentioned referral for further investigations. However, only one of the four facilities had a functional microscope. All the participants said HAT was preventable and 30% of HCW did not know how HAT is diagnosed, 40% mentioned use of a microscope, while 30% mentioned PCR. **Conclusions:** Although most HCWs knew about the condition, some did not, and only a minority were familiar with the correct diagnostic work-up for malaria-negative fever of unknown origin, which includes HAT in this endemic area. Furthermore, most HCWs did not have access to

the necessary equipment to make a HAT diagnosis. There is need to implement active surveillance of HAT to cover the tsetse fly affected belt in Zambia.

### Poster 134. Purification of Native Histidine-Rich Protein 2 (nHRP2) from *Plasmodium falciparum* Culture Supernatant, Infected RBCs, and Parasite Lysate

**J.N. McCaffery**[1], B. Singh[1], A. Kong[1], Y. Ah[1], S. Wilson[1], S. Chatterjee[2], D. Tomar[3,4], M. Aidoo[1], V. Udhayakumar[1], E. Rogier[1]
[1]Malaria Branch, Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]IHRC, Inc., Atlanta, GA, USA, [3]Department of Medicine, Division of Rheumatology, Emory University, Atlanta, GA, USA, [4]Lowance Center for Human Immunology, Emory University, Atlanta, GA, USA
**Background:** Despite the widespread use of histidine-rich protein 2 (HRP2)-based rapid diagnostic tests (RDTs), purified native HRP2 antigen is not standardly used in research applications or assessment of RDTs used in the field. **Methods:** This report describes the purification of native HRP2 (nHRP2) from the HB3 *P. falciparum* culture strain. As this culture strain lacks *pfhrp3* from its genome, it is an excellent source of HRP2 protein only and does not produce the closely-related HRP3. The nHRP2 protein was isolated from culture supernatant, infected red blood cells (iRBCs), and whole parasite lysate using nickel-metal chelate chromatography. Biochemical characterization of nHRP2 from HB3 culture was conducted by SDS-PAGE and western blotting, and nHRP2 was assayed by RDT, ELISA, and bead-based immunoassay. **Results:** Purified nHRP2 was identified by SDS-PAGE and western blot as a ~60 kDa protein that bound anti-HRP-2 monoclonal antibodies. Mouse anti-HRP2 monoclonal antibody was found to produce high optical density readings between dilutions of 1:100 and 1:3,200 by ELISA with assay signal observed up to a 1:200,000 dilution. nHRP2 yield from HB3 culture by bead-based immunoassay revealed that both culture supernatant and iRBC lysate were practical sources of large quantities of this antigen, producing a total yield of 292.4 µg of nHRP2 from two pooled culture preparations. Assessment of nHRP2 recognition by RDTs revealed that Carestart Pf HRP2 and HRP2/pLDH RDTs detected purified nHRP2 when applied at concentrations between 20.6 to 2060 ng/mL, performing within a log-fold dilution of commercially-available recombinant HRP2. The band intensity observed for the nHRP2 dilutions was equivalent to that observed for *P. falciparum* culture strain dilutions of 3D7 and US06 F Nigeria XII between 12.5 and 1,000 parasites/µl. **Conclusions:** Purified nHRP2 could be a valuable reagent for laboratory applications as well as assessment of new and existing RDTs prior to their use in clinical settings. These results establish that it is possible to extract microgram quantities of the native HRP2 antigen from HB3 culture and that this purified protein is well recognized by existing monoclonal antibody lines and RDTs.

### Poster 135. Improvements to the Universal Parasite Diagnostic Assay (UPDx): Use of A Library Preparation-free Method to Facilitate Detection in a Range of Biological Matrices

**B.A. Watson**[1,2], B. Clemons[3], M. Lane[1,4], J. Barratt[1], E. Lasek-Nesselquist[5], S. Madison-Antenucci[3], Y. Qvarnstrom[1]
[1]Parasitic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [3]Parasitology Laboratory, Wadsworth Center, NYSDOH, Albany, NY, USA, [4]Synergy America Inc., Duluth, GA, USA, [5]Bioinformatics Core, Wadsworth Center, NYSDOH, Albany, NY, USA
**Background:** UPDx is a versatile molecular tool for pan parasite identification developed by scientists at the CDC. UPDx employs universal primers to amplify a region of 18S rDNA followed by next generation sequencing (NGS) and parasite identification using an in-house database of reference sequences. This assay has many advantages over other molecular tests: no foreknowledge of the infectious agent is required and detection of coinfections (two or more parasites) in a single assay is possible. **Methods:** To reduce the time and expense of NGS, we substituted a PCR-based, Illumina adapter incorporation step for the Illumina library preparation step and applied this updated method to blood samples in a comparative study with the original UPDx assay revealing no significant differences in performance. In this study, we applied this updated method, termed Adapter UPDx Assay (Ad_UPDx), to DNA extracted from 36 samples including biological fluids (n=8), solid tissue (n=5), tapeworm segments (n=12) and formalin-fixed paraffin embedded tissue (n=11). **Results:** Using Ad_UPDx, we detected parasite signals in 33 of 36 samples either presumed to contain parasites based on patient clinical history (n=8) or confirmed via microscopy (n=11), PCR (n=13), immuno-histochemistry (n=1) or a combination of these methods (n=3). A similar Illumina adapter-incorporating modification of the original UPDx assay (using the same target amplicon and restriction enzymes) developed at New York States' Wadsworth Center has also shown good diagnostic utility for both clinical and environmental samples. **Conclusion:** Considering both methods, using an adapter-incorporating PCR step may reduce time and costs, which may facilitate wider implementation of the assay. These modifications do not appear to compromise performance and show versatility for the application of UPDx to various sample types.

### Poster 136. Application of the Universal Parasite Diagnostic (UPDx) Assay to Blood and Tissue Samples Collected from Mammals, Birds, and Reptiles

**M. Lane**[1,3], M. Kashani[1,2], J. Barratt[1], Y. Qvarnstrom[1], M.J. Yabsley[5,6], K.B. Garrett[5,6], R.S. Bradbury[4]
[1]Parasitic Diseases Branch, Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [3]Synergy America Inc., Duluth, GA, USA, [4]School of Health and Life Sciences, Federation University, Australia, [5]Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA, USA ,[6]Southeastern Cooperative Wildlife Disease Study, Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, USA

**Background:** The universal parasite diagnostic method (UPDx), which involves nested amplification of eukaryotic 18S rDNA with targeted host DNA reduction by restriction digestion and subsequent deep sequencing, is able to detect human blood parasites with a sensitivity for *P. falciparum* comparable to real-time PET-PCR. Here, we explored the potential of UPDx to detect parasites in diverse animal hosts. **Methods:** To identify parasites and adapt to the wide range needed of the assay's taxonomic spectrum, a reference sequence database was curated and an inclusive naming system was developed, starting at the species level and moving up taxonomic ranks until all species producing a 100% match to a given sequence were represented in the sequence name. Specimens (blood, tissue, or fluid) from 61 animals (birds, mammals, and reptiles) with PCR or microscopically confirmed parasitic infections, specimens from 12 animals (pet dog, wild opossum, wild raccoon, or wild skunk) that were negative for the parasite tested (PCR/morphology), and 10 specimens positive for amoebic or metamonad infections which were expected to be negative by UPDx were tested. **Results:** Of the 61 positive specimens, UPDx confirmed 47 parasitic infections: 30 at genus-level (9 of which were co-infections), 6 at species-level (2 of which were co-infections), 6 at higher-level rankings, and 5 of unknown taxonomic rank. UPDx amplified DNA in 5 of 10 specimens positive for amoebic or metamonad infections, detecting other eukaryotes (a cercozoan, 3 gregarines, and a co-infection with a gregarine plus an alveolate). Of the 12 previously negative blood specimens, 7 were negative by UPDx while 5 were positive for *Babesia* or *Theileria* and likely represent unanticipated true infections, owing to the common occurrence of these piroplasms in the species tested. In the 83 samples tested 12 co-infections were detected, 9 of which were previously undetected. **Conclusion:** These data demonstrate the potential of utilizing UPDx in the detection of parasite infections or co-infections and detection of pathogens not detected by routine diagnostic methods in blood or tissue from several animal species. A full validation panel comprising various matrices including blood, fluid, culture, and tissue is warranted to further substantiate the use of UPDx as an important diagnostic tool.

## Preparedness and Response

### Poster 137. Stakeholders' Assessment of US Centers for Disease Control and Prevention's Contributions to the Development of National Public Health Institutes in Seven Countries

**M.A. Woldetsadik**[1], K. Fitzpatrick[1], L.D. Castillo[2], B. Miller[1], D. Jarvis[1], C.R. Carnevale[1], F. Ravat[1], C.H. Cassell[1], A. Williams[1], S.K. Young[1], J. Clemente[1], H.C. Baggett[1], S. Bratton[1]
[1]Division of Global Health Protection, Center for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]RTI International, Durham, NC, USA

**Background:** National Public Health Institutes (NPHIs) can strengthen countries' public health capacities to prevent, detect, and respond to public health emergencies. This qualitative evaluation assessed the role of the US Centers for Disease Control and Prevention (CDC) in NPHI development and strengthening of public health functions. **Methods:** Among 30 countries where CDC has partnered on NPHI development and strengthening, we purposively selected countries where CDC's financial support was comparatively high, and accounted for geographic variation, institutional development stage, and how CDC support was provided (e.g., direct support or through partners). The final countries included Cambodia, Colombia, Liberia, Mozambique, Nigeria, Rwanda, and Zambia. Using MAXQDA Version 20.0.2, all recordings were transcribed verbatim and coded. We employed content analysis where coding categories were informed by the interview questions and derived directly from transcribed data. **Results:** Among 108 individuals contacted, all agreed to participate. Of the 96 people interviewed, 43 (45%) were NPHI staff, 29 (30%) were non-NPHI government staff, and 24 (25%) were non-governmental organization staff. Forty-two (98%) NPHI staff, 13 (45%) non-NPHI government staff, and 10 (42%) non-government partner staff discussed CDC's contributions to strengthening NPHIs in their country. Participants identified four areas of support that were the most important: workforce capacity building; technical assistance for key public health functions; identifying institutional gaps and priorities; and funding to support countries' priorities. Participants underscored the need for capacity building directed toward country-driven priorities during planning

and implementation. **Conclusions:** Continued support for NPHI development from CDC and other partners is vital to building stronger public health systems, improving population health, and strengthening global health security.

### Poster 138. Rethinking the Emergency Response Workforce Development Programs – Operationalizing Global Health Security Initiatives

**M. Shamout**, M. Tejan, C. Corkish, A. Hoffman, T. Stehling-Ariza, H. Lofgren, C. Giese, D. Bugli, J.C. Neatherlin, A.L. Greiner
Emergency Response and Recovery Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: Multidisciplinary Public Health Rapid Response Teams (RRT), as highlighted by the COVID-19 response, are critical to fast and effective emergency response. From 2016-2019, the United States Centers for Disease Control and Prevention (CDC) hosted multinational trainings for emergency management professionals on national RRT program establishment, management, and operations. Continued requests for RRT support and guidance indicate ongoing challenges. We aim to elucidate the factors that facilitate and challenge the implementation of sustainable RRT programs. **Methods:** In April 2021, an online survey was sent to 86 training participants regarding the status of their country's RRT program and the factors that facilitated or challenged implementation. A fully functional RRT program was defined as meeting all components outlined in CDC's Guidance for the Establishment and Management of Public Health RRTs for Outbreaks. **Results:** Fifty-six (65%) participants responded representing 24 countries across Africa (73%), Southeast Asia (13%), Middle East (7%), and East Asia (4%). Most (89%) participants supported the country's RRT program. Six (25%) countries had a fully functional RRT program and 17 (71%) had a partially functional RRT program. Supportive factors for RRT program implementation were dedicated personnel to establish the RRT program (59%), leadership understanding (59%), leadership support (52%), and the availability of RRT responders (52%). Challenges included lack of funding (68%), long-term RRT management personnel (46%), RRT medical and technological equipment (39%), and technological resources to support roster management (39%). **Conclusions:** Multisectoral RRTs are critical assets during an outbreak response but the extensive and robust requirements for an effective and sustainable program are often overlooked. The undermining factors of lack of funding, availability of long-term personnel and equipment to manage and operate the RRT program are critical areas to be addressed when establishing an RRT program to ensure effective workforce development initiatives that strengthen global health security versus training alone. Future global health initiatives should consider these sustainable factors required when implementing emergency capacity building activities.

### Poster 139. Evaluation of National Laboratory System Capabilities Using an Electronic Survey and Mapping Tool in Kenya

**B. Juma**[1], E. Ochieng[2], R. Nyaga[2], J. Mwihia[3], M. Umuro[3], E. Onyancha[4], E. Hunsperger[1]
[1]US Centers for Disease Control and Prevention, Nairobi, Kenya, [2]Association of Public Health Laboratories, Nairobi, Kenya, [3]National Public Health Laboratories Services- Kenya, Nairobi, Kenya, [4]Department of Threat Reduction Agency, Nairobi, Kenya
**Background:** Accurate and current knowledge of national laboratory capabilities is paramount in this era of improving health security to ensure preparedness for emerging and re-emerging infectious diseases. Current laboratory capacity data, and a platform to store, organize, spatially analyze, refer, and display these data, empowers the public health system to effectively manage and optimize laboratory resources. Through a collaborative effort, we developed a laboratory mapping tool to assess the capacity of diagnostic laboratories, and a platform to analyze these data in Kenya. **Methods:** A questionnaire was developed to capture 13 core capability elements of the laboratory system and services in all 47 counties in Kenya. Laboratories servicing hospitals from tier 2-6 facilities, veterinary, and Kenya government parastatal research laboratories were eligible for the assessment. Geocodes were assigned to each facility. Surveys were done on-site by Ministry of Health (MoH) trained local staff using handheld tablets to collect and upload data to a centralized database. These data were exported and analyzed using STATA and principal component analysis. **Results:** A total of 1,822 (45%) of 4,086 eligible laboratories were assessed from 4 different facility levels. A scoring system (1-4) was assigned to each core capability from all facilities to define vulnerable elements where a score <1 indicated an urgent need for intervention. From the overall scores for all laboratories, only one element (data management) was <1. We also captured the testing landscape of PCR platforms and captured referral systems available from multiple established networks such as HIV and flu. We also determined that 35% of the lab workforce was donor supported. **Conclusion:** Current mapping data guided the MoH to update sample referral networks, better utilize PCR testing platforms, and address urgent gaps to respond to the COVID-19 pandemic. The web-based questionnaire provided a timely method to monitor evolving capabilities in Kenyan laboratories as new funding and capacity became available to respond to the pandemic.

### Poster 140. Prevention is Key: Quality Control Measures for High Throughput NGS Laboratories

**J. Madden**[1], M. Sheth[1], M. Bentz[1], A. Burgin[1], M. Burroughs[1], M. Davis[1], K. Dillon[2], S. Le[3], S. Nobles[1], J. Padilla[1,4], L.A. Rowe[5], D. Batra[6], K. Knipe[3], P. Cook[7], C. Paden[7], J.K.L. Gunn[8,9], K. Lacek[3], D. Howard[3], Y. Unoarumhi[1], J. Pohl[1], J. Lee[1]

[1]Division of Scientific Resources, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Integrated Life Sciences, University of Georgia, Athens, GA, USA, [3]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]ASRT Incorporated, Atlanta, GA, USA, [5]Tulane National Primate Research Center, Covington, LA, USA, [6]Office of Advanced Molecular Detection, Centers for Disease Control and Prevention, Atlanta, GA, USA, [7]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]National Center for HIV, Viral Hepatitis, STD, and TB Prevention, Centers for Disease Control and Prevention, Atlanta, GA, USA, [9]United States Public Health Service, Washington DC, USA

**Background:** Next generation sequencing (NGS) protocols can easily amplify off target templates, leading to increased noise, false discoveries, and wasted resources. Maintaining the integrity of results generated by high throughput next generation sequencing (HT-NGS) methodologies requires a system of quality control (QC) that can circumvent sources of contamination while quickly identifying the presence of contamination without sacrificing efficiency. Our genomic sequencing lab has implemented an HT-NGS workflow that minimizes lab contamination and increases sequence integrity in our output with stringent data quality metrics. **Methods:** Samples are processed using a unidirectional workflow and a series of QC checkpoints. Automated liquid handlers are used to maintain high accuracy without losing efficiency. Nucleic acids are extracted from clinical samples by a separate lab to prevent contamination entering our lab's workflow. We use qPCR to check for the presence of unwanted template in both RNA extracts and in synthesized cDNA before moving on to library prep. Pre- and post-cDNA synthesis are not processed in the same area to minimize cross contamination during amplicon enrichment and sample indexing. Prior to sequencing, all negative controls and a panel of randomly selected library samples are assessed using fragment analysis to detect cross contamination that may have occurred during library prep. After sequencing, our bioinformatics pipeline checks that negative controls and positive controls meet our very stringent metrics and then feeds all of the sequencing data into comprehensive dashboards for review. We also resequence approximately 10% of all samples to ensure consistency across runs. **Results:** Following implementation of QC checkpoints into our workflow we saw a rapid decline in the number of samples that failed post-sequencing. Utilizing our optimized HT-NGS workflow, in under a year GSL successfully sequenced over 20,000 clinical isolate samples. **Conclusions:** The QC measures employed by our lab can be adapted to many HT-NGS workflows, facilitating rapid application in times of public health emergencies.

### Poster 141. Assessment of Standard Precaution Related to Infection Prevention Readiness of Healthcare Facilities in Bangladesh: Findings from a National Cross-sectional Survey

**M.A.A.J. Biswas**[1], M.Z. Hassan[1,2*], M.R. Monjur[3], M.S. Islam[4], A. Rahman[5], Z. Akhtar[1], F. Chowdhury[1], S. Banu[1], N. Homaira[6,7]

[1]Programme for Emerging Infections, Infectious Disease Division, International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b), Mohakhali, Dhaka, Bangladesh, [2]Nuffield Department of Medicine, University of Oxford, Oxford, UK, [3]Faculty of Health and Medicine, University of Newcastle, Callaghan, New South Wales, Australia, [4]School of Public Health and Community Medicine, University of New South Wales, Sydney, Australia,[5]Communicable Disease Control (CDC), Directorate General of Health Services, The Ministry of Health & Family Welfare, Government of Bangladesh, [6]School of Women's and Children's Health, Faculty of Medicine, University of New South Wales, Sydney, New South Wales, Australia, [7]Respiratory Department, Sydney Children's Hospital Randwick, Randwick, New South Wales, Australia

**Background:** Baseline assessment of standard precaution relating to infection prevention and control (IPC) preparedness to fight health crisis within healthcare facilities at different levels and its associated factors in Bangladesh remains unknown. **Methods:** We analyzed the nationally representative Bangladesh health facility survey (BHFS) data conducted by the MoHFW during July-October 2017 and used the World Health Organization's (WHO) Service Availability and Readiness Assessment (SARA) manual to determine the standard precaution related to the IPC readiness index. Using a conceptual framework and multivariable linear regression, we identified the factors associated with the readiness index. **Results:** We analyzed data for 1,524 surveyed healthcare facilities. On average, only 44% of the standard precaution amenities were available in all facilities. Essential elements such as guidelines for standard precaution (30%), hand-washing soap (29%), and pedal bin (38%) were not readily available in all the facilities. The tuberculosis service area was least prepared, with 85% of elements required for standard precaution deficient in all facilities. A significantly lower readiness index was found in the rural healthcare facilities (Mean difference=-13.2), healthcare facilities instructed by MoHFW (Mean difference =-7.8), and private authority

(Mean difference=-10.1) compared to corresponding reference categories. **Conclusions:** Our study suggests a severe lack of elements of standard precaution in most healthcare facilities, particularly in rural health centers. These data may serve as a baseline to measure improvement in IPC in these facilities and identify areas of gaps for targeted interventions to improve IPC strategies that can help develop a resilient health system.

### Poster 142. Towards Emergency Therapeutics for Future Pandemics and Bioterrorist Attacks

P. Prathapan
New Biochemistry, University of Oxford, Oxford, UK

Drug repositioning studies in recent decades have revealed a growing number of antimicrobials effective at treating infection types tangential to their original antimicrobial classification. Such 'pan-pathogen' antimicrobials, however, have not been formally characterized. By reviewing historical limitations of the canonical antimicrobial lexicon in light of the contemporary 'Casadevall and Pirofski' model for infectious disease, we propound a taxonomy that defines antimicrobials according to the host-pathogen interactome, not the pathogen. In doing so, antimicrobials that are effective at treating multiple infection types are highlighted, namely azithromycin, ivermectin, niclosamide, and nitazoxanide. These therapeutics not only harbor extensive repositioning profiles across a plethora of infection types but exhibit anti-inflammatory activity specific to lung tissue. Consequently, all are currently undergoing clinical trials for COVID-19. Recognition of the pan-pathogen nature of these antimicrobials can stimulate a more unified approach to antimicrobial development cognizant of generalized anti-infective mechanisms within the host-pathogen interactome and anticipatory of future pandemics and bioterrorist attacks, in accordance with the 2007 Strategic Plan for Biodefense Research by the U.S. Department of Health and Human Services.

### Poster 143. Delivering Capacity Building for a Country Infodemic Management and Response Workforce

**T.D. Purnat**[1], C. Wardle[2], T. Senft[3], C. Czerniak[1], L. Phuong[1], S. Briand[1], T. Nguyen[1]
[1]Global Infectious Hazard Preparedness, Emergency Preparedness, World Health Organization, Geneva, Switzerland, [2]First Draft News, New York, NY, USA, Media, Communications, Creative Arts, Language and Literature (MCCALL), Macquarie University, Sydney, Australia

**Background:** Infodemic management can support the management of epidemics and of epidemic risk during health emergencies. The practice requires health workforce to have multidisciplinary and cross-functional skillsets. To develop a cross-functional workforce to support pandemic response in countries, WHO, US CDC and partners have developed global copresence-based trainings in infodemic management. **Methods:** WHO has implemented two trainings and is developing two more to be implemented by early 2022. The objectives of the trainings are to introduce a range of topics and skills (both global and region-specific) to participants, including health practitioners, policymakers, and members of civil society. These include: (1) Methods and tools to identify, track health-related misinformation and disinformation on and offline. (2) Strategies and tactics for intervening in infodemics, with a focus on promoting resilience of individuals and communities. (3) Glean data-driven insights regarding capacity to listen to public and community questions and concerns, not just to improve health communication, but inform epidemic response as a whole. (4) Principles and guidance to promote individual and community self-efficacy during infodemics by encouraging self-protective health behaviors. The trainings emphasize scenario-based learning, and cross-cultural and cross-functional teamwork. **Results:** After two trainings, over 550 infodemic managers have been trained. Because the pandemic is a global health emergency with local crises, the global mix of students added a needed international perspective. Students introduced to all the 'players' in the field of emergency response during the training. Scenarios emphasized the 'value of being valuable.' To follow up on the investment in new workforce, a roster was created so that validity of training would be recognized and students with certificates deployed in the field. Students were encouraged to function as ambassadors for the field of infodemic management. One part of ambassadorship means that they seek out avenues for contribution—paper writing, webinar presentation, introduce elements of infodemic management in existing workforces. The course actively inspired and encouraged students to go behind describing what they learned about IM, but to act as co-creators of IM processes, innovating and sharing experiences back with the group to forge community of practice. Compared to traditional capacity-building events run by WHO, this training was organised faster and was cheaper. **Conclusions:** Infodemic management requires enhancement of skills and is innovating the next generation of public health system capacities and tools for more effective management of epidemics and of epidemic risk. The emergency response workforce must be equipped with essential infodemic management skills, alongside support from advanced infodemic management teams. Scenario-based trainings that are updated on a rolling basis are an effective method for building capacity for surge support in countries, as the science, knowledge, and experience of managing infodemics in the field evolves.

### Poster 144. Infection Prevention and Control Performance in Primary Health Care Facilities Following Peer-led Mentorship in Uganda

**R.R. Ayebare**[1], M. Malikisi[1], E. Katwesigye[1], A. Wailagala[1], C. Kyarisima[1], S. Ssebalamu[1], J. Bikanga[1], G. Bongole[1], G. Namyalo[1], P. Ainembabazi[1], C.W. Kaliisa[1], R. Bahatungire[2], G. Upenytho[2], J. Amone,[2] M. Lamorde[1]
[1]Infectious Diseases Institute, College of Health Sciences Makerere University, Kampala, Uganda, [2]Ministry of Health, Kampala, Uganda

**Background:** Improved infection prevention and control (IPC) practices in primary health care (PHC) facilities reduces the risk for COVID-19 and other healthcare-associated infections. In 2021, the World Health Organization released its first specific guidelines to strengthen IPC in PHC facilities. In 2020, Uganda Ministry of Health (MoH) commenced a national IPC mentorship program for COVID-19 that reached higher tier health facilities. However, most PHC facilities in have not been supported by this program. **Methods**: The Infectious Diseases Institute implemented the MoH district-led IPC mentorship and feedback program in PHCs. The project targeted 526 facilities in 33 districts to receive ten onsite mentorship and IPC assessment visits (one visit per month), and procured and distributed personal protective equipment, triage facilities and equipment and information education and communication materials. Monitoring data was captured in ODK using the MoH IPC assessment tool assessing 10 areas (IPC programs, screening and isolation, personal protective equipment, waste management, hand hygiene, instrument processing, availability of education materials, chlorine mixing, water, and environmental cleaning). Total scores per area were categorized from lower to higher scores using a red, amber, green scale. **Results**: Between February 2021 and September 2021, 526 PHCs had month 1 data and 493 (87%) month 6 data. of assessment data. Increased scores were observed from month 1 to month 6 in the following areas, overall IPC performance (61% to 82%); — IPC program score 48% to 89% mixing chlorine as an environmental disinfectant from 68% to 93% and availability of hand hygiene products 61% to 79%. Scores also increased for COVID-19 prevention measures as follows screening and isolation 22%, PPE availability 31%, and hand hygiene 18%. Seven areas improved from amber to green and three from red to amber. **Conclusion**: Using objective criteria, increased IPC scores were achieved in a large sample of primary health care facilities in Uganda. Investments are warranted to scale the national IPC mentorship program to remaining PHCs.

## Laboratory Studies and Diagnostics

### Poster 145. Withdrawn

### Poster 146. 3D Printers in Hospitals: Yay or Nay?

**K.C. Jackson**, D.R. Call, E.T. Lofgren
Washington State University, Pullman, WA, USA

**Background:** COVID-19 has presented hospitals with unique challenges. A survey of hospitals showed that 40% reported “limited” or worse levels of personal protective equipment (PPE), and 13% were self-producing PPE to address those deficits, including 3D printed items. However, we do not know how efficiently, if at all, 3D printed materials can be disinfected. We assess how these materials may be contaminated and how readily they may be disinfected. **Methods:** We used methicillin-resistant *Staphylococcus aureus*, *Staphylococcus aureus*, *Escherichia coli*, *Acinetobacter baumannii*, and *Klebsiella pneumoniae*, commonly found in hospital environments. We conducted bacterial survival assays to determine if bacteria grow on Polylactic Acid (PLA), a common 3D printed material, with and without disinfectant. We performed a time series (with dry times 3-, 8-, and 24-hours) followed by serial dilutions to attain colony forming unit (CFU) averages for each strain per disk. To determine if 3D printed material can be cleaned, we used 70% EtOH, Bleach, and UV light. We conducted the same time series followed by a disinfectant time series (with dry times 30secs, ½ dwell time, dwell time, and 2x dwell time). Again, serial dilutions were performed to attain the CFU averages with disinfectant. The CFU averages from the control group (without disinfectant) and testing group (with disinfectant) were compared to see how well each disinfectant decreased bacterial load. **Results:** 3D printed material is readily contaminated with bacteria common in hospitals and can sustain that contamination. Disinfected disks had lower CFU averages than those that were not, but the level of disinfection is relatively intensive. **Conclusion:** Proper disinfection is essential to halting the spread of HAIs. 3D printers and their products can be invaluable for hospitals, especially when supplies are low and healthcare worker safety is paramount. Environmental services should be made aware of the presence of 3D printed materials and patients should be discouraged from printing their own items for use in hospital environments.

### Poster 147. A Novel Direct to Patient Testing Program Compared to Traditional Public Health Lab Testing

**D. Shostrom**, M. Pentella, C. Cass, W. Aldous
State Hygienic Laboratory at the University of Iowa, Coralville, IA, USA

**Background:** At the beginning of the pandemic, the State Hygienic Laboratory (SHL) used paper test request forms to process all specimens. As testing volume increased, several additional staff needed to be hired for both data entry verification and testing, leading to several logistical obstacles and long turnaround times (TAT). To improve the accessibility issues, Test Iowa was established as a free COVID-19 testing program, that used a digital process including online appointment registration, a patient form and specimen matching system, and direct-to-patient result delivery. We examined differences in laboratory processes and performance between Test Iowa and SHL's COVID-19 testing workflows to identify improvements that Iowa's public health laboratory infrastructure may consider adopting. **Methods:** We compiled COVID-19 testing data on testing volume, TAT, and patient age from Test Iowa and SHL from September-November 2020 and January-March 2021, corresponding to statewide periods of high and average demand for testing, respectively. To examine differences in sample delivery time, TAT was calculated using two separate methods: 1) from time of sample collection to release of result, AND 2) from time of sample arrival time to release of result. **Results:** During the three-month period of high testing volume, Test Iowa performed 234,155 tests with an average laboratory TAT from receipt to release of 18 hours, while SHL performed 198,946 tests with a TAT of 36 hours. During the three-month period of low testing volume, Test Iowa performed 133,305 tests with a TAT of 17 hours and SHL performed 52,578 tests with a TAT of 16 hours. Average total TAT overall for all six months of data from sample collection to release was 33 and 63 hours for Test Iowa and SHL, respectively. **Conclusions:** Test Iowa's TAT was significantly lower than SHLs despite higher volume, demonstrating the efficiency of an automated data entry and result delivery system. We recommend that public health entities incorporate similar systems of digital workflows to improve performance.

### Poster 148. Using Unique Molecular Identifiers to Increase the Accuracy of Oxford Nanopore Technology MinION Sequencing for Foodborne Enteric Surveillance

**R. G. Paradis**[1,2], M. Vasquez[1,2], Y. Gao[1,3], K. C. Dillon[1,2], R. Lindsey[1], A. D. Huang[1], H. A. Carleton[1], A. J. Williams-Newkirk[1]
[1]Enteric Diseases Laboratory Branch, US Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, US Department of Energy, Oak Ridge, TN, USA, [3]ASRT, Inc., Atlanta, GA, USA

**Background:** Public health laboratories (PHLs) routinely sequence enteric bacterial isolates for surveillance to detect foodborne outbreaks. PHLs use Illumina short-read sequencing that produce fragmented assemblies and can be expensive. The Oxford Nanopore Technologies' (ONT) MinION is a small, affordable long-read sequencer that lacks the accuracy of short-read sequencers. Ligating unique molecular identifiers (UMIs) to library template molecules before amplification may improve MinION accuracy. We tested Karst et al.'s (2021) UMIs method for suitability for enteric surveillance by comparing core genome multi-locus sequence typing (cgMLST) calls from 50 isolates sequenced with Illumina, ONT native, and ONT-UMI methods. **Methods:** 25 Shiga toxin-producing *Escherichia coli* and 25 *Salmonella* isolates were used to compare ONT native and ONT-UMI to Illumina sequencing. For ONT methods, isolates were cultured using standard methods and extracted using Promega's Wizard High Molecular Weight kit. The ONT native workflow followed ONT protocols (Ligation Sequencing Kit (SQK-LSK109), Native Barcoding Expansion kit (EXP-NBD104/114) and R10.3 flowcell). The ONT-UMI workflow followed the Karst et al. (2021) shotgun protocol for sequencing and assembly. The ONT native library reads were base called, demultiplexed, and trimmed using Guppy, quality checked (QC) with NanoPlot, assembled with Flye and polished using Racon and Medaka. Illumina data was generated using DNA Prep libraries (PulseNet SOP PNL35) and sequenced on a MiSeq using 500 cycle chemistry (PulseNet SOP PNL38). FastQ files were analyzed in BioNumerics v 7.6.3 including assembly, identification using average nucleotide identity, and organism specific databases for QC and genotyping. Assemblies were compared by calling cgMLST alleles from each data set in BioNumerics, using Illumina data as the reference. **Results:** All 50 isolates were successfully sequenced and assembled using both ONT methods. The cgMLST alleles were successfully called from both assemblies for >= 85% of loci for all 50 isolates. **Conclusions:** ONT's MinION may provide PHLs a tool for foodborne outbreak surveillance, providing a cheaper option compared with Illumina sequencing while upholding data quality. A smaller footprint and lower cost could reduce resource demand by PHLs participating in foodborne enteric outbreak surveillance.

### Poster 149. NCBI's Pathogen Detection System and MicroBIGG-E Enable the Analysis of aac(6')-Ib Family Aminoglycoside Modifying Enzymes

**M. Feldgarden**, V. Brover, B. Fedorov, D.H. Haft, A.B. Prasad, W. Klimke
National Center for Biotechnology Information, US National Library of Medicine, National Institutes of Health, Bethesda, MD, USA

**Background:** The advent of genomic surveillance systems for public health also enables the comprehensive examination of the evolution and spread of important traits such as virulence and antimicrobial resistance. NCBI's Pathogen Detection System contains publicly available genome sequences from over 950,000 isolates and is used to track the spread of infectious disease outbreaks. This system also reports the genetic elements responsible for resistance to antibiotics, biocides, and other stresses, as well as virulence that are identified by AMRFinderPlus. Here, we describe features of AMRFinderPlus and its associated database, along with a publicly available browser, the Pathogen Detection Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E), which lets users download protein and nucleotide sequences of the genetic and genomic elements identified by AMRFinderPlus. We used MicroBIGG-E to examine the evolution of *aac(6')-Ib* aminoglycoside modifying enzymes (AMEs). **Methods:** *aac(6')-Ib* family AMEs are common antimicrobial resistance genes that confer clinically important phenotypes. Single or dual amino acid substitutions can yield gains and losses in susceptibility to amikacin, gentamicin, kanamycin, and tobramycin, as well as ciprofloxacin. Using MicroBIGG-E, we downloaded 26,489 full-length *aac(6')-Ib* family nucleotide sequences corresponding to one of 97 *aac(6')-Ib* family proteins. After deduplication, we reduced these 26,489 nucleotide sequences to 218 unique nucleotide sequences. We built maximum likelihood phylogenies to observe the evolution of amino acid changes that affect antibiotic susceptibility. **Results:** Transitions from amikacin resistant/gentamicin sensitive forms to the amikacin sensitive/gentamicin resistant forms have occurred multiple times within and among *aac(6')-Ib* lineages. In contrast, ciprofloxacin resistance has evolved only once followed by subsequent diversification within a single clade. We also describe how these forms are distributed among clinical and environmental isolates. **Conclusions:** This work demonstrates the need for and power of tools that enable researchers to easily find and access large scale genomic data and downstream analysis for research and epidemiological purposes.

### Poster 150. Use of Specialized Tissue-Based Diagnostic Techniques for Minimally Invasive Tissue Sampling to Determine Bacterial Causes of Death in Children under the Age of 5 in South Africa

**M.R. Bias**[1,2], T.M. Wilson[1,2], R.B. Martines[2], J.N. Seixas[2], M. Hale[3], R. Chawana[4], S. Mahtab[4], S.A. Madhi[4], V.L. Baillie[4], J. Bhatnagar[2], S.R. Zaki[2], D.M. Blau[2], J.M. Ritter[2]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Department of Anatomical Pathology, University of the Witwatersrand, Johannesburg, South Africa, [4]University of the Witwatersrand Faculty of Health Sciences, Johannesburg, South Africa

**Background:** Infectious diseases are an important, potentially preventable, leading cause of mortality in infants and children <5 years old in low-income countries. Postmortem pathological examination is useful to identify infectious etiologies of deaths in infants and children. Few data are available on how well tissue-based diagnostic assays on specimens from minimally invasive tissue sampling (MITS) are able to identify infections in this population. **Methods:** Formalin-fixed MITS samples from child deaths in South Africa were sent to the Infectious Diseases Pathology Branch (IDPB) as part of the pilot phase of the Child Health and Mortality Prevention Surveillance (CHAMPS) project in 2016. Histopathological evaluation was performed, and findings were discussed among pathologists from IDPB and South Africa through telepathology sessions, as needed, to achieve consensus diagnoses. Routine diagnostic tests, including special stains (SS), immunohistochemistry (IHC) and molecular testing by PCR and sequencing, were performed on MITS specimens that showed histopathologic evidence suggesting of an infectious etiology. **Results:** IDPB received MITS samples from 403 deaths with suspected infectious cause of mortality in children <5 years and stillbirths. Among these deaths, 55% (225) had histopathologic features suggesting of infection. Further testing at IDPB identified common infectious bacterial agents as *Klebsiella pneumoniae* (3 PCR and 41 IHC positive tests), *Pseudomonas aeruginosa* (2 PCR and 5 IHC positive tests), *Staphylococcus species*, including *Staphylococcus aureus* (12 IHC positive tests), *Streptococcus species, including Streptococcus pneumoniae* (10 PCR and 3 IHC positive tests) and *Acinetobacter species*, including *Acinetobacter baumannii* (13 PCR and 7 IHC positive tests). **Conclusions.** Tissue-based IHC and PCR assays performed on MITS samples are useful for identifying bacterial infections associated with childhood deaths in low-income countries. These infections include some that are preventable and treatable, emphasizing the potential for MITS to guide implementation of public health measures aimed at reducing childhood mortality.

### Poster 151. Mitigate Cross-Contamination Hazards by Sorting Samples within a Closed Cartridge

**C.L. Montoya**[1], R.T. Nakamoto[2], R.P. Beuk[3], A. Völkel[3], B. Ackerman[3]
[1]Miltenyi Biotec, Inc., San Diego, CA, USA, [2]Owl Biomedical, Inc., Santa Barbara, CA, USA, [3]Miltenyi Biotec B.V. & Co. KG, Bergish Gladbach, Germany

**Background:** The ability to isolate pathogens and immune cells from hazardous samples is essential to immunological and infectious disease studies. Yet, when a traditional droplet cell sorter is used there is potential for aerosol formation, exposure to infectious materials, and cross-contamination. A benchtop microfluidic instrument, the MACSQuant® Tyto® Cell Sorter mitigates these risks by utilizing a single-use and closed-sort system. In this study, we show that the MACSQuant Tyto Cell Sorter can contain 1 µm particles and sort *Escherichia coli* to a high purity without cross-contamination between samples. **Methods:** To test aerosol production, a solution of 1, 2, and 10-µm Polyscience Fluoresbrite® YG Microspheres were transferred to a cartridge at 300 mbar. After the sort, the negative-chamber air filter was excised and examined with a fluorescence microscope. Disposable Cyclex-D impactors were used to collect 1 µm microspheres during sorting with an ultrasonic atomizer positive control and PBS negative control. The Cyclex-D was positioned above the negative-sort chamber filter while flowing 5 mL of sample. Then the Cyclex-D coverslip was removed and placed adhesive-side down on a microscope slide to observe particle transfer. To test cell sorter cross-contamination, GFP-expressing *E.coli* were mixed with wild type *E.coli* (1 x $10^6$/ mL, 36% GFP+ expressing *E.coli)* and sorted. Following GFP+ bacteria sorting, a new media-containing MACSQuant Tyto Cartridge was processed for two hours. A bioburden test was performed afterwards with 14 days of culture. **Results:** The microspheres were easily distinguished from other particles at 10x due to their uniform shape, size, and bright fluorescence. When examined, the bead-containing cartridges and negative control yielded no observable beads, while the positive controls showed abundant microspheres. GFP-expressing *E. coli* were sorted to 97% purity and the bioburden test showed no cross-contamination of bacteria (<1 CFU/mL). **Conclusions:** We demonstrated the cartridge is capable of containing microspheres larger than or equal to 1 µm. This size range includes many prokaryotes, bacterium, and eukaryotic cells. Supporting this observation, we confirmed the MACSQuant Tyto Cell Sorter effectively sorted *E.coli* without cross-contamination between cartridges.

### Poster 152. *Mycoplasma genitalium* Prevalence in Clinical Samples Received at Public Health Laboratories in the Southeast United States

**S.R. Crowe[1],** Y. Totten[1], J. Heaps[1], M.C. Rowlinson[2], V. Arora[3], M. Johnson[3], T. Fields[3], R. Zinner[3], A. Young-Gunnell[3]
[1]Florida Department of Health, Jacksonville, FL, USA, [2]Wadsworth Center, New York State Department of Health, Albany, NY, USA, [3] Kentucky State Public Health Laboratory, Frankfort, KY, USA

**Background:** Laboratory testing and surveillance are critical to reduce the incidence of sexually transmitted infections (STIs). A 2019 Centers for Disease Control and Prevention report showed upward trends in STI rates in the southeastern United States with several states ranked in the top 10 for chlamydia (CT), gonorrhea (NG), syphilis and congenital syphilis. While not notifiable or reportable in the US, *Mycoplasma genitalium* (MG) should be considered an important STI since it is associated with serious sequelae, greater risk of other STIs and treatment failures related to antimicrobial resistance (AR). However, limited MG prevalence data exists. This study evaluated the prevalence of MG in clinical samples received for STI testing at eight state public health laboratories (PHL) in the southeast US. **Methods:** State PHLs in Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, and Tennessee tested de-identified, remnant samples submitted for routine CT/NG testing in Hologic® media. State, specimen source, age range and CT/NG results were recorded. Samples were tested for MG using Hologic's® Aptima *Mycoplasma genitalium* assay. Reagents for this study were funded through a grant from the Association of Public Health Laboratories (APHL) and were not provided by the manufacturer. Approximately 3,200 tests were divided among the states based on population. **Results:** In total 3,265 samples were tested. Overall MG prevalence in the study population was 13.2% (431/3265). Prevalence in individual states ranged from 10.38% (93/896) in Florida to 19.79% (37/187) in Mississippi. Of the MG positive patients, 29% (125/431) were co-infected with CT, NG or both with 18.1% (78/431) positive for MG and CT, 6.96% (30/431) positive for MG and NG and 3.94% (17/431) positive for MG, CT and NG. Chi-square tests of independence showed associations between sex and MG result, age group and MG result, and between MG and CT/NG result. **Conclusions:** Observed prevalence of MG was > 10% in all eight states and higher than NG and CT prevalence in five of eight states. Additional testing is needed to evaluate rates of MG AR in the region. This study highlights the need to perform diagnostic and surveillance testing for MG to evaluate burden of MG disease and as an indicator of STI risk.

### Poster 153. Moved to Oral Presentation E2. Laboratory Diagnostics and Systems

### Poster 154. Withdrawn

### Poster 155. Digital Pathology Systems Facilitate Remote Microscopic Diagnosis and Capacity Building for the Child Health and Mortality Prevention Surveillance Network

**T.M. Wilson**[1,2], M.R. Bias[1,2], R.B. Martines[2], J.N. Seixas[2], J.B. Swims[2], B.E. Ndibile[3], S. Sava[3], I.A. Bassey[4], C. Carrilho[5], D. Jordao[5], F.C. Fernandes[5], C.B. Traore[6], F. Arjuman[7], M. Kamal[8], M.M. Rahman[8], A. Alemu[9], M. Hale[10], P.J. Swart[11], C.G. Whitney[12], S.R. Zaki[2], J.M. Ritter[2]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Kisii Teaching and Referral Hospital, Kisii, Kenya, [4] ICAP-Columbia University, Makeni, Sierra Leone, [5]Department of Pathology, Faculty of Medicine, Eduardo Mondlane University and Maputo Central Hospital, Maputo, Mozambique, [6]Department of Pathological Anatomy and Cytology, University Hospital of Point G, Bamako, Mali, [7]National Institute of Cancer Research and Hospital, Dhaka, Bangladesh, [8]Bangabandhu Sheikh Mujib Medical University, Dhaka, Bangladesh, [9]College of Health and Medical Sciences, Haramaya University, Harar, Ethiopia, [10]Department of Anatomical Pathology, University of the Witwatersrand, Johannesburg, South Africa, [11]University of Witwatersrand, and National Health Laboratory Service, Johannesburg, South Africa, [12]Department of Global Health, Rollins School of Public Health, Emory University, Atlanta, GA, USA
**Background:** There is a need to increase in-country diagnostic pathology capacity for determining infectious causes of death in children in low-income countries. The Infectious Disease Pathology Branch (IDPB) at CDC identifies pathogens associated with deaths of children under the age of five in seven countries in sub-Saharan Africa and South Asia in partnership with the Child Health and Mortality Prevention Surveillance (CHAMPS) Network sites. We describe the use of telepathology meetings (TM) for collaborative review of histopathologic findings of infectious diseases in minimally invasive tissue samples from child deaths in this setting and implications for site pathology capacity building. **Methods:** Pathology phase 2 of the CHAMPS program emphasizes building and transferring pathology capacity to the sites. This entails review of site-processed, evaluated, and scanned digital slides by IDPB pathologists and conducting TM for real-time discussion between IDPB and site pathologists. TM are held with each site on a regular, rotating basis to discuss the pathology of select cases, and provide focused training on any other topics of interest or concern. IDPB pathologists also perform quality assessment of the site scanned slides and provide feedback on quality of site histology and scanning processes, with suggestions for improvement and standardization. **Results:** Over the past 7 months in pathology Phase 2, IDPB has reviewed site digital slides for 723 CHAMPS cases and conducted 27 TM among the 7 sites. Discussions revolved around discrepant histopathologic findings, interpretation of immunohistochemical stains, collaborative determination of diagnoses, and improvement of histologic preparation, pre-analytic slide artifacts to be resolved before scanning, and post-scan quality control to improve image quality. Varying improvements have been achieved in site pathology capacity. **Conclusion:** Efforts of IDPB and CHAMPS site pathologists in pathology phase 2 of the project have demonstrated the value of digital pathology and TM for diagnostic review, pathology capacity building, digital management of pathology slides, and image quality control. Digital slide scanning and regular TM facilitates knowledge sharing around technical preparation of specimens and interpretation of pathologic findings.

### Poster 156. Primer Creation Pipeline for an Extended MLST Approach to Culture Independent Pathogen Subtyping

**S. Lucking**[1,2], J. Hensley[1,3], A. Huang[1], R. Jin[1,2], A. Khan[1,2], H. Carleton[1], A. Jo Williams-Newkirk[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Weems Design Studio, Decatur, GA, [3]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA
**Background:** Isolate whole genome sequencing (WGS) is a powerful tool in enteric disease surveillance. The adoption of culture-independent diagnostic tests threatens culture-dependent surveillance systems and is 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 called T3Pio to design extended multi-locus sequence typing (eMLST) schemes and primers for pathogen subtyping and validating pilot results *in vitro*. **Methods:** T3Pio utilizes open-source bioinformatics software. It identifies core genes and designs primers for the user's chosen HMAS platform. As a pilot, 266 unrelated *Salmonella* were input into T3Pio. Evaluation of our pilot set revealed unacceptable resolution between isolates belonging to some common *Salmonella* outbreak serotypes. To address this, we reduced the number of genomes used to representatives of the 14 most common *Salmonella* outbreak serotypes. The impact of degenerate primer on out design was also evaluated. **Results:** Our second T3Pio analysis identified more core

genes and primer pairs and initial application of this scheme increased the resolution between previously indistinguishable isolates of the same serotype. *In vitro* testing of degenerate primers on mixtures of known isolate DNA found that all primers produced amplicons, but efficiency levels did vary, leading to allele ratios in the amplicon sequencing data that were sometimes non-representative of the ratios of the isolates in the original sample. **Conclusions:** This proof of concept demonstrates that T3Pio successfully generates candidate amplicons for use in direct-from-specimen enteric pathogen HMAS subtyping panels, potentially providing resolution between pathogen genomes similar to established *in silico* subtyping schemes for isolate WGS. The final panel of target loci will be chosen for optimal identification of outbreak-associated samples using user-provided training genomes for possible deployment to public health partners for use in outbreak surveillance.

### Poster 157. Generation of Specific Aptamers for Enzymes of the Methylerythritol Phosphate Pathway

**C. Roca Martinez**[1,2,3], S. Imperial Ródenas[1,3], X. Fernàndez-Busquets[2,3]
[1]Department of Biochemistry and Molecular Biomedicine, School of Biology, University of Barcelona (UB), Barcelona, Spain, [2]Nanomalaria Joint Unit, Institute for Bioengineering of Catalonia (IBEC) and Barcelona Institute for Global Health (ISGlobal), Barcelona, Spain, [3]Nanoscience and Nanotechnology Institute, UB (IN2UB), Barcelona, Spain
**Background:** Pathogenic microorganisms such as the bacteria *Mycobacterium tuberculosis and Pseudomonas aeruginosa,* and the protozoa of the phylum Apicomplexa, including the causing agents of malaria and toxoplasmosis, synthesize the isoprenoid precursors isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP), by the methylerythritol phosphate (MEP) pathway. This pathway is essential for most bacteria and Apicomplexa, but it is not present in humans, which synthesize IPP and DMAPP by the alternative mevalonate pathway. The essential role of the MEP pathway and its distribution in different organisms make their enzymes attractive targets for the development of new anti-infective agents. Herein, we focus on the development of aptamers against key enzymes of the MEP pathway. Aptamers are single-stranded oligonucleotides which behave as "chemical antibodies" and can bind specifically and efficiently to a given target molecule. **Methods**: Several methods have been optimized, such as: (i) the production of MEP pathway enzymes, (ii) the development of aptamers through systematic evolution of ligands by exponential enrichment, an *in vitro* selection process based on iterative cycles of binding, partitioning, and amplification of oligonucleotides from a pool of variant sequences, (iii) the cloning of aptamers, (iv) the establishment of an electrophoretic motility shift assay for the identification of interactions between selected aptamers and their target enzymes, and (v) methods for the *in vitro* evaluation of enzymatic activity. **Results:** We report the identification of a DNA aptamer which specifically binds to the enzyme catalyzing the first committed step of the MEP pathway: 1-deoxy-D-xylulose-5-phosphate reductoisomerase. **Conclusions**: The results obtained suggest that the selected DNA aptamer could be a potential candidate for the development of new therapeutic agents and for the design of novel diagnosis systems.

### Poster 158. Bactopia v2: Highly Scalable, Portable and Customizable Bacterial Genome Analyses

**R.A. Petit III**[1,2], D.J. Marcon[3,4], A. Sharma[5], T.D. Read[6]
[1]Public Health Laboratory, Wyoming Department of Health, Cheyenne, WY, USA, [2]Theiagen Genomics, Highlands Ranch, CO, USA, [3]Center of Genomics and Systems Biology, Institute of Biological Sciences, Universidade Federal do Pará, Belém, PA, Brazil, [4]Laboratory of Genetic Engineering, Guamá Science and Technology Park, Belém, PA, Brazil, [5]Faculty of Engineering and Technology, Liverpool John Moores University (LJMU), Liverpool, UK, [6]Division of Infectious Diseases, Department of Medicine, Emory University School of Medicine, Atlanta, GA, USA
**Background:** Generation of sequence data for bacterial genomes has become standardized to the point that bioinformatic analysis is the major bottleneck. There is now, more than ever, a need for bioinformatic workflows to be highly scalable and adaptable to the user's needs. In order to address this, we created Bactopia, a Nextflow workflow to provide efficient and flexible comparative genomic analyses for any bacterial species or genera. **Methods:** Bactopia can process Illumina and/or Nanopore sequences with more than 100 bioinformatic tools and many publicly available datasets. Furthermore, Bactopia includes additional workflows to select high quality samples for downstream comparative analyses, such as pan-genome, phylogenetic and functional analyses. We have rewritten the original workflow to take advantage of Nextflow DSL2, allowing users to customize Bactopia by including different tools for each step and simplifying integrations with other bacterial analysis workflows from the popular nf-core community. **Results:** Bactopia v2 is a significant step forward, as it allows users to easily adapt Bactopia to fit their organism-specific needs. To demonstrate this, we implemented Staphopia as a custom Bactopia workflow for the analysis of Staphylococcus aureus genomes. This sub-workflow supplements the standard

Bactopia workflow with additional S. aureus specific analyses such as methicillin-resistance (MRSA), spa typing, and agr typing. Using this as a model, we expect to work alongside users to create additional organism specific sub-workflows. **Conclusions:** Bactopia (v1 and v2) is an open-source system that has been shown to scale from projects as small as one bacterial genome to tens of thousands of bacterial genomes. In the latest release of Bactopia, the scalability remains, and we have introduced even greater flexibility to meet the needs of our users. The documentation and code for Bactopia can be accessed at https://bactoia.github.io/.

## Antimicrobial Resistance

### Poster 159. A Comparison of *Salmonella* Serotypes in NARMS Retail Meat (2002-2019) and in Human Clinical Cases (1996–2018)

**E. Nyirabahizi**[1], E. Hsu[2], H. Tate[1], E. Strain[1], S. Zhao[1]
[1]US Food and Drug Administration, Center for Veterinary Medicine, Office of Research, Laurel, MD, USA, [2]Walter Johnson High School, North Bethesda, MD, USA
**Background:** *Salmonella* is a zoonotic pathogen and found in a variety of environmental and animal hosts. Currently, > 2,600 serotypes are recognized, and the majority of these can live in a range of animal hosts with different prevalence. Contaminated retail meat is thought to be a significant contributor to foodborne *Salmonella* illness. Using data from the National Antimicrobial Resistance Monitoring System (NARMS), this study compared the distribution of *Salmonella* serotypes in retail meat and humans to evaluate the relative contribution of contaminated retail meat to human illness. **Methods**: A total of 8,501 retail meat isolates recovered between 2002-2019, and 46,308 human isolates recovered between 1996-2018 were analyzed. Pearson's chi-square test of association was used to assess the association between serotype and source of isolates and Mann-Kendall test was used to test for monotonic trend over time. **Results:** A total of 103 and 420 serotypes were identified in retail meat and humans, respectively. The top 10 *Salmonella* serotypes comprise over 67% and 70% of the total number of isolates from humans and retail meat, respectively. Pork, turkey, beef, and chicken isolates had 4, 5, 5, and 7 of the 10-top serotypes in common with the 10 top serotypes in humans and only *S.* Typhimurium was among the top 10 across all commodities. Humans had 332 (79%) of unique serotypes. Between 2012 and 2018, there was, a significant (p<.001) decrease in serotypes Heidelberg and Typhimurium across all commodities. There was a significant association between serotype and source. Serotypes I 4,[5], 12:i:-, Montevideo, Muenchen, Newport, and Typhimurium in humans and their counterpart in pork, beef, turkey, beef, and chicken respectively significantly contributed. **Conclusions:** Overlap in serotype distribution elucidate the food animal sources of *Salmonella*. NARMS data can narrow the scope of outbreak investigations for strains regardless of susceptibility to antimicrobial agents.

### Poster 160. The Impact of a Post-Prescription Antimicrobial Stewardship Program in Lebanon

**A. Shallal**[1,2], J. Verkler[1], C. Lahoud[3], M. Zervos[1,2], M. Matar[4,5]
[1]Division of Infectious Diseases, Henry Ford Health, Detroit, MI, USA, [2]Wayne State University School of Medicine, Detroit, MI, USA, [3]Division of Infectious Diseases, Brigham & Women's Hospital, Harvard Medical School, Boston, MA, USA, [4]Notre Dame des Secours University Hospital, Byblos, Lebanon, [5]Holy Spirit University of Kaslik School of Medical Sciences, Byblos, Lebanon
**Background:** Antimicrobial stewardship programs (ASP) are a key strategy in reducing antimicrobial resistance. The post-prescription review and feedback (PPRF) program has been shown to be effective in different countries. This project evaluated the impact of a PPRF program at a hospital in Lebanon. **Method:** Prospective cohort study from June 2020 to June 2021 at a tertiary care hospital in Lebanon, consisting of a baseline and post-intervention phase, with a one-month washout between periods. Patients aged > 15 who had received 48 hours of antibiotics were recruited for the study. During the intervention, an infectious disease (ID) physician reviewed the cases and gave alternate recommendations if appropriate. Acceptance of these was measured after 48 hours. The primary outcome was days of therapy (DOT) per patient. **Results:** 328 patients were recruited in the baseline phase, and 468 in the post-intervention phase. There was a significant reduction in antimicrobial use for gastrointestinal (13.19% to 3.85%; p<0.001), UTI (25.1% to 13.4%; p<0.0001), and post-operative prophylaxis (11% to 4.06%; p=0.0001). In the post-intervention phase, which occurred in a COVID-19 surge, empiric therapy (3.07% vs 17.5%; p<0.001) and "other" infections (9.45% vs 31.8%; <0.0001) significantly increased, likely due to empiric coverage for advanced pneumonitis. Despite this, days of therapy decreased from 8.38 during the baseline phase to 7.08 during the post-intervention phase (p <0.0016). After adjusting for age, sex, and primary disease treated, members in the baseline period were on antibiotics for 29% longer and hospitalized for 16% longer than members in the post-intervention period. Summary in Tables 1 and 2. **Conclusion:** ID physician-driven implementation of an ASP was successful in

reducing days of antibiotic therapy in an acute-care setting in Lebanon. PPRF can be used in other countries in order to build capacity and advance best practices through education.

### Poster 161. Emergence of Multidrug-Resistant *Salmonella* Serotype Kentucky in Humans—United States, 2011–2021

**L. Dorough**[1,2], M. Birhane[1], C. Snyder[1,2], K.A. Tagg[1], J.P. Folster[1], H. Caidi[1], B. Tolar[1], L. Ray[1], D. Hawkins[1,2], H.J. Shah[1], G.E. Langley[1], L. Francois Watkins[1]
[1]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA
**Background:** In the United States, Kentucky is the most common serotype of *Salmonella enterica* isolated from chicken but causes <1% of salmonellosis in humans. During 2002–2005, a multidrug-resistant (MDR) strain (Strain A) associated with travel to Africa and the Middle East emerged in Europe. We describe its emergence in the United States. **Methods:** We analyzed all human Kentucky isolates sequenced at US public health laboratories and submitted to PulseNet, the national molecular subtyping network for foodborne disease surveillance. We classified isolates as "Strain A" using core genome multi locus sequence typing of their phylogenetic position and screened for genotypic resistance determinants using a modified workflow based on ResFinder 3.0. We defined MDR as predicted resistance to ≥3 antibiotic classes. We collected epidemiologic data from state health departments for recent cases (2019–2021). We linked isolates to epidemiologic data from FoodNet (2019 and earlier), an active surveillance system tracking enteric infections in 10 US sites. We compared patient characteristics of Strain A with other Kentucky strains. **Results:** We identified 345 sequenced Kentucky isolates from humans during 2011–2021, of which 161 (47%) were Strain A (46% were detected after 2018). Epidemiologic and antibiotic resistance information were available for 65 (40%) isolates, including 44 Strain A. Strain A isolates were resistant to a median of 5 antibiotic classes; all were resistant to quinolones, and 84% were MDR. Compared with patients with other strains, those with Strain A were older (median age 50 vs. 34 years) but not more likely to be hospitalized (23% vs. 24%). However, they were more likely to have traveled internationally (58% vs. 10%, p<0.01). The 25 travelers with Strain A visited Asia (20, 80%) or Africa (5, 20%). **Conclusions:** *Salmonella* Kentucky Strain A, first identified in Europe, has emerged in the United States, and is associated with travel. Continued monitoring of human illnesses caused by Strain A is warranted to better understand exposures among those who did not travel, especially since this MDR strain may cause more severe illness.

### Poster 162. Informal Antibiotic Sales at the Community Level in Guatemala before and after Antibiotic Prescription Regulation

**N.C. Rojop**[1], M.P. Moreno[2,3], L.M. Grajeda[1,2], J.C. Romero[2], C. Cordon-Rosales[2,4], D.R. Call[4], B.M. Ramay[2,3,4]
[1]Department of Epidemiology, Faculty of Sciences and Humanities, Universidad del Valle de Guatemala, Guatemala City, Guatemala, [2]Center for Health Studies, Universidad del Valle de Guatemala, Guatemala City, Guatemala, [3]Department of Pharmaceutical Chemistry, Faculty of Sciences and Humanities, Universidad del Valle de Guatemala, Guatemala City, Guatemala, [4]Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA, USA
**Background:** Requiring a prescription for antibiotic sale is one way to mitigate potential overuse of antibiotics in communities, but any benefits of such regulation will only be achieved if alternative sources are not available. In 2019, Guatemala approved the regulation requiring a prescription for antibiotic dispensing in pharmacies. The objective of the current study was to determine if implementation of the antibiotic prescription law was effective in neighborhood corner stores in Guatemala where antibiotics were previously sold without a medical prescription. **Methods:** Two cross-sectional surveys were conducted in June of 2019 and January of 2021, respectively before and after the approved regulation, in neighborhood corner stores located in two municipalities in the highlands of Guatemala. Questionnaires were administered to document availability and types of antibiotics, and differences in antibiotic availability were assessed using a McNemer test for paired data. **Results:** Corner stores (n=145) were identified in 2019 and 2020, of which 138 (95%) had attendants available to consent in both surveys. In 2019, 47% of corner stores sold antibiotics (n=65/138), with 75% (49/65) and 83% (54/65) selling amoxicillin and tetracycline capsules, respectively. In 2021, significantly more (64%; 88/138) stores dispensed antibiotics ($P$=0.005); 61% (54/88) and 42% (37/88) amoxicillin and tetracycline capsules, respectively. The proportion of stores selling amoxicillin did not change between 2019 and 2021 ($P$>0.05), but fewer stores sold tetracycline in 2021 ($P$=0.002). These findings coincided with the onset of the SARS-CoV-2 pandemic (March 2020, Guatemala). **Conclusions:** An overall increase in the prevalence of antibiotics sold in corner stores is associated with the publication of the antibiotic prescribing legislation shifting demand for antibiotics from pharmacies to informal establishments,

although this change is confounded with unknown effects from the pandemic. Further exploration of the impacts of antibiotic legislation on informal availability of antibiotics is merited.

### Poster 163. Nontyphoidal *Salmonella* Isolated from Dogs Reveal Antimicrobial Resistance Determinants and Relatedness to Strains Found in Humans

**S. Kenney**[1], N. Mikanatha[2], E. Ganda[1]
[1]Penn State University, University Park, PA, USA, [2] Pennsylvania Department of Health, Harrisburg, PA, USA
**Background:** Non-typhoidal *Salmonella* (NTS) is a cause of foodborne illness in the United States, leading to outbreaks, food recalls, and economic losses. Of the estimated 1.35 million yearly infections, 212,500 are linked to antimicrobial resistant (AMR) *Salmonella* strains. This increasing AMR combined with the wide host range of NTS creates overlapping challenges for human and animal health, and the need for biosurveillance and outbreak tracking. Typically, human infections are acquired through consumption of contaminated food or contact with animals. Although zoonotic origin is known, comparison of AMR determinants in NTS clinical isolates from dogs and humans is limited. An estimated 48 million and 7.5 million households in the United States and Canada, respectively, own one or more dogs. However, AMR determinants in NTS clinical isolates from dogs and genetic relatedness to strains found in humans is unclear. **Methods:** Sixty-three NTS isolates from companion dog sources and 16 human clinical isolates were identified through NCBI's Pathogen Isolate Browser and collaboration with the Veterinary Laboratory Investigation and Response Network, a network of diagnostic laboratories spanning the United States and Canada responsible for investigating animal illness outbreaks and tracking AMR bacteria from sick animals. Core genome MLST, 7-gene-MLST, and SNP-based clustering schemes were used to compare strains collected from 2017-2021. AMR traits included in NCBI isolate metadata were compared within clusters. **Results:** AMR determinants for antibiotic efflux capabilities were identified in 95% of isolates, with genes associated with resistance to tetracyclines, sulfonamides, and aminoglycosides also present in specific clusters such as one of *S.* Typhimurium isolates. Of the 16 human isolates included, 14 clustered with those from dogs regardless of clustering scheme. **Conclusions:** Whole-genome sequencing has proven to be a useful epidemiological tool to investigate illness outbreaks and monitor AMR genetic elements in relevant pathogens. The strain-relatedness observed here supports the potential for NTS zoonosis between dogs and humans. Furthermore, the presence of AMR genes in isolates across sources substantiates the need for biosurveillance across a range of NTS reservoirs.

### Poster 164. Lessons Learned from Impact of the COVID-19 Pandemic on the National Antimicrobial Surveillance System in Cambodia, 2020–2021

**B. Sreng**[1], J.J. Rainey[1], J. Weiss[1], J. Letchford[2], O. Sopheap[2], R. Chanyasith[2], A. Vuth[3], V. Mom[3], S. Srun[4], K. Sidonn[5]
[1]US Centers for Disease Control and Prevention-Cambodia, Phnom Penh, Cambodia, [2]Diagnostic Microbiology Development Program, Phnom Penh, Cambodia, [3]National Institute of Public Health, Phnom Penh, Cambodia, [4]Department of Hospital Services, Phnom Penh, Cambodia, [5]Department of Communicable Disease Control, Phnom Penh, Cambodia
**Introduction:** Monitoring antimicrobial resistance (AMR) is important to detect the emergence of multi-drug resistant pathogens. In 2018, the Cambodia Ministry of Health established a national AMR surveillance system. From February-July 2021, Cambodia experienced a surge in COVID-19 transmission, increasing demand for health care services. We assessed the impact of the COVID-19 surge on AMR surveillance to identify strategies for maintaining critical systems during future public health emergencies. **Methods:** We collected inpatient data from the Cambodian Laboratory Information System (CamLIS) and four hospital laboratories from January 2018 to July 2021. We calculated two indicators: 1) mean monthly number of inpatients admitted to hospitals, and 2) percentage of inpatients from whom blood specimens were collected and cultured. We compared indicators from 2018 to 2021 using linear and binomial regressions models. Key informant interviews were conducted with nine national, hospital, and partner organization staff on the perceived impact of COVID-19. **Results:** From January 2018 to July 2021, 157,476 inpatients were registered at the four sentinel hospitals; blood specimens were collected and cultured from 28,675 (18.2%) of these inpatients. After adjusting for seasonality and hospital laboratory, the mean number of monthly inpatients remained statistically similar from 2018-2019 to January-July 2021 (p-value=0.91). The monthly percentage of inpatients with blood cultures was also statistically similar across the two time-periods (OR=1.14; 95% CI: 0.63 – 2.07). In our qualitative analysis, common challenges included: staff were infected and/or quarantined and unable to work, limited confirmation of antimicrobial susceptibility testing (AST) results, and shortages of reagents and required supplies at certain laboratories. **Conclusion:** Despite challenges resulting from the February 2021 COVID-19 surge, Cambodia maintained AMR surveillance at four hospital laboratories. The MOH could reduce AST confirmation requirements for hospitals with proven capacity, develop surge teams to

backfill shortages in skilled positions, and establish an inventory of AMR reagents to maintain core surveillance activities.

### Poster 165. Nontyphoidal *Salmonella* from Clinical and Retail Meat Reveal Increase in Genetic Mechanism for Resistance to Ciprofloxacin, Pennsylvania—2015-2018

**N. Mikanatha[1]**, Y. Fu[2], S. Sayeed[1], L. Dettinger[1], X. Yin[1,3], M. Hackman[3], E. Dudley[2], H. Tate[4]
[1]Pennsylvania Department of Health, Harrisburg, PA, USA, [2]Penn State College of Agricultural Sciences, University Park, PA, USA, [3]Penn State Hershey College of Medicine, Hershey, PA, USA, [4]Food and Drug Administration, College Park, MD, USA

**Background:** Nontyphoidal *Salmonella* (NTS) is a leading cause of bacterial foodborne illnesses in the United States. Antimicrobial drugs including ciprofloxacin are recommended for treatment of severe infections. Annually, NTS cause over 200,000 drug-resistant infections and 70 deaths in the US. Pennsylvania conducts surveillance for NTS isolates from clinical and retail meat sources in collaboration with the National Antimicrobial Resistance Monitoring System (NARMS). **Methods:** Clinical NTS isolates collected in Pennsylvania from 2015-18 were tested for antimicrobial susceptibility (AST) and analyzed by whole-genome sequencing. Concurrently, we prospectively surveyed microbiological NTS contamination in retail meat samples. NTS isolated from meat were also evaluated for AST and WGS was performed. **Results:** Of 360 clinical *Salmonella* isolates analyzed for AST, 43 (11.9%) and 14 (3.9%) were resistant to ≥3 (MDR) and ≥5 antibiotics classes, respectively. Twelve (3.3%) were ceftriaxone-resistant, 51 (14.2%) had decreased susceptibility to ciprofloxacin (DSC). Among clinical isolates, DSC increased from 3.6% (3/83) in 2015 to 16.5% (18/109) in 2018 and was correlated with a *gyr*A mutation in 30.2% (29/96) and 40.0% (8/20) of *S.* Enteritidis and *S.* Infantis respectively. Two clinical isolates (*S.* I 4,[5],12:i:- and *S.* Give) had a *qnrB19* gene and one had *gyr*A. We isolated NTS in 144 (4.1%) of 3480 meat samples tested. Twenty-seven (18.8%) and 21 (14.6%) were MDR and resistant to ≥5 antibiotics classes, respectively. Ceftriaxone resistance was detected in 22 (15.3%) of meat isolates. DSC increased from zero (0/25) in 2015 to 12.5% (6/48) in 2018 and was driven by a *gyr*A mutation in 77.8% (7/9) and 27.3% (3/11) among *S.* Infantis and *S.* Enteritidis isolates respectively. The *S.* Infantis isolates from clinical and meat sources also had $bla_{\text{CTX-M-65,}}$ which confers resistance to ceftriaxone. **Conclusions:** *Salmonella* isolated from human and meat sources in Pennsylvania were MDR including decreased susceptibility to ciprofloxacin. The increase in prevalence of genetic mechanisms that confer resistance to ciprofloxacin in NTS from clinical and meat sources undermines treatment for severe infections and highlights the need for One-Health surveillance and antimicrobial stewardship.

## Vaccines and Immunizations

### Poster 166. Association between Childhood Vaccination, Family Planning, and Healthcare Access: Analysis of Nepal, Senegal, and Zambia

**F. Castillo-Zunino**[1], P. Keskinocak[1], D. Nazzal[1], M.C. Freeman[2]
[1]H. Milton Stewart School of Industrial and Systems Engineering, Georgia Institute of Technology, Atlanta, GA, USA, [2] Rollins School of Public Health, Emory University, Atlanta, GA, USA.

**Background**: Childhood vaccination, family planning, healthcare access, and woman empowerment form part of the Millennium Development Goals (MDG). Public policy applications suggest that tackling goals holistically make larger improvements; although such studies usually lack statistical evidence. We analyzed Nepal, Senegal, and Zambia to test the association between vaccinations and other MDGs. **Methods:** The Demographic and Health Surveys (DHS) collects information across metrics and variables related to MDGs. Through ordinal logistic regressions, controlling for household/mother characteristics, we identified variables that significantly predicted the number of vaccines one-year-old children received. We analyzed DHSs from Nepal, Senegal, and Zambia. We compared children with no or few vaccines to children with 8 childhood vaccines (namely 8V children, having DTP3, MVC1, Pol3, and BCG vaccines), through bootstrapping and optimal propensity scores matching to compare children with similar living conditions. **Results:** On average, 8V mothers accessed health facilities at least once in the last year; 31.1% (16.7% to 44.4%, CI 95%) more than children with 0 to 2 vaccines in Nepal 2001, 18.8% (8.3% to 26.8%) more in Senegal 2005, and 21.7% (10.8% to 38.5%) in Zambia 2001-02. For recent years, 8V mothers accessed a health facility 16.7% (1.1% to 33.3%) more than children with 0 to 4 vaccines in Nepal 2016, 16.9% (3.9% to 31.9%) in Senegal 2019, and 23.0% (9.2% to 35.1%) in Zambia 2018. 8V mothers knew on average 0.7-1.6 (range given by all six DHSs; 0.2 to 2.1, 95% CI) more contraceptive methods than children with few or no vaccines, on all countries-years tested. **Conclusions:** Access to healthcare facilities and family planning efforts in education/accessibility were positively and significantly associated with higher vaccination rates in the last two

decades in Nepal, Senegal, and Zambia. Mother years of education was positively associated with vaccination, although evidence was not as strong.

### Poster 167. Critical Success Factors for High and Sustained Routine Immunization Coverage: A Case Study of Zambia

**K. Micek**[1], K.A. Hester[1], Z. Sakas[1], A.S. Ellis[1], E. Ogutu[1], W. Kilembe[2], R.A. Bednarczyk[1], M.C. Freeman[1]
[1]Gangarosa Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, GA, USA, [2]Center for Family Health Research in Zambia, Lusaka, Zambia

**Background:** The essential components of a vaccine delivery system are well-documented, but robust evidence on how and why the related processes and implementation strategies prove effective at driving coverage is not well-established. To address this gap, we identified critical success factors associated with advancing key policies and programs that may have led to the substantial changes in routine childhood immunization coverage in Zambia from 2000 to present. **Methods:** We conducted mixed-methods research based on an evidence-based conceptual framework of core vaccine system requirements. Additional facilitators and barriers were explored at the national and subnational levels in Zambia. We conducted a thematic analysis grounded in implementation science frameworks to determine the critical success factors for improved vaccine coverage. **Results:** The following success factors emerged: 1) the Inter-agency Coordinating Committee was strengthened for long-term engagement which, complemented by the Zambia Immunization Technical Advisory Group, is valued by the government and integrated into national-level decision-making; 2) the Ministry of Health improved the coordination of data collection and review for informed decision-making across all levels; 3) Regional multi-actor committees identified development priorities, strategies, and funding, and iteratively adjusted policies to account for facilitators, barriers, and lessons learned; 4) Vaccine messaging was disseminated through multiple channels, including the media and community leaders, increasing trust in the government by community members; 5) The Zambia Ministry of Health and Churches Health Association of Zambia formalized a long-term organizational relationship to leverage the strengths of faith-based organizations; and 6) Neighbourhood Health Committees spearheaded community-driven strategies via community action planning and ultimately strengthened the link between communities and health facilities. **Conclusion:** Broader health systems strengthening and strong partnerships between various levels of the government, communities, and external organizations were critical factors that accelerated vaccine coverage in Zambia. These partnerships were leveraged to strengthen the overall health system and healthcare governance.

### Poster 168. Safe Vaccines Against Diseases with Epidemic Potential: The Safety Platform for Emergency vACcines (SPEAC) Project

**W.T. Huang**, S. Black, C.L. Dekker, B. Law, M. Gurwith, M. Sturkenboom, R. Chen
Brighton Collaboration, Task Force for Global Health, Decatur, GA, USA

**Background.** The Coalition for Epidemic Preparedness Innovations (CEPI) is funding multiple candidate vaccines and platforms against Lassa fever, Middle East respiratory syndrome, Chikungunya, Nipah, Rift Valley fever, COVID-19, and Disease X. Harmonized assessment of adverse events across the CEPI portfolio will facilitate the identification of relevant safety issues, as a safety signal may be missed in individual small trials. In March 2019, CEPI and Brighton Collaboration launched the SPEAC project to monitor safety of CEPI funded vaccines. **Methods.** SPEAC's work includes (1) providing safety expertise on individual study data safety monitoring boards (DSMB) and implementing a meta-DSMB to oversee safety across trials; (2) creating case definitions and related tools/resources, guidelines, and vaccine technology templates to standardize safety assessment; (3) evaluating use and applicability of SPEAC products and services; and (4) scientific advising and communicating with CEPI, vaccine developers, and other stakeholders. **Results.** SPEAC created an operational meta-DSMB with 16 liaison members and a charter; maintained a pool of 26 regional, qualified DSMB members for sponsors; and trained 14 new professionals to join the DSMB pool. Six lists of adverse events of special interest (AESI) for priority pathogens were created; 6 new case definitions and 9 AESI companion guides were developed and made accessible online along with existing Brighton Collaboration safety resources; and 11 safety vaccine templates were completed. Evaluations included a systematic review of case definition use in LMIC; protocols to assess/validate performance of AESI case definitions and tools; and surveys to collect feedback from CEPI vaccine developers. SPEAC experts reviewed and provided feedback on 24 clinical trial protocols; organized 4 webinars on disease enhancement, tools, and studies for COVID-19 vaccine safety assessment; and prepared/shared 7 AEFI crisis communication sheets. **Conclusions.** Through the SPEAC project, Brighton Collaboration has the unique opportunity to harmonize safety assessment throughout the vaccine life cycle for CEPI funded vaccines. The processes developed will be extended and scaled up to support additional CEPI priority pathogens in the new vaccine development paradigm.

### Poster 169. Ethnographic Validation of Standardized Tools as a Key Component in Understanding Behavioural and Social Drivers of Vaccination in Guatemala

**M. Berger**[1], L. Barrera[2], D. Sierra[2], L. Menning[3], F. Ganter-Restrepo[3], M. Rondy[4]
[1]Universidad del Valle de Guatemala, Guatemala, Guatemala, [2]Ministerio de Salud Pública y Asistencia Social, Guatemala, Guatemala, [3]World Health Organization, Geneva, Switzerland, [4]Pan American Health Organization, Guatemala, Guatemala

**Background:** Vaccination programs prioritizing vulnerable populations are essential to increase national coverage rates. The global expert group 'Measuring Behavioural and Social Drivers of Vaccination' (BeSD) developed tools to measure and address under-vaccination in children aged ≤5 years, and to track consistent and comparable data over time. The BeSD childhood vaccination tools developed (survey, in-depth interview guides, and user guidebook) were validated in various countries, including Guatemala, where 24 different languages (in addition to Spanish) are spoken. **Methods:** Psychometric validation of the BeSD tools was conducted in four ethnolinguistic regions in Guatemala from February-April 2021, with the help of linguists fluent in each local language. Cognitive interviews with parents or caregivers of children aged ≤5 years assessed adequacy and understanding of survey questions. In-depth qualitative interviews evaluated comprehension of interview guides and user guidance tools. **Results:** We conducted 19 cognitive interviews: 79% of surveyed participants spoke languages other than Spanish (Tz'utujil, Kaqchikel, Q'eqchi'), 84% were female. In-depth qualitative interviews were conducted with 10 participants (1 National Immunization Program representative, 3 local medical professionals, 3 caregivers of children aged <5 years, and 3 community health promoters). Analyses revealed variations in dialects and language that impact respondents' interpretation of the question asked. Adapting tools to regionalized local languages is key to facilitate content understanding and participation of vulnerable groups. Results evidence the value of cognitive interviews in adapting data collection tools, the need to consider key audiences in validating tools in pandemic contexts and creating regional microadaptations prior to implementation. **Conclusions:** The language in which a questionnaire is developed may act as an exclusion factor or a factor to increase participation and visibility of vulnerable populations, especially in plurilingual settings. Local ethnolinguistic validation of internationally-developed tools is essential to guarantee participation and visibility of prioritized groups and inform national vaccination campaigns, including vaccination against COVID-19, in Guatemala.

### Poster 170. Critical Success Factors for High and Sustained Routine Immunization Coverage: A Mixed-Methods Case Study of Senegal

**Z. Sakas**[1], K.A. Hester[1], A.S. Ellis[1], E. Ogutu[1], R.A. Bednarczyk[1], M.C. Freeman[1], S.A. Diatta[2], D. Gueye[2], A.S. Mbengue[2], M. Sarr[2]
[1]Rollins School of Public Health, Emory University, Atlanta, GA, USA, [2]The Institute for Health Research, Epidemiological Surveillance, and Training (IRESSEF), Dakar, Senegal

**Background**: The core requirements for vaccine delivery systems are well-established, including strong governance and financing, evidence-based decision making, facility readiness, community-level healthcare access, and intent to vaccinate. However, existing literature lacks evidence on *how* policies and implementation strategies drive catalytic coverage improvements. To address this gap, we identified critical success factors that supported improvements in routine childhood immunization coverage in Senegal. **Methods**: We conducted mixed-methods research applying a positive deviant approach. We identified Senegal as an Exemplar in Vaccine Delivery through analysis of DTP1 and DTP3 coverage data. Through interviews and focus group discussions at the national, regional, district, health facility, and community levels, we investigated drivers of high and sustained vaccine coverage. We conducted a thematic analysis grounded in implementation science frameworks to determine critical success factors. **Results**: The following success factors emerged: 1) Strong political will and prioritization of the EPI supported resource allocation and urgency; 2) Collaboration between the MoH and external partners fostered innovation, capacity building, and efficiency; 3) Improved surveillance systems allowed for timely and evidence-based decision making; 4) Community ownership of vaccine service delivery supported financial and managerial autonomy and quick response to local needs; 5) Community health workers spearheaded the promotion and demand generation of vaccines; and 6) Equitable vaccine delivery and uptake was addressed through outreach services, health post expansion, and tailored health promotion interventions. **Conclusions**: Senegal's vaccine delivery system was supported by evidence-based strategic planning at the national level, alignment of priorities between governmental entities and external partners, and strong community engagement initiatives that fostered local ownership of vaccine delivery and uptake. High and sustained routine immunization coverage was likely driven by prioritization of the EPI, improved surveillance

systems, a mature and reliable community health worker program, and tailored strategies for addressing geographical, social, and cultural barriers.

### Poster 171. Critical Success Factors for High and Sustained Routine Immunization Coverage: A Mixed-Methods Case Study of Nepal

**K.A. Hester**[1], Z. Sakas[1], A. Ellis[1], E. Ogutu[1], A.S. Bose[2], S. Dixit[3], R.A. Bednarczyk[1], M.C. Freeman[1]
[1]Gangarosa Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, GA, USA, [2]World Health Organization, Geneva, Switzerland, [3]Center for Molecular Dynamics, Kathmandu, Nepal
**Background**: The essential components of a vaccine delivery system are well-documented, but robust evidence on how and why the related processes and implementation strategies drive catalytic improvements in vaccination coverage are not well-established. To address this gap, we identified critical success factors that may have led to the substantial improvements in routine childhood immunization coverage in Nepal from 2000 to present. **Methods**: We conducted mixed-methods research based on an analytical framework adapted from an evidence-based conceptual framework of core vaccine system requirements. Additional facilitators and barriers were explored at the national and subnational levels in Nepal. We conducted a thematic analysis grounded in implementation science frameworks to determine the critical success factors for improved vaccine coverage. **Results**: The following success factors emerged: 1) Codification of health as a human right, along with other vaccine-specific legislation, ensured the stability of vaccination programming; 2) National and multi-national partnerships supported information sharing, division of labor, and mutual capacity building; 3) Pro-vaccine messaging through various mediums, which was tailored to local needs, generated public awareness; 4) Female Community Health Volunteers educated community members as trusted and compassionate neighbors; and 5) Cultural values fostered collective responsibility and community ownership of vaccine coverage. **Conclusions**: This case study of Nepal suggests that the success of their national immunization program relied on the engagement and understanding of the beneficiaries, and is supported by consistent and reliable commitment, collaboration, communication, and collective responsibility between the government, community, and partners. These networks are strengthened through a collective dedication to vaccination programming and a universal belief in health as a human right.

## Late-breakers

### Poster LB-23. A COVID-19 and Influenza Combination Vaccine and its Administration Using Fast-dissolving Buccal Films

**S. Vijayanand**, S.R. Patil, D. Joshi, M.J. D'Souza
Vaccine Nanotechnology laboratory, Center for Drug Delivery and Research, Mercer University College of Pharmacy, Atlanta, GA, USA
**Background:** Similar to influenza, SARS-CoV-2 mutants have been shown to impact the efficacy of the currently available vaccines. Thus, vaccination against SARS-CoV-2 variants and seasonal influenza strains may be required every year. This study investigates the immunogenicity of an adjuvanted microparticulate (MP) SARS-CoV-2-influenza combination vaccine administered as one oral dissolving film (ODF) via the buccal route. We hypothesize that a combination vaccine administered via the buccal route will induce strong systemic and mucosal immunity against both viruses. Moreover, buccal vaccination is pain-free, and ODFs can be self-administered. **Methods:** Inactivated viruses (SARS-CoV-2 and Influenza A H1N1) were used as the vaccine antigens in polymeric MPs prepared using a double emulsion method, lyophilized and characterized. The MPs were assessed in vitro for immunogenicity (Griess' nitrite release assay) and safety (cytotoxicity assay). The ODFs were characterized for dissolution time, diameter, and thickness. The adjuvanted vaccine ODFs were administered to mice as one prime and two boosts via the buccal route to test the in vivo vaccine efficacy. The virus-specific serum antibodies (IgG, IgG1, IgG2a, IgM, IgA) were assessed bi-weekly using an ELISA. **Results:** The characterization assessments revealed the following 1.) size: less than 1μm. 2.) PDI range: 0.1 to 0.5. 3.) Charge: -20mV to -30mV 4.) %EE: 80% to 90%. The vaccine-loaded ODFs quickly dissolve (less than 5 mins) in artificial saliva to release the vaccine MP. The NO released by the vaccine MP was enhanced by adding adjuvant MPs (Alhydrogel®+AddaVax™+CPG 7909). The in vitro cytotoxicity assessment showed that the MPs were non-cytotoxic. SARS-CoV-2 and Influenza specific serum IgG, IgG1, IgG2a, IgM, and IgA levels increased significantly following immunization. **Conclusion:** The study has yielded promising results in terms of antibody levels. The neutralization titers, cellular immune response, and markers for mucosal immunity are yet to be assessed.

### Poster LB-24. A Large Case Series of Neurocysticercosis in Kuwait, a Non-endemic Arabian Gulf Country in the Middle East Region

**J. Iqbal**[1], S. Ahmad[1], M. Al-Awadhi[1], A. Masud[2], Z. Mohsin[3], K. Albenwan[1], N. Alenezi[4], F. AlFarsi[4]
[1]Department of Microbiology, Faculty of Medicine, Kuwait University, Safat, Kuwait, [2]Al-Sabah Hospital, Ministry of Health, Shuwaikh, Kuwait, [3]Farwaniya Hospital, Ministry of Health, Farwaniya, Kuwait, [4]Parasitology Reference Laboratory, Mubarak Al-Kabir Hospital, Jabriya, Kuwait

**Background:** Neurocysticercosis (NCC), a leading cause of severe progressive headache and epilepsy worldwide, in developed/affluent countries is mostly diagnosed among immigrants from poor/developing *Taenia solium* taeniasis-endemic countries. Taeniasis carriers in Kuwait are routinely screened by insensitive stool microscopy. **Methods:** In this study, enzyme-linked immunoelectrotransfer blot (EITB) was used as a confirmatory test for NCC. Screening was performed on 970 patients referred for suspected NCC based on relevant history and/or ring-enhancing lesions on computed tomography and/or magnetic resonance imaging during a 14-year period in Kuwait. Demographic data and clinical details were retrieved from laboratory/hospital records. Cysticercal lesions were observed in CT/MRI images. **Results:** EITB was positive in 150 (15.5%) subjects including 98 expatriates mostly originating from taeniasis-endemic countries and, surprisingly, 52 Kuwaiti nationals. Clinical details of 48 of 50 NCC cases diagnosed during 2014-2019 were available. Most common symptoms included tonic-clonic seizures, persistent headache with/without fever and fits/loss of consciousness. Cysticercal lesions were located at various brain regions in 39 of 48 patients, a vast majority (31 of 39,79.5%) of the cases showed parenchymal lesions. Multiple members of 3 families with NCC were identified; and infection was linked to domestic workers from taeniasis-endemic countries and confirmed in at least 1 family. **Conclusions:** This is the 1st large case series of neurocysticercosis from a non-endemic Arabian Gulf country in the Middle East Region. Our data show that NCC is predominantly imported in Kuwait by expatriates originating from taeniasis-endemic countries who transmit the infection to Kuwaiti citizens.

### Poster LB-25. Artificial Intelligence-empowered Screening of COVID-19 in China

**Y. Huang**[1,*], Z. Zhang[2,*], Z. Zhang[3,4,*], K. Yao[5,*], X. Li[1], B. Ye[1], J. Zheng[1], Y. Zhang[1], Z. Zhang[1], Y. Liu[1], S. Wang[1], Y. Wu[2], Q. Lv[2], H. Hu[6], Y. Zheng[1], C. Li[1,*], X. Zou[2,*]
[1]Tencent Jarvis Healthcare Lab, Shenzhen, China, [2]Shenzhen Center for Disease Control and Prevention, Shenzhen, China, [3]Institute for Hepatology, National Clinical Research Center for Infectious Disease, Shenzhen Third People's Hospital, Shenzhen, China, [4]The Second Affiliated Hospital, School of Medicine, Southern University of Science and Technology, Shenzhen, China, [5]Shenzhen Health Development Research and Data Management Center, Shenzhen, China, [6]Institute of Medical Information, Chinese Academy of Medical Sciences/Peking Union Medical College, Beijing, China
*These authors contributed equally.

**Background:** Timely detection of COVID-19 is imperative in containing the spread of the virus, especially in large population-dense cities. RT-PCR testing of COVID-19 is limited by delays in testing, turnaround time and false negatives. Identifying patients most likely to be COVID-19 positive in real-time for RT-PCR testing through cost effective means can help reduce delays and discern potential false negatives, thereby help in containing COVID-19 spread. **Methods:** An ensemble machine learning model was trained and prospectively validated using over 1.5 million electronic medical records (with a COVID-19 prevalence of 4 in 10,000) across 51 hospitals in Shenzhen, the third most densely populated city in China. Model hyper-parameters were tuned via 10-fold cross validation. Features were extracted from inpatient and outpatient entry records, routine laboratory tests and imaging reports that were measured in both COVID-19 and non-COVID-19 patients. Data collection window was restricted to within 3 days before or after inpatient visits for the COVID-19 positive patients, and within 6 days after outpatient visits for the COVID-19 negative patients. **Results:** Our model predicted COVID-19 diagnosis with a specificity near 100%, a sensitivity of 71.8%, a precision of 93.7% and the F1-score of 81.1% (SD=4.4%). The model is currently in use to monitor COVID-19 in real-time for all hospitals in Shenzhen. During the prospective validation, we detected 80.1% COVID-19 positive patients with a trade-off of 389 false positives (<0.05% total negatives) and captured one true positive patient when the RT-PCR test was negative. **Conclusion:** Our ensemble machine learning COVID-19 detection model can identify patients mostly likely to be COVID-19 positive with great accuracy using electronic health records. We are able to identify cases that were negative on RT-PCT but remain high risk to be COVID-19 positive who may benefit from repeat testing. Our approach provides real-time COVID-19 risk stratification in hospital settings and facilitates population surveillance with minimal cost.

### Poster LB-26. Centers for Disease Control and Prevention's Public Health Emergency Management Fellowship: Strengthening the International Public Health Workforce

**S. Krishnan**[1], C. Espinosa[1], M.N. Podgornik[2], S. Haile[1], J.J. Aponte[1], C.K. Brown[1], S.J. Vagi[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Peace Corps, Washington, DC, USA
**Background:** Since 2013, the United States Centers for Disease Control and Prevention (U.S. CDC) has provided the Public Health Emergency Management (PHEM) fellowship to international public health professionals. The fellowship aims to build an international workforce to establish public health emergency management programs and operations centers to increase capacity in participating countries. **Methods:** In March 2021, 141 fellowship graduates completed a web survey to examine their past and current job roles and functions, assess contributions to their country's COVID-19 response, and identify technical assistance needs for strengthening national preparedness and response systems.: **Results:** The survey response rate was 63.1% and data was summarized by geographic region and fellowship cohort. Overall, cohorts 1 and 2 had lower response rates and cohort 10 had a higher response rate compared to the other groups combined ($p<.05$). Respondents were predominately from the AFRO region (69.7%) followed by SEARO (12.4%), WPRO (10.1%), EMRO (5.6%), and EURO (2.2%). 89.9% of respondents continued to work in the PHEM discipline and served in various preparedness and response roles for COVID-19. Data were analyzed to assess the five pre-identified survey objectives. **Conclusions:** Overall, findings show that fellowship graduates play a critical role in PHEM capacity development, have served in key roles in their country's COVID-19 response, and desire continued engagement between U.S. CDC and fellowship alumni to strengthen the community of practice of public health responders.

### Poster LB-27. COVID 19 and Influenza Co-infection among Severe Acute and Influenza-like Illness in Zambia

**P. Simusika**[1], E. Chentulo[1,2], M. Mwanza[1,2], M. Monze[1,2]
[1]National Influenza Center, Lusaka, Zambia, [2]Ministry of Health, Lusaka, Zambia
**Background:** The world health designated National Influenza center in Zambia implements Influenza surveillance targeting Influenza like illness and severe acute respiratory illness cases in selected sentinel sites. Zambia has an active influenza sentinel surveillance system from 2009 to date with a yearly average detection of 10%. Several studies have reported Sars cov-2 and Influenza virus co infection. The aim of this study was to evaluate the impact of Sars cov-2 and Influenza virus co infection in ILI/SARI patients. **Methods**: Demographic data of all patients with SARI and ILI was collected. Multiplex RT PCR assay targeting both SARS COV-2 and Influenza virus genes was used. Specimens positive with both SARS –CoV-2 and Influenza were identified. Patients' characteristics with co-infection were also analyzed. **Results:** 5056 (96%) specimens were tested between March 2021-March 2022.745 (15%) specimens were confirmed SARS COV 2 while 299 (6%) specimens were confirmed Influenza; 30(%) of the ILI/SARI confirmed positive specimens were co-infected for both Influenza/SARS COV 2. The odds of getting a co-infection were higher in ILI patients than in SARI patients (OR= 6.34; 95% CI = 2.38-21.23), While the odds of co-infections were higher in children aged under 5years than those aged above 5 years (OR=3.03; 95% CI 0.76, 26.32). **Conclusion:** Influenza and COVID-19 co-infection can occur in patients. The importance of such co-infection, especially in high-risk individuals and the elderly needs to be emphasized. More studies are recommended to determine the effect of the COVID-19 and influenza co-infection in clinical outcome.

### Poster LB-28. COVID-19 Vaccine Hesitancy Trends in Kenya over 2021

**R.T. Rego**[1], A.K. Ngugi[2], A.J.S. Delius[3], S. Luchters[2], J.C. Kolars[1], F.B. Irfan[4], E. Haus[1], A. Abubakar[5], J. Zhu[6], T Hofer[1], A.K. Waljee[1]
[1]Michigan Medicine, University of Michigan, Ann Arbor, MI, USA, [2]Department of Population Health, Aga Khan University, Nairobi, Kenya, [3]World Bank Group, Washington, DC, USA, [4]Institute of Global Health, Michigan State University, Lansing, MI, USA, [5]Institute for Human Development, Aga Khan University, Nairobi, Kenya
[6]University of Michigan, LSA, Ann Arbor, MI, USA
**Background:** Vaccine hesitancy threatens COVID-19 vaccine uptake. Studies from high income countries (HICs) present several factors associated with vaccine hesitancy; but there are very few studies on the topic from low- and middle-income countries (LMICs), particularly sub-Saharan Africa. While some factors found in HICs possibly extend to LMICs, other factors are likely at play. We examine trends in and factors associated with vaccine hesitancy in Kenya. **Methods**: We analyzed data from the Kenya Rapid Response Phone Survey (RRPS), a household survey representative of the Kenyan population collected longitudinally between January and October 2021. Households were recruited through sampling of the 2015/16 Kenya Household Budget Survey and random digit dialing. We cleaned and coded the data. We plotted rates of vaccine hesitancy (if the vaccine was available easily at no cost) and performed a weighted multivariable logistic regression for vaccine hesitancy including

interactions for time. Results We found that vaccine hesitancy dropped from 32% in January 2021 to 10% in October 2021. When adjusted for other variables, we found that government distrust and recently having symptoms of COVID were positively and significantly associated with vaccine hesitancy. We further found that having education beyond the primary level, practicing increased handwashing, and responding later in the year were negatively and significantly associated with vaccine hesitancy. We found no significant association with other predictors (including geography, age, COVID-19 knowledge, and social distancing practices). **Conclusions:** Hesitancy to the COVID-19 vaccine dropped significantly over the course of 2021 in Kenya. To increase vaccine uptake among those who remain hesitant, programming should focus on those who distrust the government, report symptoms of COVID-19, and are less educated who do not practice personal COVID-19 mitigation measures.

### Poster LB-29. Developing a Global Health Science Agenda during the COVID-19 Pandemic, March 2020 — May 2022

**A. Shiver**[1], W.L. Rémy[2], R. Friedman[3], J. Barker[1,4], E. Moore[2], C.H. Cassell[1]
[1]Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]RTI International, Research Triangle Park, NC, USA, [3]Peraton, Herndon, VA, USA, [4]Oak Ridge Associated Universities, Oak Ridge, TN, USA

**Background:** In response to COVID-19, the U.S. Centers for Disease Control and Prevention (CDC) developed a COVID-19 Public Health Science Agenda. This Science Agenda highlighted the Division of Global Health Protection's need to align with the Division's Strategic Plan and develop their own Science Agenda for Global Health Security. We conducted a literature review and evaluation to identify gaps and areas of opportunity for scientific inquiry and programmatic activities. These findings were used to develop *a science agenda* to better plan and prioritize global health activities. **Methods:** To inform science agenda development and ensure alignment with CDC's priorities, we conducted literature reviews, five focus groups (n=34 people) and five interviews (n=5 people) to identify priority areas and objectives. Thirty-nine global health experts participated from diverse disciplines. A survey also was developed and distributed to all Division staff to identify science and programmatic gaps related to various technical areas. Qualitative methods and Excel were used to analyze these results. **Results:** Our findings identified the need to: develop new and improve existing scientific methods in surveillance, information, health, and laboratory systems; identify and promote best practices; continuously measure and evaluate impact; and expand and strengthen the public health workforce and National Public Health Institutes across several technical areas. The Division's Science Agenda was organized around a framework of eight priority areas with corresponding objectives and activities: 1) emergency preparedness, management, and response; 2) laboratory systems; 3) surveillance and epidemiology; 4) data modernization and information systems; 5) workforce development; 6) institutional development; 7) noncommunicable diseases; and 8) health equity. **Conclusions:** A science agenda can be a vital tool to articulate and prioritize critical areas of scientific inquiry and opportunities to advance global health security. A science agenda also can guide future implementation and monitoring and evaluation activities in these technical and priority areas.

### Poster LB-30. Development of Macrofoam Swab-based Surface Sampling Method for SARS CoV-2

**B. Relja,** A. Tamin, T.W. Brown, J. Harcourt, J. Murphy, N. Thornburg, H.L. Kirking, J.Vinjé, G.W. Park
Centers for Disease Control and Prevention, Atlanta, GA, USA

Few studies have assessed the role of contaminated environmental surfaces in transmission of with SARS-CoV-2 during the COVID-19 pandemic. This lack of information makes it hard to assess the risk of surface transmission. We developed and validated a macrofoam-based swab method for the detection of SARS CoV-2 on surfaces and applied it to investigate SARS CoV-2 contaminations on environmental surfaces in households and grocery stores. Stainless coupons of 161 $cm^2$ were inoculated in quadruplicate with 50 µL of 10- or 5-fold serially diluted ($10^{5.7}$ to $10^{0.7}$ virus particles per coupon) gamma-irradiated cell culture lysate of SARS-CoV-2 strain USA-WA1/2020. After 1-hr of drying, coupons were swabbed using PBS pre-moistened polyurethane macrofoam swabs. Virus was eluted from the swabs in PBS and 4.5 mL was concentrated to 250 µL using a Amicon Ultra-4 filter device (30,000 MWCO) by centrifugation at 4,000 × g for 10 minutes and viral RNA was extracted on a QiaCube-HT extraction system. The detection limit and viral recovery from the coupons were quantified using a SARS CoV-2 multiplex real-time reverse transcriptase (RT)-PCR assay. A total of 1,234 swab samples were collected from frequently touched environmental surfaces in 124 households as well as from 260 surfaces in 2 grocery stores and processed as described above. Real-time RT-PCR positive swab samples (Ct value ≤ 28) were further tested for infectivity by cell culture on Vero E6/TMPRSS2 cells. The recovery percentage of RT-PCR-detectable SARS CoV-2 from the coupons was 17.1% ± 5.8% and the detection limit was 1.7 $\log_{10}$ genomic copy per coupon. A total of 27.7% (342/1,232) of household samples and 3% (6/260) of grocery store samples tested positive with a median Ct value of

34.1 (range: 18.4–39.6) and 35.3 (range: 34.1–35.9) by real-time RT-PCR. Three of the 25 samples (Ct values=18.4, 20.8 and 21.5) were successfully cultured. In conclusion, we developed a macrofoam-based surface sampling method that successfully detected both viral RNA and the presence of infectious SARS-CoV-2 virus particles. This method may assist as an additional investigation tool to determine the level of environmental surface contamination during the SARS CoV-2 pandemic.

### Poster LB-50. Evaluation of Commercial Rapid Influenza Diagnostic Tests for the Detection of a Novel, Highly Pathogenic Avian Influenza A(H5N1) Virus Circulating in Wild and Domestic Birds in North America

**E. Salinas**[1,2], K.W. Radford[2], M.K. Kirby[2], J. Liddell[2], S. Thor[2], J. Jones[2], W. Sessions[2], Y. Jang[2], S. Mathew[2], R. Kondor[2], J. Steel[2], C.T. Davis[2], J.R. Barnes[2]
[1]General Dynamics Information Technology, Inc., Falls Church, VA, USA, [2]Virology, Surveillance, and Diagnosis Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** As of May 2022, a highly pathogenic avian influenza (HPAI) A(H5N1) virus belonging to clade 2.3.4.4b has spread across 35 states and has been detected in over 37 million domesticated birds and 1 person in the United States (APHIS USDA, 2022). Rapid influenza diagnostic tests (RIDTs) are a cost-effective resource to detect the presence of influenza A/B viral antigen in symptomatic individuals, but their sensitivity to the novel HPAI A(H5N1) 2.3.4.4b strain is unknown. Here, we evaluated the sensitivity of commercial RIDTs in detecting this virus in comparison to 2021 – 2022 seasonal A(H3N2) (3C.2a1b.2a.2) and A(H1N1)pdm09 (6B.1A.5a.1) influenza A viruses (IAV) circulating in the U.S. **Methods:** The sensitivity of 8 commercial RIDTs to egg- and/or cell-propagated, inactivated (in beta-propiolactone) HPAI A(H5N1) virus (A/American Wigeon/South Carolina/22-000345-01/2021), live, seasonal A(H3N2) (A/Maryland/02/2021) and live, A(H1N1)pdm09 (A/Ohio/03/2021) IAV was evaluated by endpoint dilution methods (n = 5 replicates per test per virus). IAV genome copy equivalents (GCE) for each dilution were quantified by qRT-PCR. RIDT sensitivity was defined as the lowest GCE yielding 100% positive tests. **Results:** All 8 commercial RIDTs detected the novel HPAI A(H5N1) virus with variable sensitivities, ranging from $10^{7.02}$ to $10^{8.92}$ GCE/ml with a median sensitivity of $10^{8.38}$ GCE/ml (IQR = $10^{7.66}$ GCE/ml). The median RIDT sensitivity to HPAI A(H5N1) was similar to that of seasonal viruses [median = $10^{8.46}$ or $10^{8.81}$ GCE/ml, IQR = $10^{8.70}$ or $10^{8.90}$ GCE/ml for A(H1N1)pdm09 or A(H3N2), respectively] (p = 0.15684, Kruskal-Wallis test). BinaxNow™ Influenza A&B Card 2 (Abbott) detected all 3 IAVs with the highest sensitivity, while Xpect™ Flu A&B (Thermo Scientific) had the lowest sensitivity (p =0.025, Kruskal-Wallis test). **Conclusions:** Commercial RIDTs detect the novel, HPAI A(H5N1) 2.3.4.4b virus from non-clinical samples with similar sensitivity to the dominant, seasonal A(H1N1)pdm09 and A(H3N2) IAVs circulating in the US.

### Poster LB-31. Genomic Investigation of SARS-CoV-2 Infection among Companion Animals in Households with Confirmed Human COVID-19 Cases—Arizona, 2021

**H.Y. Yaglom**[1], G. Hecht[2], A. Goedderz[1], D. Jasso-Selles[1], M. Sprenkle[1], J.L. Ely[1], I. Ruberto[2], J.R. Bowers[1], D.M. Engelthaler[1], H. Venkat[2,3]
[1]Translational Genomics Research Institute, Flagstaff, AZ, USA, [2]Arizona Department of Health Services, Phoenix, AZ, USA, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: The impact of SARS-CoV-2 on animals has been well-recognized since the start of the pandemic. Natural infection in animals, such as pets and captive wildlife is believed to occur through close contact with infected humans. There remains no evidence that animals are playing a role in spreading the virus to people. The Arizona COVID-19 and Pets Program (AZCPP) is a surveillance study being conducted to (1) characterize how SARS-CoV-2 affects companion animals living in households with COVID-19 positive people and (2) understand the dynamics surrounding how these animals become infected. **Methods:** Households with at least one confirmed, symptomatic person with COVID-19 were contacted by public health staff for study recruitment. Trained veterinary and public health staff visited enrolled households to collect blood, nasal, and fecal specimens from pets and complete a questionnaire about pet demographics and interactions with owner(s). Collected specimens were tested for SARS-CoV-2 by RT-PCR; genomic sequencing was performed on positive samples with Ct values ≤38. The GenScript cPass™ Neutralizing Antibody Assay was used for serum specimens. **Results:** During March–December 2021,110 companion animals (39 cats and 71 dogs) were sampled across 45 households. 38 pets in 21 households tested positive– 17 by PCR, 31 had evidence of neutralizing antibodies, and 10 pets were positive by PCR and serology (3 cats and 7 dogs). Positive pets had close contact with COVID-19 positive owners; 74% of positive pets slept in the same bed as the pet owner, while only 38% of negative pets did. Among 12 multi-pet households where at least one pet was positive, ten had at least one other pet test positive. Whole genome sequencing of dog, cat, and owner specimens from the same household revealed identical viral genomes of the B.1.575 lineage. **Conclusions:**

34.5% of the pets enrolled in AZCPP had evidence of infection with SARS-CoV-2. Our findings suggest a high likelihood of viral transmission in households with multiple pets and when pets had very close interactions with symptomatic humans. A collaborative One Health approach is critical during animal SARS-CoV-2 investigations to guide recommendations on how positive humans should interact with animals. Further surveillance studies are needed to characterize how new variants impact animals and understand opportunities for infection and spillover in susceptible species.

### Poster LB-32. Independent Analysis of Inclusivity and Cross-reactivity of FDA EUA Approved PCR Tests

**E.C. Chen**[1], J. Hoo[2], D. Chen[2]
[1]Program of Biomedical Sciences, College of Arts and Sciences, California Baptist University, Riverside, CA, USA, [2]Arbelos Genomics, Chino, CA, USA
**Background:** Since the outbreak of SARS-CoV-2, PCR testing is the gold standard for Covid 19 diagnosis. FDA approves these tests under EUA to increase the test availability during pandemics. However, SARS-CoV-2 virus has undergone mutations that gave rise to various strains, including Delta and Omicron variants. As result, concerns about the performance of PCR tests were raised. **Methods:** We obtained primer and probe sequences from all 269 EUA PCR kits and aligned them with 5,946,481 SARS-COV-2 sequences that were published on GISAID from January 2020 to January 2022. These sequences were then stratified by their dates, regions, and genes, and data were summarized. **Results:** Among 269 PCR kits, only 9 primer/probe sequences were available for evaluation. The results showed a decline in specificity in the perfect alignment of the primers/probes from Agena and Europhin over time, with one of the forward primer and probe sequences showing misalignment with all viral sequences collected post-Omicron. The remaining primer/probe sequences maintained their binding specificity. Additionally, at the emergence of the Delta variant, the binding specificity of the primer and probes decreased significantly. Interestingly, primer/probe alignment specificity recovered to the high 90% in the later months of the analysis timeframe that appeared to coincide with the Omicron wave. **Conclusion**: Several FDA-approved primers and probes were found to harbor mismatches to the recombinant SARS-COV-2 sequences that contributed to the instability of the PCR test results. Thus, performance of several FDA-approved PCR kits due to the rapidly mutating and emerging viral strains may be questioned. Unfortunately, since most of the sequences approved by the FDA are not publicly available, FDA holds the authority to evaluate all test performances. To safeguard public health, we recommend the FDA make available all EUA-approved primer and probe sequences for independent evaluation by the public.

### Poster LB-33. Key Learnings from Singapore's Public Health Intelligence Work during the COVID-19 Pandemic

**A.Y. Yang**, W.X. Khong, J.H.S. Chan, C.Y. Lau, Z.B.Y. Teo, M.K.C. Tan, W.Y. Leong, H. Liu, K.E. See, D.L.Y. Lim, D. Heng, W.L. Chow, A. Ty
Ministry of Health, Singapore
**Background:** The COVID-19 pandemic highlighted the vital role of public health intelligence activities e.g., risk assessment in shaping public health (PH) policy and responses. Singapore adopted an evidence-based, risk-calibrated approach to travel border policies given its position as a regional travel hub. Here, we describe a systematic approach to risk assessment and the use of tools developed by the Singapore Ministry of Health for universal periodic assessment of COVID-19 importation risk from overseas. We also share key learnings from doing so at a time of information uncertainty and evolving PH priorities. **Methods:** Throughout the pandemic, analysts went beyond the Ministry's capabilities by harnessing information from traditional and non-traditional sources to enhance its global surveillance enterprise. Multi-source information was fed into a multi-domain risk assessment framework to inform border policies. Regular refinements ensured that the framework remained relevant and fit for purpose. **Results and Conclusions:** The pandemic's evolving nature demanded a dynamic approach to risk assessment. The framework underwent 3 major iterations with growing understanding of the virus and changing PH priorities. Indicators have been rapidly adjusted from disease containment (early-2020), mitigation (mid-2021), to current open-travel posture. Where quantitative information became increasingly accessible, its tandem use with qualitative information was optimized for more robust risk assessment. The quest for reliable and timely data in the face of an 'infodemic' was another key challenge. Comprehensive horizon scanning demanded a more strategic approach using automated tools, data aggregators or web scrapping technology. Inter- and intra-government data connectivity and information sharing were key to understanding COVID-19 developments worldwide. In conclusion, we showed that adaptability and inclusivity were essential attributes for systematic risk assessments

based on open-source information to remain relevant and actionable. They are also instrumental in Singapore's dynamic stance in border policies and contributed to the country's ability to respond to global PH threats effectively.

### Poster LB-34. Minimizing COVID-19 Mortality through Smart Immunization in Capacity Limited Settings

**R. Arghal**, S.S. Bidokhti, S. Sarkar
University of Pennsylvania Dept. of Electrical and Systems Engineering, Philadelphia, PA, USA
**Background:** COVID-19 has emphasized the importance of proper prioritization of vaccination, especially during early-stage rollout or in low- and middle-income countries (LMICs) where vaccine supply is severely limited. In these settings, the public health authorities must carefully decide between vaccinating those at high risk (i.e., elderly) or those with high contacts (i.e., essential workers) or some combination. This problem is complicated by heterogeneity in risk levels, contact rates, and network topology which can dramatically and unintuitively change the efficacy of vaccination. More recently, the introduction of various strains of COVID as well as oral antiviral treatments renew questions on how to best prioritize vaccinations and/or oral treatments in presence of overall budget constraints. **Methods:** We developed a unique modeling framework that accounts for population clustering and risk and contact rate heterogeneity while maintaining computational tractability. Utilizing optimal control techniques, we obtain an optimal combination of administration of vaccine and oral treatments over all possible policies to minimize mortality or other risk factors. Our model is able to fit any network topology and population demography. **Results:** Even when considering all, potentially complex, vaccination and oral treatment policies, the optimal strategy turns out to be easily deployable. We find, somewhat counterintuitively, the commonly used strategy of prioritizing high-risk individuals need not minimize mortality, and in many realistic scenarios high contact individuals need to be vaccinated first. In case studies such as prisons and retirement homes, the optimal policy reduced mortality by over 20% when compared to default public health guidelines. **Conclusions:** Our framework provides a flexible and easy-to-use method for determining optimal vaccine strategy that public health officials can use to cater to specific communities, based on demography, contact patterns, and disease parameters, thereby more effectively mitigating the impact of the pandemic. Our framework also enables public health officials to decide how to apportion investments in vaccines vis a vis oral agents given budgetary constraints.

### Poster LB-35. Piloting Acute Febrile Illness Sentinel Surveillance in the Country of Georgia

**G. Chakhunashvili**, D. Tsereteli, Kh. Zakhashvili, E. Khmaladze, A.Machablishvili, P. Imnadze
National Center for Disease Control and Public Health (NCDC), Tbilisi, Georgia
**Background:** Acute febrile illness (AFI) represents a broad spectrum of infectious disease etiologies which frequently share common symptoms complicating accurate diagnosis based solely on clinical symptomology. AFI sentinel surveillance was initiated in August 2021 in the country of Georgia, as etiologic AFI investigations are valuable public health data sources. Such investigations are useful for understanding etiology of AFI, detecting emerging pathogens and outbreaks, guiding empiric treatment of AFI cases, and developing prevention and control measures. **Methods:** Implementation protocol (including data collection tools) was developed and approved by National Center for Disease Control and Public Health of Georgia (NCDC) and US Centers for Disease Control and Prevention (CDC) Institutional Review Boards. A list of etiologic agents was defined and one pilot site, located in Tbilisi, the capital city, has been selected. Medical personnel (site surveillance and data coordinators) were trained to enroll cases meeting the project specific AFI definition: a patient aged ≥2-years with measured fever (≥38.0°C), which lasted <7 days AND with no determined etiology that fully explains the clinical presentation. **Results:** As of April 2022, a total of 153 patients were enrolled from the pilot site. Epidemiologic information was collected through a standardized questionnaire for each enrolled patient. Blood samples were collected for multi-plex PCR and serologic testing. Nasopharyngeal and oropharyngeal swabs were collected for COVID-19 PCR testing. Samples were submitted to the NCDC's Laboratory (Lugar Center of Public Health Research) for testing. Laboratory testing results were entered into Laboratory Information Management Systems (LIMS) under NCDC. **Conclusions:** NCDC successfully implemented the AFI sentinel surveillance pilot site at the tertiary hospital, located in Tbilisi. The plan is to expand the AFI surveillance to include 6 sentinel sites located in the two additional cities - Kutaisi and Batumi. NCDC is developing a REDCap database to allow real-time monitoring of variations in AFI agent specific positivity frequency among enrolled population by geographic areas and over time. Understanding the causes of AFI could improve clinical decision-making and inform public health programming.

### Poster LB-36. Prevalence, Risk Factors, and Histopathological Studies of Cystic Echinococcosis in Northern Punjab of Pakistan

**S. Khan**[1], M. Younus[2], A. Idrees[2], H. Akbar[1], I. Rasheed[1], Q. Mehmood[3], W. Ahmad[4]

[1]Department of Parasitology, University of Veterinary & Animal Sciences, Lahore, Pakistan, [2]Department of Pathobiology, University of Veterinary & Animal Sciences, Lahore, Narowal Campus, Narowal, Pakistan, [3]Department of Epidemiology & Public Health, University of Veterinary & Animal Sciences, Lahore, Pakistan, [4]Department of Clinical Sciences, University of Veterinary & Animal Sciences, Lahore, Narowal Campus, Narowal, Pakistan

**Background**: Cystic echinococcosis (CE) is a zoonotic disease caused by the larval stage of the echinococcus parasite. This disease is a neglected tropical disease, impacting the health status and economy of many countries including Pakistan. Considering the socio-economic and zoonotic importance of disease, the current study has been designed to evaluate prevalence and risk factors of the disease. **Methods**: In this study, 1200 cattle (400/district) were grossly examined the presence of hydatid cysts in slaughtered animals from Dec 2019 to Nov 2020 through a convenient sampling method. The samples were subjected to microscopic and histopathological examinations using hematoxylin and eosin staining method. **Results**: The prevalence of hydatidosis in 3 districts was found to be 8.00%. The highest prevalence was observed in the district of Narowal (10.25%), followed by the district of Sheikhupura (8.00%) and Sialkot (5.75%), Pakistan. The age-wise prevalence was highest in the eldest age group i.e., 3,5% in 6-7 years and above followed by 3.2% in the age-group of 4-5 years, 0.9% in the age-group of 2-3 years, and 0.4% in the age-group with <1 year of age. The gender-wise prevalence was high (6.25%) in female animals as compared to male animals (1.75%). Only 70.83% of the positive animals had cysts in their lungs whereas 29.16% of the positive animals had cysts in the liver. The highest prevalence was observed in the winter season (11.3%) and lowest was in summer (5.7%). In December (15.15%), the infection rate was the highest whereas it was the lowest in March (5.05%) and July (5.05%). Histopathological changes in vital organs of the animal body affecting their structures and resulting in impairment of their functions was observed. **Conclusions**: Disease is highly prevalent in the said districts affecting the production of animals, and attention must be given to raise preventive measures.

### Poster LB-37. Role of Nucleophosmin (NPM1/B23) in Restricting Chikungunya Virus Replication

**P. Pradeep**[1], E. Sreekumar[1,2]

[1]Molecular Virology Laboratory, Rajiv Gandhi Centre for Biotechnology (RGCB), Thiruvananthapuram, Kerala, India Research Centre, University of Kerala, Thiruvananthapuram, India, [2]Institute of Advanced Virology (IAV), Bio 360 Life Science Park, Thonnakkal, Thiruvananthapuram, Kerala, India

**Background**: Chikungunya virus (CHIKV) is a positive-stranded RNA virus of the family *Togaviridae*. It is an arthiritogenic virus in nature, but often causes neurological complications in infants and immunocompromised subjects. Until now, there are no approved vaccines or any therapeutics to prevent CHIKV infection. The virus hijacks host metabolism for its genome replication, and as a result, many host proteins are differentially expressed or modulated. Whole cell proteomic analysis previously done in lab, on infected human astrocytic U-87 MG cells identified Nucleophosmin (NPM1) as one of the major host protein modulated upon CHIKV infection. NPM1 is a human histone chaperone that activates chromatin transcription in an acetylation dependent manner, while its nuclear-cytoplasmic trafficking happens during cellular stress like viral infections. Nucleophosmin (NPM1) may be a host restriction factor against chikungunya virus replication. **Methods:** Human astrocyte cell line U-87 MG was infected with CHIKV at an MOI of 1 or 10 and analyzed for the modulation of NPM1 in its transcript level through real time PCR and in protein level using immunoblotting. CHIKV infected cells were analyzed for the cytoplasmic aggregation and localization of NPM1 using immunofluorescence staining and subcellular fractionation followed by immunoblotting. The cells were treated with NSC348884, a specific NPM1 oligomerization inhibitor in a dose dependent manner and its effect on viral replication was analyzed through plaque assay in the supernatant and CHIKV specific genomic/sub- genomic RT-PCR in the cells. Knock down studies using small interfering RNA (siRNA) against NPM1 were performed and analyzed for the expression of CHIKV structural and non-structural proteins through immunoblotting as well as plaque assays were performed in supernatants for determining viral titre. Finally, LC-MS/MS analysis on NPM1 pull-down proteins and immunofluorescence staining was done to find the interacting viral partner in infected cells. **Results:** CHIKV infection in human astrocyte cell line U-87 MG resulted in the upregulation of NPM1 expression in both RNA and protein levels. Immunofluorescence staining revealed cytoplasmic aggregation of NPM1 in CHIKV-infected and subcellular fractionation followed by western blot revealed localization of NPM1 from nucleus to cytoplasm during infection. Inhibition of this aggregation using a specific NPM1 oligomerization inhibitor, NSC348884, caused a significant dose-dependent enhancement in virus replication. In addition, small interfering RNA (siRNA)-mediated knockdown of NPM1 confirmed the increase in CHIKV viral protein expression as well as an increase in viral titre. Mass spectrometry studies on NPM1 immunoprecipitated samples and immunofluorescence analysis revealed the interaction of NPM1 with CHIKV non-structural protein (nSP3), possibly in the cytoplasmic replication complex. **Conclusion:** Our studies demonstrate the antiviral role of NPM1 against CHIKV infection. Hence future studies on understanding the signaling cascade

regulated by NPM1 upon infection will help us develop a host-directed therapeutic strategy against CHIKV infection.

### Poster LB-38. SARS-Cov-2 Seroprevalence in Baja California, Mexico, February 2021

**I. Bojorquez-Chapela**[1], O.E. Zazueta[2], R.S. Garfein[3], J.O. Cano-Torres[2], C.A. Méndez-Lizárraga[2], T.C. Rodwell[3], R. Muñiz-Salazar[4], D.F. Ovalle-Marroquín[2], N.G. Yee[2], I.R. Serafín-Higuera[4], S. González-Reyes[4], J.R. Machado-Contreras[4], L. Horton[3], S.A. Strathdee[3], R. Rodríguez[1], L. Hill[3]
[1]El Colegio de la Frontera Norte, Tijuana, BC, Mexico, [2]Secretariat of Health of Baja California, Mexicali, BC, Mexico, [3]University of California San Diego, La Jolla, CA, USA, [4]Universidad Autónoma de Baja California, Ensenada, BC, Mexico
**Background:** Baja California, Mexico, has one of the highest reported rates of COVID-19 in the country. As this is a border state adjacent to California, USA, characterizing infection can inform binational public health policy. **Methods:** We conducted a survey of the prevalence of SARS-CoV-2 infection representative of the population five years of age or older in the three main cities of Baja California (Mexicali, Tijuana and Ensenada), from January 31st to February 19th, 2021. Blood samples were obtained by fingerstick and Whatman 903 protein saver cards were sent to the Broad Institute Serology Lab (BILS, Boston, USA) for determination of anti-SARS-CoV-2 IgG by ELISA assay. Participants responded a questionnaire with sociodemographic and trans-border mobility questions. **Results:** The overall prevalence of anti-SARS-CoV-2 IgG was 21.1% (95% CI 17.4-25.2). It was marginally higher among women (25.4%, 95% CI 19.7-32.1) than men (16.6%, 95% CI 12.9,21.2), and had an inverted-U shaped association with education among adults, with 21.0% for those with <=6 years of education ( 95% CI 14.7-29.3), 27.5% for those with 10-12 years of education (95% CI 20.9-35.3), 21.8% for those with some college or over 9(5% CI 16.0-29.0). 5.3% of participants reported having crossed the Mexico-United States international border in the past 6 months, of whom 10.1% (CI 95% 3.5-25.8) tested positive for anti-SARS-CoV-2, a prevalence that was not significantly different from the one among those who had not crossed the border in this period (21.9%, CI 95% 17.7-26.7). **Conclusions:** The prevalence of anti-SARS-CoV-2 antibodies in the three main cities of Baja California was similar to Mexico's national average at the time. There was no evidence that border crossing was associated with infection, suggesting that trans-border movement was not a significant driver of the epidemic in the Baja California–California binational region.

### Poster LB-39. Serologic Evidence of Exposure to Usutu and West Nile Viruses Detected on Human, Domestic Bird, and Domestic Mammals in Burkina Faso, West Africa

**B. Tinto**[1,2], O. Constant[1], T.S. Kagoné[2], J. Barthelemy[1], A. Kiba-Koumaré[3], P. Van de Perre[1], S. Salinas[1], D. Kania[2], Y. Simonin[1]
[1]Pathogenesis and Control of Chronic and Emerging Infection, Inserm, University of Montpellier, Montpellier, France, [2]Centre MURAZ, Institut National de Santé Publique (INSP), Bobo-Dioulasso, Burkina Faso, [3]Centre National de Transfusion Sanguine, Ouagadougou, Burkina Faso
**Background:** Usutu (USUV) and West Nile (WNV) viruses are phylogenetically closely related arboviruses belonging to the Flaviviridae family of the genus Flavivirus. These two viruses have long been considered viruses of African interest until their introduction into Europe. WNV has been responsible for many epidemics in Africa, Europe, and the United States. Since the discovery of USUV, only two human cases have been reported in Africa, including one case in Burkina Faso in 2004 in a ten-year-old patient with febrile jaundice. Despite this, there is no data on the circulation of the WNV and USUV viruses in either humans or potential animal reservoirs in Burkina Faso. The objective of this work is to evaluate the circulation of WNV and USUV in Burkina Faso in blood donors and domestic animals. **Methods:** Samples from blood donors and animals (horses, dogs, chicken, and pigeons) were collected in the cities of Ouagadougou and Bobo-Dioulasso from June to July 2020 (blood donors) and from November 2021 to January 2022 (animals). All samples were analyzed by competitive Enzyme-linked immunosorbent assay (cELISA) for the detection of flavivirus antibodies. Positive samples from the cELISA tests were then analyzed by Plaque reduction neutralization test (PRNT) for the quantification of antibodies directed against WNV and USUV. **Results:** In humans, we obtained a seroprevalence of 18.14% for WNV and 13.80% for USUV. In animals, seroprevalence varied from one species to another. For the WNV, we found 17.28% in horses, 1.92% in dogs and 4.76% in pigeons. The seropositivity for USUV was 6.17% in horses and 4.76% in pigeons. We also observed co-carrying of anti USUV and WNV antibodies of 12.03% and 2.46% respectively in humans and horses. **Conclusion:** The results of our study showed an active transmission of WNV and USUV in both humans and domestic animals. This highlights the importance of setting up an integrated surveillance of flaviviruses in Burkina Faso according to a global approach. Early detection of cases in animals would make it possible to

anticipate the occurrence of possible epidemics. Additional studies including vectors would be necessary to map the risk associated with flaviviruses in Burkina Faso.

### Poster LB-40. Transmission of SARS- CoV-2 in the Population Living in High and Low-density Gradient Areas in Dhaka, Bangladesh

**S.M. Satter**[1], T.R. Bhuiyan[1], Z. Abdullah[1], M. Akhtar[1], A. Akter[1], S.M.Z. Shafique[1], M.R. Alam[1], K.I.A. Chowdhury[1], A. Nazneen[1], N.A. Rimi[1], A.S.M. Alamgir[2], M. Rahman[2], F.I. Khan[2], T. Shirin[2], M.S. Flora[3], S. Banu [1], M. Rahman[1], M. Rahman[4], F. Qadri[1]
[1]icddr,b, Dhaka, Bangladesh, [2]Institute of Epidemiology, Disease Control & Research, Mohakhali, Dhaka, Bangladesh, [3]Directorate General of Health Services (DGHS), Mohakhali, Dhaka, Bangladesh, [4]Global Health Development, EMPHNET, Mohakhali, Dhaka, Bangladesh
**Background:** COVID-19 pandemic surpassed 267 million cases with 5.27 million deaths worldwide. In a country like Bangladesh, estimating secondary attack rate (SAR) and seroprevalence among contacts of confirmed COVID-19 cases following the density gradient and socio-economic status (SES) was warranted to advocate evidence-based policy on integrated infection control strategy. Our study aimed to determine the community transmission among contacts of confirmed COVID-19 cases in high and low population density areas in Dhaka city. **Methods:** This was a descriptive longitudinal study conducted at high-and low-density neighbourhood of Dhaka City between June-September 2020. Household and neighbourhood contacts of confirmed COVID-19 cases were enrolled, and we have measured SAR and SARS-CoV-2 specific antibodies in the sera of participants and analyzed serological responses based on SES of participants. **Results:** The SAR among contacts was 10% in high-density areas compared to 20% in low-density areas. People with high SES had significantly higher level of SARS-CoV-2 specific IgG antibodies on study day 1 (P=0.01) and 28 (P=0.03) in compared to low SES in high-density areas. In contrast, comparable level of SARS-CoV-2 specific antibodies were observed in low-density areas between high and low SES. In contrast, magnitude and seropositivity of SARS-CoV-2 specific IgM were comparable (P> 0.05) between people living in high and low socioeconomic status on both study day 1 and day 28 in both high- and low-density areas. **Conclusions.** Due to the similar size of household members in the high- and low-density study groups, we were not able to see any differences in the seropositivity rates between them. However, people living in high SES showed higher seroconversion rates as compared to those in the low SES. This could be due to nutritional status, behavioral practices as well as household size which needs more in-depth studies.

### Poster LB-41. Withdrawn

### Poster LB-42. Use of Antibiotic by Physicians in Bangladesh for Treating COVID-19 Patients

**U. Monda**[l], T. Haque[1], Z. Hassan[1], A. Al Jubayer Biswas[1], S. Islam[2], S. Moinuddin Satter[1], S. Debnath[1], Z. Alam[3], M. Shojon[3], M. Islam[4], H. Bin Murshid[3], N. Homaira[5]
[1]icddr,b, Dhaka, Bangladesh, [2]Australian National University, Canberra, Australia, [3]Dhaka University, Dhaka, Bangladesh, [4]Sylhet MAG Osmani Medical University, Sylhet, Bangladesh, [5]University of New South Wales (UNSW), Sydney, Australia
**Background:** Antimicrobial resistance (AMR) is one of the most serious global public health threats of this century. Despite national and international guidelines' recommendations not to use antibiotics to treat COVID-19 patients without evidence of bacterial coinfection, antibiotics are frequently used among COVID-19 patients (<2% hospital admitted patients having actual bacterial infections worldwide). This study aimed to understand antibiotic prescribing practices among Bangladeshi physicians in the treatment of COVID-19 patients. **Methods:** A cross-sectional survey was conducted among Bangladeshi physicians involved in providing clinical care to COVID-19 patients. From September to November 2021, we collected data through online surveys utilizing the Google Form web survey platform and hardcopy of self-administered questionnaires. We used descriptive statistics and a regression model to identify the prevalence of antibiotic prescribing among physicians and identify the associated factors influencing their decision making. **Results:** Out of 511 physicians, the mean years of experience as clinical practitioner was four years, and majority of them (83%) worked in general or COVID-19 dedicated hospitals. Among enrolled physicians, around 94% prescribed antibiotics to COVID-19 patients irrespective of disease severity (mild/moderate/severe). All physicians (100%) working in COVID-19 dedicated hospitals reported using antibiotics to treat COVID-19 patients. The majority (460/511) of the physicians agreed to giving antibiotics to COVID-19 patients with underlying respiratory conditions, secondary bacterial co-infections, and an elevated C Reactive Protein (CRP) count. The most prescribed antibiotics by the physicians were meropenem (80%), azithromycin (53%), and moxifloxacin (46%). **Conclusion:** The study findings demonstrated high antibiotic prescribing practices for treating COVID-19 patients which is not adherent to guidelines. Such blanket use of antibiotics during the pandemic enhances the concerns around emergence of AMR. Evidence-based interventions to

promote judicial use of antibiotics for treating COVID-19 patients in Bangladesh may help in reducing overuse of antibiotics.

## Tuesday, August 9, 2022

### Poster Session 1 Abstracts

### 12:30 PM – 1:30 PM

### Grand Hall

## COVID-19 and SARS-CoV-2

### Poster 172. Impact of COVID-19 on NCEZID Research, 2020

L. Youngblood, M. Bass
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** In May 2020, the Centers for Disease Control and Prevention (CDC), Office of Scientific Integrity (OSI) issued an agency-wide data call to assess the impact of the Coronavirus Disease 2019 (COVID-19) pandemic on CDC's ongoing human subjects research activities. Each CDC Center/Institute/Office (CIO) was requested to complete individual reports describing the impact of COVID-19 for all ongoing IRB-approved studies. This poster describes the impact of COVID-19 on research conducted by CDC's National Center for Emerging and Zoonotic Infectious Diseases (NCEZID). **Methods:** Data were collected through an electronic form. CIOs completed a form for each active study in their portfolios. Data fields included whether research activities had been paused or modified due to COVID-19 related risks. CIOs were given a two-week reporting timeframe. The NCEZID Human Studies team distributed the form via e-mail to all NCEZID principal investigators (PIs) via e-mail and assisted as needed. **Results:** As of May 2020, NCEZID had 189 open human subjects research studies. Of these, 40 (21%) studies had completed all interactions with subjects and were in data analysis. These studies are not considered in the remaining analyses. Of the remaining 149 active studies, 23 (15%) had halted some or all activities or modified activities due to COVID-19 risks. Twenty (13%) studies were put on hold due to COVID-19 reasons other than risk, such as reprioritization of resources. Twenty-eight studies (19%) were halted for other reasons not related to risk or COVID-19, such as departure of key staff prior to the pandemic. Another 78 (52%) were determined not to pose any additional risk and continued as approved, including studies that were not designed to involve contact with subjects. **Conclusions:** In total, 29% of NCEZID's active ongoing human subjects research activities were impacted by the COVID-19 pandemic because of risks to subjects or staff, reprioritization, or staffing shortages. This is likely an underestimate of the true impact, as this assessment was conducted early in the pandemic, and it does not reflect existing studies that may have been postponed later. Our findings suggest that the impact of the pandemic on existing research is not solely due to risk; the reallocation of resources and staff may also impact continuity of research operations.

### Poster 173. Emerging *Kodamaea ohmeri* and SARS-CoV-2 Co-Infection Causing Death in a Premature Neonate: A Case Report from Rural Bangladesh

**M.Z. Hossain**[1], M. Alam[1], M.I. Jahan[1], S. Jahan[1], K.M. Islam[1], A. Rahman[1], M.S. Ahmed[1], A. Rashed[1], S. Bari[1], K.H. Lee[2], S. El Arifeen[1], E.S. Gurley[2], M. Rahman[1]
[1]International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Johns Hopkins University, Baltimore, MD, USA
**Background:** A rare opportunistic pathogen, *Kodamaea ohmeri*, formerly named *Pichia ohmeri* is a yeast-like fungus that was widely used in the food industry for fermentation in the past decades. Recently, this fungus has been identified in an increasing number of serious infections in humans. Here we report a premature neonate who died due to fungemia caused by *Kodamaea ohmeri* with a SARS-CoV-2 co-infection. **Methods:** An 8-day old male baby was admitted to Bangabandhu Sheikh Mujib Medical College Hospital, Faridpur on 30$^{th}$ January 2021. Parents reported the child was unable to feed and had low body temperature. The baby was ill-looking, irritable during admission, and died after 7 days of hospitalization. The neonate was a twin and was delivered at home prematurely at 34 weeks gestation with a very low birth weight (1290 gm). Post-mortem specimens were collected using a minimally invasive tissue sampling method and tested by microbial culture (BD BACTEC and Vitek-2), immunohistochemistry and TaqMan Array Card platform based on real-time PCR. All clinical, demographic and laboratory diagnosis results were reviewed by a panel of experts to determine the cause of death. **Results:** Sepsis due to *Kodamaea ohmeri* was identified as the immediate cause of death, and SARS-COV-2, prematurity and

intrauterine growth retardation were underlying causes. *Kodamaea ohmeri* was cultured from both blood and cerebrospinal fluid (CSF). The isolate was sensitive to 7 (Amphotericin B, Clotrimazole, Nystatin, Posaconazole, Ketoconazole, Voriconazole, and Fluconazole) out of 9 antifungals tested. SARS-CoV-2 RNA (pango lineage B.1.1.25) was identified from nasopharyngeal swab, blood, CSF and lung tissue. The source of the infections and timing of acquisition were unclear. **Conclusions:** Early diagnosis of unusual fungal infections like *Kodamaea ohmeri* requires advanced laboratory techniques, and appropriate treatment is recommended for a better outcome.

### Poster 174. COVID-19 in a Refugee Camp Setting: Molecular Evidence of *Chlamydia abortus* in an Oral Swab

**D.A. Raele**, D. Galante, V. Manzulli, I. Vasco, V. Rondinone, M.A.Cafiero
Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata, via Manfredonia, Foggia, Italy
**Background:** Among zoonotic agents, a novel global pandemic coronavirus is the cause of the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). The coronavirus disease 2019 (COVID-19) is a flu-like syndrome characterized by fatigue, fever, cough, headache and, in some severe cases, by an 'atypical pneumonia' often with fatal outcome. However, other zoonotic diseases, such as Q fever or Chlamydiosis may show the same unspecific symptoms. For this the specificity and the rapidity in diagnosing individuals with clinical and/or symptomatic signs and their contacts is essential in order to limit the transmission of the COVID-19 and control the outbreak. **Methods:** The study tested a total of forty-eight DNAs extracted from oral swabs. The materials were collected and analysed during an outbreak of COVID-19 in a refugee camp sited in Poggio Imperiale (Foggia, Apulia region). In order to verify the present/absence of DNA of *Coxiella burnetii* and *Chlamydia* spp. qPCR assays targeting *IS1111* and *23sRNA* of *C. burnetii* and *Chlamydia* spp. respectively were performed. Using as a template the DNA that showed a positive signal from qPCR assay, a second step was carried out using conventional PCR targeting periplasmic oligopeptide-binding protein gene (*OppA*) and 16S ribosomal RNA gene (*16S)* of *Chlamydia* spp. DNA fragments obtained by PCRs were sequenced using the Sanger method and then they were compared with available sequences present in Genbank database. **Results:** Among the forty-eight analysed DNA, one sample was confirmed to be *Chlamydia* spp. The nucleotide sequences showed 99.79% and 99.75% homologies with *OppA* and *16S* genes of *Ch. abortus* respectively. The DNA has been linked to the oral swab collected from an adult male, asymptomatic and no fixed adobe. DNA of *C. burnetii* was not detected in any tested samples. **Conclusions:** Chlamydiae comprise a group of zoonotic obligate intracellular organisms capable of causing severe form of disease in animals and humans. Among these *Ch. abortus* is considered a cause of abortion and foetal loss in livestock. Human infections resulting from exposure to infected domestic mammals consequently, risks are limited mainly to those working with small ruminants or in contaminated sites such as farms, barns and stables. Oral swabs are a non-invasive sample type for diagnosing infectious diseases and they contains precious data to reveal the present of pathogens including, such in our case, zoonotic agents. Our result suggests to verify the presence of these zoonotic agents, especially in patients with a past linked to the care of small ruminants or those who have stayed in barns or environments connected to animal reservoirs.

### Poster 175. The Impact of COVID-19 on the TB Control Programme in England: A Quantitative Analysis

**K. Alipio**[1], B. Nozad[2], H. Watt[1], A. Majeed[2]
[1]Imperial College London, London, England, UK, [2]Public Health England, London, England, UK
**Background:** TB remains a global public health issue and leading infectious disease killing over one million people annually. Unfortunately, decades of efforts to reduce the prevalence and mortality of TB could be put at risk by the recent COVID-19 pandemic given the worldwide policies to reassign healthcare workers and lockdowns. There is no exploration of this impact on the National TB Control Programme within England in regard to progress indicators. This study aims to investigate this impact through quantitative data analysis. **Methods:** Negative binomial regression is used to analyse publicly available and NHS England datasets in order to estimate the effect of variables such as national lockdowns on TB cases nationally. The main outcome measures are the relative differences in the monthly number of culture-confirmed pulmonary TB cases and monthly rate of latent TB cases. Descriptive analysis is used to investigate the impact on TB reporting delay and treatment delay. **Results:** Reductions in TB cases during months of national lockdown (0.871 [95% CI 0.760 – 0.999]) and during the pandemic (0.770 [95% CI 0.689 – 0.862]) are found nationally. No changes are found with TB reporting delay and treatment delay. **Conclusions:** This is the first study exploring the threats posed by the pandemic on TB control in England. It is important for any future strategy to consider this study's results to ensure TB Control is prioritised nationally and internationally.

### Poster 176. Using the Human-centered Design Approach to Develop a Community-led COVID-19 Control Strategy for Informal Settlements in Kampala City

**A. Ndyabakira**[1,2], E. Katana[1,2], R. Nuwematsiko[3], J. Namayanja[1], D. Kadobera[1], A. Ario[1], R. Migisha[1], L. Bulage[1], J. Harris[4], D. A. Okello[2], R. Wanyenze[3]
[1]Uganda Public Health Fellowship Program, Ministry of Health, Kampala, Uganda, [2]Directorate of Public Health and Environment, Kampala Capital City Authority, Kampala, Uganda, [3]School of Public Health, College of Health Sciences, Makerere University, Kampala, Uganda, [4]Division of Global Health Protection, Center for Global Health, Centers for Disease Control and Prevention, Kampala, Uganda
**Background:** COVID-19 was first reported in Uganda in March 2020. By August 6, Kampala city accounted for 70% of the country's fatal cases and 40% of surviving case-patients. Informal settlements, with their crowding and inadequate sanitation, represent potential hotspots of infection. We used the human-centered design (HCD) approach to design improved interventions to address COVID-19 in informal settlements in Kampala city. **Methods:** During July-August 2020, we interviewed residents of informal settlements and community health workers (CHW) in Kampala city and used the HCD approach to identify and prioritize challenges, do root cause analysis and develop solutions. We conducted nine focus group discussions (FGDs) with 6-8 participants selected to represent the gender, educational level, and job status of settlement residents. FGDs specifically addressed challenges to uptake of COVID-19 prevention measures, ways of increasing compliance to these measures, and development of a community-led surveillance system. FGDs were audio-recorded and transcribed in English. Participants, guided by the HCD approach, brainstormed, and discussed challenges to COVID-19 prevention and surveillance within their settings, prioritized them, and did root cause analysis. A prototype solution was obtained through a plenary vote on all suggested solutions, based on feasibility and impact. **Results:** The main challenge to uptake of COVID-19 preventive measures was Ministry of Health's failure to involve community health workers (CHW) in the response. Other challenges were limited access to appropriate face masks and low awareness about social distance practices. Uncompensated CHW lacked interest in facilitating COVID-19 surveillance. Inadequate community involvement in surveillance and design of effective interventions led to low compliance to required prevention measures and poor surveillance effectiveness. Participants designed a community-based surveillance plan and a community-led response system for risk communication and sensitization, enforcement of adherence to preventive measures, and a designated facility for reporting surveillance information. However, this has yet to be adopted for use. **Conclusion:** A community-centred model offers innovative ways of controlling the spread of COVID-19. This model demonstrated a doable approach to design appropriate pandemic response for congested urban areas.

### Poster 177. Development of SARS-CoV-2 Serological Luminex Competition Assay for CDC's One Health

Moved to Poster Session 1, Monday, August 8, 12:30 PM – 1:30 PM (at end of COVID-19 and SARS-CoV-2 section, after poster 262)

### Poster 178. Evaluation of the Universal COVID-19 Admission and Pre-Surgical Testing

**X. Wang**, K. Short
Fraser Health, Surrey, British Columbia, Canada
**Background:** In response to high rates of COVID-19 prevalence, Fraser Health (FH), a regional health authority in British Columbia, Canada, implemented universal COVID-19 testing in November 2020 for all patients admitted through the Emergency Departments (ED) and all patients scheduled for non-urgent surgeries. The objective was to determine whether universal testing can identify unrecognized infections and prevent patient and healthcare worker exposures. **Methods:** All admissions through twelve EDs and all scheduled surgical bookings eligible for COVID-19 testing were extracted and linked to laboratory data, point-of-care screening and case assessment data by unique patient identifier. COVID-19 tests collected within two days of admission or one to five days prior to scheduled surgery date were included in the analysis. Analysis included percent tested, positivity rate and proportion of positive admissions or surgical bookings that did not meet point-of-care screening criteria over the study period. **Results:** Over an eight-month period, 91% (n=52,346) of eligible admissions and 81% (n=48,501) of eligible surgical bookings were tested for COVID-19. The overall positivity rate was 3% for ED admissions and 1% for surgical bookings. The positivity rates for admissions that met vs did not meet the point-of-care screening criteria were 9% and 1%, respectively. Of the cases with point-of-care screening or case assessment data, 30% (n=483) of admissions and 49% (n=112) of surgical bookings reported no COVID-19 symptoms or risk factors. Temporal trends suggest that as positivity rate decreases, the proportion of cases not meeting point-of-care screening criteria increases. **Conclusions:** Over an eight-month period, universal testing for COVID-19 on admission and prior to surgery identified 595 cases which would have been missed through traditional screening. The risk of unidentified

cases must be balanced with resources required for implementing universal testing based on local epidemiological data on COVID-19.

### Poster 179. Development and Evaluation of a Multiplex Serological Assay for Assessment of Circulating IgG Antibody Response to SARS-CoV-2 Antigens after Vaccination

**N. Venkateswaran**, J. Walker, R. Matlick, J. Sarwar, W. Nelson, K. Venkateswaran
Tetracore, Inc., Rockville, MD, USA

**Background:** WHO declared a COVID 19 pandemic caused by SARS-CoV-2 virus on March 11, 2020, and since then the clinical relevance of serological assays has been debated in the scientific community. After a year and a half, this virus is still causing a significant burden on public health worldwide. Vaccines have now proven to be a handy tool to curb the spread of this virus. In this scenario of infection and vaccination, it is imperative to understand the durability of immune response post vaccination at both individual and population levels. The assessment of circulating IgG antibodies to multiple antigens, both wild type, and variants, can provide a snapshot of immune signature in vaccinated individuals. We developed and evaluated a multiplex panel of antigens to determine the presence of circulating IgG after vaccination. **Methods:** A 36-plex panel of immobilized antigens on magnetic microspheres was developed and evaluated in this study. This panel was based on Luminex xMAP technology. This 36-plex expanded panel includes 19 different wild-type and variant proteins from SARS-CoV-2, 13 different S1 spike, and nucleocapsid proteins from other human coronaviruses. We assessed 94 serum or plasma samples from 32 vaccinated individuals immunized by different vaccines, including Moderna mRNA-1273, Pfizer/BioNTech BNT162b2, Janssen (Johnson & Johnson), Ad26.COV2.S. We also included 99 negative samples that were not vaccinated and collected between 2017-2018. **Results:** Almost all the negative samples assessed showed a positive circulating IgG response to various other human coronaviruses causing common colds but negative response to SARS-COV-2 antigens. Every individual sample displayed a unique antibody signature. This clearly demonstrates that human population was not exposed to this virus prior to COVID 19 pandemic. Data from all 94 vaccinated samples also indicate a positive response to S1-Trimeric protein, S-NTD protein, RBD, and S1 protein of SARS-CoV-2 following vaccination and a negative response to nucleocapsid proteins. **Conclusions:** This multiplex panel provides a valuable tool to monitor and assess the long-term durability of circulating IgG antibodies in case of infection and vaccination. These panels can be instrumental in retrospective studies to reconstruct the evolution of the virus and its interaction with the human immune system.

### Poster 180. How Egypt Safely Organized the First and Largest Global Mass Gathering amid COVID-19 Pandemic: Lessons Learned from Hosting the 27th Men's Handball World Championship, Egypt January 2021

**H. Magdy**, H. Hassan, S. Abu-Kamar, M. Fawzy, M. Abdullah, I. Eldeyahy, N. ElGuindy, H. Abo-ElSood, S. Sami, S. Afifi, A. Eid
Ministry of Health and Population, Cairo, Egypt

**Background:** Hosting the largest Men's Handball World Championship and the first mass gathering event in the context of COVID-19 pandemic in Egypt was challenging. "Medical Precaution Plan" was developed which included a full bubble concept with hotels exclusively reserved for participants. Bubble concept was applied for the first time to minimize COVID-19 infection transmission before, during and after the tournament. The aim of this study is to describe all aspects of the multi-sectorial plan implemented and its impact on achieving safe and healthy World Handball Championship. **Methods:** All tournament participants involved entered a full bubble without any external contact within previous three days. Medical officers, accommodation hotels, medical aid centers, isolation rooms, referral hospitals, ambulance and laboratory services were set up. Participants were accommodated in four venues where personal protective equipment, social distancing, wearing masks and continued disinfection were strictly followed. For each country team, COVID officer was assigned for early case detection through observing symptoms and reviewing PCR results on daily basis, arrange for positive patients' isolation and treatment, and ensure healthy and safe environment for the team. **Results:** Overall 3,630 participants from 32 countries entered the bubble, including 967 (26.6%) sports delegations, 1512 (41.7%) hotel staff, 164 (4.5%) medical teams and 987 (27.2%) organizers. Of them 138 (3.8%) patients were positive for SARS-CoV-2 by RT-PCR, including 110 (3.0%) Egyptian hotel staff and 28 (0.8%) non-Egyptians. Non-Egyptian patients were quarantined at designated isolation hotel under full medical care and Egyptians were isolated at home. All contacts were closely followed for up to 14 days. No secondary transmission occurred during or after the championship. Cape-Verdi team was excluded after positive results of eight players. **Conclusions:** Egypt succeeded to organize the 27$^{th}$ Men's World Handball Championship in a healthy and safe environment. With the other "Medical Precaution Plan" components, bubble

concept was effective in preventing COVID-19 transmission and is recommended in mass gatherings during COVID-19 and future pandemics.

### Poster 181. Leveraging Data from the Nationwide Commercial Laboratory Seroprevalence Survey to Characterize the Burden of COVID-19 Disease in Disproportionately Affected Populations

**C. Iwamoto**[1], Y. Kim[2], A. Lee[2], J. Thierry[1], A. Board[1], K. Anderson[1], D. Moyse[2], R. Iachan[2], K. Clarke[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]ICF, Incorporated, L.L.C., Fairfax, VA, USA
**Background:** Adults with disabilities have experienced higher levels of mental health (MH) conditions and substance use disorder (SUD) during the pandemic than those without disabilities. Despite increased risk for worse COVID-19 disease outcomes among people with SUD and some people with disabilities, lack of adequate data precludes calculation of risk of infection for these groups from case surveillance data. We used seroprevalence data and associated ICD-10-CM diagnosis codes collected through the nationwide commercial laboratory seroprevalence survey to characterize the burden of COVID-19 infection among people with disabilities, SUD, MH conditions, or combinations of these diagnoses. **Methods:** Between July 28, 2020-July 11, 2021, a total of 1,382,675 residual sera samples from commercial laboratories nationwide were tested for SARS-CoV-2 antibodies that indicate past COVID-19 infection. Deidentified data were aggregated by associated ICD-10-CM codes indicating disability, SUD, or MH condition. Prevalence ratios were obtained using log binomial regression models adjusted for age, gender, and urbanicity. **Results:** People with ICD-10-CM codes for disability, SUD, or MH conditions were less likely to test positive for COVID-19 antibodies compared to those without these diagnoses (aPRs: 0.69-0.81); seroprevalence was decreased across sex, urbanicity, and most age groups. Adults >65 years with a diagnosed disability (aPR: 1.09; 95%CI: 0.95-1.2) or SUD (0.91; 0.71-1.14) had a seroprevalence not significantly different than those without these diagnoses. Among people with disabilities, seroprevalence was significantly higher among those >65 years than other age groups. On assessment of comorbidity, only those with diagnosis codes indicating both disability and MH condition (0.73; 0.57-0.92) had a decreased seroprevalence compared with those without these conditions. **Conclusion:** The nationwide seroprevalence survey is unique in capturing SARS-CoV-2 serology data associated with ICD-10-CM codes. An ICD-10-CM code indicating disability, SUD, or MH condition was associated with a decreased likelihood of past SARS-CoV-2 infection in most groups. To better understand burden and trends of COVID-19 and other diseases among these populations, improved capture of related variables in infectious disease surveillance systems are needed.

### Poster 182. A Systematic Review of Seroprevalence of SARS-CoV-2 Antibodies across the WHO European Region, January - December 2020

**A. Vaughan**[1], E.F. Duffell[2], G.S. Friedl[1], D.S. Lemos[1], T. Funk[2], A. Nardone[3], M. Valenciano[3], L. Subissi[4], I. Bergeri[4], E. Broberg[2], P. Penttinen[2], R. Pebody[1], M. Keramarou[2]
[1]World Health Organization Regional Office for Europe, Copenhagen, Denmark, [2]European Centre for Disease Prevention and Control, Stockholm, Sweden, [3]Epiconcept, Paris, France, [4]World Health Organization, Geneva, Switzerland
**Background:** Seroprevalence surveys are essential to assess the age-specific prevalence of pre-existing cross-reactive antibodies in the population with the emergence of a novel pathogen; to measure population cumulative seroincidence of infection, and to contribute to estimating infection severity. With the emergence of SARS-CoV-2, ECDC and WHO Regional Office for Europe have supported Member States in undertaking standardized population-based SARS-CoV-2 seroprevalence surveys across the European Region. **Objectives:** The objective of this study was to undertake a systematic literature review of SARS-CoV-2 population seroprevalence studies undertaken in the WHO European Region in 2020 since the start of the SARS-CoV-2 pandemic to measure pre-existing and cumulative seropositivity. This review aimed to describe seroprevalence in relation to time since start of pandemic and cumulative disease incidence until the introduction of national COVID-19 vaccination programmes. **Methods:** We systematically searched MEDLINE, ELSEVIER and the pre-print servers medRxiv and bioRxiv within the “COVID-19 Global literature on coronavirus disease” database using a predefined search strategy. We included seroepidemiology studies published before the widespread implementation of COVID-19 vaccination programmes in January 2021 among the general population and blood donors, at national and regional levels. Study risk of bias was assessed using a quality scoring system based on sample size, sampling and testing methodologies. Articles were supplemented with unpublished WHO-supported Unity seroprevalence studies and other studies reported directly to WHO Regional Office for Europe and ECDC. **Results:** In total, 115 studies involving 796 900 participants from 27 countries undertaken between 01/01/2020 and 31/12/2020 across the European Region were included. A significant heterogeneity in implementation was noted across the studies, with a bias towards studies in high-income countries in Western Europe. Eighty-one (70%) studies were assessed to be of high or medium quality.

Overall, SARS-CoV-2 seropositivity prior to widespread community circulation was very low. National seroprevalence estimates after circulation started ranged from 0% to 48% (median 2.2 (0 – 48.4); n=105), while sub-national estimates ranged from 0% to 52% (median 5.5 (0 – 52); n=97), with the highest estimates in areas following widespread local transmission. **Conclusions:** The review found evidence of low national SARS-CoV-2 seroprevalence (<10%) across the WHO European Region, before and after the emergence of SARS-CoV-2. The low levels of SARS-CoV-2 antibody in most populations in Europe prior to the start of vaccine programmes highlights the critical importance of vaccinating priority groups at risk of severe disease while maintaining reduced levels of transmission to minimize population morbidity and mortality.

### Poster 183. Transmission Dynamics and Short-Term Forecast of COVID-19 in Nepal in 2020/2021

**S. Dahal,** G. Chowell
Department of Population Health Sciences, School of Public Health, Georgia State University, Atlanta, GA, USA
**Background:** Nepal was hard hit by the third wave of COVID-19 in 2021. Low testing rates, weak social distancing guidelines, open border with India, and poor economy have impacted pandemic management in the country. We investigated the transmission dynamics of COVID-19 at the national and provincial level. **Methods:** We obtained data on laboratory-confirmed RT-PCR positive cases from the country situation reports. We performed 8 week-to-week sequential forecasts of 10-days and 20-days at national level using three dynamic phenomenological growth models from 3/5/2021-5/22/2021. Performance of the models was assessed using five different performance metrics. We estimated effective reproduction number and instantaneous reproduction number at national and provincial level. We also assessed the mobility trend using Google's mobility data. **Results:** Our forecast estimates indicated a declining trend of COVID-19 cases in Nepal in mid-May 2021 for most of the models. While sub-epidemic model performed better during calibration phase and forecast phase in the initial forecast periods, Richards model performed better during forecast phase in the later forecast periods. We report almost a linear pattern of COVID-19 incidence trajectory during the first and second waves in Nepal (deceleration of growth parameter (p)=0.41-0.43, reproduction number (Rt) at 1.1 (95% CI: 1.1, 1.2)), and a sub-exponential growth pattern in the third wave (p=0.61 (95% CI: 0.58, 0.64)) and Rt at 1.3 (95% CI: 1.3, 1.4). At the provincial level, Rt during the early growth phase of third wave ranged from 1.2 to 1.5. The instantaneous reproduction number fluctuated around 1 since January 2021 indicating a sustained transmission. Our analysis of mobility trend showed that the peak in mobility across different areas correspond to rise in COVID-19 cases. **Conclusions:** The sub-epidemic and Richards model provide reasonable short-terms projections of COVID-19 trajectory in Nepal and indicate a declining trend of the cases until June 2021. The country saw a slight resurgence of cases in August 2021. We recommend the careful planning of mobility strategies to prevent resurgence of cases.

### Poster 184. Seroprevalence of IgG and IgA Antibodies against SARS-CoV-2 in Vendors from Community Markets of Guatemala

**L.M. Grajeda,** R. Mendizábal-Cabrera, M.R. López, C. Cordón-Rosales
Center for Health Studies, Universidad del Valle de Guatemala, Guatemala City, Guatemala
**Background:** The seroprevalence of antibodies against SARS-CoV-2 is used in the surveillance of infections and to better understand the risk of transmission. Studies have focused on healthcare personnel, but the seroprevalence in other populations conducting essential activities, as market vendors, is unknown. This study aimed to estimate the seroprevalence of IgG and IgA antibodies against SARS-CoV-2, and the prevalence of infection in market vendors of Guatemala during July-September 2021. **Methods:** We conducted a cross-sectional survey in two markets from urban communities; initial recruitment focused on adults (aged 18+) who had not received the COVID-19 vaccine. From all participants we collected nasopharyngeal (NP) swabs to detect SARS-CoV-2 infection by RT-PCR, and a blood sample to assess IgG and IgA antibodies against the S viral protein by a commercial ELISA test. We also collected demographic and clinical information by an electronic questionnaire. **Results:** We recruited 102 market workers. At baseline 86% provided a NP swab and a blood sample. Most (71%) were aged 18-40 years, and 76% were women. Seventy-two (75%) reported working in the market 6-7 days a week. We found active SARS-CoV-2 infection in 14% (IC 95%: 7% to 22%) and a seroprevalence of 46% (IC 95%: 36% to 56%) and 58% (IC95%: 48% to 68%) for IgG and IgA against SARS-CoV-2, respectively. Bivariate analysis showed higher seroprevalence of IgG in woman (52%, IC95%: 40% to 64%) than men (26%, IC95%: 10% to 48%). Self-reported anosmia and ageusia were associated with IgG seroprevalence (p<0.005 and 0.002), however, only 13 (30%) reported these two symptoms at any time since March 2020, the official reported onset of the epidemic in the country. **Conclusions:** Results indicate that vendors were exposed to the virus but suffered mild or asymptomatic illness of which they were not aware, and thus increased the risk of transmission in markets. Data suggest that COVID-19 was under

diagnosed and underreported in this population, highlighting the need to reinforce routine surveillance of vendors and the practice of personal protection measures.

### Poster 185. SARS-CoV-2 Mortality Surveillance among Community Deaths brought to University Teaching Hospital Mortuary in Lusaka, Zambia, 2020

**A. Hamukale**[1], J.Z. Hines[2], N. Sinyange[3], S. Fwoloshi[4], W. Malambo[2], S. Sivile[4], S. Chanda[1], L.A. Mucheleng'anga[5], N. Kayeyi[3], C.M. Himwaze[6], A. Shibemba[4], T. Leigh[2], M.L. Mazaba[3], N. Kapata[3], P. Zulu[3], K. Zyambo[4], F. Mupeta[4], S. Agolory[2], L.B. Mulenga[4], K. Malama[4], M. Kapina[3]
[1]Zambia Field Epidemiology Training Program, Lusaka, Zambia, [2]Centers for Disease Control and Prevention, Lusaka, Zambia, [3]Zambia National Public Health Institute, Lusaka, Zambia, [4]Zambia Ministry of Health, Lusaka, Zambia, [5]Ministry of Home Affairs, Office of the State Forensic Pathologist, Nationalist Road, Lusaka, Zambia, [6] University Teaching Hospitals, Department of Pathology and Microbiology, Nationalist Road, Lusaka, Zambia
**Background***:* During March-December 2020, Zambia recorded 20,725 confirmed COVID-19 cases, with the first wave peaking between July and August. Of the 388 COVID-19-related deaths occurring nationwide, most occurred in the community. We report findings from COVID-19 mortality surveillance among community deaths brought to the University Teaching Hospital (UTH) mortuary in Lusaka. **Methods***:* In Zambia, when a person dies in the community, and is brought into a health facility mortuary, they are recorded as 'brought in dead' (BID). The UTH mortuary accepts persons BID for Lusaka District, the most populated district in Zambia. We analysed data for persons BID at UTH during 2020. We analysed two data sources: weekly *SARS-CoV-2* test results for persons BID and monthly all-cause mortality numbers among persons BID. For all-cause mortality among persons BID, monthly deaths during 2020 that were above the upper bound of the 95% confidence interval for the historic mean (2017-2019) were considered significant. Spearman's rank test was used to correlate the overall percent positivity in Zambia with all-cause mortality and *SARS-CoV-2* testing among persons BID at UTH mortuary. **Results***:* During 2020, 7,756 persons were BID at UTH (monthly range 556-810). SARS-CoV-2 testing began in April 2020, and through December 3,131 (51.9%) of 6,022 persons BID were tested. Of these, 212 (6.8%) were SARS-CoV-2 positive with weekly percent test positivity ranging from 0-32%, with the highest positivity occurring during July 2020. There were 1,139 excess persons BID from all causes at UTH mortuary in 2020 compared to the 2017-2019 mean. The monthly number of persons BID from all causes was above the upper bound of the 95% confidence interval during June-September and December. **Conclusion***:* Increases in all-cause mortality and SARS-CoV-2 test positivity among persons BID at UTH mortuary corresponded with the first peak of the COVID-19 epidemic in June and August 2020, indicating possible increased mortality related to the COVID-19 epidemic in Zambia. Combining all-cause mortality and SARS-CoV-2 testing for persons BID provides useful information about the severity of the epidemic in Lusaka and should be implemented throughout Zambia.

### Poster 186. Immunoassays Used in SARS-CoV-2 Seroprevalence Surveys Worldwide: A Descriptive Analysis of Assay Use, Testing Algorithms, and Performance

**X. Ma**[1,2], Z. Li[2,3], M. Whelan[2], C. Cao[2], T. Yan[4], M. Yanes-Lane[5], L. Subissi[6], N. Bobrovitz[4], R. Arora[2,7]
[1]Institute of Health Policy Management and Evaluation, University of Toronto, Toronto, Ontario, Canada, [2]Centre for Health Informatics, Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada, [3]Faculty of Engineering, University of Waterloo, Waterloo, Ontario, Canada, [4]Temerty Faculty of Medicine, University of Toronto, Toronto, Ontario, Canada, [5]COVID-19 Immunity Task Force, McGill University, Montreal, Quebec, Canada, [6]World Health Organization, Geneva, Switzerland, [7]Institute of Biomedical Engineering, University of Oxford, Oxford, UK
**Background:** During the start of the COVID-19 pandemic, many commercial SARS-CoV-2 serological assays were rapidly developed and mobilized. However, differences in detection mechanism and target of immunoglobulin (Ig) subclasses limit comparability of the regional prevalence of SARS-CoV-2. In this study, we synthesized the evidence on immunoassay usage and their validations in serosurveys to inform future testing strategies.
**Methods:** Data on serological assays (test type, manufacturers, Ig targets, sensitivity/specificity [Sn. /Sp.], multiple testing algorithms) was extracted as part of an ongoing living systematic review of global serosurveys (Jan 1, 2020 - Sep 3, 2021). We mapped our data in manufacturer, third-party head-to-head (*NRL*, *Doherty*, *FIND*, *FDA*, and a Dutch multicenter evaluation), and independent field evaluations. Descriptive statistics on assay characteristics, performance, and multiple assay combinations were conducted and summarized by WHO-defined geography regions. **Results:** Among 1751 serosurveys, 87.0% used commercial assays; 19.9% developed assays at the lab; and 21.2% used multiple assays. Global usage follows a power-law distribution, with the top 25 assays accounting for 75.4% of total use in serosurveys. 58.0% of commercial assays were evaluated in third-party head-to-head laboratory comparisons, while 39.4% of assays were evaluated by research groups in the field. According to

manufacturers, 24.4% of commercial assays (n = 193) met the WHO criteria for emergency use (i.e., Sn. >= 90.0%, Sp. >= 97.0%), while 70.0% of the 50 most frequently used assays met the criteria. Third-party (criteria met among top 50: 43.6%) and independent evaluations (59.0%) indicated that manufacturers tended to overstate the performance of their assays. **Conclusions:** Independent evaluations showed that immunoassays have generally low field performance. Study investigators are encouraged to use well-performing assays that have been evaluated by third parties, conduct independent evaluations using common reference panels to allow for robust comparison between immunoassays and study results. Due to the high number of unique immunoassays used, and the high variation in test performance, adjustments based on test Sn. /Sp. are recommended to standardize results.

### Poster 187. Epidemiology of SARS-CoV-2 Variants at a Large Private University

**C. Stafylis**[1], A. Kovacs[2], J. Emerson[3], P.M. Ward[3], S. Van Orman[4], F. Gilliland[1], D. Conti[1], O. Pernet[2], M. Weisenhaus[2], A. Ghanem-Uzqueda[4], C. Hernandez-Tamayo[1], S. Stellar[1], A. Tadanki[1], J. Kravitz[1], T. Chu[1], H. Hu[1], J.D. Klausner[1]
[1]Department of Population and Public Health Sciences, University of Southern California, Los Angeles, CA, USA, [2]Maternal, Child and Adolescent Center for Infectious Diseases, University of Southern California, Los Angeles, CA, USA, [3]Department of Clinical Pathology, University of Southern California, Los Angeles, CA, USA, [4]Department of Family Medicine, University of Southern California, Los Angeles, CA, USA
**Background:** SARS-CoV-2 variants with different infectivity, transmission potential and morbidity change the characteristics of local epidemics and affect vaccine effectiveness. As part of the University of Southern California COVID-19 Pandemic Research Center's (USC CPRC) efforts to understand, control the ongoing pandemic and inform local community, we implemented a surveillance of SARS-Cov-2 variants among students, employees, and USC medical center patients. **Methods:** We analyzed stored remnant specimens of cases infected with SARS-CoV-2 that tested at the USC laboratories between September 2020 - July 2021. Samples were analyzed using droplet digital Reverse Transcriptase PCR. Samples were tested for 8 SARS-CoV-2 variants: wild-type, α (B.1.1.7, Q.1-Q.8), β (B.1.351, B.1.351.2, B.1.351.3), γ (P.1, P.1.1, P.1.2), δ (B.1.617.2), δ+ (or δ417N), ε (B.1.427 and B.1.429), η (B.1.525), λ (C.37). We reviewed medical records from positive cases and collected demographics, history of COVID-19 infection, COVID-19 vaccination, test results. **Results:** We extracted data from 449 cases. The majority of the cases were among students (234/449; 54.2%) and USC patients (100/449; 23.1%); 48.5% (218/449) self-identified as white and 11% (50/449) as Latinx. The most common comorbidities among those with underlying health conditions (117/449; 26.1%) were: hypertension (29.9%; 35/117), cardiovascular disease (15.4%; 18/117). Among symptomatic individuals (29.8%;134/449), commonly reported symptoms were fever (32/134; 23.9%), headache (19/134; 14.2%), shortness of breath (21/134; 15.7%), loss of smell or taste (19/134; 14.2%), cough (18/134; 13.4%). No repeat infections were recorded. Among the 75 samples analyzed to date, 56 were classified as the original strain, 10 as 'Delta', 4 as 'Alpha', 1 as 'Gamma' and 3 were 'inconclusive'. **Conclusions:** Case surveillance at a large university with variant determination is feasible. Repeat infection was very rare. Local variant monitoring could inform prevention and control efforts.

### Poster 188. SARS-CoV-2 Seroprevalence and Reported COVID-19 Cases in U.S. Children, August 2020— May 2021

**A. Couture**[1], B.C. Lyons[1], M.L. Mehrotra[2], N. Ezike[3], I.A. Azzam[4], B.J. Katić[5], A. Copea[6], K. Dickerson[7], L. BrTraxler[8], J. Dunn[9], C. Reed[1], K. Clarke[1], B. Flannery[1], M.D. Charles[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]California Department of Public Health, Fresno, CA, USA, [3]Illinois Department of Public Health, Springfield, IL, USA, [4]Nevada Division of Public and Behavioral Health, Carson City, NV, USA, [5]New Jersey Department of Health, Trenton, NJ, USA, [6]North Carolina Department of Health and Human Services, Raleigh, NC, USA, [7]Ohio Department of Health, Columbus, OH, USA, [8]South Carolina Department of Health and Environmental Control, North Charleston, SC, USA, [9]Tennessee Department of Health, Nashville, TN, USA
**Background:** Case-based surveillance of pediatric COVID-19 cases underestimates the prevalence of SARS-CoV-2 infections among children and adolescents. Our objectives were to estimate monthly SARS-CoV-2 antibody seroprevalence and calculate ratios of SARS-CoV-2 infections to reported COVID-19 cases among children and adolescents in 8 U.S. states. **Methods:** This analysis of data from the Nationwide Commercial Laboratory Seroprevalence Survey compared cumulative incidence of SARS-CoV-2 infection extrapolated from monthly seroprevalence estimates from August 2020 through May 2021 with reported COVID-19 cases among children aged 0-17 years in California, Illinois, Nevada, New Jersey, North Carolina, Ohio, South Carolina, and Tennessee. Convenience samples of residual serum specimens provided by children aged 0-17 years and tested for antibodies to SARS-CoV-2 and COVID-19 case reports were used. **Results:** Of 41 583 residual serum specimens tested, children

aged 0-4, 5-11 and 12-17 years accounted for 1619 (3.9%), 10 507 (25.3%) and 29 457 (70.8%), respectively. Median SARS-CoV-2 antibody seroprevalence among children increased from 8% (range, 6% to 20%) in August 2020 to 37% (range, 26% to 44%) in May 2021. Estimated ratios of SARS-CoV-2 infections to reported COVID-19 cases in May 2021 ranged by state from 4.7-8.9 among children and adolescents to 2.2-3.9 for all ages combined. **Conclusions:** Through May 2021 in selected states, it is likely that greater than five times more SARS-CoV-2 infections occurred in children than the number of reported pediatric COVID-19 cases; most children with serum specimens included in serosurveys did not have detectable antibodies suggesting previous SARS-CoV-2 infection. Case-based surveillance underestimated the number of children infected with SARS-CoV-2 more than among all ages. Continued monitoring of pediatric SARS-CoV-2 antibody seroprevalence should inform prevention and vaccination strategies.

### Poster 189. Seroprevalence of SARS-CoV-2 Antibodies in Four Cities in Thailand, December 2020-September 2021

**S. Nakphook**[1,2], W.W. Davis[3,4], K. Prasert[5], D. Ditsungnoen[3], H. Lerdsamran[6], P. Puthavathana[6], M. Shrestha[6], S. Iamsirithavorn[1], E. Azziz-Baumgartner[4], B. Skaggs[3,4], P. Praphasiri[3], J.A. Mott[3,4]
[1]Ministry of Public Health, Nonthaburi, Thailand, [2]Thammasat University, Pathum Thani, Thailand, [3]Thailand MOPH-US CDC Collaboration, Nonthaburi, Thailand, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Nakhon Phanom Provincial Hospital, Nakhon Phanom, Thailand, [6]Mahidol University, Nakhon Pathom, Thailand
**Background:** From January 13, 2020, to September 9, 2021, Thailand reported 28,734 laboratory-confirmed coronavirus-19 (COVID-19) infections to the World Health Organization (WHO), placing it in the 10$^{th}$ percentile of countries for numbers of cases reported. To better understand the proportion of persons who developed antibodies to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2, the virus that causes COVID-19), and to identify populations most at risk of COVID-19, we implemented a sero-epidemiological survey of SARS-CoV-2 antibodies in an age-stratified sample of people in four major cities in Thailand. **Methods:** We used two-stage sampling or stratified random sampling using official residence lists to recruit 1200 people in three age strata in Bangkok, Chiang Mai, Nakhon Phanom and Phuket cities. We interviewed consented participants about demographics, risk factors and symptom history and took serum samples. Serum was screened for SARS-CoV-2 antibodies with enzyme-linked immunosorbent assay (ELISA) and microneutralization assays. After enrolment, participants were asked weekly if they had symptoms of COVID-19-like illness (CLI, defined as presence of any one of: fever, cough, shortness of breath, chills, myalgia, sore throat, loss of taste or smell, or diarrhea). If they reported CLI, nasopharyngeal swab was taken and tested by RT-PCR. **Results:** At baseline, of 1,200 people enrolled during December 2020-January 2021, 5 had antibody detection by ELISA (0.4%; 95% confidence interval (CI): 0.16-1.16), and none were positive by microneutralization. By September 16, 2021, 1200 participants reported 251 CLI events, 211 had swabs tested for SARS-CoV-2, and 31 (2.6%, 95% CI: 1.8%-3.7%) were positive, including 1 (0.1%) in Nakhon Phanom, 24 (2.0%) in Bangkok, 6 (0.5%) in Phuket, and 0 in Chiang Mai. **Conclusions:** Low SARS-CoV-2 seroprevalence at baseline suggests that Thailand successfully prevented COVID-19 infections through non-pharmaceutical interventions during the first year of the pandemic and may have valuable examples to share with other countries. Thailand's susceptible populations should receive COVID-19 vaccine to prevent continued pandemic activity.

### Poster 190. SARS-Cov-2 and Respiratory Symptom Surveillance in a School-Based Cohort after Shut-Down of In-Person Classes in March 2020

**C. He**[1], M. Goss[1], D. Norton[2], J.L. Temte[1], S. Barlow[1]
[1]Department of Family Medicine and Community Health, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]Department of Biostatistics, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA
**Background**: Surveillance of respiratory viruses among school-aged children can serve as a predictor for future virus circulation in the community. During the 2020 SARS-CoV-2 pandemic, many surveillance systems were limited during due to implementation of public health measures. We demonstrate the feasibility of a survey tool to effectively monitor the prevalence of acute respiratory infections (ARIs) in households (HHs) within a school community. **Methods:** The Great ORCHARDS Vaccine Effectiveness Study (GROVES) tracks ARIs and influenza vaccine effectiveness in the Oregon School District (Oregon, WI). Participating HHs complete weekly online surveys to enumerate ARIs. To assess if the pandemic driven school closure on 3/13/2020 was associated with a change in reported ARIs, we compared weekly responses in the 16 weeks prior to the closure (pre-COVID period) to the 16 weeks immediately following closure (COVID period) using interrupted time-series logistic regression. To

assess if the slope / intercept interrupt was associated with a change in family illness probability, a likelihood ratio test was conducted versus a model without the interrupt. Slope and intercept change coefficients were individually examined. **Results:** From 11/25/2019 - 7/5/2020, 204 (197-204) GROVES HHs participated. Weekly survey response rates ranged from 97-100%. During pre-COVID weeks, 44.4% (1437/3234) of responses indicated ≥1 HH member with ARI during the previous week. In the COVID period, 10.2% (318/3130) indicated ≥1 HH member with ARI during the previous week. The slope / intercept interrupt was statistically significant ($\chi 2$=133, df=2, p<0.0001). Regression coefficients revealed both intercept and slope changes were statistically significant, with an intercept interrupt estimate indicating an immediate drop in HH ARI odds corresponding to an OR of 0.51 (95% CI: 0.30-0.85) and a weekly slope reduction corresponding to an OR of 0.89 (95% CI: 0.83-0.95) week-to-week. **Conclusions:** The cessation of in-person K-12 education on 3/13/2020 was strongly associated with a reduction in reported ARIs in HHs, suggesting school closure can reduce transmission. Surveys can effectively be used to monitor respiratory activity in a school community.

### Poster 191. AGRI-CASA: Operationalizing a Community-based Cohort in Rural Guatemala to Describe SARS-CoV-2 Household and Household-Workplace Transmission Dynamics

**J. Monzon**[1], D.M. Calvimontes[2], E. Barrios[2], M.M. Lamb[3], K. Arias[2], M. Gomez[2], M. Fineman[4], A. Chacon[2], G. Guzman[2], G.An. Bolanos[2], L. Duca[5], C. Iwamoto5, N. Vuong[5], E. Azziz-Baumgartner[5], E. Zielinski-Gutierrez[1], E. Asturias[2,4,6,], D. Olson[4,6]

[1]Centers for Disease Control and Prevention, Division for Global Health Protection (CDC-DGHP), Guatemala City, Guatemala, [2]Center for Human Development, Fundacion para la Salud Integral de los Guatemaltecos, FSIG, Retalhuleu, Guatemala, [3]Department of Epidemiology and Center for Global Health, Colorado School of Public Health, Aurora, CO, USA, [4]Department of Pediatrics, Division of Infectious Disease, University of Colorado School of Medicine, Aurora, CO, USA, [5]Centers for Disease Control and Prevention, National Center for Influenza and Respiratory Diseases Division, Atlanta, GA, USA, [6]Department of Epidemiology and Center for Global Health, Colorado School of Public Health, Aurora, CO, USA

**Background:** The difficulties in conducting research in rural, resource-limited settings challenge high-quality assessment of COVID-19 burden in such areas. We describe the design, methods, rapid operationalization, and lessons learned from the AGRIcultural worker COVID-19 Asymptomatic and SymptomAtic transmission in the Home and Workplace (AGRI-CASA) Study, which began enrollment in September 2021. **Methods:** AGRI-CASA's primary objectives are to evaluate household and household-workplace burden and transmission dynamics of SARS-CoV-2 in a community in rural Guatemala. In an iterative process with high community engagement, we rapidly developed and operationalized a protocol and adapted data collection tools to local context. We present the final study methodology outlining adaptations from the parent study design. **Results:** AGRI-CASA will enroll 70 households near an agribusiness engaged in another study evaluating the burden of COVID-19 among plantation workers (AGRI). The inclusion of only AGRI study participant households was added when preliminary analysis found 81.8% of AGRI study COVID-19 cases reported being the index case within their households, highlighting the workplace as a potential household transmission source. Households are visited twice weekly for symptom surveys and once-weekly saliva sample collection from all household members. Visitation periodicity and subject reimbursement were determined via community consultation. Subjects meeting the case definition for COVID-like illness (CLI), or recent exposure, are tested for SARS-CoV-2. A positive test activates all household members intensive surveillance with frequent data collection over 6-weeks , followed by long-COVID surveys at 3-month intervals. **Conclusions:** AGRI-CASA adapted the study design to operationalize lessons learned from a community-based cohort. The study methods may inform research occurring during a rapidly evolving public health emergency in similar resource-limited settings.

### Poster 192. Identifying Associations between Variant and Vaccine Breakthrough Infection Using Case-Only Data: Evidence of Elevated Risk Associated with Circulating Beta, Delta, and Gamma Variants in Europe

**J. Brown**[1], P. Mook[1], J. Hagan[1], I. Singini[1], J. Mossong[2], M. Sadkowska-Todys[3], N. Bundle[4], G. Spiteri[4], R. Pebody[1]

[1]World Health Organization (WHO) Regional Office for Europe, Copenhagen, Denmark, [2]Health Directorate, Luxembourg, Luxembourg, [3]National Institute of Public Health NIH – National Research Institute, Warsaw, Poland, [4]European Centre for Disease Prevention and Control (ECDC), Stockholm, Sweden

**Background:** Effective vaccination is a key component of strategies to reduce morbidity and mortality. Emerging SARS-CoV-2 variants may affect the effectiveness of vaccination. We aim to identify any signals of increased risk of vaccine breakthrough by variant using case-only surveillance data. **Methods:** We analysed case-only surveillance

data reported by four European Countries (Estonia, Latvia, Luxembourg and Poland) to a regional surveillance platform. Using multivariable logistic regression, we estimated the odds ratio comparing partially and fully vaccinated cases to unvaccinated cases for Beta (B.1.351), Delta (B.1.617.2) and Gamma (P.1) variants relative to Alpha (B.1.1.7) variant. We adjusted for country, calendar time, age and sex. **Results:** In total, we analysed data on 1,304; 840; and 41,364 partially vaccinated, fully vaccinated, and unvaccinated COVID-19 cases. There was strong evidence that partially vaccinated cases were more likely infected with Gamma (adjusted OR [aOR] 2.53; 95% CI 1.06-6.16) or Delta (aOR 1.92; 95% CI 1.16-3.12) than Alpha. For full vaccination, there was strong evidence after adjustment that fully vaccinated cases were more likely infected with Beta (aOR 4.52; 95% CI 1.61-11.49) or Delta (aOR 2.74; 95% CI 1.39-5.34) than Alpha. There was little evidence that partially vaccinated cases were more likely Beta (aOR 1.27; 95% CI 0.65-2.30) or fully vaccinated cases were more likely Gamma (3.25; 95% CI 0.84-12.88) than Alpha. **Conclusions:** We identified evidence for increased risk of vaccine breakthrough with Gamma and Delta variants in cases with partial vaccination, and with Beta and Delta variants in fully full vaccinated cases, relative to Alpha. Such case-based surveillance data analyses offer a promising approach for the rapid identification of increased vaccine breakthrough risk with emerging SARS-CoV-2 variants.

### Poster 193. Factors associated with Receipt of COVID-19 Vaccination and SARS-CoV-2 Seropositivity among Healthcare Workers in Albania, February-May 2021

**P. Jorgensen**[1], I. Preza[2], I. Hatibi[2], J. Sulo[3], E. Kissling[4], A. Schmid[5], A. Fico[2], S. Sridhar[5], J. Rubin-Smith[5], G. Bejtja[6], A. Robo[2], M. Kota[2], A. Vasili[2], R. Daja[2]. E. Nelaj[2], R. Pebody[1], M. Katz[1], S. Bino[2]
[1]High Threat Pathogen Team, Health Emergencies Program, World Health Organization Regional Office for Europe, Copenhagen, Denmark, [2]Institute of Public Health, Tirana, Albania, [3]Southeast European Center for Surveillance and Control of Infectious Diseases, Tirana, Albania, [4]Epiconcept, Paris, France, [5]Boston Children's Hospital Global Health Program, Boston, MA, USA, [6]Country Office, World Health Organization, Tirana, Albania
**Background:** Healthcare workers (HWs) were the first group to receive COVID-19 vaccination in Albania. We identified factors associated with SARS-CoV-2 seropositivity and vaccination among HCWs enrolled in a 12-month prospective cohort study on COVID-19 vaccine effectiveness. **Methods**: Between 19 Feb-7 May 2021, we enrolled 1504 HCWs at 3 hospitals (Tirana, Durres, and Fier) by convenience sampling. At enrollment, participants provided serum (≤4 days after vaccination for vaccinated HCWs), which were tested for anti-spike SARS-CoV-2 antibodies, and completed a survey on demographics, occupation, prior SARS-CoV-2 infection and COVID-19 vaccination. We excluded participants who reported SARS-CoV-2 infection ≤90 days prior to enrolment from the vaccine analysis, due to a national policy that people infected in the previous 3 months to postpone vaccination. Using multiple logistic regression analysis, we explored factors associated with being vaccinated and SARS-CoV-2 seropositivity at enrollment. **Results: M**edian age was 44 years (IQR 33-55), 1181 (79%) were female, and 535 (36%) reported prior SARS-CoV-2 infection. 1085 (72%) participants were seropositive, of whom 495 (46%) reported prior infection. In multivariable analysis, factors associated with seropositivity (adjusted odds ratio and 95% CI) were: female (1.40; 1.1-1.9), BMI 25-29.9 (1.4; 1.1-1.8), working in Tirana hospital (1.4; 1.1-1.9), and performing aerosol generating procedures (AGPs) (1.6; 1.3-2.0). Smokers had reduced odds of seropositivity (0.6; 0.4-0.8). 1292 participants were included in the vaccination analysis, 829 (64%) were vaccinated, all with BNT162b2. In the adjusted analysis, being vaccinated was associated with previous influenza vaccination (3.2; 2.0-5.0), patient contact (2.5; 1.2-5.0), and being clinical staff (5.4; 3.2-9.2). Tirana HWs were less likely to be vaccinated (0.3; 0.2-0.4) than other HWs. We found strong interaction between age and sex, with females (<35-years) less likely vaccinated than females >35 year and males (any age). **Conclusion**: AGPs were associated with SARS-CoV-2 seropositivity highlighting the importance of PPE use. HWs vaccinated with seasonal influenza were >3 times as likely to accept COVID-19 vaccine. Identifying reasons for non-vaccination among young female HWs is a priority.

### Poster 194. Insights into SARS-CoV-2 Transmission based on a Household Survey, Georgia

**O. Tarkhan-Mouravi,** A. Machablishvili, K.H. Zakhashvili, M. Shakhnazarova, P. Imnadze
National Center for Disease Control and Public Health, Tbilisi, Georgia
**Background:** COVID-19 pandemic caused by SARS-CoV-2 virus continues to have major impact on public health worldwide. To control virus spread it is crucial to better understand virus spread among population. **Methods:** In order to evaluate factors influencing SARS-CoV-2 transmission among close contacts household (HH) survey was conducted in Georgia between November 1, 2020 and April 1, 2021. Data were collected using special questionnaire. Nasopharyngeal and blood specimens were obtained from study participants to confirm COVID-19 diagnosis by PCR and/or serology tests (IgA/IgG). Index case was defined as a person first tested positive on SARS-CoV-2 in the HH. **Results:** Totally 112 HHs were included in the survey with 112 index cases and 359 household contacts. 74/112 (66%) of index cases were women. Almost 60% of index cases were aged 30-60 years. In around

32% (114/359) of HH members COVID-19 was confirmed by laboratory investigations. 33 out of 114 cases (29%) mentioned having respiratory symptoms prior to index case tested positive on SARS-CoV-2 but did not go to laboratory for testing. In total only 47 out of 114 HH contacts with laboratory confirmed COVID-19 diagnosis had symptoms before or after 14 days contact with index case. 83% of close contacts with COVID-19 shared the living room with the index case. The most HHs (56%) had less than one all kind and less than one bedroom per capita. **Conclusions:** Asymptomatic cases play important role to SARS-CoV-2 spread among close contacts. HH members who during the period of illness, take care of the case, embrace the case, touch the case, share food with the case, eat from the same plate, share a cup with the case, have a shared toilet with the case have got an increased risk of contracting COVID-19 in the HH.

### Poster 195. Revised Interim Guidance on Integrated Sentinel Surveillance for Influenza and SARS-CoV-2

**A. Hammond**[1], S. Hirve[1], D. Pereyaslov[1], M. Medina[1], V. Cozza[1], B. Maharjan[1], W. Zhang[1], I.A. Asante[2], S.O. Badaru[3], C. Bancej[4], S. Bino[5], J.-M. Heraud[6], E.A. Karlsson[7], J. Leite[8], A. Melidou[9], K. Nahapetyan[10], A. Rodriguez[8], S. Walaza[11]

[1]Global Influenza Programme, World Health Organization, Geneva, Switzerland, [2]University of Ghana, Noguchi Memorial Institute for Medical Research, Virology Department, Accra, Ghana, [3]Nigeria Centre for Disease Control, Abuja, Nigeria, [4]Centre for Immunization and Respiratory Infectious Diseases, Public Health Agency of Canada, Ottawa, Canada, [5]Institute of Public Health, Tirana, Albania, [6]Virology Department, Institut Pasteur de Dakar, Dakar, Senegal, [7]Virology Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia, [8]Health Emergencies Department, Pan American Health Organization (PAHO/WHO), Washington, DC, USA, [9]European Centre for Disease Prevention and Control, Solna, Sweden, [10]WHO Regional Office for Europe, Copenhagen, Denmark, [11]Centre for Respiratory Diseases and Meningitis, National Institute for Communicable Diseases of the National Health Laboratory Service, Johannesburg, South Africa and School of Public Health, faculty of Health Sciences, University of Witwatersrand, Johannesburg, South Africa

**Background:** In March 2020, the Global Influenza Surveillance and Response System (GISRS) incorporated SARS-CoV-2 into laboratory diagnostic algorithms for testing specimens from sentinel surveillance to monitor trends in the circulation of influenza and SARS-CoV-2 viruses. Guidance encourages the reporting of this information to the global database (FluNet) managed by the WHO Global Influenza Programme. Interim guidance on integrated surveillance was published in November 2020 and guidance on expediting GISRS genomic surveillance in February 2021. In October 2021, the interim guidance on end-to-end integrated sentinel surveillance was revised. **Methods:** A working group of global, regional and national influenza surveillance and laboratory professionals revisited and updated sections of the interim guidance. The ILI/ ARI/SARI case definition performance for detecting SARS-CoV-2 was reviewed through a literature review and analyses of unpublished data. A compendium of country experiences in integrating surveillance complemented the revised guidance. **Results:** The updated interim guidance includes surveillance objectives closely aligned with those for influenza and are tiered by country priority and capacity. The specificity of ILI for detecting SARS-CoV-2 ranged between 38 and 90% and that for SARI between 31 and 77%. The sensitivity ranged from 20 – 55% for ILI and 33-62% for SARI and thus the use of the ILI/SARI case definitions to monitor trends in both SARS-CoV-2 and influenza continues to be recommended. Updated considerations on sourcing specimens, laboratory algorithms and procedures, monitoring and evaluation and informing policy are also included. **Conclusions:** Two years of the COVID-19 pandemic reinforces the need for longer-term health emergency preparedness. Low seasonal influenza activity in 2020-2021 and frequent detections of zoonotic influenza infections heighten the continued threat of influenza. The revised interim guidance enables agile and resilient surveillance systems which are effective in addressing the concurrent public health needs for influenza and SARS-CoV-2 at the same time.

### Poster 196. Cohort Study to Measure Covid-19 Vaccine Effectiveness among Health Care Workers in Albania (COVE-AL)

**I. Preza**[1], A. Schmid[2], A. Fico[1], I. Hatibi[1], J. Sulo[3], E. Kissling[4], R. Daja[1], A. Vasili[1], M. Kota[1], A. Robo[1], M. Nika[5], A. Strakosha[5], E. Dabaj[6], N. Jani[6], A. Moci[7], A. Xhaferi[1], E. Ndreu[3], S. Sridhar[2,8], J. Rubin-Smith[2], R. Ibrahim[9], D. Lemos[9], M. Rojas[4], P. Jorgensen[9], R. Pebody[9], K. Lafond[10], M. Katz[9], S. Bino[1]

[1]Institute of Public Health, Tirana, Albania, [2]Boston Children's Hospital Global Health Program, Boston, MA, USA, [3]Southeast European Center for Surveillance and Control of Infectious Diseases, Tirana, Albania, [4]Epiconcept, Paris, France, [5]University Hospital Center “Mother Theresa” Tirana, Albania, [6]Durres Regional Hospital, Durres, Albania, [7]Fier Health Care Unit, Fier, Albania, [8]Brigham and Women's Hospital, Boston, MA, USA, [9]

WHO Regional Office for Europe, Copenhagen, Denmark, [10]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** COVID-19 vaccination is critical to reducing the impact of the COVID-19 pandemic. In real-world settings, particularly outside of high-income countries, factors like vaccine storage, transport capacity, and vaccine administration may vary, which can impact vaccine effectiveness (VE). In Albania, an upper middle-income country (UMIC), two doses of Covid-19 vaccine were offered to health workers (HWs) beginning on January 11, 2021. **Methods**: On February 19, 2021, we initiated a prospective 12-month cohort study of COVID-19 VE in HWs in one public university hospital and two public regional hospitals in Albania. All HWs at the three hospitals were invited to participate, regardless of their intention to get vaccinated. At enrolment, participants provided a nasopharyngeal specimen, which was tested for SARS-CoV-2 by RT-PCR, and a serum sample, which was tested for anti-spike SARS-CoV-2 antibodies to determine prior SARS-CoV-2 infection. Participants complete a weekly symptom questionnaire, and symptomatic participants provide a nasopharyngeal swab, which is tested for SARS-CoV-2 by RT-PCR. Serology is collected at enrolment, and months 3, 6, 9, 12. We will measure adjusted VE as (1-Hazard Ratio) x 100 for all participants, and for those with and without previous infection. An interim VE analysis will be conducted in November 2021. **Results**: From 19 February to 7 May 2021, we enrolled 1502 HWs from Tirana [940 (62.6%)], Durres [300 (20.0%)], and Fier [262 (17.3%)] Hospitals. Of these, 841 (56.0%) were vaccinated with one dose of BNT162b2 at enrollment, and 98% were enrolled within 5 days of their first vaccine. The median age was 44 years (range 22-71) and 1182 (78.6%) were female. Overall, 20.3% were doctors, 46.1% were nurses, and 34.2% were in other occupations. At enrolment 1081 (72.0%) participants had evidence of prior SARS-CoV-2 infection by serology, and 18 (1.7%) were SARS-CoV-2-positive by RT-PCR. **Conclusions**: Our prospective COVID-19 VE study will provide useful COVID-19 VE estimates in an UMIC during a 12-month period among HWs who were and were not previously infected with COVID-19.

### Poster 197. Estimating Pfizer-BioNTech COVID-19 Vaccine Effectiveness among Hospitalized Adults >=75 years old in Lebanon Using a Case Control Design, Lebanon, April 1st – May 31st, 2021

**Z. Farah**[1], N. Haddad[1], H.A. Naja[1], M. Saleh[1], P. Mrad[2], N. Ghosn[1]
[1]Ministry of Public Health, Beirut, Lebanon, [2]UNICEF country office, Beirut, Lebanon
**Background:** Soon after COVID19 vaccine introduction worldwide, effectiveness studies were implemented to assess vaccines' performance in real-world settings. In Lebanon, national COVID19 vaccination campaign was launched in February 2021 using Pfizer-BioNTech vaccine and prioritizing elderly, persons with comorbidities and healthcare workers. Our study aims to estimate the post-introduction effectiveness of Pfizer-BioNTech vaccine in preventing COVID-19 hospitalization among ≥75 years in Lebanon. **Methods:** A case-control study design was used. Cases were Lebanese, ≥75 years, diagnosed with COVID-19 by RT-PCR between April and May 2021 and hospitalized. They were randomly selected from COVID-19 surveillance database of the epidemiological surveillance program at the Ministry of Public Health(MOPH). Each case was matched by age and locality to 2 controls. Controls were hospitalized non-COVID-19 patients with negative PCR result admitted for other reasons and randomly selected from MOPH hospital admission database. Data was collected using structured interview and digitalized using DHIS2 tracker program. Univariate and multivariate conditional logistic regression analyses were performed using R version 4.0.4 and R studio version 1.4.1103. Primary and secondary VE analyses accounted for partial vaccination at different time periods. **Results:** 345 cases and 814 controls were recruited. Almost half were females, with a median age of 82 years. 12 cases(4%) and 139 controls(21%) received 2 doses ≥14 days before illness onset or hospitalization, respectively. Univariate analysis showed significant association with gender, general health, chronic medical conditions, socioeconomical status and crowding index. However, none contributed with more than 5% changes in OR in multivariable analysis, based on "change-in-estimate" approach used for selection of confounders. Vaccine effectiveness was estimated at 84%(95%[CI]=70%–91%) for full vaccination. **Conclusions:** Our study showed that Pfizer-BioNTech vaccine is effective in reducing risk for COVID-19–associated hospitalization in older adults. Additional studies are warranted to explore vaccine effectiveness in reducing hospitalization in younger age groups, as well as in reducing covid-19 infections.

### Poster 198. Immunogenicity of Adjuvanted Psoralen-Inactivated SARS-CoV-2 Vaccine in Nonhuman Primates

**A.K. Sundaram**[1,2], D. Ewing[1], Z. Liang[1,2], M. Blevins[3], V. Jani[1,2], Y. Cheng[1,4], P. Sun[1], K Raviprakash[1], S.-J. Wu[1], N. Petrovsky[5], M. Williams[6], J.W. Sanders[3], K.R. Porter[7]
[1]Viral and Rickettsial Diseases Department, Naval Medical Research Center, Silver Spring, MD, USA, [2]Henry M. Jackson Foundation for the Advancement of Military Medicine, Bethesda, MD, USA, [3]Section on Infectious Diseases, Wake Forest School of Health Sciences, Winston-Salem, NC, USA, [4]Leidos, Reston, VA, USA, [5]Vaxine

Pty Ltd., Warradale, SA, Australia, [6]Naval Research Laboratory, Washington, DC, USA, [7]Infectious Diseases Directorate, Naval Medical Research Center, Silver Spring, MD, USA
**Background:** The World Health Organization declared COVID-19, caused by the severe acute respiratory coronavirus-2 (SARS-CoV-2), a global pandemic in March 2020. Although vaccines against COVID-19 targeting the SARS-CoV-2 spike protein are currently available, several SARS-CoV2 variants of concern (VOCs) with mutations in the spike protein have since emerged. Efficacy of these COVID-19 vaccines against the VOCs is not clear. Mutations in the receptor binding domain (RBD) of the spike protein could potentially lead to immune evasion of any of these vaccines. Development of a safe and effective vaccine that protects against SARS-CoV-2 VOCs is a high priority. Inactivated whole-virus vaccines target several viral antigens and can elicit broader immune responses to potentially overcome this issue. **Methods:** We have prepared purified psoralen-inactivated whole-virus SARS-CoV-2 vaccine (SARS-CoV2 PsIV), formulated it with Advax-2 adjuvant and evaluated its immunogenicity in nonhuman primates. First, we evaluated the immunogenicity of SARS-CoV-2 PsIV at 108 particles/dose. We also evaluated prime/boost regimen where the animals received two doses of DNA vaccine encoding the spike protein and a booster dose of SARS-CoV-2 PsIV. Currently, we are evaluating the efficacy and immune responses in NHPs vaccinated with 108 – 5x1010 particles/dose. **Results:** After two doses of 108 particles/dose, SARS-CoV-2 PsIV did not elicit any neutralizing antibody responses in NHPs. However, low titers of Abs against the spike protein RBD and the nucleocapsid protein were present in the sera of NHPs immunized with SARS-CoV-2 PsIV while higher titers of Abs against the spike protein RBD and nucleocapsid protein were present in the sera of NHPs in the prime/boost group. Preliminary results from the ongoing dose escalation study indicates the presence of SARS-CoV-2 neutralizing Abs in sera of animals after one dose at 5x1010 particles/dose. **Conclusions:** SARS-CoV-2 PsIV, with Advax-2 adjuvant, elicits a dose dependent neutralizing Ab response in NHPs. SARS-CoV-2 PsIV also elicits immune responses to more than one antigen (spike and nucleocapsid proteins) suggesting that SARS-CoV-2 PsIV has the potential to protect against COVID-19 from emerging SARS-CoV-2 variants either by itself or as a booster shot to other nucleic acid vaccines.

### Poster 199. Effectiveness of COVID-19 Vaccines in Preventing SARS-CoV-2 Infection Among Frontline Workers Before and During B.1.617.2 (Delta) Variant Predominance — Eight U.S. Locations, December 2020–August 2021

**A. Fowlkes**[1], M. Gaglani[2], Kimberly Groover[3], M.S. Thiese[4], H. Tyner[5], K. Ellingson[6], HEROES-RECOVER Cohorts
[1]CDC COVID-19 Response Team, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Baylor Scott and White Health, Texas A&M University College of Medicine, Temple, TX, USA, [3]Abt Associates, Inc., Rockville, MD, USA, [4]University of Utah, Salt Lake City, UT, USA, [5]St. Luke's Regional Health Care System, Duluth, MN, USA, [6]Mel and Enid Zuckerman College of Public Health, University of Arizona, Tucson, AZ, USA
**Background:** During December 14, 2020–April 10, 2021, data from the HEROES-RECOVER Cohorts,* a network of prospective cohorts among frontline workers, showed that the Pfizer-BioNTech and Moderna mRNA COVID-19 vaccines were approximately 90% effective in preventing symptomatic and asymptomatic infection with SARS-CoV-2, the virus that causes COVID-19, in real-world conditions. This report updates vaccine effectiveness (VE) estimates including all COVID-19 vaccines available through August 14, 2021 and examines whether VE differs for adults with increasing time since completion of all recommended vaccine doses. **Methods:** Health care personnel, first responders, and other essential and frontline workers in eight U.S. locations across six states were tested weekly for SARS-CoV-2 infection by reverse transcription–polymerase chain reaction (RT-PCR)† and upon the onset of any COVID-19–like illness. VE before and during SARS-CoV-2 B.1.617.2 (Delta) variant predominance, which coincided with an increase in reported COVID-19 vaccine breakthrough infections, were compared. **Results:** During Delta variant–predominant weeks at study sites, 488 unvaccinated participants contributed a median of 43 days (IQR = 37–69 days; total = 24,871 days) with 19 SARS-CoV-2 infections (94.7% symptomatic); 2,352 fully vaccinated participants contributed a median of 49 days (IQR = 35–56 days; total = 119,218 days) with 24 SARS-CoV-2 infections (75.0% symptomatic). Adjusted VE during this Delta predominant period was 66% (95% CI = 26%–84%) compared with 91% (95% CI = 81%–96%) during the months preceding Delta predominance. **Conclusion:** During December 14, 2020–August 14, 2021, full vaccination with COVID-19 vaccines was 80% effective in preventing RT-PCR–confirmed SARS-CoV-2 infection among frontline workers, further affirming the highly protective benefit of full vaccination up to and through the most recent summer U.S. COVID-19 pandemic waves.

### Poster 278. Individual Factors associated with Early Uptake of COVID-19 Vaccination among Health Workers in Georgia, 2021

**C.J. McKnight**[1], H. Lucaccioni[2], G. Chakhunashvili[3], M. Rojas[4], T. Zardiashvili[5], P. Jorgensen[6], R. Pebody[6], E. Kissling[4], M.A. Katz[6], L. Sanodze[3]
[1]South Caucasus Hub, World Health Organisation Regional Office for Europe, Tbilisi, Georgia, [2]European Programme for Intervention Epidemiology Training, European Centre for Disease Prevention and Control, Stockholm, Sweden, [3]National Center for Disease Control and Public Health, Tbilisi, Georgia, [4]Epiconcept, Paris, France, [5]Country Office, World Health Organisation, Tbilisi, Georgia, [6]World Health Organisation Regional Office for Europe, Copenhagen, Denmark
**Background:** In Georgia, COVID-19 vaccine roll-out began on March 15 2021 via the COVAX facility mechanism. Health workers (HW) were among the initial priority groups for vaccination. Enrolment data from a cohort study of vaccine effectiveness among hospital-based HWs was analysed to evaluate factors associated with early uptake of vaccine. **Methods:** Study enrolment was offered to clinical and non-clinical staff over 18 years old at six large hospitals in Tbilisi and Batumi, regardless of vaccination status or intention to vaccinate. Data on socio-demographic, clinical, and behavioral factors were collected by written questionnaire. Descriptive and multivariable analysis was done to assess factors associated with vaccination. **Results:** Between March 21 and June 21, 2021, 1331 participants were enrolled, of which 1186 (89.1%) were included with complete data for this analysis, and 101 (7.6%) excluded due to previous SARS-COV-2 infection occurring less than 120 days before enrolment, the minimum time recommended between infection and immunization. The median age was 40 years old, with 11.7% >60 years old and 83.9% female. More than half (51.9%) were nurses/midwives, 19.7% medical doctors, and 28.2% other HW categories. The majority (76.6%) did not report any comorbidities; 44.1% reported a previous laboratory-confirmed SARS-CoV-2 infection. Only 240 (20.2%) were vaccinated. After adjusting for hospital study site, multivariable analysis revealed previous vaccination against influenza (adjusted OR (aOR): 2.7; 95% CI: 2.0-3.7), worker occupation as physician (aOR: 5.7; 95% CI: 4.0-8.1) and providing hands-on care (aOR: 1.8; 95% CI: 1.3-2.4), as strong, independent predictors of early vaccine uptake. A unique variable of safe COVID-19 vaccine perception measured by Knowledge, Attitudes, and Practices scores was significant (aOR: 1.4; 95% CI: 1.3-1.6). Previous infection was negatively associated with receiving the vaccine (aOR: 0.6; 95% CI: 0.4-0.8). **Conclusions:** Low Covid-19 vaccine uptake was observed among HWs enrolled in a hospital-based study during the early stages of the vaccination campaign in Georgia. Occupational category and perception of vaccines likely play an important role in COVID-19 vaccine acceptance. Health promotion campaign directed towards HWs could help addressing these issues to contribute to higher vaccine uptake.

## Zoonotic and Vector-borne Diseases

### Poster 200. Detection of Hantavirus during the COVID-19 Pandemic in Arizona, 2020

**A.P. Dale**[1,2], G. Hecht[2], I. Ruberto[2], G. Adame[2], R. Close[3], S.-J. Snyder[3], N. Lemmon[3], M. Madsen[4], C. Cossaboom[5], T. Shoemaker[5], M.J. Choi[5], D. Cannon[5], I. Krapiunaya[5], S. Zaki[5], J.D. Klena[5], H. Venkat[2,5]
[1]Epidemic Intelligence Service, Division of Scientific Education and Professional Development, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Arizona Department of Health Services, Phoenix, AZ, USA, [3]Indian Health Service, White Mountain Apache Tribe,, Whiteriver, AZ, USA, [4]Coconino County Health Department, Flagstaff, AZ, USA, [5]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: COVID-19 can complicate the diagnosis of respiratory illnesses (e.g., hantavirus pulmonary syndrome [HPS]), because clinical presentations are similar. Exposure to saliva, urine, or feces from hantavirus infected rodents can cause HPS in humans. In March 2020, two deaths with pneumoniae were reported in eastern Arizona. On May 15, postmortem tissue samples were sent to CDC as part of the pandemic response; cause of death determination was delayed pending laboratory results. Pathology review determined a suspicion of hantavirus; tissues for both decedents tested positive on September 15. One patient was coinfected with SARS-CoV-2. These results prompted further public health investigation. **Methods**: After hantavirus identification, federal, state, and local partners collaborated to investigate by medical record review and environmental investigation of patients' residences. **Results**: Patient 1 was a woman aged 25 years living at a fourplex, Residence A. On March 18, she was transported to the emergency department (ED) because of shortness of breath since March 12, and abdominal pain and hemoptysis. Her condition declined and she died on March 19. Patient 2 was Patient 1's son aged 11 years. He lived at Residence B, and frequently visited Residence A. On March 20, after feeling ill for two days, Patient 2 experienced emesis followed by difficulty breathing, a collapse, and unresponsiveness. He was transported to the ED, where he died on March 21. In October 2020, after identification of hantavirus, serum samples were collected from 16 of 17 Residence A occupants. All samples tested negative for hantavirus IgM and IgG. Four traps set at

Residence A had house mice, which are not a hantavirus reservoir. No trapping could be performed at Residence B. **Conclusions**: HPS likely contributed to both patients' deaths. Delays in case identification because of the COVID-19 pandemic caused a 6-month lag in investigation and community education regarding HPS. Although a vector or exposure was not identified, in HPS endemic areas, medical providers should consider both alternative and concurrent diagnoses in patients with respiratory distress syndrome. Timely case investigations should be prioritized for prompt public health action.

### Poster 201. HantaNet: A MicrobeTrace Application for Variant Classification and Outbreak Investigations of Hantaviruses

**R. Cintron-Moret**, S. Whitmer, K.W. Chiu, E. Moscoso, E. Talundzic, M. Mobley, J. Montgomery, J. Klena, E. Campbell, W.M. Switzer
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Hantaviruses cause human infections worldwide and are transmitted by infected rodents that shed virus in urine and feces. Genetic evidence suggests that viral sub-strains are geographically confined, but the lack of an organized clearinghouse for hantavirus data integration and sharing hinders virus surveillance and outbreak response. To overcome this challenge, we developed HantaNet, a new MicrobeTrace application for rapid variant classification of hantaviruses. CDC and public health labs use MicrobeTrace for HIV and COVID-19 cluster detection and response by combining genomic and epidemiologic data for visualization and analysis of transmission networks. **Methods:** We built three reference modules in MicrobeTrace for the nucleocapsid (S), glycoprotein (M) and RNA-dependent RNA polymerase (L) for the hantavirus segmented genome. First, we searched the NCBI nucleotide database for hantaviruses collected since 1982, curated the metadata in Tableau and performed sequence alignments using MAFTT. Hantavirus strain-specific references were selected based on good sequence quality and completeness and were imported into MicrobeTrace to generate clusters with the Tamura-Nei 93 (TN93) nucleotide substitution model. To validate the HantaNet reference modules, the genetic threshold was changed to modify cluster size and specificity compared to published S, M and L gene phylogenies. Transmission networks in HantaNet were validated using contact tracing data and hantavirus sequences collected during a recent Andes virus (ANDV) outbreak in Argentina. **Results:** We determined a TN93 distance threshold of 15-20% (0.15-0.20 nucleotide substitutions/site) was optimal for viral strain-specific clustering in HantaNet. Lower genetic thresholds resulted in specific clustering of ANDV viruses isolated during the 2018-19 outbreak in Argentina. With HantaNet, users can classify, build and visualize outbreak clusters and transmission networks, and save and share datasets. **Conclusions:** HantaNet is a new adaption of MicrobeTrace for the classification of hantaviruses and analysis of transmission networks making it a versatile tool for rapid deployment during surveillance and outbreak response of viruses containing segmented genomes, such as hantavirus and influenza.

### Poster 202. Successful Implementation of a Rapid Screening Tool for Hantavirus Cardio-Pulmonary Syndrome: 5 Years of Experience from a Community Hospital in an Endemic Region

**T.T. Oliver**[1], J.W. Dyal[2], D.L. Talker[1], S. Safaeian[1], D. Yazzie[3], S.M. D'Andrea[1], M. Saleki[1], G.B. Ingall[4], M.J. Choi[2]
[1]Tséhootsooí Medical Center, Fort Defiance, AZ, USA, [2]National Center for Emerging and Zoonotic Infectious Diseases, CDC, Atlanta, GA, USA, [3]Navajo Epidemiology Center, Window Rock, AZ, USA, [4]University of New Mexico Health Science Center, Albuquerque, NM, USA

**Background:** Hantavirus Cardiopulmonary Syndrome (HCPS) due to Sin Nombre virus is a severe respiratory disease with average case fatality rates as high as 35%.[1] Diagnostic options are limited to real-time reverse transcription polymerase chain reaction or serology. However, these tests may not be readily available and can take considerable time to complete. In 2016, Tsehootsooi Medical Center (TMC) on Navajo Nation adapted and implemented a rapid screening test. Initially developed by the University of New Mexico Health Sciences Center, the screen categorizes patients into low, intermediate, and high risk for HCPS based on the presence of five criteria seen on a peripheral blood smear (PBS). **Methods:** The 5-pt screen is initiated by provider request or by reflex due to thrombocytopenia (platelet counts <120,000/µL) for patients presenting to the emergency department. A complete blood count is performed and a PBS slide is created to calculate the 5-pt screen score. A score of 4 or 5 is considered high-risk and serological testing is recommended; 3 is intermediate-risk and a repeat screen in 12 hours is recommended; 1 or 2 is low-risk. **Results:** From May 2016 - September 2020, 189 screening tests were performed on 172 patients. The median score was 1; mean 1.7. High-risk screens constituted 5.8% (11/189) of all screens. Serology results were available for 12 patients. Of these, 5 (42%) were positive by serology. One patient who tested IgM positive received a score of 1/5 on the screen and was considered a false positive. Four patients scored 3/5 on their initial screen and had a second screen performed within 24 hours. The 5pt-screen score increased to 4/5 for

three patients. Of these, one tested positive on hantavirus serology. **Conclusions:** Although hantavirus infection is rare even in high-risk areas, this tool resulted in the rapid detection of four confirmed hantavirus patients. Importantly, the screen was implemented in a resource-limited setting without incurring additional implementation costs.

### Poster 203. Epidemiological and Clinical Characteristics of Acute Dengue Virus Infections Detected through Acute Febrile Illness Surveillance, Belize 2020

**A. Ly**[1,2], R. Manzanero[3], A. Maliga[2], S.M. Gunter[2,4], S.E. Ronca[2,4], E. Zielinski-Gutierrez[5], F. Morey[3], K. Bautista[3], A. Espinosa-Bode[5], B. López[5], L. Cadena[5], R. Chacon-Fuentes[5], T.A. Erickson[2], F. MunozRivas[2], J. Mackey[6], G.H. Morazan[2,3,7], K.O. Murray[2,4] on behalf of the Belize Acute Febrile Illness Surveillance Team
[1]Department of Epidemiology and Environmental Sciences, The University of Texas Health Science Center at Houston, Houston, TX, USA, [2]Department of Pediatrics and National School of Tropical Medicine, Baylor College of Medicine and Texas Children's Hospital, Houston, TX, USA, [3]Belize Ministry of Health and Wellness, Belmopan, Belize, [4]The William T. Shearer Center for Human Immunobiology, Texas Children's Hospital, Houston, TX, USA, [5]Centers for Disease Control and Prevention—Central America Region, Division of Global Health Protection, Center for Global Health, Guatemala City, Guatemala, [6]Emergency Medicine, Department of Medicine, Baylor College of Medicine, Houston, TX, USA, [7]Central Medical Laboratory, Belize Ministry of Health and Wellness, Belize City, Belize

**Background:** Dengue is a global health threat, especially for many low- and middle-income countries in the tropical and subtropical regions. With a tropical climate, high rates of poverty, and lack of resources, Belize is at increased risk for transmission of infectious diseases including dengue. The Acute Febrile Illness (AFI) Surveillance Network in Belize is a countrywide active surveillance program aimed at diagnosing vector-borne, respiratory, and enteric pathogens among patients presenting with new onset fever to 11 participating hospitals and clinics throughout the country. **Methods:** This study describes the epidemiology of dengue virus (DENV) infections in Belize diagnosed through AFI surveillance in 2020. Patients > 60 days of age with a fever of unknown cause were invited to participate. Enrolled patients were interviewed to collect demographic, clinical, and epidemiological information. Blood samples were collected to test for DENV along with other vector-borne pathogens by real-time multiplexed polymerase chain reaction (PCR). Samples positive for DENV were then tested with an additional real-time PCR to determine the DENV serotype. Univariate and multivariate analyses were used to determine risk factors for infection and to describe clinical features of cases. **Results:** Of 894 patients enrolled and PCR-tested for DENV in this period, 44 DENV-positive cases (5%) were identified. All four DENV serotypes were detected, with two cases testing positive for DENV serotype 4, which is the first report of this serotype in Belize since 2004. Among the cases, 29 (66%) were diagnosed in Belize District, which contains Belize City, the nation's largest urban area. Positive cases were detected between January and September 2020, with 39 (89%) diagnosed during the January to April dry season, unlike years prior when cases were more often diagnosed during the wet season. Two cases (5%) were hospitalized, both of whom were infected with DENV serotype 2. **Conclusion:** Active surveillance of DENV among AFI cases provides insight into the epidemiologic and clinical characteristics of DENV in Belize including variation from previous seasonality and presence of all four DENV serotypes. This information is critical to inform public health interventions to mitigate DENV transmission in Belize, where DENV is endemic.

### Poster 204. Descriptive Epidemiology of Dengue Fever Cases in Islamabad Capital Territory (ICT) Pakistan, October 2021

**N. Noreen**[1], I. Naveed[2], S. Dil[3]
[1]Directorate of Central Health Establishments, Islamabad, Pakistan, [2]PIMS, Islamabad, Pakistan, [3]Livestock, and Diary Development Department, Rawalpindi, Pakistan

**Background:** Dengue is a crucial vector-borne viral human disease widespread throughout the tropical region, with local risk variations affected by rainfall, temperature, humidity, and unplanned rapid urbanization. The dengue epidemic is a major public threat in Pakistan since 2005. Dengue fever is now endemic in Pakistan throughout the year circulation of four dengue serotypes with a peak incidence in the post-monsoon period (September-November). The study aimed to analyze the epidemiology of dengue fever cases in Islamabad Capital Territory (ICT). **Methods:** A descriptive analysis was undertaken from January 1 to October 16, 2021. A case of dengue fever was defined as any person resident of ICT with fever and any of these three symptoms: headache, retro-orbital pain, myalgia, arthralgia, rash, hemorrhagic manifestation, leucopenia, abdominal pain, and restlessness. Confirmation was by positive NS1 (Non-structural Protein 1) antigen detection in serum. Population estimates of Islamabad from the Federal Bureau of Statistics were used to calculate attack rates. **Results:** From January 1 to October 2021, a total of 15,790 suspected cases were reported and 1,948 were confirmed. Out of cases 1,469 (75.4%) were males and 06

deaths were reported with a CFR of 0.3%. Out of the total 1948 cases, the majority n=1249 were reported from rural areas of ICT. The mean age was 35.7 years±14.9 (range 73 years). Attack Rate was 16.7/10,000. The most affected age group was from 30 to 45 years of age with an AR of 1.6%. The cases started increasing in September (342), with the highest single-day cases( n=152) reported on 16th October. Area-specific vector control, indoor residual sprays (IRS), and health education activities were initiated by local health authorities to control the outbreak. **Conclusion:** The analysis showed the predominant involvement of adult males. Moreover, the highest number of cases was reported in the post-monsoon months of September and October. Age, gender-specific health education, and area-specific larvae and vector control activities need to be ramped up since pre-monsoon season for effective control.

### Poster 205. Epidemiological Determinants Associated with the Spread of Dengue Fever in Tarlai Kalan Islamabad--September 2021

**N. Noreen**[1], I. Naveed[2], N.U. Khan[3]
[1]Directorate of Central Health Establishments, Islamabad, Pakistan, [2]PIMS, Islamabad, Pakistan, [3]FGPC
**Background:** Dengue has emerged as a vector-borne disease with an increase in the number of cases with multiple outbreaks throughout Pakistan and hospitalization each passing year. It is one of the important public health emergencies of international concern as per International Health Regulations (IHR). In recent years the number of cases in peri-urban areas of Islamabad has increased significantly in the post-monsoon season. In the first week of September 2021, five suspected cases of dengue fever were reported from UC Tarlai (rural population 26,769) to the health department. The study was conducted with objectives to identify risk factors and to recommend control measures. **Methods:** House to house search for active case finding was done from 2nd September to 10th October 2021. A suspected case was defined as “any resident of Tarlai presented with fever and two or more of the following signs and symptoms: headache, retro-orbital pain, joint/bone pain myalgia and petechial rash during 1st September to 10th October 2016”.Confirmation was by positive NS1 (Non-structural Protein 1) antigen detection in serum. Age and sex-matched controls were recruited from the same area. **Results:** Total 1547 houses were surveyed and 399 confirmed cases were identified based on case definition. The mean age was 34.7 years ± 14.5 (range 2-73 years).Mostly affected age group was 31-45 years (Attack Rate 0.52%). The overall attack rate was 1.5%. Male gender being more exposed to vector were predominantly involved n=276 (69.2%). Out of total cases,121(30.3%) had stagnant water inside and around their houses (OR 3.7), indoor larvae (OR 3.1), which was a significant risk factor. Not using repellent (OR 2.7) was an independent determinant of dengue infection (P<0.01 for all). Use of insecticide spray (OR 0.35) and use of full protective clothing (OR 0.11) had a protective effect. **Conclusion:** Dengue has emerged in the poor peri-urban Islamabad typically in post-monsoon seasons reaching a peak during September due to rain-water pooling in and around houses acting as breeding grounds for Aedes aegypti mosquitos. Health education campaigns for improved water storage practices, residual sprays in high-risk areas one month before the transmission period, and community-based environmental management were recommended.

### Poster 206. An Epidemic of Dengue Fever in District West Karachi, July — October 2021

**A. Hussain**, M.A. Syed
Field Epidemiology Laboratory Training Pakistan, Health Department, Government of Sindh, Karachi Pakistan.
**Background:** The first dengue fever case of district West Karachi has been reported by a local private secondary hospital. This outbreak investigation was conducted to evaluate children with serologically confirmed Dengue fever in order to identify common clinical features, progress of disease, grades of severity and outcome of cases to take action and counter the future outbreaks. **Methods:** A descriptive study was conducted on serologically positive children with Dengue fever (DF) admitted in two secondary level hospitals from July to October 2021, in district West Karachi. Demographics, clinical signs and symptoms and laboratory parameters were collected for data analysis utilizing Epi Info version-7. Data was also assessed to identify the common clinical types and grades of infection as classified by World Health Organization. **Results:** A total of 153 children were evaluated in the study. Mean age of children was 9.6 +/- 4.7 years and majority was male (63%). Frequent clinical features included fever (98%), vomiting (72%), abdominal pain (69%) and rashes (67%). Gastrointestinal bleeding (64%) and epistaxis (28%) were commonest haemorrhagic manifestations. Thrombocytopenia (89%), anaemia (55%) and Leucopenia (52%) were common laboratory findings. Leukocyte count improved in 2 to 8 days and Platelet count in 2 to 9 days. Dengue haemorrhagic fever (DHF) was seen in 86 children (56.2%). Majority had Grade-II severity. Case specific fatality was (2.6%). **Conclusion:** Current ongoing outbreak of Dengue infection in district West Karachi have shown slight difference in clinical features, course and outcome of disease compared to epidemics in other regions, thus warranting the need for continuous sero-epidemiological surveillance.

### Poster 207. Eastern Equine Encephalomyelitis in Michigan: Historical Review of Equine, Human, and Wildlife Involvement, Epidemiology, Vector Associations, and Factors Contributing to Endemicity

**M.G. Stobierski**[1], K. Signs[1], E. Dinh[1], T.M. Cooley[2], J. Melotti[2], M. Schalow[3], J.S. Patterson[4], S.R. Bolin[4], E.D. Walker[5]
[1]Michigan Department of Health and Human Services, Lansing, MI, USA, [2]Michigan Department of Natural Resources, Wildlife Disease Laboratory, Lansing, MI, USA, [3]Michigan Department of Agriculture and Rural Development, Lansing, MI, USA, [4]Michigan State University, College of Veterinary Medicine, Veterinary Diagnostic Laboratory, Lansing, MI, USA, [5]Department of Microbiology & Molecular Genetics, and Department of Entomology, Michigan State University, East Lansing, MI, USA
**Background:** Eastern equine encephalomyelitis (EEE) is a mosquito-borne viral disease that is an emerging public health concern in the state of Michigan. Although Michigan has one of the highest incidence rates of EEE in the US, much of the information known about cases in humans, equines, and other animals in Michigan is unpublished. This article summarizes such information and explores spatial trends in the historic distribution of EEE in Michigan. **Methods:** A review of extant case records and literature was conducted to tally known confirmed and suspect cases of EEE in Michigan. Exploratory spatial analyses of historical EEE cases in Michigan began with detection of spatial clustering of cases throughout the state. In addition, we tested the associations of case locations with glacial landscapes and landforms. **Results:** Outbreaks in Michigan have occurred over a span of 80 years, involving only horses in 1942-43 and 1973-1976, and then episodically from 1980 to 2020 and involving horses, humans, and wild and domestic animals. An estimated 1,036 equine cases (confirmed and suspected) and 36 confirmed human cases have occurred, including ten in 2019 (6 deaths) and four in 2020 (two deaths). Human cases ranged in age from 1-81 years; 70% were male, and fatality rate of 34.3%. Equine and human cases occurred from July-October, peaked in August, and cluster in space in southwestern and southeastern lower Michigan. Cases occurred in glacial outwash and ice-contact landscapes in glacial interlobate zones. Virus was recovered from *Culiseta melanura, Coquillettidia perturbans, Aedes* species, and other mosquito species near horse and human case sites. **Conclusions:** Virus isolations or presence of neutralizing antibodies in several passerine species of birds suggest broad EEEV-bird associations. White-tailed deer and other wildlife were also affected. Geographic spread to northern areas of the state suggest expansion of this disease system into unsuspected foci.

### Poster 208. Zika Virus Presentation in Symptomatic Women, Dominican Republic, 2016 in 8 Intervals from 0 to 86 Days

**F.L. Kiechle**[1], A. Freddo[1], H. Quezada[2]
[1]Boca Biolistics, Pompano Beach, FL, USA, [2]Hosp. Gen. de la Plaza de la Salud, Santo Domingo, Dominican Republic
**Background**: Zika virus (ZIKV) is a *Flavivirus* transmitted to humans by *Aedes* mosquitoes. To assess the clinical presentation of ZIKV over time in pregnant (PR) and nonpregnant (NP) symptomatic women during a ZIKV outbreak in Dominican Republic (DR) in 2016, we evaluated the presence of 6 symptoms and 3 lab tests over 8 time intervals (12 to 36 repeat PR or NP patients per interval). The intervals (days) were I-1 (0–7); I-2 (8-15); I-3 (16–23); I-4 (24-31); I-5 (32-39); I-6 (40-47); I-7 (48-55) and I-8 (56-86). **Methods**: Corresponding clinical symptomology reports were reviewed for each PR and NP patient. The Aptima ZIKV assay (Hologic, San Diego, CA) was used to detect ZIKV by transcription-mediated amplification in serum. ZIKV IgG by ELISA (Euroimmun, US; Mountain Lakes, NJ) and ZIKV IgM by MAC-ELISA from CDC performed by the Florida Department of Health, Jacksonville, FL. **Results**: The prevalence of 4 symptoms were less frequent in PR women vs. NP, including fever, severe eye pain, head pain and join and muscle pain (exception I-2 [PR 82% vs. NP 73%]). Conjunctivitis occurred more frequently in PR vs. NP with one exception (I-4 PR 60% vs. NP 66%). Rash occurred with equally high frequency in both groups. ZIKV PCR results were positive for all 8 intervals (87.5% to 72.2%) in PR patients and in NP (55.2% in I-1 to 0.0 to 4.0% in I-2 to I-8). ZIKV IgG and MAC-ELISA IgM were positive with similar frequency in both groups in I-1 to I-8. **Conclusion**: In I-1 to I-8, PR exhibited a lower prevalence of fever, severe eye pain, head pain and joint and muscle pain compared to NP ZIKV symptomatic patients. Conjunctivitis occurred with greater prevalence in PR vs. NP cohorts and rash exhibited a similar frequency for both groups in I-1 to I-8. The finding of ZIKV persistence in high frequency in I-1 to I-8 for PR vs. NP is consistent with Driggers RW, et al. N Eng J Med. 2016; 174: 2142-51. ZIKV IgG and IgM had a similar prevalence in both groups from I-1 to I-8. The results suggest that PR provides protection from clinical symptoms compared to NP during the ZIKV infection cycle in spite of the persistent viremia in PR vs. NP.

### Poster 209. Characterization of Family Planning and Decision-Making after the Zika Virus Pandemic in a Cross-Sectional Survey of Guatemalan Women of Reproductive Age, 2017-2018

**V.J. Hicks**[1], L. Gosdin[1], M. Palmieri[2], M. Sagastume[3], M.E. Jefferds[1], C.Y. Rao[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Instituto de Nutrición de Centro América y Panamá, Guatemala City, Guatemala, [3]Ministerio de Salud Pública y Asistencia Social, Guatemala City, Guatemala
**Background**: In Guatemala, human Zika virus (ZIKV) was first detected in 2015 and annual cases peaked at 3,214 in 2016. By April 2016, congenital ZIKV infection was a known cause of microcephaly and birth defects. Policies and prevention activities launched globally to protect pregnant women from infection. We characterize family planning and decision-making in Guatemalan women of reproductive age before and after the 2016 ZIKV pandemic. **Methods**: The Integrated Reproductive Health and Nutrition Surveillance System (SIVESNU) is a routine survey of women aged 15-49 in Guatemala that provides nationally representative health, nutrition, and sociodemographic data through a multi-stage cluster sampling design. Family planning data from the 2013 to 2018-19 surveys were analyzed. ZIKV-related perceptions and family planning considerations were added to the 2017-18 and 2018-19 surveys. Data were weighted and accounted for the complex sampling. **Results**: The percentage of non-pregnant women of reproductive age using a family planning method modestly increased from 39.6% (95% confidence interval [CI], 36.6%–42.7%) in the 2013 survey to 44.3% (95% CI, 40.9%–47.6%) in the 2018-19 survey (p=0.05). Common methods were hormonal injections, sterilization, condoms, and oral contraceptive pills. In the 2017-18 survey, 71.5% (95% CI, 66.8%–76.2%) of 1729 women were not planning to conceive in the previous 12 months, 8.8% (95% CI, 7.1%–10.6%) did not change their plans due to ZIKV, 19.0% (95% CI, 14.5%–23.5%) were unaware of ZIKV, and 0.7% (95% CI, 0.3%–1.1%) changed their plans due to ZIKV. In the 2017-18 and 2018-19 surveys, of the women desiring a child, none described ZIKV family planning considerations. In the 2017-18 and 2018-19 surveys, 16.3% (95% CI, 10.5%– 22.1%) of 190 pregnant women were educated on how to prevent ZIKV infection during pregnancy from a healthcare provider. **Conclusions**: Though the use of family planning methods increased overall from 2013 to 2018, ZIKV did not appear to influence family planning or decision-making for Guatemalan women of reproductive age. Few women referenced ZIKV in describing current or future family planning. Most pregnant women lacked preventative ZIKV education. In endemic countries, prenatal education programs or campaigns should consider promoting ZIKV awareness and prevention.

### Poster 210. The First Serological Evidence of Zika Virus Transmission based on IgG Antibodies in Ethiopia

**M.M. Tsegaye**[1], B. Beyene[2], A. Abebe[2], S. Yactayo[3], A. Sall[4], M. Eshetu[5], W. Ayele[2], I. Tareke[6], D. Belay[2], A. Lilay[2], A. Alemu[2], E. Alemu[2], A. Kume[2], M. Tefera[2], E. Staples[7], A. Bekele[2], D. Jima[2], A. Kebede[2]
[1]Armauer Hansen Research Institute, Addis Ababa, Ethiopia, [2]Ethiopian Public Health Institute, Addis Ababa, Ethiopia, [3]WHO, Genève, Switzerland, [4]Institute Pasteur, Dakar, Senegal, [5]WHO, Harare, Zimbabwe, [6]WHO, Addis Ababa, Ethiopia, [7]CDC, Atlanta, GA, USA
**Background:** Zika virus, member of the flavivirus family, was generally believed to have a more limited geographical range and to cause few infections annually. This belief has been refuted by the more recent 2015-2016 large Zika virus epidemics. Here, we present the first serological evidence of Zika virus transmission in Ethiopia. **Methods:** The serological evidence of Zika virus transmission was generated as part of the Yellow Fever risk assessment study done in Ethiopia, in which the laboratory investigation required differential diagnosis for flavi viruses, including Zika virus. As a methodological approach, the country was divided in to five Ecological Zones based on factors that affect the distribution and abundance of flavi virus vectors. Serum samples were collected from a total of 1643 study participants and tested for flavi viruses; namely, Yellow Fever, Dengue Fever, Zika and West Nile viruses specific IgG antibody first by enzyme-linked immunosorbent assay (ELISA) and then confirmed by Plaque Reduction Neutralization Test (PRNT). Demographic and laboratory data was analyzed. **Results:** Of the total serum samples tested, 7 (0.43%) showed a confirmed PRNT IgG positivity for Zika virus exposure. Three of the five Ecological Zones of the country (Zones 2 with one case, Zone 3 with 5 cases and Zone 5 with 1 case) showed IgG positivity for Zika virus. Five of the total 7 positive cases (71.4%) were females and the median age for the positive cases was 28. **Conclusions:** This is the first serological evidence showing Zika virus transmission in Ethiopia. Further studies are required to see if there is active circulation in the areas with Zika positivity and understand the risk factors for infection and transmission. This study also warrants existing surveillance system in Ethiopia to consider and follow Zika virus infection more closely.

### Poster 211. Serological Evidence of Zika Virus in Non-human Primates in Kenya

**A. Makio**[1], E. Hunsperger[2], P. Ambala[3], H. Ozwara[3], P. Munyua[2], M. Widdowson[2]

[1]Kenya Medical Research Institute, Nairobi, Kenya, [2]Centers for Disease Control and Prevention, Nairobi, Kenya, [3]Institute of Primate Research, Nairobi, Kenya
**Background:** Zika virus (ZIKV), first described in 1947 is an arthropod borne virus associated with sporadic outbreaks and interepidemic transmission. In 2015, outbreaks of ZIKV in humans in the Americas and Asia were associated with multiple congenital fetal malformations and declared a Public Health Event of International Concern in 2016. Recent studies have implicated non-human primates (NHPs) as the probable reservoir hosts. We tested archived serum samples of NHPs collected from selected locations in Kenya for evidence of neutralizing ZIKV antibodies using a high throughput microneutralization test (MNT). **Methods:** We randomly selected 212 archived serum samples from Institute of Primate Research in Kenya collected between 1992 and 2017. These specimens were tested by MNT. Briefly, two-fold serum dilutions were mixed with titred ZIKV at known concentration, infected onto confluent Vero cell monolayer, and incubated for three days. Following incubation with ZIKV, the cells were fixed and an enzyme-linked immunosorbent assay was performed to detect the presence of anti-ZIKV envelope protein. Optical densities were determined and analyzed using an automated program. Samples with reciprocal neutralizing titers of ≥ 1:20 were considered positive while samples with a titer of < 1:20 were considered negative. **Results:** The 212 serum samples were collected from 87(41.0%) Olive baboons, 69 (32.5%) Vervet monkeys, and 49(23.1%) Sykes monkeys. Half (50.9%) were male and 56.4% were adult. Serum samples had been collected from 7 counties with 31.3% collected from Kajiado and 29.9% from Nairobi county. Thirty six percent of the samples were collected in 2012. We detected ZIKV antibodies in 38 (17.9%; 95% Confidence Interval: 13.3%—23.6%) samples including 16 (18.4%) Olive baboons, 15(19.7%), Vervet monkeys and seven (14.3%)Sykes monkeys. The highest proportion of samples with ZIKV antibodies were from 2012 (59.4%), followed by 2015 (33.5%). Over a third (34.2%) of the positive sera were from Kajiado county. **Conclusions:** These results suggest ZIKV transmission and potential maintenance in nature by NHPs in Kenya.

### Poster 212. External Quality Assessment at Veterinary Laboratories in Armenia

**H. Danelyan**, P. Tumanyan, V. Isahakyan, A. Avagyan
Reference Laboratory of Especially Dangerous Pathogens (RLEDP), Republican Veterinary Sanitary and Phyto-Sanitary Center for Laboratory Services State Non-Commercial Organization (RVPCLS SNCO), Yerevan, Armenia
**Background:** *Brucellosis* is endemic in Armenia and is most often tested by veterinary laboratories. Since laboratory diagnosis is considered a final step in disease diagnosis, proper laboratory quality assurance and quality control become very important. External Laboratory Assessment (EQA) is one of the most effective tools in laboratory Quality Control. National EQA on *Brucella* serology has been implemented at the veterinary laboratories in the country for the first time to identify weaknesses and gaps. **Methods:** The Quality Control Team of RVPCLS conducted the EQA survey with the RLEDP and 10 Marz laboratories of RVPCLS. The EQA panel was prepared from positive and negative cattle serum samples and was tested and confirmed at the RLEDP using RBT, SAT, CFT and ELISA methods. We prepared 7 samples (3 negative and 4 positive samples), out of which 3 positive samples were diluted with respective ratios of 1:0.5, 1:1, 1:1.5 to have samples ranging from weak positive to strong positive. All laboratories used RBT to test the prepared EQA panel. Samples were transported to Marz laboratories observing cold chain conditions. The duration of the survey was set to 14 days. In addition, reserve samples were prepared for QC at RLEDP within 14 days of the survey. The passing score for the survey was set at 100%. A special web interface designed for laboratory EQA in Armenia was used for input and analysis of the survey results. **Results:** Out of 11 participating laboratories, 10 successfully passed the survey, with 1 Marz laboratory that failed by recording all samples as negative. A corrective Action Plan has been developed and implemented by the laboratory that failed to identify, correct, and prevent source(s) of nonconformities. Corrective Actions included the following directions: 1. Reagents used for the survey; 2. SOPs; 3. provision of adequate environment; 4. personnel: skills, knowledge, motivation, etc. **Conclusions:** We conducted the national Laboratory EQA among veterinary Marz laboratories in Armenia for the first time. Since brucellosis is an important issue for Armenia, it is necessary to monitor laboratory diagnostic performance and to implement national EQA on regular basis to provide reliable results through implementation of quality control measures.

### Poster 213. Spatiotemporal Diversity and Population Growth of Powassan Virus in the United States

**N. Raytselis**[1], E. Normandin[2], R. McMinn[3], H.K. Goethert[4], R.M. Robich[5], P.C. Sabeti[6], R.P. Smith[5], S.R. Telford[4], G.D. Ebel[3], A. Piantadosi[7]
[1]Graduate Program in Population Biology, Ecology and Evolution, Emory University, Atlanta, GA, USA, [2]Department of Systems Biology, Harvard Medical School, Boston, MA, USA, [3]Department of Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA, [4]Department of Infectious Disease

and Global Health, Tufts University, North Grafton, MA, USA, [5]Maine Medical Center Research Institute, Vector-borne Disease Research Laboratory, Scarborough, ME, USA, [6]Broad Institute of Harvard and MIT, Cambridge, MA, USA, [7]Department of Pathology, Emory University School of Medicine, Atlanta, GA, USA
**Background:** Powassan virus (POWV) is a tick-borne flavivirus that causes severe encephalitis and is endemic to the Northeast and Midwest United States. Reports of human infection with POWV lineage 2 (Deer Tick Virus, DTV) are increasing, which we hypothesize is partly due to expansion of the viral population. **Methods:** *Ixodes scapularis* ticks were collected across five states (Maine, Massachusetts, New Jersey, New York, and Rhode Island) between 2018 and 2020. RNA was extracted and tested for POWV/DTV by RT-PCR. Positive samples underwent full viral genome sequencing using random hexamer cDNA synthesis, Nextera XT library indexing and amplification, and Illumina sequencing. Viral genome sequencing was also performed from 10 culture supernatants derived from ticks collected in Wisconsin in 2008. Viral genome sequences were assembled using a reference-based approach and were aligned with reference genomes available from GenBank. Maximum-likelihood phylogenetic analysis was performed using IQtree, and time-scaled phylogenetic analysis and estimation of effective population size over time were performed using BEAST. **Results**: We generated 61 new full-length DTV genome sequences directly from ticks and an additional 10 sequences from cultured viruses. Phylogenetic analysis recapitulated the two known lineages of POWV/DTV and provided further support for large-scale geographic population structure of DTV, with separate sub-lineages observed in the Midwest and Northeast U.S. These two sub-lineages diverged 506 years ago (95% HPD 202-873); sequences from the Northeast shared their most recent common ancestor (MRCA) 85 years ago (95% HPD 53-124), and those from the Midwest 58 years ago (95% HPD 36-85). Within the Northeast sub-lineage, many sequences clustered by geographic location, though we also observed closely related sequences that were dispersed across states. Population size was relatively constant over time. **Conclusions:** Our results suggest that POWV lineage 2, DTV, has been present in the U.S. at relatively stable population size for several hundred years. Distinct sub-lineages are present in the Midwest and Northeast, and further work is needed to understand phylogeography at finer scale.

### Poster 214. Development of Novel Molecular and Serological Assays for Chapare Virus, Bolivia, 2019-2021

**R.L. Mafayle**[1], C. Romero[2], M. Morales-Betoulle[3], S. Whitmer[3], C.M. Cossaboom[3], A. Leach[3], K. Patel[3], J.C.A. Ardaya[1], S. Sasias[1], J.R. Guzmán[1], N. Mendoza Loayza[1], J. Mendez-Rico[4], J. Brignone[5], J. Garcia[5], C.-F. Chiang[3], J. Graziano[3], T. Sealy[3], B. Amman[3], J. Towner[3], S.T. Nichol[3], C.F. Spiropoulou[3], T. Shoemaker[3], J. Klena[3], J.M. Montgomery[3]
[1]Centro Nacional de Enfermedades Tropicales, Santa Cruz de la Sierra, Bolivia, [2]Unidad de Epidemiología, Ministerio de Salud, La Paz, Bolivia, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Pan American Health Organization, Washington, DC, USA, [5]Instituto Nacional de Enfermedades Virales Humanas Dr. Julio I. Maiztegui, Pergamino, Argentina
**Background**: In 2004, a novel rodent-borne New World arenavirus (NWA), Chapare virus (CHAPV), was identified as the cause of one fatal case of hemorrhagic fever, known as Chapare hemorrhagic fever (CHHF) in Cochabamba, Bolivia. No additional cases were identified for 16 years. In 2019, we investigated five CHHF cases in North La Paz that involved nosocomial transmission among healthcare workers and a case-fatality rate of 60%. Initially, lack of CHAPV diagnostics was a challenge to surveillance and early case detection. In response, we developed novel molecular and serological assays to improve NWA laboratory capacity in Bolivia. **Methods:** Using next generation sequencing and virus isolation, we identified and characterized the CHAPV strains circulating in humans and rodents in Bolivia in 2019. We designed primers and probes for specific real-time RT-PCR (RT-qPCR) assays for the S and L segments of the virus. Using viral isolates obtained at CDC's biosafety level 4 laboratory and blood specimens from CHHF survivors, we developed enzyme linked immunosorbent assays (ELISA) to detect anti-CHAPV IgM and IgG antibodies. **Results:** After the 2019 outbreak, CHHF surveillance was improved, enabling detection of additional human cases. The novel RT-qPCR detected CHAPV RNA in specimens from 13 patients (N=7 in 2019, N=3 in 2020 and N=3 in 2021). The assays also detected CHAPV in rodent specimens (N=9 in 2019, N =5 in 2020) collected in areas where human CHHF cases lived and worked. The novel serological assays allowed the detection of IgM and IgG seroconversion in CHHF survivors, with positive IgM and IgG antibody titers detected up to 6 months post-symptom onset. **Conclusions:** This collaborative work resulted in the development of novel molecular and serological diagnostic tools for CHAPV and improved surveillance and characterization of viral hemorrhagic fevers caused by NWA in Bolivia. Molecular assays enable detection of active infection, isolation of acutely ill patients, early supportive care, and prevention of secondary, including nosocomial, transmission. Serological assays are valuable to understand the immune response to CHAPV infection and can be used for

serosurveys to assess the CHAPV distribution in Bolivia. Both tools could be used to support CHHF survivor follow-up as part of survivor monitoring and support programs.

## Respiratory Diseases and Influenza

### Poster 215. Enhanced Laboratory Capacity for Molecular Detection of Respiratory Pathogens and Other Infectious Diseases in Public Health Laboratories in Ghana

**B. Nkrumah**[1], M. Owusu[2], G. Acheampong[2], P. Angra[3], D. Sambian[2], P.O. Boadi[2], A.B. Amoasah[2], J.A. Frimpong[1], D.T. Barradas[1]
[1]Division of Global Health Protection, US Centers for Disease Control and Prevention, Accra, Ghana, [2]Centre for Health System Strengthening, Kumasi, Ghana, [3]Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, USA
**Background:** Public health laboratories (PHLs) in Ghana are incorporating molecular techniques for the detection, surveillance, and genotypic characterization of pathogens. These methods are accurate, reliable and provide timely information more quickly than conventional methods. However, molecular diagnostics require dedicated laboratory areas with special requirements that can be daunting for a resource-limited country like Ghana. We describe molecular capacities building of two PHLs to detect respiratory pathogens including SARS-CoV-2. **Methods:** Between October 2020 and September 2021, we designed and implemented strategies to enhance the molecular diagnostic capabilities and capacities of Sekondi and Tamale PHLs in Ghana. Previously, Sekondi PHL was not testing for COVID-19, and Tamale PHL did not have adequate resources for standard laboratory workflow. Implemented project activities included creating distinct rooms for clinical specimen reception, sample preparation including DNA/RNA extractions, master-mix preparation, equipment room for amplification, analysis, and reporting. These laboratories were equipped, resourced, and trained on molecular techniques to detect respiratory and other pathogens including SARS-CoV-2 using real time-PCR. Pre and post assessments were done to determine staff improvement. **Results:** Capacity building for molecular testing was successfully completed in both laboratories. Systematic checks, controls, and test runs were implemented. These PHLs can now detect pathogens of epidemic concern. Both laboratories have been operationalized, commissioned, and handed over to GHS. The Sekondi PHL now has testing capacity of 500 samples per day and serves diagnostic facilities for the Western and Western North regions. The workflow at Tamale PHL has significantly been enhanced to improve quality of laboratory testing. The competency levels of laboratory staff at both PHLs have been improved to over 90%. **Conclusion:** With in-country partnerships and international collaboration, the diagnostic capability and testing capacity of two PHLs have been greatly enhanced for timely detection of pathogens for appropriate action by the introduction of RT-PCR. Our work demonstrates a model that can be applied in other similar settings.

### Poster 216. Incidence of Respiratory Virus Illnesses in a Panama and El Salvador Birth Cohort, 2014–2018

**L.M. Duca**[1], E. Azziz-Baumgartner[1], R. Gonzalez[2], A. Calvo[2,3], N.K. Daniels[1], N. Olson[1], A. MacNeil[1], V. Veguilla[1], R. Domingüez[4], A. Vicari[5], R. Rauda[4], N. Vuong[1], A.M. Ropero[5], N. Sosa[2], J. Armero[4], R. Porter[1], D. Franco,[2] J.M. Pascale[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Gorgas Institute, Panama City, Panama, [3]University of South Florida, Panama, [4]National Institute of Health of El Salvador, [5]Pan American Health Organization
**Background:** The COVID-19 pandemic provided public health officials experience with non-pharmaceutical interventions to prevent contagion, accelerated the production of vaccines, and rekindled interest in the control of respiratory viruses among pediatric populations. We estimate the burden of such viruses among children <2 years. **Methods:** We enrolled neonates of mothers in a pregnancy cohort and followed them for two years. Weekly calls were conducted to ask parents if the child had acute respiratory infection (ARI) defined as cough, rhinorrhea, difficulty breathing, asthenia, anorexia, irritability, or vomiting. Children had nasopharyngeal swabbing performed when they had ARI and fever. Samples were tested for respiratory viruses (influenza, RSV, parainfluenza 1-3, adenovirus, HMPV, and rhinovirus) through singleplex RT-PCR using Centers for Disease Control and Prevention protocols. Incidence was calculated by dividing the number of laboratory-confirmed infections by the person-time each child accrued during weeks when that particular virus was detected through national surveillance and corrected for under-ascertainment among the untested. **Results:** From December 2014 until November 2017, we enrolled 1,561 neonates who contributed 2,165.9 person-years (py). All children developed ARI (2,476 total ARIs). The incidence of RSV ARI among children aged <2 years was 24.7 (95% CI 22.9–26.4) per 100py, higher than incidence for rhinoviruses (20.8, 95% CI 20.7–21.0), parainfluenza 1-3 (14.3, 95% CI 12.4–16.3), HMPV (9.4, 95%

CI 7.8–10.9), influenza (6.0, 95% CI 4.1–7.8), adenoviruses (5.2, 95% CI 5.1–5.3), bocaviruses (1.8, 95% CI 0.7–3.0), and seasonal coronaviruses (1.6, 95% CI 0.6–2.7 per 100py). Children aged <3 months had the highest rates of RSV ARI (74.7, 95% CI 69.6–79.7 per 100py) followed by those aged 3–5 (25.1, 95% CI 20.1–30.0), 6–11 (17.6, 95% CI 13.2–21.9), and 12–23 months (11.9, 95% CI 10.7–13.0 per 100 py). One in ten children <2 years with RSV was hospitalized (2.5 [95% CI 2.1–2.8] per 100py). **Conclusions:** Birth cohort children frequently developed viral ARI before age 2 and a substantive proportion required inpatient care. Such findings suggest the importance of exploring the value of pharmaceutical (e.g., mRNA vaccines) and non-pharmaceutical interventions to mitigate this burden.

### Poster 217. Investigation of an Outbreak of Pertussis in the Health Area of Barkoissi, Oti District, Togo, June 2019

**S. Alidou**[1], R. Kinde-Sossou[2]
[1]Ministère de la santé, Lome, Togo, [2]AFENET-Togo, Lome, Togo
**Background:** In Togo, pertussis is a disease under surveillance, aiming at elimination through vaccination; it is in this context with good vaccination coverage that an epidemic of pertussis cases was reported in the health zone of Barkoissi. The objective of this study is to investigate the pertussis epidemic in the village of Kong and Barkoissi in the Barkoissi health zone, Oti district, Togo, June 2019. **Methods:** We conducted a descriptive study from 11 to 14 June 2019 on pertussis cases occurring in the Barkoissi health area (Kong and Tankatchil). A suspected case of pertussis was defined as anyone living in the Barkoissi health area or anyone presenting with a cough associated with at least one of the following symptoms: rhinitis, coughing fits (attacks), vomiting and subconjunctival haemorrhage. We actively sought out cases in the community and at the Centre Médico-Social Barkoissi. For each case, we collected socio-demographic information, clinical information, information on vaccination status and other information, and we took an oropharyngeal swab in some cases. The information collected was analysed by Epi-info 3.5.4. We calculated proportions, median and ratios. **Results:** A total of 75 cases were recorded, representing an attack rate of 69 cases per 100,000. The index case was a 10-year-old boy, school-going with no notion of travel or regrouping, who had received 3 doses of pertussis vaccine (PENTA). The majority of cases were male, 23 were female. The median age was 8 years with an interquartile range of 2 years. Symptoms observed were coughing fits in all cases, associated with subconjunctival haemorrhage in 26 (34.7%) cases, vomiting in 09.33% (n = 07). Of the children, 70 (93.33%) were school children. Forty-one point three percent (n = 31) of the sick children had been vaccinated against 58.66% not vaccinated (p = 0.5). The majority of vaccinated cases 26 (83.87%) received 3 doses of pertussis vaccine. Oropharyngeal swab was taken from 10 (13.33%) patients and was Gram stained and 08 (80%) cases showed Gram negative bacilli suggestive of Bordetella. **Conclusion:** This study highlighted that pertussis remains a public health problem in Togo and the urgency of finding an adequate strategy to strengthen diphtheria-tetanus-pertussis-hepatitis-Haemophilus influenzae B vaccination coverage. We recommend that the necessary equipment for the confirmation of pertussis be put in place and that the cold chain be strengthened during advanced vaccination strategies.

### Poster 218. Agreement between Different Real time-PCR Assays in Identification of *Bordetella pertussis* in the United States

**M. Cole**, A. Simon, A. Faulkner, T.H. Skoff, M.L. Tondella, M. Williams
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The most common method for detecting *Bordetella pertussis*, the causative agent of whooping cough, is Real-time PCR (RT-PCR). Most U.S. testing is performed at commercial laboratories that use highly sensitive RT-PCR assays that target insertion sequences *481* (IS*481*), which is present in multiple copies of the *B. pertussis* genome, and *1001* (pIS*1001*), a *B. parapertussis*-specific target. Because other pathogenic *Bordetella* species also contain IS*481*, we evaluated possible species misidentification by comparing results of assays used by commercial labs with a more specific multi-target assay. **Methods:** Two large, commercial laboratories sent a convenience sample of de-identified, positive *B. pertussis* or *B. parapertussis* clinical specimens from 49 states collected between 2012 and 2020 to the Centers for Disease Control and Prevention (CDC). Specimens were retested with CDC's multi-target RT-PCR assay, which identifies *B. pertussis, B. parapertussis,* and *B. holmesii* with targets IS*481*, pIS*1001*, and hIS*1001*, respectively, through specific criteria of cycle threshold (CT) values. For *B. pertussis* identification, CDC classified IS*481* CT values <35 as positive, 35 to <40 as indeterminate, and ≥40 as undetected. The additional target ptx*S1* provided confirmation of *B. pertussis*. *B. parapertussis* was identified with p*IS1001* and ptx*S1* CT values <40, and *B. holmesii* with IS*481* and hIS*1001* CT values <40. Specimens with only a ptx*S1* CT value <40 signaled detected *B. bronchispetica.* Specimens that met the criteria for multiple interpretations were considered co-detections. **Results:** Overall, CDC found 87.1% agreement between commercial and CDC assays in

*Bordetella* species identification among 3998 clinical specimens (Cohen's κ =0.52, 95% CI: 0.49-0.56). Agreement was found with CDC's assay for 86.4% (3162/3661) of specimens identified as *B. pertussis* or undifferentiated *B. pertussis/B. holmesii* at the commercial laboratory. For 2940 submitted specimens with IS*481* or IS*1001* <33 CT detected by the commercial laboratories, 95.5% of specimens produced similar interpretations when retested with CDC's assay, indicating good agreement (Cohen's κ =0.77, 95% CI: 0.73-0.80). The majority (389/499, 78.0%) of submitted *B. pertussis* specimens considered discordant were indeterminate for *B. pertussis* in CDC's assay. **Conclusion:** These results show moderate to good agreement between the assays identifying *B. pertussis* at CDC and two, large commercial laboratories in the United States and reinforce the validity of large-scale commercial *B. pertussis* PCR testing across the United States.

### Poster 219. Pneumococcal Carriage in Burkina Faso 4 and 7 Years after 13-Valent Pneumococcal Conjugate Vaccine Introduction and before a Schedule Change

**L. Childs**[1], L. Kaboré[2], F. Tarbangdo[3], S. Ouangraoua[4], I. Medah[5], I. Ouedraogo[5], A. Sidibe[5], R.L. Zoma[3], H.F. Aké[3], M. Kobayashi[6], L. McGee[6], T. Pilishvili[6]
[1]National Foundation for the Centers for Disease Control and Prevention, Inc., Atlanta, GA, USA, [2]Agence de Médecine Préventive, Ouagadougou, Burkina Faso, [3]Davycas International, Ouagadougou, Burkina Faso, [4]Centre Muraz, Bobo-Dioulasso, Burkina Faso, [5]Ministère de la Santé, Ouagadougou, Burkina Faso, [6]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The 13-valent pneumococcal conjugate vaccine (PCV13) was introduced in Burkina Faso using three primary doses and no booster (3+0) in 2013. PCV13 led to reductions in disease and vaccine type (VT) carriage in vaccinated children but indirect effects were limited. Emerging evidence suggests a schedule of two primary doses with a booster dose (2+1) may have a larger impact by providing a longer duration of protection against VT carriage. In June 2021, Burkina Faso changed the PCV13 schedule from 3+0 to 2+1. We implemented two pneumococcal carriage studies in Burkina Faso in 2017 and 2020 to evaluate VT carriage 4 and 7 years after PCV13 introduction and prior to the schedule change. **Methods:** We conducted cross-sectional, age-stratified pneumococcal carriage studies in Bobo-Dioulasso among healthy children aged 1-59 months and 5-14 years and adults. Nasopharyngeal (all ages) and oropharyngeal (≥5 years) swabs were collected, and pneumococcal colonization was identified by culture. Pneumococcal serotypes were identified by polymerase chain reaction (PCR), and a subset of isolates were tested by Quellung reaction. We evaluated overall and VT pneumococcal carriage and serotype distribution by age. **Results:** We enrolled 604 and 601 children <5 years in 2017 and 2020, respectively, and 401 older children and adults in each study. From 2017 to 2020, overall pneumococcal carriage decreased from 61% (95% CI: 57, 64) to 56% (53, 59; p=0.03) among all ages. In both studies, overall pneumococcal carriage was higher in children <5 years (2017: 69% 2020: 66%) and older children (2017: 64% 2020: 52%) when compared to adults (2017: 37% 2020: 27%) (2017, 2020 p<0.0001). Among those colonized with pneumococci, the proportion of VT strains remained unchanged in 2020 compared to 2017 in all age groups and ranged from 25 – 44% by age group. In 2017 and 2020, the most common VT strains in children <5 years old were 19F (9%) and 6A/6B (5%), and the most common non-VTs were 35B (9%) and 15B/15C (7%). **Conclusions:** VT strains continue to colonize children <5 years, older children, and adults seven years after PCV13 introduction in Burkina Faso. If a booster dose further decreases VT colonization, the PCV13 schedule change has the potential to lead to larger public health benefits through both direct and indirect effects.

### Poster 220. Hepatorenal Syndrome is Associated with Poor Outcomes in Patients Admitted with Pneumonia

**H. Laswi**[1], I. Maghari[1], A. Alhabhbeh[2], M. Al-Khateeb[3]
[1]John H. Stroger Hospital of Cook County, Chicago, IL, USA, [2]East Tennessee State University, Johnson City, TN, USA, [3]Lincoln Medical Center, Bronx, NY, USA
**Background:** Both pneumonia and cirrhosis pose a significant burden on the healthcare system. Hepatorenal syndrome (HRS) is common in patients with cirrhosis and is associated with poor prognosis. The goal of this study is to examine the effect of HRS on outcomes of cirrhotic patients admitted with pneumonia. **Method:** The nationwide inpatient sample databases (2016 – 2018) was utilized. The International Classification of Diseases, 10th Revision (ICD-10) codes were used. All patients with a secondary diagnosis of cirrhosis admitted with pneumonia were included. The primary outcome was in-hospital mortality. Secondary outcomes included: length of stay (LOS), total hospital charges (THC), and the development of respiratory failure. Multivariate regression analysis was used to adjust for confounders. **Results:** 33394 patients with cirrhosis and a primary diagnosis of pneumonia were included in the study. On multivariate analysis, the development of HRS was associated with 2.7 day increase in mean LOS (P=0.020) and 51905 USD increase in mean THC (P=0.026). Moreover, HRS was associated with 4.8-

fold increase in the inpatient mortality (P=0.000) and 2.1-fold increase in the risk of respiratory failure (P=0.003). **Conclusion:** The development of HRS in patients admitted with a primary diagnosis of pneumonia was associated with worse outcomes in terms of LOS, THC, inpatient mortality, and the development of respiratory failure.

### Poster 221. Early Re-emergence of Invasive Pneumococcal Disease in Germany During the Summer of 2021

**S.R. Perniciaro**[1], M.P.G. van der Linden[2], D.M. Weinberger[1]
[1]Yale School of Public Health, New Haven, CT, USA, [2]University Hospital RWTH Aachen, Aachen, Germany
**Background:** The incidence of invasive pneumococcal disease (IPD) decreased worldwide in 2020 and through the first quarter of 2021, concurrent with non-pharmaceutical interventions (NPIs) intended to stymie transmission of SARS-CoV-2. In 2021, the stringency of these NPI strategies have varied locally. We investigated age- and serotype-specific variations in IPD incidence in Germany in relation to local trends in mobility and stringency of NPIs. **Methods:** IPD cases through July 31, 2021, were stratified by age group, vaccine serotype, or geographic location. IPD surveillance data in 2020-2021 were compared with: 1) IPD surveillance data from 2015-2019, 2) mobility data during 2020 and 2021 and 3) NPI stringency data in 2020 and 2021. **Results:** IPD incidence was lower than expected from March 2020 through mid-2021. IPD increased over baseline values (a 9% increase over the average monthly values for 2015-2019) beginning in June 2021 in children 0 to 4 years old and continued increasing during the summer of 2021. Children 5 - 14, adults aged 15 - 34 and adults ≥80 years showed increases over baseline values starting in July 2021 (200%, 15%, 20%, respectively). Age distribution and the proportion of vaccine serotypes remained comparable to previous years despite lower overall case counts in 2020 and 2021. Serotype 3 remained the most common cause of adult IPD throughout the study period, while in children <15, serotype 10A was most common pre-pandemic and serotype 23B was most common during the SARS-CoV-2 pandemic. IPD incidence returned to baseline values in 6 out of 16 federal states by July of 2021. The percent decrease in IPD incidence (as compared to the previous five years) correlated with percent decreases in transit, work and retail mobility (Spearman's ρ: 0.82 (95% CI: 0.53, 0.96); 0.69 (0.28, 0.89); 0.85 (0.56, 0.96), respectively, and with NPI stringency (Spearman's ρ:-0.74, 95% CI: -0.93, -0.36). **Conclusions:** IPD decreased steeply and uniformly concurrent with nonpharmaceutical interventions (NPIs) adopted as part of SARS-CoV-2 pandemic response efforts in 2020. Proportions of vaccine serotypes remained largely consistent throughout 2020-2021. Potential disruptions to routine immunization programs could have unknown consequences, further complicated by the arrival of new pneumococcal vaccines.

### Poster 222. Validation of Case-Based Bacterial Meningitis Data in Burkina Faso from 2018 to 2020

**T.F. Tarbangdo**[1], J.L. Kibler[2], R. Novak[2], S. Ouattara[3], I. Yaméogo[3], G. Sawadogo[1], F. Kambou[3], F. Acho[1], Y. Donnou[1], D.O. Konaté[1], M. Tamboura[3], K. Ouattara[3], A. Da[3], A. Kaboré[3], S. Palm[3], H.F. Ake[1]
[1]Davycas International, Ouagadougou, Burkina Faso, [2]Division of Bacterial Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Ministère de la Santé, Ouagadougou, Burkina Faso
**Background:** Burkina Faso, a Sub-Saharan country situated in the meningitis belt of Africa, experiences a high burden of bacterial meningitis each year. Thus, strong case-based surveillance in Burkina Faso is critical to provide evidence for new vaccine introduction, monitor existing vaccine impact and examine on-going meningitis epidemiology. The objective of this analysis was to outline the importance of data validation in creating a high-quality case-based dataset for subsequent research, analysis, and planning. **Methods:** Using the national real time case-based surveillance (CBS) and aggregate data management systems, meningitis surveillance data were collected for each district across Burkina Faso from 2018 to 2020. National, district and laboratory health staff conducted data validation for all three years in 2021. Data validation consisted of data review and comparison with case investigation forms and laboratory registries to assess data completeness, consistency, accuracy, and cleanliness. Case-based surveillance was compared with aggregate meningitis case counts by year and district. Completeness of several key variables, such as 'Age', 'Sex' and 'Outcome', was assessed to understand improvements after data validation. **Results:** After validation, 6,316 total cases were recorded in the case-based dataset for 2018-2020 (97.7% of aggregate case total). 523 missing cases were added to the CBS data and 733 duplicates were removed during validation. Completeness for key variables increased from 47-100% before validation to 95-100% afterwards. Validation of laboratory resulted in an additional 58 cases being classified as confirmed cases and completeness of the final result data improved by 24.7%. **Conclusions:** Validation of these data significantly enhanced the completeness and quality of data collected. The national exercise of validating case-based data is an effective method to assess the sensitivity of CBS data systems, improve meningitis surveillance, and better target data management activities. While resource intensive, the process results in high-quality data that serves as a foundation

for strong comprehension of bacterial meningitis epidemiology and can inform effective resource allocation and future vaccine development. This exercise can serve as a valuable model for countries across the meningitis belt.

### Poster 223. Laboratory Diagnosis of Bacterial Meningitis by Direct Detection, Serotyping, and Next Generation Sequencing: How 10 Years of Testing in New York State Has Evolved to Improve Laboratory Diagnosis and Public Health

**J. Long**[1], K. Mitchell[1], J. Edwards[1], D. Wroblewski[1], E. Luke[1], M. Dickinson[1], A. Kidney[1], N. Dumas[1], P. DelRosso[2], M. Dorsinville[2], M. Antwi[2], D. Weiss[2], E. Nazarian[1], R.J. Limberger[1], K. Musser[1], T.A. Halse[1]
[1]Wadsworth Center, New York State Department of Health, Albany, NY, USA, [2] Bureau of Communicable Disease, New York City Department of Health & Mental Hygiene, New York City, NY, USA
**Background:** Diagnosis of bacterial meningitis is difficult. While culture is the gold standard, the success of isolation is reduced once antibiotic treatment is initiated. Molecular testing and next generation sequencing (NGS) can rapidly determine the causative agent even when no viable organism is present. The Wadsworth Center has provided molecular testing to identify causative agents of bacterial meningitis since 2005 and is continually exploring new methods to identify these agents. **Method:** Our laboratory utilizes a molecular testing algorithm to detect bacteria that cause meningitis. Real-time PCR targeting bacterial agents known to cause meningitis and their serogroup/serotype are utilized to detect the presence of *Neisseria meningitidis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Streptococcus agalactiae* DNA in cerebrospinal fluid (CSF) and blood samples. If negative by real-time PCR, 16S rDNA Sanger sequencing can be performed upon request. Additionally, a retrospective NGS study was performed on CSF samples that previously tested negative by real-time PCR. **Results:** Over a 10-year period we tested 831 CSF and blood samples from 634 patients. Bacterial DNA was detected in 223 (27%) samples from 183 patients (29%) and 55% of those positive were further serogrouped/serotyped. Among 131 paired specimens (CSF and blood received from the same patient) 88% of the positive pairs had a lower CT value for CSF than blood. Additionally, 16S rDNA Sanger sequencing identified bacteria in 16% of samples negative by real-time PCR while NGS identified bacteria in 26%. **Conclusions:** In ~30% of the culture-negative samples, this algorithm was successful for providing rapid results used to inform decisions regarding treatment, prophylaxis, surveillance, and infection control. Serogroup/serotype determination in culture-negative specimens can inform disease burden estimates and vaccine preventable disease surveillance. Data suggests CSF is the preferred sample type but blood should also be tested in cases where CSF volume is insufficient, unavailable, or meningococcal bacteremia alone is suspected. Results of the NGS study suggest it is a more sensitive test than 16S rDNA sequencing and may be useful in identifying emerging infectious agents which cause bacterial meningitis.

### Poster 224. Estimates of the National Burden of Respiratory Syncytial Virus in Kenyan Children Aged under 5 Years, 2010-2018

**B.O. Nyawanda**[1], N. Murunga[2], N.A. Otieno[1], G. Bigogo[1], J.U. Nyiro[2], D.J. Nokes[2], P. Munywoki[3], G.O. Emukule[3]
[1]Kenya Medical Research Institute, Center for Global Health Research, Kisumu, Kenya, [2]Kenya Medical Research Institute-Wellcome Trust Research Programme, Kilifi, Kenya, [3]U.S. Centers for Disease Control and Prevention, Nairobi, Kenya
**Background:** Respiratory syncytial virus (RSV) is among the leading causes of viral pneumonia worldwide. Establishing RSV-associated morbidity and mortality is important in informing the development, delivery strategies and evaluation of impact of interventions. **Methods:** Using data collected during 2010-2018 from population-based surveillance studies in western Kenya and the Kilifi Health and Demographic Surveillance Study, we estimated age-specific base rates of acute respiratory illness (ARI), severe acute respiratory illness (SARI - defined as hospitalization with cough or difficulty breathing with onset within the past 10 days) and SARI-associated deaths. We extrapolated the base rates to other regions of Kenya while adjusting for risk factors of ARI and healthcare seeking behaviour, and finally applied the proportions of RSV positive cases to these rates to obtain regional age-specific rates of RSV-associated ARI and SARI. We applied age-specific RSV case fatality ratios on SARI to obtain estimates of RSV-associated in- and out-of-hospital deaths. **Results:** Among Kenyan children aged <5 years, the annual incidence of outpatient and non-medically attended RSV-associated ARI was 206 (95% Credible Interval, CI; 186-229) and 226 (95% CI; 204-252) per 1,000 children, respectively. The annual rates of hospitalized and non-hospitalized RSV-associated SARI were 349 (95% CI; 303-404) and 1,077 (95% CI; 934-1,247) per 100,000 children respectively. The estimated annual number of in- and out-of-hospital deaths associated with RSV infection in Kenya were 539 (95% CI; 420-779) and 599 (95% CI; 420-839), respectively. Children aged <1 year had the highest burden of RSV; 302 (95% CI; 272-336) per 1,000 children for outpatient ARI, and 1,303 (95% CI; 1,122-1,507) and 35 (95% CI 24-51) cases per 100,000 children for hospitalized SARI and in-hospital deaths, respectively. **Conclusion:** Our findings suggest a substantial disease burden due to RSV infection, particularly among younger

children. Prioritizing development and use of maternal vaccines and affordable long-lasting monoclonal antibodies could help in reducing this burden.

### Poster 225. Significance of the WHO EQA 2019-2020 for the Molecular Detection of Respiratory Syncytial Virus

**S. Jackson**[1], T. Williams[2], I. Barr[3], M. Zambon[4], M. Viegas[5], A. Von Gottberg[6], S. Hirve[1], J. Bhiman[5], E. Vega[7], B. Whitaker[7], S. Rughooputh[8], S. Bi[8], W. Zhang[1] ([1]on behalf of the WHO RSV Surveillance Network; A. Ahad, M. Albeaini, L. Ariqi, A. Barakat, N. Bastien, E. Baumeister, P. Couto, P. Coyle, B. Darmaa, N. Dia, P. Dussart, J. Ellis, R. Fasce, M. Gazo, K. Herve, B. Herring, F. Inbanathan, R. Jha, J. Leite, V. Lacoste, M. Lumandas, J. Moyes, A. Naguib, Nahapetyan, J. Namulondo, N. Razanajatovo, P. Okada, H. Oumzil, M. Pisareva, V. Potdar, M. Siqueira, P. Tang, A. Tivane, A. Vicaria, P. Wijesinghe, E. Yanndoko)
[1]World Health Organization, Geneva, Switzerland, [2]University of Edinburgh, Edinburgh, UK, [3]Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, [4]Virus Reference Department Respiratory Virus Unit, Public Health England, Colindale, London, UK, [5]Hospital de Niños Dr Ricardo Gutiérrez, Buenos Aires, Argentina, [6]National Institute for Communicable Diseases, Johannesburg, South Africa, [7]Centers for Disease Control and Prevention, Atlanta, USA, [8]UK NEQAS for Microbiology, Health Security Agency, Colindale, UK
**Background:** This study describes the second of the World Health Organization (WHO) External Quality Assessment (EQA) 2019-2020 for the molecular detection of Respiratory Syncytial Virus (RSV). Regular updated EQA's are necessary to ensure a high level of accuracy. **Methods:** This EQA 2019-20 assessed laboratory proficiency for the detection and typing of RSV. The panel included 12 samples (10 RSV positives and two negatives) characterized and matched against Centers for Disease Control and Prevention (CDC) and the Victorian Infectious Diseases Reference Laboratory (VIDRL) primer/probe sets. One historical and nine recent RSV viruses collected from 2015-2019 were distributed by UK NEQAS to 28 laboratories in 25 countries. Countries were given the option to use RSV singleplex or multiplex RT-qPCR assays provided by the CDC, USA or VIDRL Australia, commercial assays or in-house assays. **Results:** Panel RSV-A isolates belonged to the ON1 lineage within the GA2 genotype and RSV-B to genotype BA. Analysis of whole genome sequences (WGS) of isolates and WGS on GISAID EpiRSV showed no mismatches likely to impact the effectiveness of the CDC and VIDRL primer/probe sets. Twenty-eight laboratories submitted detection results and 26 reported for typing. Samples were correctly identified in 99% for detection (N=336) and typing (N=260). Severn laboratories reported Ct values above two standard deviations from the mean Ct value of reporting laboratories. Performance in RSV EQA 2019-20 improved compared to 85.7% all correct detection results of RSV EQA 2016-17. **Conclusions:** The RSV EQA 2019 for countries participating in Phase II of the WHO Global RSV Surveillance Program, showed that the laboratories performed at high standards. Varying mean Ct values indicated possible decreased sensitivity of some methods Accurate testing of clinical samples is fundamental to the WHO RSV Surveillance that aims to better understand the impact and burden of RSV globally particularly in vulnerable age groups.

### Poster 226. RSV Surveillance in the Context of the COVID-19 Pandemic

**S. Hirve**[1], I. Barr[2], S. Jackson[1], E. Vega[3], M. Viegas[4], A. Von Gottberg[5], T. Williams[6], M. Zambon[7], W. Zhang[1] on behalf of the WHO RSV Surveillance Network (A. Ahad, M. Albeaini, C. Bancej, E. Baumeister, P. Coyle, B. Darmaa, N. Dia, J. Ellis, R. Fasce, M. Gazo, K. Herve, R. Jha, V. Lacoste, M. Lumandas, J. Moyes, A. Naguib, J. Namulondo, P. Okada, H. Oumzil, M. Pisareva, V. Potdar, M. Siqueira, A. Tivane, .E Yanndoko)
[1]World Health Organization, Geneva, Switzerland, [2]Peter Doherty Institute for Infection and Immunity, Melbourne, Australia, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Hospital de Niños Dr Ricardo Gutiérrez, Buenos Aires, Argentina, [5]National Institute for Communicable Diseases, Johannesburg, South Africa, [6]University of Edinburgh, Edinburgh, UK, [7]UK Health Security Agency, Colindale, UK
**Background:** With the prospects of RSV becoming a vaccine preventable infection, WHO initiated a sentinel surveillance strategy that leverages the capacities of the Global Influenza Surveillance and Response System (GISRS) in 25 countries across all six WHO regions to better understand seasonality, global circulation, disease burden and age groups at risk for RSV infection. Combined with establishing the infrastructure for a molecular epidemiology approach based on RSV whole genome sequencing, the overall aim of the program is to develop the evidence-base to inform guidelines for the introduction of RSV vaccines and long-acting monoclonal antibodies. **Methods:** Each country used an extended SARI or ARI case definition that did not require fever as an entry criterion and included apnea or sepsis in infant less than 6 months age, to test 400 upper respiratory specimens all year round, for RSV detection and typing by using RT-PCR assays in children less than 2 years age. **Results:** Like for influenza, the COVID-19 pandemic resulted in significant disruptions to RSV surveillance as resources were repurposed, fewer specimens available as patients avoided seeking care or were diverted to designated COVID-19

testing and treatment facilities. Sixteen of the 25 countries sustained RSV surveillance with temporary disruptions in 2020, and seven countries shared RSV positive samples with reference laboratories for whole genome sequencing. RSV circulation was low in 2020 with few RSV hospitalizations as countries implemented strict mitigation measures to control the spread of SARS-CoV-2 but resurged in 2021 with atypical seasonal patterns according to the lifting of the restrictive mitigation measures in each country. **Conclusions:** It is critical to maintain and strengthen RSV surveillance to monitor transmission dynamics, age shifts in burden over the next few years to inform RSV vaccine development and introduction and prepare for different scenarios for RSV circulation as the pandemic progresses and beyond.

### Poster 227. Risk Factors for Diphtheria in Sana'a Capital, Yemen, 2019: A Matched Case-Control Study

**A.A. Nassar**[1], M.A. Al-Amad[2]
[1]Ministry of Public Health and Population, Sana'a City's Public Health and Population Office, Sana'a, Yemen, [2]Ministry of Public Health and Population, Field Epidemiology Training Program, Sana'a, Yemen
**Background:** The ongoing war in Yemen has caused the collapse of the health system, which led to low immunization coverage and re-emerge of diphtheria in 2017 and is still reported to the end of 2019. Sana'a city is one of the most affected governorates, therefore this study aims to identify diphtheria risk factors related to sociodemographic, immunization and household status, and source of infection in Sanaa city. **Methods:** A retrospective matched case-control study design (1:2 ratio) was conducted. Case defined as any person who met the WHO definition of confirmed diphtheria living in Sana'a city during Jan.-Nov. 2019. Control was any person did not have a history of diphtheria infection, living in the same neighborhood and matched with case by age and sex. A structured questionnaire was used for collecting data. Epi info version 7.2. was used for data entry and analysis. Univariate and multivariate conditional logistic regression with an odds ratio (OR) and 95% confidence intervals (CI) were calculated. *P* value < 0.05 was considered as the cut point for significance. **Results:** A total of 76 confirmed cases and 152 controls were enrolled. The median age (interquartile range) of cases and controls was 12.5 years (22 years) and 13 years (22 years), respectively. 60% of participants were female. Multivariate analysis shows that there were significant associations between diphtheria infection and shared a bedroom with ≥ 2 persons (OR= 2.3; 95% CI: 1.1 – 5.0), non-vaccination (OR= 2.3; 95% CI: 1.1 – 4.9) and contact with diphtheria case (OR= 8.9; 95% CI: 2.4 – 32.3). **Conclusions:** This study emphasizes the vaccination, not sharing a bedroom with ≥ 2 persons, and isolation of cases to prevent contact with diphtheria cases were the main important measures for protecting the community from diphtheria. Raising community awareness regarding vaccination, transmission and preventive measures is recommended.

### Poster 228. Cause-specific Student Absenteeism Monitoring In K-12 Schools for Detection of Increased Influenza Activity in the Surrounding Community - Dane County, Wisconsin, 2014-2020

**J.L. Temte**[1], S. Barlow[1], M. Goss[1], E. Temte[1], A. Schemmel[1], C. Bell[1], E. Reisdorf[2], P. Shult[2], M. Wedig[2], T. Haupt[3], J.H. Conway[4], R. Gangnon[5], A. Uzicanin[6]
[1]Department of Family Medicine and Community Health, University of Wisconsin School of Medicine and Public Health, Madison, WI USA, [2]Wisconsin State Laboratory of Hygiene, Madison, WI USA, [3]Division of Public Health, Wisconsin Department of Health Services, Madison, WI USA, [4]Department of Pediatrics, Division of Infectious Diseases, University of Wisconsin School of Medicine and Public Health, Madison, WI USA, [5]Department of Biostatistics, University of Wisconsin School of Medicine and Public Health, Madison, WI USA, [6]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Schools are primary venues of influenza amplification with secondary spread to communities. We assessed K-12 student absenteeism monitoring as a means for early detection of influenza activity in the community. **Methods:** Between September 2014 and March 2020, we conducted a prospective observational study of all-cause (a-TOT), illness-associated (a-I), and influenza-like illness–associated (a-ILI) absenteeism within the Oregon School District (OSD), Dane County, Wisconsin. Absenteeism was reported through the electronic student information system. Students were visited at home where pharyngeal specimens were collected for influenza RT-PCR testing. Surveillance of medically-attended laboratory-confirmed influenza (MAI) occurred in five primary care clinics in and adjoining OSD. Poisson general additive log linear regression models of daily counts of absenteeism and MAI were compared using cross correlation analysis. **Results**: Influenza was detected in 723 (30%) of 2,378 visited students, and in 1,327 (27%) of 4,903 MAI patients. Over the combined six influenza seasons, a-ILI was significantly correlated with MAI in the community (r = 0.57; 95% CI: 0.53—0.63) with a one-day lead time and a-I was significantly correlated with MAI in the community (r = 0.49; 0.44-0.54) with a 10-day lead time, while a-TOT performed poorly (r = 0.27; 0.21—0.33), following MAI by six days. **Conclusions:** Surveillance using cause-

specific absenteeism was feasible and performed well over a study period marked by diverse presentations of seasonal influenza. Monitoring a-I and a-ILI can provide early warning of seasonal influenza in time for community mitigation efforts.

### Poster 229. Clinical and Epidemiological Profile of Hospitalized Influenza-Associated Pneumonia Cases Among Older Adults in India – A Multi-Center Study

**S. Kanungo**[1], B. Manna[1], A.K. Chakrabarti[1], K. Sarda[1], A.O. Prabhakaran[2], R. Kumar[3], R. Amarchand[3], A. Choudekar[3], G. Gopal[3], P. Rajkumar[4], G. Kumar[4], S.D. Bhardwaj[5], V. Potdar[5], K.E. Lafond[6], E. Azziz-Baumgartner[6], S. Saha[2], L. Dar[3], A.Krishnan[3]
[1]National Institute of Cholera and Enteric Diseases, Kolkata, India, [2]US Centers for Disease Control and Prevention-India Office, New Delhi, India, [3]All India Institute of Medical Sciences, New Delhi, India, [4]National Institute of Epidemiology, Chennai, India, [5]National Institute of Virology, Pune, India, [6]US Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Pneumonia is one of most common causes of hospitalization and deaths among older adults; however, in India it's unclear what fraction might be associated with influenza. **Methods:** From December 2019 to March 2020, we conducted surveillance for pneumonia among older adults (≥60 years) within 48 hours of hospitalization in 16 secondary and tertiary level public and private hospitals in four locations in India. Pneumonia was defined as presence of cough along with dyspnea or chest pain, a respiratory rate of >20 breaths/minute, and either measured fever or a reported symptom complex of fever, sweating, headache, and myalgia. Trained nurses collected demographic and clinical data of participants and took nasal/oropharyngeal specimens for influenza testing using RT-PCR. Cases were followed for 30 days after hospital discharge. We used multivariable logistic regression using factors showing significant association in univariate analysis to estimate adjusted odds ratios to identify risk factors for ICU admission and death. **Results:** We enrolled 1109 pneumonia cases with 112 from secondary and 997 from tertiary care hospitals; among these, we completed 30-day follow-up among 1018. The mean age of participants was 70 years (SD: ± 8), and 38% (425) were female. Forty percent (445) were admitted to the ICU. Of all pneumonia cases, 134 (12.3%) tested positive for influenza, of which 62 (46.3%) required ICU admission. Pneumonia case fatality was 16.4% (95% CI 14.2-18.7), and influenza-associated fatality was 21.6% (95% CI 14.6-28.6). The multivariable analysis of pneumonia cases showed unconsciousness at admission (aOR 3.7; 95% CI 1.2-11.6), pulse rate >80/minute (aOR: 1.1; 95% CI 1.1-2.9) and hypoxia (SpO2 <94%) (aOR 4.0; 95% CI 2.7-6.1) as significant risk factors for ICU admission. Hypertension (aOR 2.1; 95% CI 1.1-3.8), unconsciousness at admission (OR 4.3; 95% CI 1.3-13.9), anemia (Hb<10gm/dl) (aOR 1.7; 95% CI:1.0-3.0) and hypoxia (SpO2 <94%) (aOR: 2.2; 95% CI:1.2-4.2) were identified as significant risk factors for death. **Conclusion:** In our study almost half of the influenza-associated pneumonias among adults ≥60 aged years required ICU care and almost one in four died. These results may help inform policy for implementing influenza prevention like vaccination among older adults in India.

### Poster 230. Incidence and Epidemiological Characteristics of Influenza Associated with Hospitalized Acute Respiratory Illness, Damanhour, Egypt, 2009-2017

**H. BahaaEldin**[1], A. Mansour[2], H. Mansour[3], S. El Alkamy[1], S. Samy[1], E. Reaves[4], E. Dueger[4], N. Schaad[4], I. Abbass[1], H. Abu El Sood[1], A. Eid[1]
[1]Ministry of Health and Population, Cairo, Cairo, Egypt, [2]Rumph and Associates P.C, Cairo, Cairo, Egypt, [3]Global Health Development, Cairo, Cairo, Egypt, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Influenza is of global public health concern. Globally, influenza causes 290,000 to 650,000 deaths annually. Limited influenza incidence data are available in the Middle East or Egypt. We aim to describe the epidemiology of influenza associated with hospitalized acute respiratory illness (ARI-Influenza) in Damanhour district, Egypt. **Methods:** From 2009-2017, population-based ARI surveillance was conducted in Damanhour district. ARI cases were eligible if they were hospitalized, had ≥1 signs of acute infection and ≥1 respiratory symptoms. Nasopharyngeal/oropharyngeal (NP/OP) specimens were analyzed by real-time, reverse transcription polymerase chain reaction for influenza types and subtypes. A health utilization survey conducted in 2012 was used to estimate the incidence rate (IR) of hospitalized ARI-Influenza. **Results:** Of the 16,782 ARI cases enrolled, 15,984 NP/OP specimens (95.2%) were tested for influenza and 16.7% were positive: 9.7% for influenza A and 7.0% for influenza B. The median age of hospitalized ARI-Influenza cases was 25 years (IQR 5.2-48.0). Males and rural residents represented 53.3% and 79.6% of cases, respectively. The median duration of illness and hospitalization were 5 (IQR 4-7) and 3 (IQR 2-5) days, respectively. Twelve (0.5%) cases died during hospitalization. The overall hospitalized ARI-influenza IR was (44.9/100,000 persons) with the lowest annual IR in 2011 (21.5/100,000 persons) and the highest in 2016 (84.7/100,000 persons). The highest IR was among children <5 years (102/100,000 persons). **Conclusion:** There is a considerable burden of Hospitalized ARI-influenza in Damanhour district. Incidence data

are critical to direct prevention and control strategies, including the development of national guidelines for high-risk group vaccination and treatment.

### Poster 231. Countries Archetypes as a Reference Model for LMICs Public Health Managers to Develop a Tailored Influenza Vaccine Demand Plan that Aligns with Country's Resources

**M. Mazur**[1], I. Gorodnichev[2], M. Jagga[3], J. Bresee[4]
[1]Ready2Respond, Philadelphia, PA, USA, [2]PricewaterhouseCoopers, New York, NY, USA,
[3]PricewaterhouseCoopers, Mumbai, India, [4]The Task Force for Global Health, Atlanta, GA, USA
**Background:** Influenza vaccines remain underused in low- and middle-income countries (LMICs). In 2019, 50% of the world's population accessed only 6% of distributed seasonal influenza vaccine doses. Facing scarce resources and competing health priorities, many LMICs lack a structured approach for developing a reliable influenza vaccine demand forecast to support better access to vaccine doses. We developed a methodology that allows the distinction of LMIC archetypes as a reference model for countries to gain insights on realistic target immunization rates, improve their influenza vaccine demand projections and align their resources strategically, based on their current situation and archetype. **Methods:** Multiple defining characteristics were used to identify the countries' archetypes, including the GDP, the healthcare spending per capita, the size of the population, the healthcare infrastructure, influenza vaccination recommendations or lack of thereof, strength of existing vaccination programs, the access of influenza vaccine doses, the importance of vaccine hesitancy in the population. Where data were unavailable (due to differing coverage across sources) the model uses income-based averages. The model defines countries archetypes based on an aggregate scoring of key demand indicators and an aggregate scoring of factors influencing a country's ability to execute vaccination campaigns. **Results:** Four country archetypes were identified, with each providing a framework to set baseline target vaccination rates, determine vaccination campaign target populations, predict wastage and to suggest year on year vaccine demand /vaccination target growth rates. Mapping countries and analyzing them against the three different GNI groups (LIC, LMIC and UMIC) for each archetype provided a more accurate assessment of each country's projected influenza vaccination performance compared to its closest peers. **Conclusions:** The archetype approach could support countries' public health managers in their planning and help articulate the countries' strengths, core capabilities, and unique differentiators. Recognition of each country's archetype is the critical first step towards developing a tailored influenza vaccine programming strategy that incorporates long range vaccine demand forecasting as a key capability to achieve both their short-term objectives and longer-term ambitions for influenza vaccination coverage.

### Poster 232. Seasonal Influenza Vaccination in the Eastern Mediterranean Region: Policy Status and Vaccination Coverage (2015-2020)

**S. Mohammed,** S. Tempia, W. Khan, A. Abubakar, L. AL-Ariqi, R. Kawafha, H. Abou-Elnaja, A. Aman, A. Barakat, A. Elkholy
The WHO/Regional Office of the Eastern Mediterranean, Cairo, Egypt
**Background:** Annually, seasonal influenza causes more than three million cases and half a million deaths globally. Acknowledging the disease's high infectivity and the availability of safe vaccines, WHO recommended annual vaccination for five high-risk groups, however vaccine uptake remains suboptimal in many parts of the world. We aim at providing an update on the influenza vaccination policy status and coverage in the Eastern Mediterranean Region. **Methods:** We used data from the WHO-UNICEF Joint Reporting Form on immunization (2015-2020) and the Eastern Mediterranean Region survey on seasonal influenza vaccination (2016-2017). For each country, we used the most recent available data and used the two sources to validate countries' responses and complement the missing data. **Results:** Of 22 member states, 15 (68%) reported having a national influenza vaccination policy. Countries without a policy were Afghanistan, Djibouti, Pakistan, Somalia, Sudan, Syria, and Yemen. All 15 member states (100%) with a policy had vaccination recommendations for health workers and older persons, 93% had recommendations for people with chronic medical conditions, and 80% had recommendations for pregnant women and young children. Influenza vaccination coverage rate (VCR) was available from only six countries. Among countries with coverage data, only one country reported VCR for pregnant women (90%) and children (2%). Six countries reported 39-100% VCR for health workers and three countries reported 2-70% VCR for people with chronic medical conditions. 4-8.5 million doses of influenza vaccine were distributed in 10-13 countries during 2015-2020. In 2020, the vaccine doses distributed in nine countries were 5-129 doses per 1000 population. **Conclusions:** In the Eastern Mediterranean Region, most of the emergency-affected countries have no influenza vaccination policy. With fragile health systems, these countries cannot tolerate an extra burden of influenza. Uptake of influenza vaccine in the member states reported having a vaccination policy is poor and documentation of vaccination coverage is sub-optimal. Advocating for vaccination, providing technical and financial support, and

addressing reasons for vaccine hesitancy might enhance the introduction and increased uptake of influenza vaccine in the region.

### Poster 233. Influenza Activity in the Eastern Mediterranean Region in 2020-2021 amidst the COVID-19 Pandemic

**H. Abou El Naja**, A. Barakat, A. El Kholy, A. Aman, S. Tempia, W. Khan, A. Abu Bakar
World Health Organization, Eastern Mediterranean Regional Office, Cairo, Egypt
**Introduction:** A reduction of influenza virus activity during the COVID-19 pandemic has been observed globally, including in the Eastern Mediterranean Region (EMR). However, these changes have not been thoroughly evaluated in the Region. We aimed to describe seasonal influenza virus circulation during the pre-pandemic period (2016-2019) and assess changes during the pandemic years (2020 and 2021 as of week 33) in countries of the EMR. **Methods:** Epidemiologic and virologic influenza surveillance data were retrieved from both WHO FLUNET and EMFLU networks. Four pre-pandemic seasons are used in the comparison analysis. We described weekly aggregated data of number of enrolled patients, number of tested specimens, and number of positive influenza specimens. **Results:** Of the 22 countries in the Region, on average 79% (range: 68% in 2016 - 86% in 2019) of countries reported to FLUNET and EMFLU during the four pre-pandemic years. Number of enrolled patients and tested specimens increased gradually from 55,234 and 54,755 respectively in 2016 to 138,781 enrolled patients and 137,511 tested specimens in 2019. In 2020, number of enrolled patients increased significantly to 257,849; however, number of tested specimens decreased to 68,289. In 2021, both enrolled patients and tested specimens reduced to very low levels (30,856 and 29,067 respectively). For percent influenza positivity, it fluctuated between 2016 and 2019 on an average of 21.5% (range 18.7%-23.9%) to decrease to 12% and 2.6% in 2020 and 2021 respectively. **Conclusion:** The implementation of non-pharmaceutical interventions to control the COVID-19 pandemic may have also impacted the spread of influenza viruses. The low circulation of influenza viruses during 2020-2021 and the associated potential immunity gap may result in increased transmission and severity of post-pandemic influenza seasons. This necessitates high vigilance to continuous data and virus sharing to timely monitor circulating viruses and the intensity and severity of future influenza epidemics.

### Poster 234. Knowledge, Attitudes, and Practices towards Seasonal Influenza among Adults with Chronic Diseases in Kyrgyzstan

**R. Akmatova**[1], A. Omuralieva[2], M.S. Ebama[1], D. Otorbaeva[2]
[1]Center for Vaccine Equity, Task Force for Global Health, Atlanta, GA, USA, [2]Department of Disease Prevention and State Sanitary and Epidemiology Surveillance, Bishkek, Kyrgyzstan
**Background:** Influenza is an acute viral respiratory disease of major global health concern and poses a threat to future pandemics. High morbidity and mortality from influenza were found among elderly people. Strengthening the influenza vaccination program is the most effective strategy to prevent seasonal influenza. This study aims to assess knowledge, attitude, and practice as well as to understand the factors associated with barriers to vaccine uptake among patients with underlying diseases in Kyrgyzstan. **Method:** A cross-sectional study was conducted from December 2018 to March 2019 for patients with chronic conditions attending the public health facilities in all regions of Kyrgyzstan. A total of 1200 participants aged from 18 to 92 years old with at least one underlying disease were recruited for interview. Multivariate regression analysis was used to determine the association between variables and outcomes of interests. **Results:** Among 1118 participants enrolled in this study, the majority (63.2%) were vaccinated against influenza in the previous year. People with university degrees had a significant intention for vaccination ($p<0.02$). Concerning marriage status, being divorced was an indicator of intention to be vaccinated ($p<0.03$). Geographically, there was a significant difference among residences living in the North ($p=0.003$) and Osh city ($p<0.001$) in the intention of vaccination. Regarding knowledge of influenza vaccination, 6.9% of participants disagreed with the statement that the influenza vaccine helps patients with chronic conditions ($p<0.000$). Only 42.1% of interviewees knew that the influenza vaccine is not a source of influenza infection ($p<0.000$). Almost half of the participants (44.5%) indicated that healthcare workers did not offer vaccination the last year. **Conclusion:** Our study revealed the higher vaccine uptake depends on educational and marriages status. The main barriers of vaccine uptake were a lack of awareness of vaccines effectiveness, fear of vaccine harmful effects, bad experiences among their family.

### Poster 235. Biennial Seasonal Activity of Human Metapneumovirus among a Clinical Pediatric Cohort in Managua, Nicaragua

**K. Hacker**[1], G. Chowell-Puente[2], J. Mousa[3], H. Maier[1], A. Gordon[1]
[1]University of Michigan, School of Public Health, Department of Epidemiology, Ann Arbor, MI, USA, [2]Georgia State University, School of Public Health, Department of Population Health Sciences, Atlanta, GA, USA,

[3]University of Georgia, College of Veterinary Medicine, Center for Vaccines and Immunology, Department of Infectious Disease, Athens, GA, USA
**Background:** Human metapneumovirus (hMPV) is an important cause of lower respiratory infection in children. Few non-hospital-based studies exist, and none have taken place in the tropics. In this study, we leveraged the Nicaraguan Pediatric Influenza Cohort Study (NPICS) to assess the burden, seasonality, and clinical characteristics of hMPV. **Methods:** NPICS is an ongoing community-based prospective study of children aged 0-14 years located in Managua, Nicaragua aimed at assessing the burden of pediatric influenza and other important respiratory viruses. Participants receive free medical care at a study health clinic and are asked to come to the clinic at the first sign of illness where they are tested for influenza and other clinically relevant diseases, including hMPV using real-time (RT)-PCR. We specifically assessed those that tested positive for hMPV via RT-PCR including those that presented clinically for Acute-Lower Respiratory Infection (ALRI). We used a classical multiplicative decomposition analysis to assess the temporal trend of hMPV by extracting seasonal patterns and assessing remaining temporal patterns. Generalized Growth Models (GGMs) were used to estimate effective reproduction numbers. **Results:** From 2011-2016, 564 children tested positive for hMPV or an Incidence Rate of 5.74% (5.3, 6.2 CI) per 100 person-years. Of those 564 children, 160 met the clinical criteria for Acute-Lower Respiratory Infection (ALRI) (Incidence Rate of 2.1 (1.9, 2.4 CI) per 100 person-years. When seasonality was extracted from the overall temporal trend, a noted decrease in anticipated hMPV infection was observed in 2012, 2014, and 2016, which resulted in a notable biennial seasonality. Positive participants with ALRI followed the same biennial pattern. **Conclusions:** Among those enrolled in NPICS, hMPV incidence rate varied dramatically year to year, with a distinct biennial pattern typically occurring in the early rainy season and diminishing throughout the dry season. This pattern, while only observed across the 5-years of the study, was distinct and not captured by regular seasonal variation indicating that other mechanisms may be driving this unique seasonality.

### Poster 52. Improvements in Influenza Surveillance, Specimen Testing, Sharing, and Reporting Globally, 2013–2019

**M. McCarron**[1], R. Kondor[1], C. Fuster[2], K. Vandemaele[2], J. Bresee[1], X. Xu[1], V.G. Dugan[1], V. Weatherspoon[1], A. Vance[1], K. Zureick[1], A.M. Fry[1], M. Samaan[2], A. Hammond[2], J. Fitzner[2], W. Zhang[2], A. Moen[2], D.E. Wentworth[1], E. Azziz-Baumgartner[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Global Influenza Programme, World Health Organization, Geneva, Switzerland
**Background:** Many gains were made in global respiratory virus surveillance following the 2009–2010 H1N1 pandemic. We assessed the sustainability of those gains among CDC partners following reductions in CDC funds. **Methods:** We quantified gains in molecular testing, participation in World Health Organization (WHO) reporting systems, samples genetically and antigenically characterized, and global representativeness of surveillance in 64 countries using data from several sources from 2013 to 2019. We also quantified statistical power for identification of signals of unusual influenza activity. **Results:** We analyzed data for countries funded in 2019, representing 41% of countries reporting to FluNet. While CDC reduced per-country influenza funding by approximately 79% over 10 years, the number of specimens tested annually remained consistent (mean 2,261). The number of partner countries shipping specimens to a WHO Collaborating Center (CC) increased from 68% in 2013 to 88% in 2019 (p=0·02). Partner countries accounted for 71% (range 61–75%) of specimens included in WHO Consultations on the Composition of Influenza Virus Vaccines meeting data package submissions. Limitations in our study include our reliance on publicly available data, which may not represent the entirety of a country's surveillance data, potentially biasing our estimates for power to detect unusual events and gains. Our exclusive use of partner data results in estimates from only low- and middle-income countries. Our analyses may be biased by the volume of data from China. **Conclusions:** Major strides have been made in the global understanding of influenza trends and seasonality; to optimize surveillance to identify atypical influenza viruses and to integrate SARS-CoV-2 molecular testing, sequencing, and reporting into existing systems work and funding must continue.

### Poster 236. Engaging the National Postal Service in Burkina Faso to Strengthen Bacterial Meningitis Specimen Transport

**J.F. Chen**[1], T.F. Tarbangdo [2], I. Yameogo[3], J. Kibler[1], S. Porgho[2], S. Ouattara[3], I. Ouedraogo[3], X. Wang[1], N. Cureau[1], H.F. Aké[2], M. Kamaté[2], R. Novak[1], L.A. McNamara[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Davycas International, Ouagadougou, Burkina Faso, [3]Ministère de la Santé, Ouagadougou, Burkina Faso
**Background:** A rapid specimen delivery system is critical for confirming etiology of bacterial meningitis and informing prevention strategies. In January 2020, the Burkina Faso Ministry of Health engaged the national postal

service to implement SITEB (Integrated System of Biological Specimen Transport) to promote rapid delivery of suspected bacterial meningitis cerebrospinal fluid (CSF) samples to centralized national reference labs (NRL). This analysis assesses the impact of this new system on the completeness and timeliness of CSF specimen transport to an NRL. **Methods:** "Consistent SITEB districts" (CSD) were defined as districts where, of the total specimens delivered to the NRL, ≥70% were transported by SITEB. CSDs were compared to "inconsistent SITEB districts" (ISD), all other districts relying more on prior specimen transport methods. The Chi-Square and Mann-Whitney U tests evaluated completeness and timeliness of specimens received by an NRL using national case-based meningitis surveillance data from 2020. Descriptive analyses of these outcomes by region were also conducted. Specimen transport times were assessed against the World Health Organization's performance indicator (≤7 days from specimen collection to arrival at NRL). **Results:** Fifteen districts were identified as CSD and 53 as ISD. Among specimens collected in CSDs, 78% (259/332) arrived at an NRL, versus 70% from ISDs (1,033/1,479; p=0.003). There was no difference in percent of deliveries meeting the ≤7 days indicator (25%, p = 1), but a significant difference in median specimen transport times was observed (CSD: 28 days, ISD: 38 days; p = 0.02). The Sahel region delivered the lowest percent of CSF samples to an NRL (21%). Under 20% of specimen deliveries in Centre-Nord, Cascade, Nord, and Sud-Ouest regions met the ≤7 days indicator. **Conclusion:** Use of SITEB was associated with higher proportions of CSF samples received at an NRL and shortening the period from specimen collection to NRL arrival, but not with meeting the ≤7 days indicator. Findings of this analysis will inform further investigation of gaps leading to specimen transport delays and identify districts to be targeted for assistance. Additional analyses are needed to understand the impact of and potential for confounding by other factors that may affect specimen transport, such as political insecurity and distance from an NRL.

## Antimicrobial Resistance

### Poster 237. Trends in Antimicrobial Resistance amongst Pathogens Isolated from Blood and Cerebrospinal Fluid Cultures in Pakistan (2011-2015): A Retrospective Cross-sectional Study

**N. Javid**
Lahore University of Management Sciences, Lahore, Pakistan
**Background:** While antimicrobial resistance (AMR) continues to be a major public health problem in Pakistan, data regarding trends of resistance among pathogenic bacteria remains scarce, with few studies presenting long-term trends in AMR. **Methods:** This study was therefore designed to analyze long-term AMR trends at a national level in Pakistan. We report here results of a comprehensive analysis of resistance, among pathogens isolated from blood and cerebrospinal fluid (CSF), between 2011 and 2015. Susceptibility data was obtained from a local laboratory with collection points all across Pakistan (Chughtai Laboratory). Resistance proportions to most commonly used antimicrobials were calculated for each pathogen over a period of five years. **Results:** While Acinetobacter species demonstrated highest resistance rates to all tested antimicrobials, a sharp increase in carbapenem resistance was the most noticeable (50%95%) between 2011–2015. Our results also highlight the presence of third and fourth generation cephalosporins resistance in Salmonella enterica serovar Typhi in Pakistan. Interestingly, where rise in AMR was being observed in some major invasive pathogens, decreasing resistance trends were observed in *Staphylococcus aureus*, against commonly used antimicrobials. **Conclusion:** Overall pathogens isolated from blood and CSF between 2011–2015, showed an increase in resistance towards commonly used antimicrobials.

### Poster 238. Risk Factors for Methicillin-resistant *Staphylococcus aureus* (MRSA) Carriage in MRSA-exposed Household Pets

**C.J. Cotter**[1], C. Ferradas[1,2,3], S. Ludwig[1], K. Dalton[1], J. Larsen[4], D. Laucks[1], S.A. Iverson[1], P. Baron[1,5], P.C. Tolomeo[6], A.M. Brazil[1], J.M. Ferguson[1], E. Lautenbach[6], S.C. Rankin[7], D.O. Morris[7], M.F. Davis[1]
[1]Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD, USA, [2]Emerging Diseases and Climate Change Research Unit, School of Public Health and Administration, Universidad Peruana Cayetano Heredia (UPCH), San Martin de Porres, Lima-Perú, [3]School of Veterinary Medicine, Universidad Peruana Cayetano Heredia (UPCH), San Martin de Porres, Lima-Perú, [4]Department of Bacteria, Parasites and Fungi, Statens Serum Institut, Copenhagen S, Denmark, [5]Department of Health and Human Values, Davidson College, Davidson, NC, USA, [6]Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA, [7]School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA, USA
**Background:** Household pets can carry methicillin-resistant *Staphylococcus aureus* (MRSA), typically introduced to the home by their human companions, but specific factors promoting pet carriage of this pathogen have not been fully elucidated. This study evaluated MRSA cultured from pets and home environments, given exposure to human infection, to inform design of further studies to identify risk factors for pet carriage in household pet populations

without known exposure. **Methods:** In the context of a human household member diagnosed with community-associated MRSA (CA-MRSA) skin or soft-tissue infection in the mid-Atlantic United States, we enrolled 142 dogs and cats from 57 households at baseline, of which 134 (94.4%) were sampled for bacterial culture, PCR confirmation, and *spa*-typing for MRSA strain determination. **Results:** At baseline, 12 (9.0%) of pets carried MRSA. Potential risk factors associated with carriage included pet bed (environmental) MRSA contamination, flea infestation, and antimicrobial use in the pet. Pets tended to carry human-adapted CA-MRSA strains, and *spa*-types of MRSA isolates cultured from pets were concordant with strains cultured from the home environment in seven of eight homes (87.5%) at baseline. **Conclusions:** Results may inform risk-based veterinary clinical recommendations and provide evidence for selective pet testing as a possible alternative to early removal of pets from the homes of humans infected with CA-MRSA. MRSA contamination of the home environment is likely an important risk factor for pet MRSA carriage, and future studies of household interventions should consider indoor environmental reservoirs to reduce risk of MRSA carriage in exposed pets.

### Poster 239. Extensively Antibiotic-resistant *Acinetobacter* spp.: A Life-threatening Infectious Agent for Neonatal Deaths and Illnesses in Bangladesh

**M. Alam**[1], M.I. Jahan[1], K.H. Lee[2], S. Jahan[1], M.Z. Hossain[1], A. Rahman[1], M.S. Ahmed[1], A. Rashed[1], S. Bari[1], S.E. Arifeen[1], M. Rahman[1], E.S. Gurley[1,2]
[1]icddr,b, Dhaka, Bangladesh, [2]Johns Hopkins University, Baltimore, MD, USA
**Background**: *Acinetobacter baumannii* resistant to carbapenem, the last resort of antibiotics, is listed as a priority-1 critical pathogen by the WHO and is a cause of nosocomial infection due to its ability to form biofilms on biotic and abiotic surfaces. **Methods**: Child Health and Mortality Prevention Surveillance (CHAMPS) aims to understand the causes of stillbirths and under-5 deaths by a panel of experts using laboratory and clinical data in Bangladesh. Bacterial isolates from post-mortem blood specimens and routine clinical specimens of under-5 children with suspected sepsis at a pediatric ward were tested for antibiotic susceptibility using Kirby-Bauer method. Bacteria resistant to ≥1 antibiotic from 3 antibiotic classes were considered multidrug resistant (MDR). **Results**: From Aug 2017- Jun 2021, pathogens were isolated from 126 (50% of 254) post-mortem samples and 93 (77% of 121) suspected sepsis cases. *Acinetobacter* spp. were isolated from 2 stillbirths and 12 neonates who died (11% of 126) and in 9 were considered in the causal chain of death or as co-morbid factor. In 12 (13% of 93) suspected-sepsis cases (11 neonates and 1 child) *Acinetobacter* spp. were found. Among 14 isolates collected from post-mortem samples, 12 were MDR with 8 XDR (extensively drug resistant). Isolates from 12 suspected-sepsis cases were MDR with 8 XDR. All isolates were resistant to first-line antibiotics used in neonates (ampicillin and gentamicin) and >80% against second-line antibiotics (meropenem and amikacin). All MDR isolates were resistant to at least one carbapenem group antibiotic. Isolates were all susceptible to tigecycline, colistin and polymyxin B. **Conclusions**: A concerning proportion of neonatal deaths and suspected sepsis were caused by carbapenem-resistant Acinetobacter infections. Whole genome sequence analysis for serotypes and virulence factors is necessary to develop vaccines and infection control measures focusing on biofilm forming capacity of *Acinetobacter* spp.

### Poster 240. Trends of Antimicrobial Susceptibility Pattern in Bangladesh 2017-2021: Findings from a National Sentinel Surveillance System

**Z.H. Habib**[1], S.B.G. Rasul[1], J. Sujan[2], M. Nasrin[3], M. Rahman[1], N. Afreen[1], A.N. Alam[1], A.S.M. Alamgir[1], T. Shirin[1]
[1]Institute of Epidemiology, Disease Control & Research (IEDCR), Dhaka, Bangladesh, [2]International Vaccine Institute (IVI), Seoul, South Korea, [3]Uttara Adhunik Medical College, Dhaka, Bangladesh
**Introduction**: Antimicrobial resistance (AMR) is an evolving public health issue. Surveillance and research in order to track its current situation and trend are vital for its containment. Since 2017, the National AMR surveillance is being conducted in Bangladesh to find out the causative organisms with their antimicrobial susceptibility pattern in different infectious conditions and to understand the trend. **Methods:** In nine tertiary care facilities across Bangladesh, a case-based surveillance system is being implemented. We analyzed data from March 2017 to June 2021 to see if there were any trends in antibiotic susceptibility patterns. Six types of specimens were obtained from individuals with five different clinical conditions and microorganisms were isolated and identified according to protocol. To determine the AMR trend, we used a total of 25 antimicrobials. Statistical data analysis tools Stata version 16.0 and Python 3.0 were used to analyze data. We performed simple linear regression to establish the significance of antibiotic susceptibility patterns across time, with a p- value of 0.05 considered statistically significant. **Results**: A total of 5,647 isolates were selected for this study. Of these 36.27%, 35.17%, 8.50%, 8.38%, 7.47%, and 4.21% isolates were from urine, wound swab, blood, sputum, endotracheal aspirate, and stool sample respectively. The most common organism was E. coli (29.57%, n=1,670) followed by Pseudomonas aeruginosa

(19.85%, n=1,121), Klebsiella pneumoniae (16.11%, n=910), Staphylococcus aureus (10.38%, n=586) and others. Among the selected antimicrobials, susceptibility of Doxycycline (52.58% - 71.11%; R2=0.756, p=0.055) and Tetracycline (41.64% - 46.08%; R2=0.968, p=0.003) increased over the period whereas Cefuroxime (37.84% - 15.77%, R2=0.791, p=0.043) showed decreasing trend. All of them were statistically significant. The susceptibility of most other antibiotics like Ceftriaxone, Imipenem, and Ciprofloxacin decreased over time but it was not statistically significant. **Conclusion**: Although the sensitivity shown here is irrespective of specimen and organisms, most of the antimicrobials tested showed lower trends of susceptibility over the years which is alarming. It is high time we take appropriate measures to curb the rising trend of antimicrobial resistance in Bangladesh.

### Poster 312. Machine Learning Models for Predicting Decreased Susceptibility to Ceftriaxone in *Neisseria gonorrhoeae*

**S.M. Ha**[1], P.C. Adamson[2], E.Y. Lin[3], J.D. Klausner[4]
[1]Department of Integrative Biology and Physiology, UCLA, Los Angeles, CA, USA, [2]Division of Infectious Diseases, David Geffen School of Medicine at UCLA, Los Angeles, CA, USA, [3]David Geffen School of Medicine at UCLA, Los Angeles, CA, USA, [4]Departments of Population and Public Health Sciences and Medicine, Keck School of Medicine of University of Southern California, Los Angeles, CA, USA
**Background:** Antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* is an emerging global health threat. Ceftriaxone is the only empiric treatment option that remains. Machine-learning (ML) algorithms can be coupled with next-generation sequencing (NGS) to predict antibiotic susceptibility using genetic mutations. ML can also be leveraged to improve diagnostic testing and surveillance for AMR. **Methods:** PathogenWatch, a public, online database of pathogen genomes, was used to download all available *N. gonorrhoeae* genome sequences and associated antibiotic susceptibility data on 11/17/20 (n=12,936). Decreased susceptibility to ceftriaxone was defined as a minimum inhibitory concentration of >0.064 mg/mL; values ≤0.064 mg/mL were susceptible. We used 97 SNPs known to be associated with ceftriaxone resistance from four genes (*penA, ponA, penB,* and *mtrR*) using BLAST and FA1090 reference genes. For the ML analysis, the total dataset of genomes was partitioned by random sampling into training (70%) and testing (30%) datasets. The performance of six different ML models were evaluated for predicting ceftriaxone susceptibility. Shapley additive explanations (SHAP) analysis was used to understand how each of the 97 individual SNPs contribute to ceftriaxone susceptibility. **Results:** The ML model trained with a random forest classifier (RFC) using all 97 SNPs achieved the highest area under the curve (AUC) 0.965. The top 10 SNPs from the SHAP analysis were: penA-501, penB-120, ponA-421, penB-121, penA-545, mtrR_Promoter_delA, penA-551, penA-542, penA-406, and penA-512. The RFC models trained with top 1, 3, 5, and 10 SNPs from the SHAP analysis achieved AUCs of 0.622, 0.901, 0.947 and 0.963, respectively. **Conclusions:** The results demonstrate how ML models using 5 or 10 SNPs could achieve performance similar to a model using all 97 SNPs. ML might be useful to predict decreased susceptibility to ceftriaxone in *N. gonorrhoeae* and identify SNPs contributing to resistance, for future diagnostic assays or surveillance efforts.

## Surveillance and Surveillance Systems

### Poster 241. A Multisectoral Digital Platform to Enable One Health Disease Surveillance in Albania

**K. Mersini**[1,5], A. Vasili[2], J. Sulo[1], D. Çela[3], L. Agolli[1], J. Mantero[4], N. Divi[4], S. Bino[1,2]
[1]South East European Centre for Disease Surveillance and Control, Tirana, Albania, [2]Institute of Public Health, Tirana, Albania, [3]ArkIT, Tirana, Albania, [4]Ending Pandemics, San Francisco, California, USA, [5]Agricultural University of Tirana – Faculty of Veterinary Medicine, Tirana, Albania
**Background:** In Albania, disease surveillance data are collected by multiple specialized electronic systems in the human and animal health sector and used separately by each stakeholder. Analysis is not performed jointly to detect early warning signals of potential outbreaks, preventing timely and coordinated actions. To improve and enhance the one health disease surveillance activities across sectors, an electronic platform has been created to enable the interoperability and visualization of multi-sectoral surveillance data and link all sectors. **Methods:** The One Health platform has been built around the existing data exchange routines during health events. Various components include: i) integrating indicator-based surveillance data from both human and animal systems; ii) assimilating information from media reports utilizing the Medical Information System (MEDISYS), a media monitoring system providing event-based surveillance for both human and animals; and iii) incorporating community-based event notifications (web based or mobile text messaging) from community health workers, local veterinarians, and the general public. **Results:** Currently, the One Health platform exhibits data from human health disease surveillance system, laboratory information system, vaccine information system, syndromic surveillance, health events collated by media scanning, notifications from community-based event surveillance, and will be completed

with the addition of animal health surveillance information system and vector distribution information system by mid-2022. The Public Health authorities have already used this platform to control the COVID-19 epidemic and the Animal Health authorities are slated to utilize it routinely in 2022. The platform will enhance data exploration and visualization by summarizing the information through customizable graphs, maps and tables featuring epidemiological indicators, thresholds and one health timelines metrics for different diseases, species, demographic strata, habitats, etc. **Conclusions:** This dynamic platform is a promising and pioneering tool to enhance the collaboration across sectors and inspires a holistic view of One Health perspective by interconnecting health events.

### Poster 242. Trends of Key Surveillance Performance Indicators of Acute Flaccid Paralysis, Uganda, 2015 - 2020

**B.O. Amodan**[1,2], A. Kisakye[3], P.T. Okumu[1], S.R. Ahirirwe[1], D. Kadobera[1], A. Driwale[2], A.R. Ario[1,2]
[1]Uganda Public Health Fellowship Program, Kampala, Uganda, [2]Ministry of Health, Kampala, Uganda, [3]World Health Organization, Country Office-Uganda, Kampala, Uganda
**Background:** Poliomyelitis is caused by poliovirus and can cause lifelong paralysis, presenting as acute flaccid paralysis (AFP). A sensitive AFP surveillance system, in which AFP cases are evaluated to determine if they are true AFP or non-polio AFP (NPAFP), is key for tracking polio eradication. We describe Uganda's AFP surveillance performance by district from 2015-2020, based on WHO recommended indicators. **Methods:** We performed a descriptive analysis of national AFP surveillance data from 2015-2020. We evaluated proportion of AFP cases reported that were true AFP and changes in NPAFP and stool adequacy (SA) rate. NPAFP rate was defined as NPAFP cases/100,000 population <15 years (targeted at ≥4/100,000). SA rate was the percentage of AFP cases with 2 adequate stool samples collected ≥24 hours apart ≤14 days after onset of paralysis and arriving at the laboratory in good condition. **Results:** Of 3,605 AFP cases investigated countrywide, 3,475 (96%) were true AFP cases. Between 97-100% of districts reported each year. Overall, the mean NPAFP rate declined (3.1/100,000 in 2015 and 2.1/100,000 in 2020). Less than 40% of districts met the NPAFP target rate in all years. The proportion of districts with NPAFP rate ≥4/100,000 declined from 35% to 20% from 2015-2020 (OR=0.47; 95% CI: 0.26-0.83). Only 66% of districts achieved the SA target of ≥80%. The proportion of districts with SA rate ≥80% significantly increased from 68% to 80% from 2015-2020 (OR=1.9; 95% CI: 1.1-3.4). **Conclusion:** SA rates were adequate and improved over time, and most districts reported AFP cases. However, there was a decline in NPAFP rate from 2015-2020 and few districts achieved the target rate. The suboptimal AFP surveillance system performance leaves the country at risk of missing ongoing poliovirus transmission. We recommend health worker training on active AFP searches, intensified supportive supervision, and periodic review meetings with districts to assess AFP surveillance performance.

### Poster 243. Outbreaks Near Me: An Online Crowdsourced Syndromic Surveillance System Tracking Influenza and COVID-19

**A. Gertz**[1], S. Thompson[1], K. Sewalk[1], J. Hawkins[1], M. Oglia[1], J.S. Brownstein[1,2]
[1]Boston Children's Hospital, Computational Epidemiology Lab, Boston, MA, USA, [2]Harvard Medical School, Boston, MA, USA
**Background:** Outbreaks Near Me (ONM) is a crowdsourced syndromic surveillance system tracking influenza, COVID-19, and other respiratory disease activity. ONM leveraged the technology of Flu Near You (FNY), a decade-running crowdsourced surveillance system for influenza. Novel surveillance systems like ONM complement existing surveillance by providing real-time estimates and detecting non-care seeking cases that may be missed by traditional public health surveillance. **Methods:** ONM launched in March 2020, capturing symptom reports by participants across North America. ONM users are sent weekly email or text reminders to report if they feel healthy or sick. Sick users share any observed symptoms, type of care sought, and diagnoses. All users self-report about COVID-19 testing, and influenza and COVID-19 vaccination status. Influenza-like-illness (ILI, defined as fever and cough or sore throat), and COVID-like-illness (CLI, defined as fever and shortness of breath or cough) are both assessed mapped by zip code on ONM. **Results:** ONM has collected over 6,700,000 unique user entries, with 1.58% of all submissions reporting illness. All 50 states and D.C. are represented, and a small proportion of users reside in Canada and Mexico. The ONM population skews female (62.7% reports, 65.5% registered users), and older (median reporting age 59, median registered user age 64). For the 2020-2021 influenza season, 0.08% ILI, and 0.07% CLI was detected. Between June and August 2021, 0.39% ILI and 0.35% CLI was detected. Reported vaccination rates among ONM users for influenza (77.1%) and COVID-19 (89.4%) were higher than average US estimates. **Conclusions:** ONM crowdsources symptoms to track ILI, CLI, and other respiratory disease activity. In addition to syndromic surveillance, ONM captures healthcare utilization, testing, and vaccination data. With a dedicated user

base, ONM complements traditional surveillance by capturing real-time estimates and longitudinal trends across North America.

### Poster 244. The One Health Surveillance Readiness and Requirements Tool (OHSRRT): Establishing the Groundwork for Successful Multi-sectoral Surveillance Systems

**K.L. Meidenbauer,** S.V. Patel
Johns Hopkins Applied Physics Laboratory, Laurel, MD, USA
**Background:** The Tripartite (WHO, OIE and FAO) recognizes that many determinants of health outcomes are outside of the human health sector. The development and implementation of coordinated multi-sectoral One Health surveillance solutions to support timely data sharing between sectors is essential to rapidly identify disease events. Data from human, animal, environmental and other relevant sectors within a country should be included in a coordinated surveillance system to support disease prevention, detection, response, and mitigation. **Methods:** One of the greatest challenges for countries seeking to adopt a coordinated One Health surveillance system is determining how to structure the proposed system and if quality data exists within the individual sectors that can be utilized for coordinated surveillance efforts. Many countries also struggle to determine best methods to establish a system that is sustainable within their government organization and funding structure. The One Health Surveillance Readiness and Requirements Tool (OHSRRT) was developed to determine country readiness and gather requirements to develop a One Health surveillance system based on defined critical success factors. **Results:** The prototype of OHSRRT was successfully piloted in June-July 2018 in Uganda. The tool includes a stakeholder engagement guide and questionnaire, data collection and characterization sheet, and the OHSRRT landscape assessment. The tool is structured so the results collected can be used to write a Requirements Analysis Report and develop functional requirements for an operational One Health surveillance system. **Conclusions:** Building upon the tool's initial success, and the findings and recommendations of the joint Tripartite Surveillance and Information Sharing Operational Tool (SISOT) workgroup, the Johns Hopkins Applied Physics Laboratory plans to continue to evolve the existing manual paper-based OHSRRT prototype to an open-source, electronic tool that countries can easily access and utilize to help establish a functional coordinated surveillance solution.

### Poster 245. Establishing a One Health Surveillance System: Results of a Gap Analysis in Bangladesh

**M.S. Uzzaman**[1], A.S.M. Chowdhury[1], M. Rahman[1], M.G. Osmani[2], F. Rahman[3], A. Atanda[4], J. Mantero[4], N. Divi[4], T. Shirin[1]
[1]Institute of Epidemiology, Disease Control & Research (IEDCR), Dhaka, Bangladesh, [2]Department of Livestock Services, Dhaka, Bangladesh, [3]Bangladesh Forest Department, Dhaka, Bangladesh, [4]Ending Pandemics, San Francisco, CA, USA
**Background:** Bangladesh, with its fast-growing economy, dense population, and subjection to climate change makes it a hotspot for emerging infectious diseases. Seventy-five percent of emerging infectious diseases jump from animals to humans highlighting the importance of a One Health (OH) approach to prevent and respond to disease outbreaks. The COVID-19 pandemic is a recent example of the devastating impact of zoonotic diseases. Enhanced and shared data feeds from human, animal and wildlife sectors enable a OH approach to improve situational awareness, enable early detection, and ensure rapid response. An analysis of the current disease surveillance systems in Bangladesh was conducted to document OH-related activities, identify existing data sources, and identify gaps in information sharing and collaboration between sectors. **Methods:** The gap analysis was conducted between May and July 2021 as a virtual focus group with 23 multisectoral stakeholders from human, animal, and forestry departments, followed by a survey that included a OH mapping & assessment tool. **Results:** The main gaps identified include a limited commitment to OH promotion; limited coordination and leadership on OH activities; non-standardized data collection; and issues with data quality and storage. Current systems are also non-digital causing inefficient utilization. Furthermore, the indicator-based surveillance systems within each sector operate in parallel, and data is rarely shared due to a lack of clear guidance and limited autonomy of managers. **Conclusions:** Sector leads report a strong willingness to work together to improve early detection through better coordination, integrated data sharing and institutionalization of OH surveillance. The COVID-19 pandemic created some cross-sectoral collaboration that requires the establishment of guidelines for sustainability. These findings support the need for a true OH approach to disease surveillance.

### Poster 246. One Health Participatory Surveillance – Role of Afyadata in Early Detection and during COVID-19 in Tanzania

**E. Karimuribo**[1,2], E. Beda[1], M. Mwabukusi[1], [3]O.F. Inlamea, M. Rweyemamu[1], [4]N. Divi

[1]SACIDS Foundation, Morogor, Tanzania, [2]Sokoine University of Agriculture, Morogoro, Tanzania, [3]National Institute of Health, Maputo, Mozambique, [4]Ending Pandemics, San Francisco, CA, USA
**Background:** Early detection includes detection of zoonotic diseases in animals before they infect humans and also at the community level. SACIDS Foundation has pioneered Afyadata, an open-sourced digital disease surveillance tool that eases the collection, analysis, and documentation of human and animal health events from the community. Afyadata allows trained community health workers in remote areas to transmit health information to local surveillance systems; information is then verified, and then acted upon. The tool can be customized based on language and system integration needs. **Methods**: Tool utilization between November 2016 and September 2020 was analyzed. The tool was modified to support cross border surveillance in 2018. The tool was further expanded to capture data using USSD (Unstructured Supplementary Service Data) for livestock keepers and/or pastoralists who did not have access to smartphones. **Results:** Between 2016 and 2021, over 700 community volunteers and health professionals have been trained on the use of Afyadata. From 2015 to September 2019, more than 6,866 reports related to human health were submitted; nearly 22,000 reports (1,419 using mobile app, over 29,300 using USSD) related to veterinary health were submitted, and 1,430 reports related to environmental events were reported. The tool has improved timeliness of reporting from the community level from an average of 10 days to an average of 3 days. During COVID-19, the tool was adapted for use in Mozambique for cross-border surveillance of COVID-19. **Conclusions**: Countries benefit from participatory surveillance systems operating year-round. Due to the existence of this Afyadata tool prior to COVID-19, it was feasible to quickly modify the tool to enable cross-border surveillance. The Food and Agriculture Organization of the United Nations is already working toward integrating the tool with its mobile field reporting application.

### Poster 247. Building a One Health Surveillance System in Pakistan: Results of a Gap Analysis

**S. Mursalin**[1], A. Zaeer[2], S. Zareen[3], A. Atanda[4], J. Mantero[4], N. Divi[4]
[1]Pak One Health Alliance, Islamabad, Pakistan, [2]University of Health Sciences, Lahore, Pakistan, [3]Department of Health Punjab, Ludhiana, Punjab, India, [4]Ending Pandemics, San Francisco, CA, USA
**Background:** Three out of four emerging infectious diseases spread from animals to humans, emphasizing the importance of a multisectoral One Health (OH) approach to outbreak prevention. No comprehensive mapping of OH surveillance capabilities had previously been done in Pakistan. **Methods:** A mapping and gap analysis exercise was conducted with multisectoral stakeholders to evaluate data sources for existing disease surveillance systems and identify gaps in information sharing between sectors. A two-part, 12-item structured questionnaire was used to collect quantitative and qualitative data from May to July 2021. **Results:** A total of 51 responses were received from federal and provincial level stakeholders from human (39%), animal (39%), and environmental health (14%); and the food and agricultural (8%) sectors. The majority of respondents (78%) were familiar with the term OH yet 55% reported poor coordination across sectors and lack of a designated OH focal person. Regulatory frameworks and guidelines for OH are unavailable across sectors. Indicator-based surveillance systems exist in each sector but operate in parallel without regular data sharing. Guidelines for standardized operations of routine health information systems are unavailable and data collection is non-digital, leading to issues with data quality. System managers have limited authority to share data. The public health sector had better established surveillance systems, training plans and curriculums than other sectors. **Conclusions:** No robust OH-event-based surveillance (EBS) or joint surveillance initiatives exist between sectors, though there's a strong desire to work together on OH-EBS capabilities. This current momentum, however, provides an opportunity for multi-sectoral coordination and data sharing for early disease detection. A true OH approach to disease surveillance will help fill the gaps identified in this analysis.

## Hepatitis

### Poster 248. All Cause Death Trend Analysis of Hepatitis B Virus and Hepatitis C Virus Infections in Tennessee; 2016–2020

**P. Shoup**, H. Wingate, P. Talley, L. Sizemore
Tennessee Department of Health, Nashville, TN, USA
**Background:** Chronic hepatitis B virus (HBV) and hepatitis C virus (HCV) infection are associated with liver damage, cirrhosis, and liver cancer. The purpose of this study was to assess all cause death trends based on laboratory identified HBV and HCV investigations in Tennessee (TN). **Methods:** HBV and HCV investigations created between January 1, 2016, and December 31, 2020, from the TN NEDSS Base System (NBS) were matched to the TN vital statistics final death data from 2016–2020 to ascertain number of deaths among persons with diagnosed HBV and/or HCV. Cases were matched on an individual identifier consisting of current last name, first

name, and date of birth. Investigations are classified based on the CDC/CSTE case definitions. **Results:** During 2016–2020 there were 392,568 total deaths in TN. Of these, 8,587 (2.2%) had an HCV investigation and 889 (0.2%) had an HBV investigation. The highest proportion of all TN deaths occurred in persons over the age of 85 (24.3%); however, the highest proportion of HBV and HCV deaths were aged 60-69 (28.7% and 31.3% respectively). Females accounted for 47.9% (188,182) of TN deaths and males 52.1% (204,386). Most deaths among persons with HBV and HCV were male (66.2% and 66.7% respectively). Despite most deaths occurring in males, the percentage of HCV deaths among females increased 0.4% every year. On average, 2.7% of persons with a past HCV investigation die annually, with half expiring less than a year after their investigation start date (49.7%). Similarly, HBV deaths accounted for 3.7% of HBV cases, with 63.5% expiring within a year of their investigation start date. **Conclusion:** This analysis demonstrates lower life expectancy among individuals with HBV and HCV in TN. The short time frame between investigation start date and death highlights the need for earlier testing and prompt linkage to treatment and harm reduction resources.

### Poster 249. The Development of a Machine Learning Algorithm for Early Detection of Viral Hepatitis B Infection in Nigerian Patients

**B.I. Ajuwon**[1,2], A. Richardson[3], K. Roper[1], M. Sheel[1], R. Audu[4], B.L. Salako[5], M.O. Bojuwoye[6], K.A. Ibrahim[6], B.A. Lidbury[1]
[1]National Centre for Epidemiology and Population Health, Research School of Population Health, ANU College of Health and Medicine, the Australian National University, Acton, Australian Capital Territory, Australia, [2]Department of Biosciences and Biotechnology, Faculty of Pure and Applied Sciences, Kwara State University, Malete, Nigeria, [3]Statistical Support Network, the Australian National University, Acton ACT, Australia, [4]Microbiology Department, Centre for Human Virology and Genomics, Nigerian Institute of Medical Research, Yaba, Lagos State, Nigeria, [5]Director-General's Office, Nigerian Institute of Medical Research, Yaba, Lagos State, Nigeria, [6]Department of Medicine, Gastroenterology Unit, University of Ilorin Teaching Hospital, Ilorin, Kwara State, Nigeria, [6]Department of Medicine, University of Ilorin Teaching Hospital, Ilorin, Kwara State, Nigeria
**Background:** Approximately 300 million people live with hepatitis B virus (HBV) worldwide, a leading cause of liver cancer and death with significant burden in low-resource settings. In Nigeria, where at least one in ten people are infected with most of them unaware of their infection status, late detection of HBV is a fundamental problem, and therefore a machine learning-enabled diagnostic model based on patterns in routine pathology data are required to detect HBV infection earlier and provide linkage to care. **Methods:** De-identified patient data consisting of 20 routine pathology and clinical attributes in 916 individuals who underwent hepatitis B surface antigen (HBsAg) immunoassay testing within 2010-2020, were used to develop a predictive model of HBV infection. Supervised machine learning algorithms were evaluated using 10-fold cross-validation for assessment of model performance, and the algorithm with the best performance was adopted for use. **Results:** Among the patients, 540 (58.9%) were male, and 376 (41.1%) were female. People who were positive for HBsAg accounted for 69% of these patients, and the proportion of negative HBsAg category was 31%. Random forest algorithm (Accuracy = 95.9%, Sensitivity =97.8%, Specificity = 91.6%, Precision = 96.3%, F1-Score = 97.1%, AUC = 98.0%) proved to be highly accurate for discriminating HBsAg positive from negative patients, and thus rivals with immunoassay in accuracy. Aspartate aminotransferase (AST), white blood cell (WBC), and age were the highest ranked predictive markers in the Nigerian patient cohort. **Conclusions:** We proposed a potential combination of pathology data and pattern recognition algorithm for accurate diagnosis of HBV, which is a valuable response to WHO's Global Hepatitis B Strategy to have 90% of infected persons diagnosed by 2030**. Early prediction of HBV infection via pathology markers** potentially represents significant savings on time, cost, and patient anxiety, and will support early intervention for rural and remote laboratories that do not have easy access to specialised immunoassay.

## Fungal Diseases

### Poster 250. Genomic Description of within-host Diversity for Patients with Aspergillosis

**E. Misas**[1], J.Z. Deng[2], J.A.W. Gold[1], L. Gade[1], N.S. Nunnally[1], O. Georgacopoulos[1], M. Bentz[1], E. Berkow[1], J.D. Klausner[3], A. Litvintseva[1], N.A. Chow[1]
[1]Mycotic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]David Geffen School of Medicine, University of California at Los Angeles, Los Angeles, CA, USA, [3]Department of Preventive Medicine, University of Southern California, Los Angeles, CA, USA
**Background:** Invasive aspergillosis, primarily caused by the environmental mold *Aspergillus fumigatus*, is a life-threatening disease that affects immunocompromised patients. Whole-genome sequencing (WGS), an advanced genotyping method, can supplement epidemiologic investigations of fungal disease outbreaks; however, data are

lacking on its use for healthcare-associated aspergillosis outbreaks. For these investigations, it is unclear whether a single isolate per patient is sufficient to determine relatedness. To address this question, we conducted a molecular epidemiologic study of aspergillosis reported during February–March 2020 in nine facilities in Southern California, USA. **Methods:** We performed WGS analysis of 24 *A. fumigatus* isolates derived from 18 patients; we analyzed within-host diversity of isolates from five patients who had multiple isolates. We identified single nucleotide polymorphisms (SNPs) using MycoSNP workflow and calculated pairwise distances and a maximum parsimony tree using the MEGA-X program. **Results:** Phylogenetic analysis of WGS data identified 128,243 SNP positions among the 24 *A. fumigatus* isolates. Minimum pairwise distance between patients was 195 SNPs, and maximum was 70,681 SNPs. We did not observe genetic clustering by facility. For the five patients with multiple isolates, 7 pairwise comparisons representing within-host diversity were generated; 4 of 7 pairs ranged from 6-21 SNPs. The remaining three pairwise comparisons had 17,126 SNPs, 11,752 SNPs, and 11,756 SNPs. The pairwise comparison of 17,126 SNPs corresponded to a patient that had two samples that were collected at two different facilities. The other two were from a patient with three samples, two from sputum and one from bronchoalveolar-lavage (BAL). The two sputum samples were separated by 11,752 SNPs, and the sputum and BAL samples were separated by 11,756 SNPs. **Conclusion:** Two patients had substantial within-host diversity with pairwise comparisons ranging from 11,752 to 17,126 SNPs. Our findings indicate that sequencing a single isolate per patient may not be sufficient to determine relatedness in an outbreak investigation of healthcare-associated aspergillosis.

### Poster 251. Geographic Range and Epidemiologic Characteristics of Blastomycosis: A Systematic Literature Review

**K. Wu**[1,2], K. Benedict[2], S. Le[2], S. Williams[2], M. Toda[2], I. Schwartz[3], B. Jackson[2]
[1]Epidemic Intelligence Service, Atlanta, GA, USA, [2]Mycotic Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Division of Infectious Diseases, Department of Medicine, University of Alberta, Edmonton, Alberta, Canada
**Background:** The fungus *Blastomyces* lives in the environment and can cause blastomycosis in humans and animals. The rarity of the disease, limited public health surveillance, and challenges to environmental detection limit the understanding of its geographic distribution. Clinicians frequently use maps showing the range of *Blastomyces* to inform patient testing and diagnosis, and missed diagnoses are common. We characterized the epidemiologic features of published cases of blastomycosis, including geographic range, to help inform clinical and public health decisions. **Methods:** We conducted a systematic literature review of cases of human and animal blastomycosis in the United States and Canada from 1970–2020. Data on patient demographic characteristics, hospital location, patient residence, and travel were abstracted from full reports. States were classified as endemic based on CDC's published map from 2020, which shows a wider range than CDC's previous map. **Results:** We identified 527 publications involving 942 cases of blastomycosis (778 human, 164 animal). Cases were reported from 41/51 US and 7/13 Canadian jurisdictions; 47% of cases occurred in five jurisdictions. Less than half (n=393, 42%) of cases were diagnosed in locations where blastomycosis is reportable. The range of the 2020 map captured the diagnosis location of 96% of cases. Compared with the previous map, an additional 71 cases were captured, including cases diagnosed in Saskatchewan (32), Texas (11), and Florida (8). Seven cases identified outside of the geographic range (from California, Colorado, Oregon, Alberta, and New Brunswick) did not travel in the previous year. **Conclusions:** Published cases of blastomycosis primarily occurred in areas within the previously recognized range of *Blastomyces*; 4% of cases were diagnosed outside of the current estimated range, including those without recent travel history. More data are needed about the fungus' range, particularly since over half of cases occurred in jurisdictions without public health surveillance. That almost half of the cases occurred in five jurisdictions highlights the existence of blastomycosis hotspots, which are not well explained. Further study of *Blastomyces'* range and habitat are needed to inform clinical decisions and reduce misdiagnosis.

### Poster 252. In Vitro Activity of Novel Antifungal Olorofim against Filamentous Fungi and Comparison to Eight Other Antifungal Agents

**O. Georgacopoulos**[1], N.S. Nunnally[1], E.M. Ransom[2], D. Law[3], M. Birch[3], S.R. Lockhart[1], E.L. Berkow[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Association of Public Health Laboratories, Silver Spring, MD, USA, [3]F2G Ltd., Manchester, UK
**Background:** Olorofim is a novel antifungal drug that belongs to the orotomide drug class which inhibits fungal dihydroorotate dehydrogenase (DHODH), thus halting pyrimidine biosynthesis and ultimately DNA synthesis, cell growth and division. It is being developed at a time when many invasive fungal infections exhibit antifungal resistance or have limited treatment options. **Methods:** The goal of this study was to evaluate the in vitro effectiveness of olorofim against a large collection of recently isolated, clinically relevant mold isolates. In vitro

antifungal activity was determined for 246 azole-susceptible *Aspergillus fumigatus* isolates, five *A. fumigatus* with TR34/L98H-mediated resistance, 19 *Rhizopus* species isolates, 21 *Fusarium* species isolates, and one isolate each of six other species of mold. Olorofim minimum inhibitory concentrations (MICs) were compared to antifungal susceptibility testing profiles for amphotericin B, anidulafungin, caspofungin, isavuconazole, itraconazole, micafungin, posaconazole, and voriconazole. **Results:** Olorofim MICs were significantly lower than those of the echinocandin and azole drug classes and amphotericin B. *A. fumigatus* wild type and resistant isolates shared the same MIC50 = 0.008 µg/mL. In non-*Aspergillus* susceptible isolates (MIC ≤2 µg/mL), the geometric mean (GM) MIC to olorofim was 0.54 µg/mL with a range of 0.015–2 µg/mL. Olorofim had no antifungal activity (MIC ≥ 2 µg/mL) against 10% of the collection (31 in 297), including some isolates from *Rhizopus* spp. and *Fusarium* spp. **Conclusions:** Olorofim showed promising activity against *A. fumigatus* and other molds regardless of acquired azole resistance.

## Special Populations

### Poster 253. Seroprevalence and Associated Factors of Maternal Cytomegalovirus in Southern Ethiopia

**M. Hailemariam**[1,2,3], Z. Mekonnen[2], E. Loha[4], E. Padalko[3,5]
[1]School of Medical Laboratory Sciences, Hawassa University College of Medicine and Health Sciences, Hawassa, Ethiopia, [2]School of Medical Laboratory Sciences, Jimma University Institute of Health, Jimma University, Jimma, Ethiopia, [3]Department of Diagnostic Sciences, Ghent University, Ghent, Belgium, [4]Centre for International Health, University of Bergen, Bergen, Norway, [5]Laboratory of Medical Microbiology, Ghent University Hospital, Ghent, Belgium
**Background**: Maternal cytomegalovirus (CMV) infection continue to be a public health problem largely due to congenital transmission of the infection to the developing fetus. The study assessed the rate of maternal anti-CMV IgG and IgM antibodies and associated factors in Southern Ethiopia. **Methods**: A total of 600 consecutive pregnant women attending the delivery ward were recruited for the study at Hawassa University comprehensive and specialized hospital, Ethiopia. Mothers' sera were tested serologically for anti-CMV IgM and IgG by EUROIMMUN ELISA. Pregnant women responded to a questionnaire about their previous and current obstetric history and socio-demographic characteristics. Possible associated factors were assessed by bivariable and multivariable logistic regression. **Results:** Seropositivity for active CMV infection during pregnancy, IgM antibodies was 8.2% (49/600) (95% CI: 6 -10.5%), whereas the CMV IgG was 88.7% (532/600), (95% CI: 89.5 - 94.0%). Seroprevalence was higher in women of older age, currently unmarried and having nursery schooled children. Although, the significance of CMV-STI co-infections during pregnancy and whether co-infections increase intrauterine transmission of CMV remains unclear, our study showed active CMV seropositivity has a significant association with curable STIs among pregnant women. **Conclusion**: In the present study, we identified a high rate of CMV IgM and CMV IgG seroprevalence among pregnant women in southern Ethiopia. Given that there is no existing CMV diagnosis, special attention should be designed to pregnant women in parallel to the existing antenatal care facility. Besides, training health care professionals will support awareness conception among pregnant women concerning the sequels of CMV infection during pregnancy.

### Poster 254. Racial and Ethnic Differences in Potential Drivers of Mask Use Among Adults ≥18 Years — United States, May – November 2020

**G. Earle-Richardson**[1], K. Fisher[1], C. Nestor[1], C. Craig[1], D. Yee[1], R. Soelaeman[1], R. Calanan[1], P. Reese[1], G. Sunshine[1], M. Gakh[2], C. Prue[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]University of Nevada, Las Vegas, NV, USA
**Background:** While studies have identified a range of factors associated with mask wearing in the U.S., less is known about possible drivers of mask-wearing among racial and ethnic minority groups. This analysis assessed whether factors positively associated with wearing a mask (defined as having reported always wearing a mask in public during the prior week) differed between participants grouped by race/ethnicity (Hispanic, non-Hispanic Asian, non-Hispanic Black, non-Hispanic White). **Method:** Data were obtained from a U.S. internet panel survey of 3,217 respondents during May – November 2020 (weighted by race/ethnicity, age, gender and education). Within each of the four racial/ethnic groups, crude and adjusted odds ratios (COR, AOR) were calculated using logistic regression to assess factors (potential drivers) associated with wearing a mask. Nine psychosocial constructs were tested. Adjusted models controlled for age, gender, education, county COVID-19 case count, presence of a state-issued mask mandate and interview month. **Results:** The following variables were most strongly positively associated with mask wearing ($p<0.05$) in each racial/ethnic group: *Hispanic* (n=381) - seeing others wearing masks

(AOR: 6.7), importance of wearing a mask combined with social distancing (3.0); *non-Hispanic Black* (n= 345) - reporting hearing that one should wear a mask (AOR: 3.6), belief that wearing a mask would protect others from coronavirus (AOR: 5.1); *non-Hispanic White* (n=2,240) - seeing others wearing masks (AOR: 3.1), importance of wearing a mask to respondent (AOR: 2.3); *non-Hispanic Asian* (n=158) - belief that people important to them believe they should wear a mask (COR: 5.1, not significant). Across all four groups, variables relating to the idea that others wear masks or believe the respondent should were positively associated with mask wearing, however, the specific variables differed. **Conclusion:** Public health efforts to encourage mask wearing should consider the diversity of behavioral influences within different population groups.

### Poster 255. Raising Awareness of Neglected Tropical Diseases (NTDs) to Improve Healthcare for Migrants

**F. Berghenti**[1], A. Conciatori[2], M.A. Bandello[1], S. Banzola[1], R. Costantino[3], A. Balestrino[4]
[1]Spazio Salute Immigrati Azienda USL, Parma, Italy, [2]ICARE Project Azienda USL, Modena, Italy, [3]ICARE Project Regione Emilia-Romagna, Bologna, Italy, [4]Primary Care Department Azienda USL, Parma, Italy
**Background:** The study was performed in a primary care setting targeting migrants' health in Parma, Italy. Since 2016, 3435 newly arrived migrants from more than 50 countries were screened for STDs and NTDs in the Local Health Authority (LHA). Among them, 120 NTDs were diagnosed: 21 intestinal schistosomiasis, 27 urinary schistosomiasis, 52 soil-transmitted helminthiasis; 1 cutaneous leishmaniasis; 1 loa loa filariasis; 18 strongyloidiasis. Furthermore, 77 positive serologic tests for schistosomiasis were detected. The population was either from the Indian Subcontinent or Sub-Saharan Africa. NTDs are common among immigrants from endemic countries, yet there is lack of awareness among general practitioners (GPs) and paediatricians. The team planned activities within the I.C.A.R.E. European project (Integration and Community Care for Asylum and Refugees in Emergency) to raise awareness of these diseases through a culturally competent and health literate approach, and to improve primary healthcare for migrants. **Methods:** Twelve meetings involving 9 GPs and 3 paediatricians were carried out to highlight the importance of a culturally competent approach to healthcare in accordance with the National Guidelines. An experiential learning activity in the primary care setting followed. **Results:** The participants agreed on the importance of a thorough epidemiological assessment and an evaluation of the patient's medical history to prevent misdiagnosis. As a result, they identified key factors to consider when looking for NTDs: country of origin; living conditions and environment (e.g., poverty, rural origin); history of migration; migration route; education level; different expression of symptoms depending on the individual's culture. Secondly, the participants recognized the need to identify refugees and victims of human trafficking or torture among patients, since traumatic experiences could undermine patient's confidence. Lastly, they agreed on the need for an effective communication to deliver safe treatments to migrants. **Conclusions:** The meetings and the experiential learning activity improved knowledge of NTDs and pointed out the impact of patients' health literacy on the expression of symptoms. The I.C.A.R.E. team suggests providing a structured course on NTDs within LHAs.

### Poster 256. COVID-19 Vaccination Status and Willingness to Vaccinate in Guatemala-Mexico Transborder Crossers

**I. Bojorquez**[1], R. Leyva-Flores[2], R. Cortés-Alcalá[3], M. Arévalo[4], C. Rodriguez-Chavez[5], G. Rodriguez-Elizondo[3], S. Ward[6], R. Merrill[6], N. Bustamante[6]
[1]El Colegio de la Frontera Norte, Tijuana, BC, Mexico, [2]Instituto Nacional de Salud Pública, Cuernavaca, MOR, Mexico, [3]Secretaría de Salud, Ciudad de México, México, [4]Facultad Latinoamericana de Ciencias Sociales, Guatemala, Guatemala, [5]Research assistant, Sin Fronteras, Mexico City, Mexico, [6]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** A binational, multi-institutional transborder survey evaluating the impact of the COVID-19 pandemic on mobile populations at the Guatemala-Mexico border began implementation in September 2021. Transborder crossers include asylum-seekers, voluntary and involuntary repatriated migrants, and local nationals. COVID-19 vaccination status, willingness to be vaccinated, and associated factors are being evaluated. **Methods:** Through a time-venue sampling design, a cross-sectional questionnaire is administered to transborder crossers entering three Guatemalan border cities from Mexico (El Carmen, La Mesilla, and Tecún Umán) from September-November 2021. Eligibility criteria: age 18 years or older and having crossed from Mexico into Guatemala within the previous 12 hours. Preliminary data from September 15-October 8, 2021, are presented. **Results:** In total, 1,658 participants (85% eligible) were interviewed. Mean age was 36 years (SD=12.7), 39% were female, 32% indigenous and 0.3% afrodescendants. A majority reported being from Guatemala (90%) with 8% from Mexico. Fifty-one percent reported having received at least one dose of a COVID-19 vaccine. Of those who had not received a vaccine (49%), 53% were unwilling to receive a COVID-19 vaccine for reasons including fear of COVID-19 vaccine side effects

(50%), disbelief in vaccines (18%), fear of side effects of vaccines in general (17%), and disbelief in the effectiveness of the COVID-19 vaccine (11%). Multivariate analysis demonstrated people who had received at least a high school education were more willing to be vaccinated than those with no education (OR 4.29, p<.000). Compared to non-religious respondents, those who identified as Catholic (OR 0.59, p=.009) or affiliated with other religions (OR 0.55, p=.002) were less willing to be vaccinated. Sex, age, identification with an indigenous group, and main source of COVID-19 risk communications had no statistical significance in willingness to be vaccinated. **Conclusions:** Although 51% of respondents had received at least one dose of a COVID-19 vaccine, 26% of respondents were unwilling to receive a COVID-19 vaccine. Responses provide an opportunity on the use of data to improve education and messaging around safety and effectiveness of COVID-19 vaccines.

## Waterborne Diseases and Hand Hygiene

### Poster 302. Hand Hygiene Resources and Hand Hygiene Adherence among Healthcare Workers at Two Large Healthcare Facilities in the Dominican Republic

**C.D. Schnorr**[1,2], M. Lozier[3], M.J. de St. Aubin[1,2], C.J. Then Paulino[4], YV Cornelio Puello[4], D. Dumas[1,2], W. Duke[5], E. Zielinski Gutiérrez[6], R. Skewes-Ramm[4], E.J. Nilles[1,2,7]
[1]Brigham and Women's Hospital, Boston, MA, USA, [2]Harvard Humanitarian Initiative, Cambridge, MA, USA, [3]National Center for Emerging Zoonotic and Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Dirección General de Epidemiología, Santo Domingo, Distrito Nacional, Dominican Republic, [5]Universidad Nacional Pedro Henríquez Ureña, Santo Domingo, Dominican Republic, [6]Centers for Disease Control and Prevention, Central America Regional Office, Guatemala City, Guatemala, [7]Harvard Medical School, Boston, MA, USA
**Background:** Poor water, sanitation, and hygiene (WASH) conditions increase the risk of healthcare-associated infections (HAI). Healthcare facilities (HCFs) in low- and middle-income countries (LMICs) are more likely to lack essential WASH infrastructure and suffer high burdens of HAIs. Reaching 100% coverage of WASH infrastructure in HCFs in LMICs is among the 2030 Sustainable Development Goals. In preparation for initiating local production of alcohol-based hand rub (ABHR) in HCFs in the Dominican Republic, we assessed hand hygiene resources and adherence among healthcare workers (HCWs). **Methods:** Between April and July 2021, all patient care areas in two large hospitals were assessed using standardized electronic forms for availability and functionality of hand washing stations and ABHR dispensers. Trained enumerators directly observed WHO-defined hand hygiene adherence (HHA) among HCWs before and after contact with five patients per HCW. Hand hygiene adherence was defined as hand washing with soap and water or ABHR use for each observed hand hygiene opportunity. **Results:** Of 134 patient care areas assessed, 130 (97%) contained at least one hand hygiene resource and 58 (43%) contained a hand hygiene resource that was functional at the time of assessment. Among the patient care areas, 36 (27%) contained an ABHR dispenser and 30 (22%) contained an ABHR dispenser that was functional. HHA of 137 HCWs was observed during a total of 1,394 hand hygiene opportunities. HHA was 4.0% before patient contact and 27.4% after patient contact. Composite HHA was 14.4% for all hand hygiene opportunities. **Conclusion:** Most observed patient care areas and HCW/patient interactions did not meet standards for hand hygiene, indicating the need to strengthen HCW HHA and decrease the risk for HAIs. Limited hand hygiene resources likely contributes to low adherence.

## Late-breakers II

### Poster LB-43. *Angiostrongylus cantonensis* Meningoencephalitis in Three Pediatric Patients in Florida, USA

**M. Chance**[1], F. Bula[2], A.B. Thompson[1], C. Horvat[3], J. Green[3], J.E. Armstrong[1], A. Noel[1], F. Levent[1], R. Dudas[2], S. Martin[2], A. Samide[2], N. Marrero[2], K. Martinez[3], K. Stockdale[4], R.J. Chancey[5]
[1]AdventHealth for Children, Orlando, FL, USA, [2]Johns Hopkins All Children's Hospital, St. Petersburg, FL, USA, [3]St. Joseph's Children's Hospital, Tampa, FL, USA, [4]Florida Department of Health, Tallahassee, FL, USA, [5]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Eosinophilic meningoencephalitis caused by *A. cantonensis* has been reported in several southern U.S. states, but most human infections in the U.S. occur in Hawai'i. Exposure is typically via ingestion of infected snails or slugs. Definitive diagnosis requires visualization of larvae or positive cerebrospinal fluid (CSF) polymerase chain reaction (PCR). In Florida, *A. cantonensis* has previously been reported in rats and snails. The first published report of *A.* (*Parastrongylus) cantonensis* infection in Florida was in a non-human primate at a Miami zoo in 2003. We present the first known locally acquired human cases of *A. cantonensis* meningoencephalitis in Florida. **Methods**: Three meningoencephalitis cases were investigated by review of medical records. **Results:** Case 1: A 19-

month-old male presented in June 2021 with eleven days of malaise, fever, irritability, and inability to walk. At least one episode of pica with sand ingestion at a beach was reported. Initial CSF had pleocytosis with 8% eosinophils. Karius microbial cell-free DNA (mcfDNA) next generation sequencing (NGS) detected *A. cantonensis*. Confirmatory CSF PCR testing by CDC was positive. He recovered without sequelae after a 3-week steroid course. Case 2: A 10-year-old male presented in October 2021, one month after eating a snail, with symptoms of meningoencephalitis. He had CSF pleocytosis with 18% eosinophils. He required an external ventricular drain for increased intracranial pressure. Karius mcfDNA NGS detected *A. cantonensis*. He received steroids and albendazole and was discharged to rehabilitation. Case 3: A 9-month-old female presented in January 2022 with six days of emesis, lethargy, left-sided esotropia, and fever. She had no known exposures. CSF revealed pleocytosis with 41% eosinophils. Karius mcfDNA NGS detected *A. cantonensis*. She recovered without neurologic sequelae. None had pertinent out-of-state exposures during the time frame prior to illness. **Conclusions:** These patients represent the first known locally acquired human cases of *A. cantonensis* infection in Florida and were identified using a novel diagnostic method, plasma-based mcfDNA NGS. A. cantonensis should be considered for any patient with an appropriate clinical history and possible exposure risk, even in areas without previously known cases.

### Poster LB-44. Animal Models for the Study Therapeutics against Hantaan Virus Infection

**Y.J. Song,** C.H. Yu, S.H. Gu, J.E. Kim, H.S. Yun, S.H. Lee, G.H. Hur, Y.H. Lee
Agency for Defense Development, Yuseong, Daejeon, Korea

**Background**: Hantaan virus (HTNV) causes hemorrhagic fever with renal syndrome (HFRS). Effective antiviral treatments against HTNV infection are limited. The development of antiviral strategies for HTNV has been partly hampered by the lack of efficient animal models to evaluate the efficacy of the candidate antiviral drugs. In this study, we presented a lethal animal model and an asymptomatic animal infection model of HTNV. **Methods**: The animal experiments were performed at the bio safety level 3 facility. ICR mice were inoculated with HTNV via intracranial (IC) or intraperitoneal (IP) route. The median lethal dose value of HTNV was calculated by probit analysis of deaths occurring within two weeks. Animals were monitored daily signs of morbidity and mortality throughout the study. Mice were sacrificed and lung tissues were harvested every week after challenge. Viral RNAs were analyzed by RT-PCR. Indirect fluorescent antibody test was performed on serum samples taken on weeks 0 to 4 post-infection. **Results**: 20-day-old ICR mice began to die 8 days after intracranial inoculation of HTNV. The lethal dose required to kill 50% of the mice ($LD_{50}$) was calculated to be 2.365 PFU/head. Serum samples from adult ICR mice injected with HTNV were positive for HTNV specific antibody two weeks after IP challenge, indicating that the animals were infected when challenged with HTNV. Viral RNA began to be detected in lung tissue a week after infection. **Conclusions**: In this study, we established animal models for HTNV. In adult ICR mice, HTNV intraperitoneal challenge led to asymptomatic infection and seroconversion. Infection of 20-day-old ICR mice with HTNV by intracranial route led to lethal neurological disease. These *in vivo* models are helpful to evaluate the efficacy of therapeutics against HTNV.

### Poster LB-45. Assessment of the Acceptability of the Vaccine against SARS-CoV-2 Virus Infection in DR Congo

**I.L. Nkwalabote**[1,2], R.M. Badiambile[3,4]
[1]National Dracunculiasis Eradication Program, Kinshasa, Democratic Republic of Congo, [2]African Centers for Disease Control and Prevention, Addis Ababa, Ethiopia, [3]Faculty of Medicine and Public Health, Official University of Mbujimayi, Kasaï Oriental, Mbuji Mayi, Democratic Republic of Congo [4]Democratic Republic of the Congo, Regional Research and Medical Benefit, Atlanta, GA, USA

Background: Vaccination is one of the pillars of good population health, especially when you consider that vaccines are often the best. Equitable access to safe and effective vaccines is essential to ending the pandemic of the SARS-CoV-2 virus infection. This study aims to assess the knowledge and acceptability of the vaccine against the SARS-CoV-2 virus infection in Mbujimayi. Methods: This was a descriptive & cross-sectional study conducted from December 18, 2021 to February 18, 2022 including 962 investigated. Data analysis was achieved with SPSS software package, version 25.0. Results: In this study 99.2% investigated know about the new SARS-CoV-2 virus as well as the mode of contamination; 76.2% were for modern treatment and 51.3% were for prayer; 83.6% were informed of the availability of the SARS-CoV-2 virus vaccine and 61.2% did not accept to be vaccinated and to have these family members vaccinated once the vaccine available in mbujimayi; 58% were concerned about side effects; 70.5% believed the vaccine cannot be safe; 71.5% believed in traditional remedies; 43.5% believed the process of developing a vaccine should be 25 months and more for them to be comfortable accepted a vaccine; 63.6% thought that the new vaccine is not effective and has dangers; 53.4% had not chosen the vaccine, 27.2% was for Astrazeneca , 10.1% for Moderna,5.7% for Pfeizer, 3.5% for Johnson and

Johnson; 47.5% preferred if studies prove the vaccine is safe and effective can encourage them to get vaccinated; 51.7% preferred oral vaccine and 72.6% preferred if vaccine was developed in Africa would make them feel comfortable getting vaccinated. Conclusion: According to the results, sensibilization should be focused on the importance of the vaccine against SARS-CoV-2 virus infection.

### Poster LB-46. Characterization of Household SARS-CoV-2 Transmission in Minnesota for Alpha, Delta, and Omicron Variant Waves

**Z. Zirnhelt**, A. Markelz, A. Fell, K. Morris, S. Seys, K. Como-Sabetti, S. Meyer
Minnesota Department of Health, Saint Paul, MN, USA

**Background:** Over 925,000 COVID-19 cases, including more than 5,000 deaths were reported to the Minnesota Department of Health from 03/2021 – 03/2022. Although children have a lower risk of severe COVID-19 disease than adults, understanding of transmission between adults and children within households is limited. This analysis sought to characterize transmission in households during Alpha, Delta, and Omicron variant of concern (VOC) waves. **Methods:** Using a multivariate logistic regression, we examined the odds of an adult index case compared to a child index case within a household for each VOC wave. VOC waves were defined as consecutive weeks when a VOC represented ≥50% samples sequenced among MN residents, and most children were in-person learning. Households were defined as private residences with ≥1 child and ≥1 adult with laboratory confirmed COVID-19 at the same address. Addresses with >6 cases were excluded as they may represent unknown congregate living settings. If households had multiple separate transmission events, only the first was included. **Results:** A total of 680,427 cases were included (106,434 Alpha, 233,656 Delta, 340,337 Omicron). After identifying households with transmission events, 54% of household index cases were adults and 48% of all subsequent cases were adults. As transmission progressed within households, there was a significant increase in the proportion of child subsequent cases. During the Alpha wave, adult cases had 2.98 (95% CI: [2.78, 3.19]) higher odds of being an index case after adjusting for race/ethnicity, gender, geographical region, and total household cases. However, during Delta and Omicron waves, there were no differences between the odds of adult and child household members being the index case. **Conclusions:** We characterized household transmission for the three VOC waves of COVID-19 disease in Minnesota. Adjusted odds ratios indicated adults had higher odds of being the household index case during the Alpha wave but did not have higher odds during Delta and Omicron waves. This analysis provides insight about COVID-19 transmission within households during the Alpha, Delta, and Omicron VOC waves. Future analyses should be conducted to further examine potential contributors to household transmission including uptake of COVID-19 vaccine

### Poster LB-47. Comparison of Pediatric Influenza- and COVID-19-Associated Hospitalizations in Two Counties in Connecticut, FluSurv-NET and COVID-NET

**T. Carter**, K. Yousey-Hinde
Connecticut Emerging Infections Program, Yale School of Public Health, New Haven, CT, USA

**Background:** Rates of COVID-19-associated hospitalizations increased in children during the Omicron period of the pandemic. Our objective was to compare characteristics of influenza- and COVID-19-associated hospitalizations among pediatric cases (<18 years). **Methods:** FluSurv-NET and COVID-NET are population-based active surveillance networks that collect data on influenza- and COVID-19-associated hospitalizations. A case was defined as a pediatric resident of New Haven or Middlesex County, Connecticut, admitted to an acute-care hospital, with a positive influenza or SARS-CoV-2 test within two weeks before admission or during hospitalization. Data from FluSurv-NET for the 2017-18, 2018-19, and 2019-20 surveillance seasons (October-April) were compared to COVID-NET data from March 2020 to April 2022. Data included demographics, length of stay, intensive care unit (ICU) admission, underlying medical conditions, and signs and symptoms present at admission. **Results:** During the surveillance periods, 177 influenza- and 215 COVID-19-associated hospitalizations were identified. The highest monthly rate of COVID-19 cases was 24.8 per 100,000 children in January 2022, during the omicron period. For influenza, it was 14.9 per 100,000 children in February 2020. The median age of influenza cases was lower than COVID19 cases (5 vs 9 yrs,; $p<0.001$). Cases differed by race/ethnicity ($p=0.039$). The largest influenza group was non-Hispanic White (36.2%), while the largest COVID-19 group was Hispanic of any race (40.9%). COVID-19 cases were more likely to report no signs or symptoms compatible with acute viral infection at admission than influenza cases (24.2% vs 0%; $p<0.001$). Comparing the 161 COVID-19 cases with symptoms to the influenza cases, no additional differences were found. ICU admission, mechanical ventilation, length of stay, and outcome were not significantly different. **Conclusions:** Hospital course and death were similar between influenza and COVID-19 cases. However, demographic characteristics differed between the groups with influenza cases more likely to be younger and non-Hispanic White. All influenza cases were symptomatic at admission while many

COVID-19 cases were not. This could be due to screening practices detecting infections in patients admitted for other reasons.

### Poster LB-48. Delivering Actionable Infodemic Insights and Recommendations for the COVID-19 Pandemic Response

**T. Purnat,** A. Ishizumi, B. Yau, B. White, C. Bertrand-Ferrandis, S. Briand, T. Nguyen
World Health Organization, Geneva, Switzerland

**Background:** The COVID-19 infodemic has manifested itself in the rapid spread of questions, concerns and misinformation that can affect population attitudes and behavior harmful to health—from promoting stigma and discrediting science, to promoting alternative, non-recommended treatment and cures to politicizing public health programs and eroding trust in healthcare personnel and health systems. WHO's COVID-19 incident management support team's Pillar 2 (risk communication, community engagement and infodemic management) developed an integrated public health infodemic analysis and insights methodology for weekly analysis of social media, traditional media data and other data sources to identify, categorize, and understand the key concerns and narratives expressed, and inform risk communication and response activities. **Methods:** The infodemic characterization, integrated analysis and insights generation consisted of a 3-step mixed-methods approach. First, data was collected from publicly available social and news media sources and categorized into categories of conversations as per a COVID-19 public health taxonomy to quantitatively identify potential topics of concern and information voids. Second, the dataset was analyzed qualitatively and compared week-on-week to identify narratives and their changes, characterize sentiment changes in the conversation, and supplemented with user searches in google trends to produce a digital infodemic intelligence report. Third, the digital infodemic intelligence was reviewed by a group of subject matter experts and triangulated with other data sources to derive infodemic insights and provide recommendations for action for the week. The methodology has been applied to COVID-19 response, specifically for COVID-19 vaccine demand promotion, and to inform preparing for acute public health events around mass gatherings or mass immunization campaigns. **Results:** By 25 April 2022, 107 weekly digital infodemic intelligence reports were produced and disseminated. Over time, they were improved with increased data segmentation to ensure that narratives outside of regions and countries with high-volume conversations are more readily detectable. In addition, multiple ad-hoc digital intelligence reports were produced based on emerging topics of interest. The public health taxonomy for analysis of COVID-19 conversations was further adapted and localized to deliver digital infodemic intelligence reports in 18 countries across four WHO Regions, including the Philippines, Indonesia, Canada, and Mali among others. The taxonomy was also tested and implemented for automated social listening approaches on the pilot WHO platform EARS (Early AI-supported response with social listening). **Conclusions:** The development and application of analytical methodologies for infodemic intelligence generation and integration during WHO's COVID-19 response has introduced evidence-based analytical practices for generation of infodemic insights and recommendations for action into the work of WHO IMST's Pillar 2. The methodology must be further adapted for use by different health programmes and preparedness functions and is expanded in the first version of the US CDC and WHO Field Infodemiology Manual.

### Poster LB-49. Effect of COVID-19 Vaccination on COVID-19 Mortality in Georgia

**B. Bogdanovich**[1], J. Pollock[2], M.E. Maloney[1], L. Langston[1], J. Yu[1]
[1]Medical College of Georgia, Augusta, GA, USA, [2]Edward Via College of Osteopathic Medicine, Auburn, AL, USA

**Background:** As with most infectious diseases, the elderly have a higher mortality rates with the coronavirus disease 2019 (COVID-19) due to increased comorbidities. Therefore, vaccination efforts prioritized immunizing older individuals. The purpose of this study was to determine the association between vaccination and age as a risk factor for COVID-19 mortality. **Methods:** Data pertaining to COVID-19 cases, deaths and vaccinations were obtained from the Georgia Department of Public Health's COVID-19 Status Report from February 1st, 2020 to March 23rd, 2022. The data was then organized based on three discernable periods of increased mortality rates, corresponding to alpha, delta, and omicron variant disease. Comparative analyses between mortality rates for each wave were conducted to identify gross trends and assess relative mortality burden between age groups. Superimposing vaccination trends allowed mortality rates during the omicron wave to serve as the vaccination mortality group. **Results:** Arranged temporally, relative mortality burden among each age group remains statistically constant with a predilection for older populations during the first two variant waves. This trend breaks during the period associated with the omicron wave. During this period, the data show a skewed distribution with the greatest relative mortality in the 60–69-year-old group, accounting for 24.57% of omicron deaths. Further, there was no statistical difference in mortality between age groups after age 59. **Conclusions:** Before widespread availability of

the COVID-19 vaccine, increasing age demonstrated a positive relationship with mortality rate. The omicron variant was the first COVID-19 wave after most Georgia residents had been vaccinated, and it is during this time that survival rates could not be predicted based on age. Vaccination eliminated age as a risk factor after the 50-59 age group in the omicron variant with no statistically significant difference between groups after that age.

### Poster LB-50. Withdrawn

### Poster LB-51. Exploring the Thermal Limits of Malaria Transmission in the Western Himalaya

**F. Mozaffer**[1,2], G.I. Menon[1,2,3,4], F. Ishtiaq[5]
[1]The Institute of Mathematical Sciences, CIT Campus, Taramani, Chennai, Tamil Nadu, India, [2]Homi Bhabha National Institute, Training School Complex, Anushaktinagar, Mumbai, Maharashtra, India, [3]Departments of Physics & Biology, Ashoka University, Rajiv Gandhi Education City, National Capital Region, Sonepat, Haryana, India, [4]Centre for Climate Change and Sustainability (3CS), Ashoka University, Rajiv Gandhi Education City, National Capital Region, Sonepat, Haryana, India, [5]Tata Institute for Genetics and Society, New InStem Building, Bangalore, Karnataka, India
**Background**: Malaria transmission dynamics is highly driven by the environmental temperature. Using detailed temperature records from four sites (1800-3200m) in the western Himalaya, we studied how temperature regulates parasite development rate (the inverse of the extrinsic incubation period, EIP) in the wild. We study the thermal limits of transmission for avian (*P. relictum*) and human Plasmodium parasites (*P. vivax* and *P. falciparum*) as well as for two malaria-like avian parasites, Haemoproteus and Leucocytozoon. **Methods**: A thermodynamic model that describes the nonlinear relationship between developmental rate and temperature, for five blood-borne parasites and their arthropod hosts is employed to understand the effect of mean temperature and diurnal temperature range on transmission dynamics. For this we use a parametrization of the EIP proposed by Briére et al. (1999), using Bayesian inference methods to estimate the relevant parameters using prior knowledge assembled using an extensive literature search. **Results:** We demonstrate that temperature conditions can substantially alter the incubation period of parasites at high elevation sites (2600-3200m) leading to restricted parasite development or long transmission windows. We then compare estimates of EIP based on measures of mean temperature versus hourly temperatures to show that EIP days vary in cold versus warm environments. We use temperature projections from a suite of climate models to predict that by 2040, high elevation sites (~ 2600 m) will have a temperature range conducive for malaria transmission, albeit with a limited transmission window. **Conclusions**: Using measures of mean temperature versus the diurnal fluctuating temperature in the field, we demonstrated both spatial and temporal variation in malaria transmission risk in the western Himalayan region. Our study highlights the importance of accounting for fine-scale thermal effects in the expansion of the range of the malaria parasite with global climate change.

### Poster LB-52. Fatality Assessment and Variant Risk Monitoring for COVID-19 Using Three New Hospital Occupancy-related Metrics

**P.W. Zhang**[1*], S.H. Zhang[1,4], W.F. Li[1], C.J. Keuthan[1], S. Li[1], F. Takaesu[1], C.A. Berlinicke[1], J. Wan[2], J. Sun[3], D.J. Zack[1*]
[1]Wilmer Eye Institute, Johns Hopkins University School of Medicine; Baltimore, MD, USA, [2]Department of Medical and Molecular Genetics, Center for Computational Biology and Bioinformatics, Indiana University School of Medicine, Indianapolis, IN, USA, [3]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [4]Department of Computer Science, University of Maryland at College Park, College Park, MD, USA
**Background:** Though case fatality rate (CFR) is widely used to reflect COVID-19 fatality risk, it's use is limited by large temporal and spatial variation. Hospital mortality rate (HMR) is also used to assess the severity of COVID-19, but HMR data is not directly available except 35 states of USA globally. Alternative metrics are needed for COVID-19 severity and fatality assessment. To address this need, and improve existing methods, we here propose three new, alternative and complementary measurements for COVID-19 fatality risk evaluation, early CFR variation analysis, and dynamic monitoring. **Methods:** New metrics and their applications in fatality measurements and risk monitoring are proposed here using publicly available data including daily hospital occupancy. We also introduce a new mathematical model to estimate average hospital length of stay for death (L-dead) and discharges (L-dis). Multiple data sources were used for our analysis. **Results:** 1. We propose three new metrics, hospital occupancy mortality rate (HOMR), ratio of total deaths to hospital occupancy (TDHOR) and ratio of hospital occupancy to cases (HOCR), for dynamic assessment of COVID-19 fatality risk. 2. Estimated average hospital length of stay for death (L-dead) and discharges (L-dis) for 501,079 COVID-19 hospitalizations in US 34 states between Aug 7, 2020 and Mar 1, 2021 were18.2 (95%CI:17·9-18·5) and 14.0(95%CI:13·9-14·0) days respectively. 3. We found that TDHOR values of 27 countries are less spatially and temporally variable and more capable of detecting changes in COVID-

19 fatality risk. The dramatic changes in COVID-19 CFR observed in 27 countries during early stages of the pandemic were mostly caused by undiagnosed cases. 4. Compared to the first week of November 2021, the week mean HOCRs (mimics hospitalization-to-case ratio) for Omicron variant decreased 34.08% and 65.16% in the United Kingdom and USA respectively as of Jan 16, 2022. **Conclusions:** 1. Our new metrics, HOMR and TDHOR, mimic HMR for COVID-19 fatality risk assessment but utilize readily available data for many US states and countries around the world. HOCR mimics hospitalization-to-case ratio for COVID-19. 2. The results of this study can aid county, state, and national leaders in making informed public health decisions related to the ongoing COVID-19 pandemic. 3. We provide evidence that explains why COVID-19 CFR has such dramatic changes at the beginning of a COVID-19 outbreak. 4. We have additionally provided new metrics for COVID-19 fatality risk dynamic monitoring including Omicron variant and showed that these metrics provided additional information.

### Poster LB-53. Intradermal Vaccination with F-VLP Microparticles Elicits Th-1 Biased Immune Response

**S.R. Patil**[1], I.J. Menon[1], S.M. Kang[2], M.J. D'Souza[1]
[1]Mercer University, Vaccine Nanotechnology Laboratory, Center of Drug Delivery Research, College of Pharmacy, Atlanta, GA, USA, [2]Georgia State University, Center for Inflammation, Immunity and Infection, Atlanta, GA, USA
**Background:** Respiratory syncytial virus (RSV) causes thousands of cases and deaths in infants and older adults annually. Past vaccine trials for RSV using the formalin-inactivated virus ended in tragic failure triggering Th-2 skewed immune response and causing more susceptibility to the virus in infants. Our vaccine utilizes microneedles incorporating a non-virulent subunit antigen candidate like F-protein virus-like particles (F-VLP) which induces a Th-1 skewed immune response. This approach will be more patient compliant as opposed to invasive intramuscular route of administration. **Methods:** Formulation of microparticulate vaccine was done with double emulsion method using a biodegradable polymer, F-VLP, and adjuvants. Microparticles were incorporated in dissolving microneedles and mice were immunized with the microneedle vaccine. Microparticulate vaccine was tested for immunogenicity, antigen uptake and antigen presentation in vitro in immune cells. Further, mice were challenged with RSV A2 virus after immunization. Mice serum and lung homogenates was analyzed for the presence of IgG, IgG subtypes, and IgA using ELISA. Mice Spleen and lymph nodes were analyzed for presence of CD4 and CD8a T cells using flow cytometer. **Results:** In vitro testing showed an upregulation of MHC I, II, and autophagosomes in the cells treated with vaccine microparticles. These are critical innate and adaptive immune markers. Ratio of IgG2a/IgG1 indicated significantly elevated levels of IgG2a in serum and lung homogenates of vaccinated mice signifying Th-1 skewed immune response. High IgA levels in the lung homogenates of vaccinated mice revealed humoral immunity. CD8a T cells which play a critical role in viral clearance were significantly higher in vaccinated mice further signifying Th-1 skewed response. **Conclusion:** The F-VLP microparticle-loaded microneedles were able to induce a robust humoral and cellular immune response. Thus, in the absence of a licensed vaccine, the microparticle-loaded microneedles will be a powerful tool for pain-free immunization against RSV, especially in infants.

### Poster LB-54. Investigation of Patient and Viral Characteristics Associated with SARS-CoV-2 Vaccine Breakthrough Infections in Atlanta, GA

**L.R. Carmola**[1], A. Roebling[2,3], D. Khosravi[1], R.M. Langsjoen[1], E. Wang[1], Y. Lu[1], Z. Zheng[4], R. Zhang[4], P. Nguyen[5], R.A. Arthur[6], E. Fitts[1], D.A. Gulick[7], D. Higginbotham[7], K. Openo[3], A. Taz[1], C. Kraft[1,5], J.J. Waggoner[5], A. Babiker[1,5], A. Piantadosi[1,5]*
[1]Department of Pathology and Laboratory Medicine, Emory University School of Medicine, Atlanta, GA, USA, [2]Georgia Emerging Infections Program, Georgia Department of Health, Atlanta, GA, USA, [3]Atlanta Veterans Affairs Medical Center, Atlanta, GA, USA, [4]Department of Biostatistics and Bioinformatics, Rollins School of Public Health, Emory University, Atlanta, GA, USA, [5]Division of Infectious Diseases, Department of Medicine, Emory University School of Medicine, Atlanta, GA, USA, [6]Emory Integrated Computational Core, Emory University School of Medicine, Atlanta, GA, USA, [7]Georgia Clinical & Translational Science Alliance, Emory University School of Medicine, Atlanta, GA, USA
**Background:** SARS-CoV-2 vaccines are highly effective. Nevertheless, infections occur in vaccinated individuals. Studies investigating post-vaccine infections during periods of multiple circulating variants of concern and variants of interest have been limited, and the results have been mixed. Here, we characterized host and viral features of post-vaccine infection caused by two predominant lineages, alpha and delta, during a period of co-circulation in Atlanta, GA. **Method:** Between March 22 and July 16, 2021, forty-four vaccinated and 147 unvaccinated SARS-CoV-2 positive individuals were identified within the Emory Healthcare System. Residual nasopharyngeal swabs were used for full viral genome sequencing, and medical records were reviewed. **Results:** The median time from final vaccine dose to positive COVID-19 test was 94 days (range 15-176). Vaccinated individuals with post-vaccine

infections, compared to unvaccinated individuals, were significantly older (median 57.5 years vs 42.0 years, p<.0001) and immunocompromised (13.5% were immunocompromised and 35.9% had diabetes vs 3.3% and 15.4%, respectively). Full SARS-CoV-2 genomes were analyzed from 29 vaccinated and 147 unvaccinated individuals. Phylogenetic analysis revealed that sequences from vaccinated individuals did not cluster together and generally belonged to the predominant lineage of the time: alpha (March 22- June 19) and delta (June 20-July 16). No mutations, insertions, or deletions across the SARS-CoV-2 genome were associated with post-vaccine infections. There was no difference in SARS-CoV-2 RT-PCR cycle threshold ($C_T$) between vaccinated (n=32, median Ct=20.7, interquartile range (IQR)- 10.3) and unvaccinated individuals (n=94, median Ct=24.0, IQR= 7.0; p=0.34), however, sgRNA abundance was proportionally lower in vaccinated compared to unvaccinated individuals (p=0.0001); further studies are needed to understand the implications of this finding. **Conclusions:** Overall, the results of this study suggest that there is little to no association of specific viral genomic factors with post-vaccine infections of SARS-CoV-2 alpha and delta lineages in Atlanta, GA. Host factors including age and immunodeficiency are clearly risk factors, and the role of sgRNA in post-vaccine infections warrants further study.

### Poster LB-55. Modelling the Impact of Mobility Restrictions and Vaccination on the COVID-19 Epidemic in Sri Lanka

**P. Jayasundara**[1], S. Dhanapala[2], M. Kato[2], S. Shinde[2], P. Wijesinghe[2], P. de Silva[2], C. Wijesundara[2], M. Abayawardana[1], E.S. McBryde[3], M.T. Meehan[3], A. Hughes[1], R. Ragonnet[1], J.M. Trauer[1]
[1]School of Public Health and Preventive Medicine, Monash University, St. Kilda, Australia, [2]World Health Organization Regional Office for Southeast Asia, New Delhi, India, [3]Australian Institute of Tropical Health and Medicine, James Cook University, Townsville, Australia
**Introduction:** With the spread of Alpha and Delta variants of concern (VoC), Sri Lanka experienced a substantial increase in COVID-19 cases that prompted the government to implement mobility restriction measures and a COVID-19 vaccination campaign to regain epidemic control. In this study, we aim to assess the impact of imposing movement restrictions and vaccination in curtailing the COVID-19 epidemic in Sri Lanka, to inform future public health policy development. **Methods:** A modified susceptible-exposed-infectious-recovered compartmental model was developed that included two sequential incubation and infectious periods, with stratification by clinical state. The model further captured processes such as contact tracing, the interaction of multiple VoC and waning of vaccine- and infection-induced immunity. We implemented scenarios reflecting mobility restrictions introduced at different time points and lasting for different durations than to the actual restrictions implemented in Sri Lanka and also counterfactual scenarios reflecting no vaccination or no mobility restrictions being implemented. **Results:** The model successfully captured the changes in notifications and infection deaths observed in Sri Lanka through the second and third epidemic waves. The model results indicated that the high COVID-19 vaccination rates and the mobility restrictions imposed in Sri Lanka contributed substantially towards controlling the COVID-19 epidemic. Simulations further suggested that implementing restrictions earlier and shortly after the resurgence in case numbers was identified or maintaining restrictions for longer resulted in better control of the epidemic without overwhelming health care capacity. **Conclusions:** Despite their major social and economic consequences, our counterfactual scenario projections found a substantial epidemiological effect of the interventions implemented in Sri Lanka, including the high vaccination rates and the movement restrictions.

### Poster LB-56. Persistence of Antibody Responses to SARS-CoV-2 in COVID-19 Patients: A Report up to 06 Months after Infection

**S.A.H.M. Abdullah**[1], S.C.K. Daniels[2], N. Jubaida[3], R. Raihan[4], M.S. Islam[4], M. Murshed[4], M.M. Anwar[2], M.G.D. Harun[5]
[1]South Asia Field Epidemiology &Technology Network (SafetyNet) Bangladesh Country Office, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention (CDC), Bangladesh Country Office, Dhaka, Bangladesh, [3]Armed Forces Institute of Pathology, Dhaka, Bangladesh, [4]American Society of Microbiology (ASM), Dhaka, Bangladesh, [5]icddr,b, Dhaka, Bangladesh
**Background:** Limited information is available about antibody persistence and correlated factors in COVID-19 survivors, which limits the serological diagnosis and prognosis prediction. We aimed to estimate the presence and persistence of anti-SARS-CoV-2 specific antibodies among COVID patients. **Methods:** We tested 161 RT-PCR positive COVID-19 patients of two hospitals on the 5th, 8th, 14th days, and 2$^{nd}$ and 6$^{th}$ months after symptom onset or RT-PCR positivity for asymptomatic cases. **Results:** Clinically there were 32% asymptomatic (having contact history), 43% mild, 16% moderate and 9% severe COVID-19 cases; 27% had at least one co-morbidity. At 5$^{th}$ day, IgM was positive in 40% and 48% in two rapid kits respectively whereas IgG was found 35% and 24%. IgM was higher until 2 months, but at six months, IgG was higher than IgM in both kits (70% and 55%). Both IgM and IgG

decreased by 25% from two months to six months. At 14 days, IgM positivity was observed among severe cases, above 50 years and in patients with co-morbidities ($p>0.05$). **Conclusions:** Project results suggest that antibody tests can be helpful for disease confirmation two weeks after infection and in the formulation of vaccination strategies.

### Poster LB-57. Preventing Vector-borne Diseases at Major Sport Events: Addressing the Challenges for FIFA22 in Qatar

**D. Bansal**[1], F. Schaffner[1], M.H.J. Al-Thani[1], H. Al-Romaihi[1], E.A.B. Abd Farag[1]
[1]Health Protection & Communicable Diseases Division, Ministry of Public Health, Doha, Qatar, [2]Francis Schaffner Consultancy, Riehen, Switzerland

**Background:** The 2022 FIFA World Cup Qatar has necessary requirements for the prevention and preparedness for any potential disease transmission, including vector-borne diseases (VBDs). VBDs have re-emerged worldwide due to urbanization, increase in travel and climate change, becoming a major and serious threat to global public health. **Methods:** We examined the current status of vectors and VBDs of public health importance in Qatar, based on a systematic literature review and snapshot survey. **Results:** The literature reveals that no locally transmitted VBD cases recorded in Qatar, but cases were recorded among expatriate workers and travellers who returned from an endemic country. The results of the adult mosquito trappings show that southern house mosquito *Culex quinquefasciatus* is the most widespread and abundant mosquito species, followed by *Cx. perexiguus*, both representing a risk of West Nile virus transmission. *Anopheles stephensi* is widespread in urbanized areas, suggesting a risk of local malaria transmission. The wetland mosquito *Aedes caspius* is also widespread, representing a risk of Rift Valley fever virus transmission. The dengue vector *Ae. aegypti* was not detected, suggesting a minimal risk for local transmission of dengue, chikungunya and Zika viruses. Interestingly, the study detected *Culiseta longiareolata* for the first time in Qatar. **Conclusions:** Overall, Qatar benefits currently from a good surveillance of VBDs and has some capacities in vector control. Regular field studies are needed to further address the knowledge gaps in terms of distribution, ecology, and biting habits of different mosquito species currently present in Qatar to accurately assess the risk of mosquito-borne diseases.

### Poster LB-58. Role of Cross-reactive Dengue and Japanese Encephalitis Antibody in Zika Virus Infection: A Prospective Study during Zika Epidemic in Thailand 2017

**R. Buathong**[1], H. Kanjanasombut[1], S. Wacharapluesadee[2]
[1]Department of Disease Control, Ministry of Public Health, Bangkok, Thailand, [2]Thai Red Cross Emerging Infectious Diseases Clinical Center, Chulalongkorn University, Bangkok, Thailand

**Background:** Zika virus is a global public health issue. Sporadic cases of Zika virus have been reported annually in Thailand since 2010 in limited areas during the rainy season. However, it is not apparent why there has been no big outbreak of Zika virus in Thailand as is the case in Brazil. It has been proposed that this is due to cross reactivity of viruses within the flavivirus family such as dengue and Japanese encephalitis viruses due to high similarity of antigens. This may be resulting in reduced infectivity of zika virus in Thai population. **Methods:** We conducted a prospective study in Thailand 2017 during outbreak. Subjects in the study included any Zika virus patient, and all the contacts, including villagers from their village older than 15 years of age from 7 provinces cover all parts of the country. Urine, blood and patient data from subjects were collected at once on screening day (Day 0) and second time on Day 21 during follow-up. Specimens were tested for Zika and Dengue virus using real-time PCR, and Dengue virus and JE virus serology was performed in Zika PCR positive specimens by ELISA. **Results:** Specimens were successfully collected on both Days 0 and 21 in 400 of 464 (86.4%) enrolled subjects. Of these, 53 subjects (13.2%) were infected with Zika virus but negative Dengue virus by real-time RT-PCR. Almost half of these subjects were asymptomatic (26/53; 49.05%). The most common symptoms included rashes (96.2%), joint pains (74.1%), myalgia (52.0%), fever (48.1%), and conjunctivitis (24%). Average age of Zika patients found in this study was 45 years [15-79 years], with more female patients (58.5%). Anti-dengue IgM performed by ELISA on positive specimens from first and second visit were 5.66% and 7.55%, respectively. But as forecast, anti-dengue IgG by ELISA, the positive specimens from the first and second visit were 98.11% and 98.11%, respectively. For anti-JEV IgM by ELISA revealed positive in first and second samples were 39.62% and 43.40% respectively. And anti-JEV IgG by ELISA from first and second samples were 100.00% and 98.11% respectively. **Conclusions:** The high rate of dengue IgG in Zika positive cases suggests secondary flavivirus infection. Further, the number of asymptomatic cases of zika in Thailand was lower than the rate in Yap Islands, Micronesia (80%) in 2007, where the first zika virus outbreak was reported. From this, it may be hypothesized that the lower rate of asymptomatic cases in Thailand may be because Thai people have existing antibodies against Zika virus. Further serological study is needed, and high accuracy method to detect Zika virus and the antibodies is required, for better understanding of the pathogenesis of zika virus and congenital zika syndrome.

### Poster LB-59. SARS-CoV-2 Omicron Variant Outbreak and Response in a High School, Houston, Texas – December 2021

**A.M. Oladimeji,** M. Stancil, R. Polara, L. Kunney, M. Mark-Osondu, S. Bhandari, C. Hundley, T. Olumuyiwa, K. Short
Houston Health Department, Houston, TX, USA

**Background:** The Houston Health Department (HHD) received call from a school nurse on 17th December 2021. The nurse reported receiving an increased number of COVID-19 positive results among students. HHD deployed epidemiologists to the school to verify the occurrence of an outbreak, investigate and institute control measures. **Methods:** Epidemiological investigation was conducted, nurse's record was reviewed, cases interviewed, and contacts identified. Testing teams were deployed onsite to obtain nasal swabs from exposed persons. SARS CoV-2 Polymerase Chain Reaction (PCR) Reverse Transcriptase test was conducted with sequencing of all positive results to determine variant. Environmental cleaning with disinfection was also conducted. Data was collected and analyzed. **Results:** School held an indoor games event on December 11, 2021, with COVID-19 transmission precautionary measures unobserved. School nurse's records revealed a total of 54 positive athletes and cheerleaders testing positive between Dec13-17, 2021. Their mean age was 16±2 years. Eleven (34%) girls from the female basketball team, 9 (15%) track/cross country and 11 (10%) cheerleaders/dance group members reported positive COVID-19 PCR test result. Forty-four (81%) were symptomatic. Common symptoms reported were headache and sore throat. Onsite testing was conducted among 162 students, 34 (21%) were positive for COVID-19. Sequencing revealed Omicron variant in all 34. Two-thirds of the positive students were yet to receive a complete series of COVID-19 vaccine. Games and athletic events were suspended until after the holiday break. **Conclusion:** COVID-19 spreads fast in congregate indoor settings, close contact games can be a predisposing factor. Occurrence of COVID-19 is higher among unvaccinated individuals. Surveillance testing and vaccination are important tools that need to work together.

### Poster LB-60. Spatial and Temporal Dynamics of Cholera Epidemics in Lake Tanganyika Areas from 2008 to 2021

**S. Mako Mbokolo**[1], N. Taty[2,3], D. Batumbo[4] , P. Welo[2], T. Vita [4], N. Meschnet de Richmond[3], D.Bompangue [4]
[1]Master 1 in Ecology of Infectious Diseases, University of Kinshasa, Kinshasa, Democratic Republic of the Congo, [2]National Program for the Elimination of Cholera and the Fight against Other Diarheic Diseases, Ministry of Health, Kinshasa, Democratic Republic of the Congo, [3]Montpellier Geography and Planning Laboratory, University of Paul Valéry, Montpellier, France, [4]Research and Training Unit on Ecology and Control of Infectious Diseases, University of Kinshasa, Kinshasa, Democratic Republic of the Congo

**Background:** Lake areas in Tanganyika province are reporting cholera cases continuously. Three of these Zones out of the total of 11 zones in this province (Kalemie, Moba and Nyemba) constitute the Kalemie sanctuary site. Despite the implementation of numerous response activities, the epidemiological profile does not appear to be improving. The present study aims to identify the micro-hotspots in these sanctuary areas as well as the factors of persistence of cholera epidemics. **Methods:** A descriptive cross-sectional study was conducted in Tanganyika. Epidemiological, environmental and biological data were collected. The field investigation was carried out from July 29 to September 4, 2021. **Results:** The lake areas of Tanganyika recorded 80% of cases and 50.5% of deaths from 2008-week 30.2021. In these areas, during periods of lull, cases retract in 14 micro-hotspots (6 in Kalemie, 5 in Nyemba and 3 in Moba) out of the 94 health areas in this region. The persistence of cholera epidemics in these micro-hotspots suggests the existence of potential environmental and human reservoirs. Five strains of Vibrio cholerae were found in samples taken from Lake Tanganyika and 2 stool samples taken from asymptomatic fishermen came back positive out of 44 samples taken during the lull. The health areas adjacent to the lake are the most affected at the level of sanctuary areas. The presence of a train station and a large market with significant activity make these areas particularly vulnerable to cholera epidemics. **Conclusion:** The association of "water-hygiene and sanitation" type actions with community sensitization primarily targeting micro-hotspots of persistent epidemics could avoid the seasonal trend of cholera epidemics highlighted by this study. The continued epidemiological and environmental monitoring of parameters of the yaw and the genetic characterization of strains of Vibrio cholerae in the environment should contribute to the early

### Poster LB-61. TB Treatment Non-adherence and its Associated Factors among School-Going Children with TB: Meru County, Kenya, 2021

**R. Pola**[1], A. Abade[1], L. Diero[2], E. Kanana[1]
[1]Field Epidemiology Training Program, Ministry of Health, Nairobi, Kenya, [2]Moi University School of Public Health, Eldoret, Kenya, [3]Department of Health, Meru County Government, Meru, Kenya

**Background**: Tuberculosis (TB) remains a public health problem in developing countries. Globally 7.1 million people were diagnosed with TB, and 4.1 million deaths were reported in 2020. Children have a higher risk of developing severe forms of tuberculosis. Treatment non―adherence can lead to prolonged illness and further TB transmission in the community, development of drug resistance or death. We sought to determine the level of TB treatment non-adherence and its associated factors among school-going children in Meru county. **Methods**: A hospital based cross-sectional study among school-going children was conducted in Meru county, January―July 2021. Our definition for adherence was one who kept all clinic appointments, took correct number of tablets each day. Children were randomly selected from the TB register and enrolled into the study. A structured questionnaire containing socio-demographic, clinical, school related and health system factors was administered. Data was cleaned and analysed on Ms. Excel, categorical variables summarised using proportions and continuous variables using mean and standard deviation. Crude and adjusted odds ratio and 95% CI were calculated. Factors with p-values less than 0.05 at multivariate level were considered significant. **Results**: A total of 207 school―going children with TB were interviewed, mean age was 14.5 years (S.D.=±4), females were 105 (50.7%) and 96 (46.4%) were found to be non-adherent. The adjusted odds of TB treatment non―adherence were 3.01 (95% CI=1.65–7.09) among those in secondary school. Other factors associated with non-adherence included waiting times of more than 30―minutes at the health facility (AOR=3.02; CI 1.37–6.66), not received health education (AOR=15.04; CI=3.89–58.09) and not having someone reminding the patient to take treatment (AOR=6.95; CI=2.64–18.28). **Conclusion**: The level of non-adherence to anti-TB drugs among school going children in Meru County was high, health system and school related factors were significantly associated with non―adherence.

### Poster LB-62. The CDC IRAT at 10 Years: Assessing Influenza Viruses for Pandemic Potential, 2011-2021

**J.C. Kile**
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Surveillance and assessment of animal viruses to evaluate the potential for human infection supports pandemic preparedness. Influenza A viruses have caused four major global pandemics with significant morbidity and mortality. The Influenza Risk Assessment Tool (IRAT) is an evaluation tool developed by CDC and external influenza experts that assesses the potential pandemic risk posed by influenza A viruses that circulate in animals but not in humans. The IRAT cannot predict the next pandemic influenza virus but provides a means to rank and compare viruses on perceived pandemic potential. **Methods:** IRAT evaluations are initiated by CDC for influenza A viruses that are representative of a particular subtype or group that are of unique interest due to their pandemic potential. The IRAT uses 10 elements to measure the potential pandemic risk based on two different scenarios: "emergence", or the risk of an animal or novel influenza virus acquiring the ability to spread in people, and "public health impact", or the potential severity of human disease caused by the virus. Influenza experts evaluate animal and novel human influenza viruses based on each of the 10 elements, calculating a composite risk score for each virus based on each scenario. **Results:** From 2011 through 2021, 22 animal and novel human influenza A viruses were assessed for pandemic potential. A Eurasian avian-like swine influenza A(H1N1) virus scored the highest potential emergence of 7.5, with potential public health impact of 6.9, scoring within the moderate risk range on a scale from 1 to 10. A low pathogenicity avian influenza A(H7N9) virus scored the highest potential public health impact of 7.5, with potential emergence of 6.5, also within the moderate risk range. Comparing all viruses assessed, 5 scored within the low-risk range for both emergence and impact, and 15 scored within the moderate range. The remaining 2 viruses scored low emergence and moderate impact. From 2016 through 2021, an average of 21 influenza experts from 4 to 5 U.S. Government agencies assessed 13 of the 22 viruses, scoring from 1 to 3 risk elements per expert. **Conclusions:** Over 10 years, IRAT evaluations have identified animal and novel human influenza viruses that should be monitored for their pandemic potential when they cause animal outbreaks and human infections.

### Poster LB-63. Tuberculosis Spells Death Knell in Patients with SARS-CoV-2 Infection

**K. Bala**[1], P. Grover[1], R Bir[1], J. Biswas[1], N. Jamshed[3], A. Mohan[2], P. Agarwal[3], R. Chaudhry[1], U.B. Singh[4]
[1]Department of Microbiology, New Delhi, India, [2]Department of Pulmonary Critical Care & Sleep Disorder, New Delhi, India, [3]Department of Emergency Medicine, New Delhi, India, [4]Department of Medicine, New Delhi, India.

**Background:** Concomitant infections due to COVID-19 and tuberculosis (TB) have been reported to lead to high morbidity and mortality. Current study enrolled patients diagnosed with SARS CoV-2 infection, presenting with signs, symptoms suggestive of TB to demonstrate association and outcome of patients. **Materials & Methods:** The admitted COVID-19 positive patients were categorized as symptomatic and asymptomatic. Both groups were investigated to rule out TB. Detailed demographic findings, symptoms/ signs, and microbiological tests used for confirmation of diagnosis, presence of primary pulmonary focus, treatment received, and treatment response was

noted. Various pulmonary & extrapulmonary samples from COVID positive patients were subjected to Ziehl Neelsen stain, Gene Xpert, PCR (MPT 64), MGIT liquid culture. **Results:** Tuberculosis was diagnosed in 15.5% (24/155) patients, 2 to 41 days after diagnosis of COVID suggesting pre-existing undiagnosed TB in those detected early and possible reactivation/reinfection following COVID in those detected later. All COVID-19 positive patients were categorised into symptomatic 135 (87%) and asymptomatic 20 (12.9%) group. Pulmonary TB and Extrapulmonary TB was diagnosed in 66.67% and 33.3% respectively (pulmonary TB (16 cases), CNS TB (3 cases), Lymph node TB (1 case), Peritoneal TB (1 case), Pleural TB (1 case) and Spinal TB (2 cases). Diagnosis was confirmed by GeneXpert in 17/24 cases, rifampicin resistance detected 1 patient, by PCR in 6/24 cases, MGIT 960 (liquid culture) in 1/8 cases tested. Twenty-eight patients with TB responded to Anti-Tubercular-Treatment (15 microbiologically confirmed,13 clinically diagnosed). Mortality was higher among COVID patients co-infected with TB (9/24,37.5%) compared to those with COVID alone (24/131, 4.4%) (p value < 0.0397, odds ratio 2.67) demonstrating causal association. **Conclusion:** Mortality was higher among TB -COVID co-infected patients (37.5%). Rifampicin resistance does not seem to increase with COVID-19 co-infection.

### Poster LB-64. Using Google-Apple Exposure Notification (GAEN) and Exposure Notification Private Analytics (ENPA) To Support COVID-19 Pandemic-Response—13 U.S. Jurisdictions, July–April 2022

**A.N Hankus**[1], E. Kim[1], D. Eisert[1], C. Cho[1], S. Gran[2], M. Raykova[3], R. Palekar[1]
[1]The MITRE Corporation, McLean, VA, USA, [2]Internet Security Research Group, San Francisco, CA, USA, [3]Google, Mountain View, CA, USA

**Background:** Infectious disease contact tracing is time and labor intensive for public health authorities (PHAs) and relies on the infectious person attempting to recall their contacts. During the COVID-19 pandemic, Apple and Google, along with their partners, developed a protocol that leverages smartphone Bluetooth capabilities, to perform digital contact tracing, in a privacy-preserving way, called Google-Apple Exposure Notification system (GAEN). When two smartphones running GAEN come within range of each other, they exchange information that allows a person, who later tests positive for COVID-19, to anonymously notify those who might have been exposed. MITRE developed and operates the national and international GAEN analytics server, Exposure Notification Private Analytics (ENPA). ENPA collects data from GAEN users, who have opted-in to share their data, in a privacy preserving manner, and conducts analytics to provide insights to jurisdictions. **Methods:** We analyzed data from participating jurisdictions (29.1% of U.S. population) during July through April 2022. We conducted descriptive analyses of the following metrics: exposure notifications (ENs) sent to users, user interactions with ENs, user vaccination status, server-key uploads to notify contacts, and encounter characteristics. **Results:** A total of n= 2.10 billion device days were analyzed. In total, n=2,762,617 ENs were sent to users, of which 74.1% were viewed, rather than dismissed or ignored. Among the users who tested positive for COVID-19 and shared their vaccine status (n=3,101), 55% reported being vaccinated. Among users with COVID-19 who uploaded a server-key to notify their contacts of possible exposure (n= 227,663), 14.7% had received an EN within the prior 14 days. Among all encounters (n= 2.82 billion), 59.2% were <5 minutes, and 2.2% had attenuations of 0-60dB (proxy for short distance). **Conclusion:** The use of GAEN and ENPA demonstrate how digital tools can be deployed to effectively support pandemic response. Future analyses should examine the acceptability of these tools among users and cost-benefit to PHAs.

## Oral Presentation Abstracts

## J1. Respiratory Diseases

**3:15 PM – 4:45 PM**

**Centennial Ballroom I**

### Performance of a Commercial Rapid Influenza A and B Diagnostic Test in a Community Sample of School-aged Children: ORCHARDS – Wisconsin 2015-2020

**J.L. Temte**[1], S. Barlow[1], M. Goss[1], C. Bell[1], E. Temte[1], J. Birstler[2], G. Chen[2], A. Uzicanin[3]
[1]Department of Family Medicine and Community Health, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [2]Department of Biostatistics, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA, [3]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** School-based outbreaks often herald accelerated influenza (flu) activity in communities. Rapid testing may facilitate timely detection of increased flu activity in schools. We evaluated performance a commercial Fluorescent Immunoassay (FIA; SofiaR by Quidel) in a community sample of school-aged children participating in a longitudinal cohort study. **Methods:** The ORegon CHild Absenteeism due to Respiratory Disease Study (ORCHARDS), a prospective study of absenteeism and flu in students aged 4—19 years, in Oregon, WI, conducts home visits for children with acute respiratory infections. Nasal swab (NS) and orophanygeal (OP) specimens were collected during 1/15/2015—3/12/2020, with demographic and symptom data. NS specimens were tested using FIA within 4 hours of collection. OP swabs were tested for flu using RT-PCR and other respiratory viruses using a respiratory pathogen panel. We calculated odds ratios of true (+) and true (-) FIA results versus RT-PCR result based on age and sex, days from illness onset, presence of influenza-like illness (ILI) signs and symptoms, vaccination status, and flu type. **Results:** Of 2378 recruited students, 2368 (99.6%) had paired FIA and RT-PCR results. The mean age of children was 10.2 years and 58.8% met ILI case definition (fever plus ≥1 respiratory symptom). Flu A and B were detected by RT-PCR in 447 (19%) and 363 (15%) children, respectively. Relative sensitivity and specificity of FIA were 76.1% (95% CI: 72.8—79.1) and 97.2% (96.2—97.9), respectively. Factors associated with sensitivity included coryza (OR=3.0, p<0.001), nasal congestion (1.59, p=0.045), days from symptom onset (per day; 0.75; p<0.001), myalgia (0.61; p=0.014), age (per 5 years; 0.55; p=0.001), and detection of another virus (0.50; p=0.042). None of the explored factors were associated with relative specificity. **Conclusion:** Moderately high sensitivity and high specificity were found for FIA for a cohort of school-aged children tested in home settings. Age, time from symptom onset, detection of non-flu virus, and the presence of some symptoms may affect relative sensitivity. Rapid testing for flu in home settings is associated with favorable performance characteristics and merits further study for use in school settings for faster detection of accelerated influenza activity in communities.

### Incidence of Influenza and Other Respiratory Viruses among Pregnant Women; a Multi-Country, Multiyear Cohort

**E. Azziz-Baumgartner**, A. Hall, V. Veguille
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Pregnant women seem to underutilize influenza vaccines because they and their providers often are unaware of illness risks and uncertain about the benefits of vaccination. To address a gap in knowledge about the risk of influenza, and better understand the benefits of influenza vaccination, we established mother/baby cohorts in Panama and El Salvador. **Methods:** We established a multi-center longitudinal prospective cohort study of pregnant women in four primary health care centers. Upon enrollment, study staff documented demographic, socioeconomic, and clinical histories using standardized survey. Pregnant women were followed each week by phone or text to identify acute respiratory infections (ARI). Participants were instructed to come to the clinics for testing if they developed any ARI symptoms including cough, sore throat, or rhinorrhea. Nasopharyngeal swabs obtained from women with febrile ARI were tested by reverse-transcription polymerase chain reaction for respiratory viruses. **Results:** We enrolled 2,556 women between October 2014–April 2017. Sixteen percent developed at least one ARI; 59 had two ARI, and five had three ARI for a total of 463 ARI. Women in El Salvador and Panama contributed 297 person-years (py) and 293py, respectively, during influenza circulation. Twenty-one (11%) of 196 sampled women tested positive for influenza. Influenza incidence was 5.0/100py (4.3/100py in Panama and 5.7/100py in El Salvador). Only 13% of women in El Salvador and 43% in Panama had been vaccinated against influenza before influenza epidemics (p<0.0001). The incidence of rhinovirus during weeks when this virus was detectable nationally was 7.3/100py (95%CI 7.0–7.7/100py), parainfluenza viruses 3.3/100py (95%CI 3.1–3.5/100py), RSV 2.4/100py (95%CI 2.2–2.5/100py), and human metapneumovirus 0.9/100py (95%CI 0.8–1.1/100py). Based on the only laboratory-confirmed RSV hospitalization, the RSV hospitalization rate in El Salvador was 3.0/1000py. **Conclusions:** One in six pregnant women developed ARI and more than one in ten ARI were attributable to vaccine-preventable influenza. While women were at risk of influenza, few had vaccinated before each epidemic. The incidence of other respiratory viruses also suggests the value of self-protection through non-pharmaceutical interventions.

### The Incidence of Acute Respiratory Illness before and during COVID-19 Era in Kibera, Nairobi, Kenya: The Potential Impact of Non-pharmaceutical Interventions

**G. Bigogo**[1], A. Ouma[1], S. Ronoh[1], A. Audi[1], A. Herman-Roloff[2], P. Munyua[2], P. Munywoki[2]
[1]Centre for Global Health Research, Kenya Medical Research Institute, Kisumu, Kenya, [2]US Centers for Disease Control and Prevention, Nairobi, Kenya

**Introduction:** The first case of SARS-CoV-2 was detected in Kenya on March 12th, 2020. In April 2020, the government instituted various non-pharmaceutical interventions (NPIs) including travel bans, social distancing and use of face masks to minimize virus transmission. We examined the relationship between NPIs and the incidence of acute respiratory infections (ARI) in Kibera, a densely populated urban informal settlement in Nairobi, Kenya. **Methods:** Using demographic and clinical data from an ongoing longitudinal population-based infectious disease surveillance project providing free care at Tabitha Medical Clinic in Kibera, we compared the number of sick visits and ARI incidence in the period after introduction of NPIs (May 2020 – June 2021) to the baseline period (January 2017 – April 2020). ARI was defined as presence of cough, difficult breathing, runny nose, or sore throat with acute onset (<2 weeks). Person-years of observation (PYO) were calculated from participants' residency period in Kibera. ARI incidence was calculated as the number of ARI episodes per PYO, stratified into three age categories; <5, 5-17, and ≥18 years. Incidence rate ratios (IRR) compared ARI incidence during the intervention period relative to the baseline. **Results:** The number of sick visits for 2017, 2018, 2019 and 2020 was 12,365, 14,325, 19,802 and 13,671 respectively. January – June 2021 had 7413 sick visits. At baseline, ARI incidence was 0.40 (95% confidence Interval (CI), 0.39 – 0.40) per PYO overall, and 1.15 (95% CI, 1.13 – 1.17), 0.34 (95% CI, 0.34 – 0.35) and 0.24 (95% CI, 0.23 – 0.24) per PYO for the <5, 5–17 and ≥18-year age categories, respectively. After introduction of NPIs, ARI incidence was 0.19 (95% CI, 0.19-0.20) overall, 0.53 (95% CI, 0.51 – 0.55) for <5 years, 0.16 (95% CI, 0.15 – 0.17) for 5-17 years and 0.13 (95% CI, 0.12 – 0.14) for ≥18 years per PYO. The IRR overall was 0.49 (95% CI, 0.47-0.50). For persons aged <5, 5 – 17 and ≥18, the IRR was 0.46 (95% CI, 0.44 – 0.48), 0.46 (95% CI, 0.43 – 0.49) and 0.54 (95% CI, 0.52 – 0.57), respectively. **Conclusion:** While the number of sick visits remained stable over time, ARI incidence declined by 46 – 54% after introduction of NPIs suggesting moderate effectiveness of the NPIs on all-cause ARIs in this densely populated setting.

### Healthcare-seeking Behavior for Respiratory Illnesses in Kenya: Implications for Burden of Disease Estimation

**G.O. Emukule**[1], E. Osoro[2], B.O. Nyawanda[3], I. Ngere[2], D. Macharia[1], G. Bigogo[3], N.A. Otieno[3], S.S. Chaves[1,4], M.K. Njenga[2], M.-A. Widdowson[1,5]
[1]Centers for Disease Control and Prevention - Kenya Country Office, Nairobi, Kenya, [2]Washington State University Global Health, Nairobi, Kenya, [3]Kenya Medical Research Institute, Kisumu, Kenya, [4]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Institute of Tropical Medicine, Antwerp, Belgium
**Background:** Understanding healthcare-seeking patterns for respiratory illness can help improve estimations of disease burden and inform public health interventions to control acute respiratory disease in Kenya. **Methods:** We conducted a cross-sectional survey to determine healthcare utilization patterns for acute respiratory illness (ARI) and severe pneumonia in four diverse counties representing urban, peri-urban, rural mixed farmers, and rural pastoralist communities in Kenya using a two-stage (sub-locations then households) cluster sampling procedure. Healthcare seeking behavior for ARI episodes in the past 2 weeks and severe pneumonia in the past year was evaluated. Severe pneumonia was defined as reported cough and difficulty breathing for ≥3 days with at least one of hospitalization, danger sign (unable to breastfeed/drink, vomiting everything, convulsions, unconscious) for children <5 years, or report of inability to perform routine chores. **Results:** From August through September 2018, we interviewed 28,072 individuals from 5,407 households. Of those surveyed, 9% (95% CI 8-11) reported an episode of ARI, and 4% (95% Confidence Interval [CI] 4–5) reported an episode of severe pneumonia. Of the reported ARI cases, 40% (95% CI 37-43) sought care at a health facility. Whereas 74% (95% CI 70–78) of those who reported severe pneumonia visited a medical health facility, 29% (95% CI 26–33) of these were hospitalized, and 7% (95% CI 5–9) whom clinicians referred to the hospital were not hospitalized. Twenty-one percent (95% CI 18–24) of self-reported severe pneumonias were hospitalized. Children aged <5 years and persons in households with a higher socio-economic status were more likely to seek care for respiratory illness at a health facility. **Conclusions:** Our findings suggest that hospital-based surveillance capture less than one quarter of severe pneumonia in the community. Multipliers from community household surveys can account for underutilization of healthcare resources and under-ascertainment of severe pneumonia at hospitals.

### Children as Surrogates for Cumulative History of Infections with Endemic Coronaviruses: Impact on Severity of Parental SARS-CoV-2 Infections

**J.W. Leung**[1], S. Saydah[1], R. Harpaz[2]
[1]COVID-19 Response Team, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Harpaz-Herman Consultants, Atlanta, GA, USA
**Background:** Many clinical and epidemiological aspects of COVID-19 are unexplained. A host-factor that may be relevant is one's cumulative history of infections with the 4 endemic coronaviruses (ECs), or "EC experience."

Young children are a reservoir for ECs and sources of repeated parental exposures. There is evidence for immunological cross-reactivity between SARS-CoV-2 and the ECs, but the implications are unknown and there are no direct methods to assess EC experience. We used presence of young children as a proxy for risk of cumulative EC exposure in persons diagnosed with COVID-19 to assess its impact on subsequent severity of illness. **Methods:** We used data from IBM® MarketScan® to follow adults aged 25-45 years with emergency department diagnoses of COVID-19 during Jan. 2020 – Jan. 2021, comparing COVID-19 severity in cases with vs. without young children. The exposed cohort consisted of cases having ≥1 young children (co-beneficiaries) aged ≤7 years; the comparators were those having children aged 13 – 17 years only, or no children aged ≤17 years. We assessed severity via proportions requiring hospitalization, prolonged hospital stay, intensive care, or mechanical ventilation. We compared pre-pandemic (2019) rates of hospitalization across cohorts to assure that underlying health status did not confound the results. **Results:** Pre-pandemic, likelihood of hospitalization was higher in the cohort with young children vs. those with teenaged or no children (11% vs 6%), increasing with number of children (9% in parents with 1 child to 18% with ≥3 children). In contrast, in persons diagnosed with COVID-19, most measures of COVID-19 severity were modestly but significantly diminished in parents of young children, 17% hospitalized and 6% admitted to the ICU in adults with young children vs 19–22% and 7–8% without young children ($p$<0.01). Severity also declined by number of children. **Conclusions:** Using methods to complement other ways for comparing EC experience, our results hint that cross-reactive immunity to SARS-CoV-2 mediated by EC experience can affect the clinical features of COVID-19. Studies are needed to confirm our findings and to see if EC experience (or future exposures) can affect related SARS-CoV-2 phenomena, such as susceptibility, contagiousness, or vaccine performance, safety, and durability.

### The Real-World Impact of 13vPCV on Invasive Pneumococcal Pneumonia in Australian Children: A National Study

**N. Homaira**[1,2], R. Strachan[2], H. Quinn[3], S. Beggs[4,5], M. Bhuiyan[6], L.K. Fawcett[1,2], G.L. Gilbert[7], S.B. Lambert[8,9], K. Macartney[3,9], H.S. Marshall[10,11], A. Martin[12], G. McCallum[13], A. McCullagh[14,15], T. McDonald[16], H. Selvadurai[9], P. McIntyre[3,17], S. Oftadeh[18], S. Ranganathan[19,20], S. Suresh[20,21], C.E. Wainwright[20,21], A. Wilson[22], M. Wong[23], A. Jaffe[1,2], T. Snelling[24]

[1]School of Women's and Children's Health, Faculty of Medicine, UNSW Sydney, Sydney, New South Wales, Australia, [2]Respiratory Department, Sydney Children's Hospital Randwick, NSW, Australia, [3]National Centre for Immunisation Research and Surveillance (NCIRS), Sydney Children's Hospital's Network, Westmead, NSW, Australia, [4]Paediatric Department, Royal Hobart Hospital, Hobart, Tasmania, Australia, [5]College of Health and Medicine, University of Tasmania, Tasmania, Australia, [6]Wesfarmers Centre of Vaccines and Infectious Diseases, Telethon Kids Institute, Perth, Australia, [7]Children's Health Queensland, Queensland Paediatric Infectious Diseases Laboratory, Brisbane, Queensland, Australia, [8]UQ Child Health Research Centre, The University of Queensland, Brisbane, Queensland, Australia, [9]The Children's Hospital at Westmead, Westmead, New South Wales, Australia, [10]Women's and Children's Health Network, North Adelaide, South Australia, Australia, [11]Robinson Research Institute and Adelaide Medical School, The University of Adelaide, Adelaide, South Australia, Australia, [12]Department of General Paediatrics, Perth Children's Hospital, Nedlands, Western Australia, Australia, [13]Child Health Division, Menzies School of Health Research, Charles Darwin University, Casuarina, Northern Territory, Australia, [14]Respiratory Department, Monash Children's Hospital, Melbourne, Australia, [15]Respiratory Department, Royal's Children's Hospital, Melbourne, Australia, [16]The Centenary Hospital, Canberra, [17]Women's and Children's Health, University of Otago—Dunedin Campus, Dunedin, New Zealand, [18]Pneumococcal Reference Laboratory, Institute of Clinical Pathology and Medical Research, Westmead, New South Wales, Australia, [19]Department of Paediatrics, The University of Melbourne, Parkville, Victoria, Australia, [20]Infection and Immunity, Murdoch Children's Research Institute, Melbourne, Victoria, Australia, [21]Respiratory and Sleep Medicine Children's Health Queensland Hospital and Health Service , Queensland Children's Hospital, South Brisbane, Queensland, Australia, [22]Department of Paediatrics, Alice Springs Hospital, Alice Springs, Northern Territory, Australia, [23]Department of Allergy and Immunology, The Children's Hospital at Westmead, Westmead, New South Wales, Australia, [24]School of Public Health, The University of Sydney, Sydney, New South Wales, Australia

**Background:** The 13-valent pneumococcal conjugate vaccine (13vPCV) was introduced in Australia's National Immunisation Program in July 2011 with 3 routine schedule at 2, 4 and 6 months, without a booster dose We aimed to assess the effect of 13vPCV against hospitalisation for pneumonia in Australian children. **Methods:** In a prospective nationwide case-control study across 11 paediatric tertiary hospitals all children <18 years old admitted with pneumonia were eligible for enrolment. An invasive pneumococcal pneumonia (IPP) case had *Streptococcus pneumoniae* (SP) cultured or detected by polymerase chain reaction from blood or pleural fluid. Causative SP serotype (ST) was determined from blood or pleural fluid SP isolates, by molecular method in PCR positive

specimens or else inferred from nasopharyngeal isolates. For each IPP case, 20 age and socio-economic status matched population controls were sampled from the Australian Immunisation Register (AIR). 13vPCV immunisation status was ascertained from AIR. We used logistic regression to estimate the adjusted odds ratio (aOR and 95% CI; adjusted for sex and Indigenous status) of being fully vaccinated with 13vPCV among IPP cases compared to controls. **Results:** Between February 2015-September 2018, we enrolled 1,168 children with pneumonia; 779 were 13vPCV-eligible and were matched to 15,580 controls. Of vaccine-eligible children, 195 (25%) had IPP and 126 had 13vPCV-type IPP; STs 3 and 19A accounted for 52% (101/195) and 11% (21/195) of IPP cases. A total of 87% controls and 88% IPP cases were fully vaccinated. Compared to controls, the aOR of being fully vaccinated (versus 0, 1 or 2 doses) was 0.8 (0.6-1.0) for IPP, and 0.9 (0.5-1.7) for 13vPCV-type IPP: ST3 0.9 (0.5-1.9) and ST19A 0.8 (0.2-2.8). **Conclusion:** Several years after introduction of 13vPCV, we were unable to demonstrate a protective effect of 13vPCV which is consistent with reduced protection of an unboosted 13vPCV schedule against IPP caused by residual 13vPCV-serotypes.

## J2. Surveillance and Outbreak Response

**3:15 PM – 4:45 PM**

**Centennial Ballroom II**

### Detecting SARS-CoV-2 Cases using Sentinel Influenza Surveillance in Bangladesh

**Z. Akhtar**[1], A. Islam[1], M.A. Aleem[1], S. Mah-E-Muneer[1], M.K. Ahmmed[1], P.K. Ghosh[1], M. Rahman[1], M.Z. Rahman[1], M. Rahman[1], M. Rahman[1,2], T. Shirin[3], J.A. Mott[4], W.W. Davis[4], F. Chowdhury[1]
[1]International Center for Diarrheal Diseases, Bangladesh, (icddr,b) Programme for Emerging Infections, Dhaka, Bangladesh, [2]Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh, [3]Global Health Development/EMPHNET, Amman, Jordan, [4]Influenza Division, Centers for Disease Control and Prevention Regional Influenza Program, Bangkok, Thailand
**Background**: The WHO recommends using influenza sentinel surveillance (ISS) to monitor COVID-19. We leveraged our hospital-based ISS in March 2020 to also detect cases of COVID-19. We describe characteristics of influenza cases and COVID-19 cases identified and the challenges of implementing the modified surveillance. **Methods**: We analyzed data from March 2020 - August 2021 from patients admitted with severe acute respiratory illness (SARI cases: reported or measured fever of ≥38 C° and cough with onset ≤10 days prior). Surveillance staff recorded demographic, clinical, and laboratory data and took nasopharyngeal and oropharyngeal swabs to test for influenza virus and SARS-CoV-2 by real time reverse transcription–polymerase chain reaction (rRT-PCR). We performed multiple regression analysis to estimate the odds of death due to SARS-CoV-2 infection, controlling for age and preexisting chronic conditions. **Results**: We enrolled 4,987 SARI cases with a median age of 30 years (IQR: 1.2 55 years); 62.9% were male. Among SARI cases, 992 (19.9%) were positive for SARS-CoV-2, 350 (7.0%) were positive for influenza virus, and 8 (0.2%) were co-infected. SARS-CoV-2-positive SARI cases had a median age of 50 years (IQR: 35-60); 261 (26.3%) had hypertension and 117 (11.8%) had diabetes. SARI cases with influenza had a median age of 8 years (IQR: 1.2-32); 17 (4.9%) had hypertension and 10 (2.9%) had diabetes. There were 261 deaths among SARI cases; 111 (11.2%) were SARS CoV-2 positive, 3 (0.9%) were influenza-positive and none were co-infected. SARI cases positive for SARS CoV-2 had 2.5 times higher odds of death compared to negatives (95% CI: 1.9-3.3; p<0.001), controlling for age and chronic conditions. Challenges of maintaining surveillance during the pandemic included staff shortages and shipping disruptions for samples during lockdowns. Fewer samples (2,361 in 2020 and 2,626 up to August 2021) were tested compared 5,001 tested in 2019; however, engaging additional resources helped to maintain surveillance. **Conclusions**: Our findings suggest that our sentinel ISS can detect SARS-CoV-2 cases. Age and comorbidities are likely factors influencing high mortality among SARS-CoV-2 positive cases, indicating a need for continued prevention strategies, including vaccines and nonpharmaceutical interventions.

### The Global Pathogen Analysis System: Making Processing SARS-CoV-2 Genetic Data Cheaper, Simpler, and More Consistent

**DW Crook**[1], GPAS Consortium
[1]University of Oxford, Oxford, UK
**Background:** There is no standard way to take the raw genetic reads output from a genetic sequencing machine and produce a consensus genome, from which important public health information (lineage, Spike protein mutations and relatedness) can be obtained. A ten-year donation of free access to the ORACLE cloud has enabled us to build the

Genome Pathogen Analysis System (GPAS) to assist with SARS-CoV-2 surveillance. **Methods:** GPAS is a globally accessible, secure and accurate genetic processing service. A local client removes all personally identifiable genetic reads before uploading the remaining reads to the ORACLE cloud where the reads are quality checked and mapped to the SARS-CoV-2 reference genome before variants, including indels are called. Standard tools (e.g., pango) are then used to infer the sample lineage. Related samples previously uploaded are returned in <1s to aid outbreak, importation and new variant detection using a novel algorithm called FindNeighhbour4. **Results:** We show that GPAS is able to rapidly and accurately process genetic reads generated using the ARTICv3 protocol using both Illumina and Oxford Nanopore genetic sequencing machines. We shall describe how GPAS has been rapidly taken up by a range of public health bodies worldwide to enable and/or simplify their SARS-CoV-2 surveillance. Finally, we shall describe ongoing efforts to add additional pathogens, focusing on *M. tuberculosis* in the first instance. **Conclusions:** GPAS is the first globally accessible service backed by a world-leading technological company to offer free processing of raw pathogen genetic data by low- and middle-income countries.

### Estimating Excess Mortality during the COVID-19 Pandemic in the Largest Township in Gauteng, South Africa: Results from a Health and Demographic Surveillance System

**P.C. Mutevedzi**[1,2], P. Ndagurwa[1], D. Thaela[1], N. Mutanda[1], C. Hwinya[1], S. Tloubatla[1], C. Herrera[1], S. Madhi[1,3]
[1]South African Medical Research Council Vaccines and Infectious Diseases Analytics Research Unit, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa, [2]School of Pathology, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa, [3]African Leadership in Vaccinology Expertise, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa
**Background:** Since December 2019, the COVID-19 pandemic has caused varying but devastating levels of mortality. South Africa has experienced three epidemic waves since March 2020 when the first COVID-19 case was reported. Like many African countries, excess mortality owing to COVID-19 is likely underestimated because mortality estimates are largely based on health facility death counts excluding community deaths. We utilised data from a health and demographic surveillance system (SaT-HDSS), in Soweto the largest township in South Africa, to estimate excess mortality during the Covid-19 pandemic. **Methods:** SaT-HDSS was established in 2017 as part of the Child Health and Mortality Surveillance (CHAMPS). Currently, the HDSS has a dynamic population cohort of approximately 123000 individuals in 35000 households. Enrolled households are visited twice a year to collect demographic and epidemiological data from all household members. We used the mortality data to compute year-specific mortality rates per 100,000 population stratified by age. Mortality rates were compared pre- (2018 & 2019) and during Covid-19 era (2020 & 2021). Population denominators and death counts were annualised to account for the twice a year data collection. **Results:** A total of 4183 deaths were recorded; 33% (1604) and 29% (1419) in 2020 and 2021 compared to 16% (796) and 22% (1077) in 2018 and 2019 respectively. Mortality rate (per 100,000) increased by 57% from 2019 (945) to 2020 (1486) and 2021 (1352). Mortality rate increased two-fold increase in those aged >65years (7338 vs 13811) and <1year (3139 vs 7235) comparing 2019 to 2020 respectively, $p<0.01$. Mortality rates marginally decreased in the 5-17years age group (2019=90; 2020=72; 2021=71). For deaths occurring in 2021, 40% (356) occurred at home compared to only 9% in 2019 and 14% in 2020 ($p<0.01$). **Conclusions:** We report significant excess mortality since the onset of Covid-19 in South Africa with increasing number of deaths occurring at home that are unlikely to be accounted for in national and regional mortality estimates. As of July 2021, the South African government had reported a crude mortality rate of 870 in 2020, increasing to 1160 in 2021, a possible underestimate due to the high number of home-based deaths.

### Molecular Epidemiology of Hepatitis A Virus Infections during the Recent Multistate Outbreaks, United States (2016 – 2020)

**S. Ramachandran**, Z. Dimitrova, Y. Lin, G.L. Xia, Y. Khudyakov
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Decrease in number of hepatitis A virus (HAV) cases was observed in the USA since 1996. However, since 2015, with the onset of multi-state outbreaks, a 294% increase in HAV cases among people who use drugs, are experiencing homelessness, and men who have sex with men have been reported. **Methods:** Specimens from the HAV outbreaks (2016-2020) were tested using next generation sequencing (NGS) and web-based Global Hepatitis Outbreak and Surveillance Technology (GHOST). The novel protocol was deployed to state health laboratories to track HAV strains. **Results:** Among specimens (n=3727) analyzed using GHOST, 695 (18.6%) were from patients infected with HAV subtype IA, 2937 (78.8%) IB, and 95 (2.6%) IIIA. The HAV IIIA variants were organized in one genetic cluster. The HAV IB variants formed one unique major cluster whereas a second smaller HAV IB cluster and numerous HAV IA clusters intermixed with HAV variants detected in the USA before 2016. Intra-host HAV heterogeneity varies broadly, with mean entropy and percent of polymorphic nucleotide sites ranging between

$2.6\times10^{-3}$ – $13.6\times10^{-3}$ and 1.2% - 47.9%, correspondingly. Detection of many cases infected with variants from both IB clusters and cases with mixed IA/IB infections (n=8) indicate existence of complex intra-host HAV populations. **Conclusions:** Predominance and genetic heterogeneity of HAV subtype IB, demonstrated by total number of cases and breadth of spread during the recent outbreaks in multiple states in the USA suggest >1 introduction and effective dissemination of HAV IB strains, which were infrequently detected in the USA before 2016. Patients with mixed strain and subtype indicate the importance of NGS and novel molecular surveillance tools like GHOST for uncovering genetic complexity of HAV population and intensity of transmission operating for 5 years during these outbreaks and underscores the need for timely detection of transmissions and assistance in guiding public health interventions.

### Overview of the Circulation of Two Arboviruses in the South of France: Usutu and West Nile

**O. Constant,** K. Bolloré, J. Barthelemy, S. Salinas, Y. Simonin
Pathogenesis and Control of Chronic and Emerging Infection, Inserm, University of Montpellier, Montpellier, France

**Background:** Among the (re-)emerging arthropod borne viruses (arbovirus), Usutu (USUV) and West-Nile virus (WNV) are two closely related flaviviruses, belonging the Japanese encephalitis virus (JEV) serocomplex which distribution area is increasing in Europe and which co-circulates in certain regions. These flaviviruses are mainly maintained in the environment through an enzootic cycle involving mosquitoes and birds and are occasionally spreading to mammals. Mostly asymptomatic, the infection can lead to neurological impairments in humans. In the south of France, the region called Camargue is particularly exposed to USUV and WNV circulation. It is a wetland that houses a large diversity of wild bird species, including migratory birds, and various mosquito population. Close to this place, Montpellier is an urban area allowing tight circulation of these two arboviruses between captive mammals, birds and human. **Methods:** We performed a serological analysis to estimate the prevalence of USUV and WNV in this area. We have been able to evaluate the seroconversion of these two arboviruses in mosquitoes, wild and captive birds, but also in captive mammals (animals from zoo and domestic dogs) and humans from hospitals of Montpellier. First, sera samples were tested with a competitive enzyme-linked immunosorbent assay (cELISA) against flaviviruses. Then, positive samples were tested in seroneutralization assays against USUV and WNV to avoid cross reaction between these two viruses. **Results:** Ours studies showed a greater proportion of USUV seroprevalence than WNV. For example, in the zoo of Montpellier, we have found 1.45% and 0.73% of samples positive for WNV and 14.59% and 6.57% positive for USUV in bird and animal populations respectively. **Conclusion:** These results disclose how the contact between these viruses and populations is tighter than it appears and illustrate the importance of surveillance of these flaviviruses known for recurrent epidemic events as in the United States (US). In 2018, Europe has experienced a major WNV epidemic and an important USUV epizootic. Thus, their distribution in the south of France, and elsewhere, illustrate the importance of acute surveillance, in sentinel animals from zoo for example to anticipate the spread in human population.

### Turning Farmers into Disease Detectives – How Participatory Surveillance Can Prevent Future Pandemics

**P. Susumpow**[1], M. Parker[1], Nomita Divi[2]
[1]Opendream, Bangkok, Thailand, [2]Ending Pandemics, San Francisco, CA, USA

**Background**: In 2014, a participatory surveillance tool was launched in Northern Thailand as an early warning system to prevent zoonotic spillover. Chiang Mai University operationalized the open-source tool within local communities and contributed veterinarian oversight. The technology was developed by Opendream, a private technology company who maintains the software. Ownership of the tool was transferred to local governments in 2016 and sustained with local resources. In 2018, the system was modified to support environmental health events such as wildfires, and further adapted in 2019 for mosquito surveillance. The tool was also used during COVID-19 lockdowns to track non-resident mobility in and out of communities. Nearly 20,000 volunteers have been trained to use the tool. In 2020, a team was established to share the technology with other countries. **Methods**: Data submitted via the participatory surveillance tool between 2014 and 2021 was analyzed. **Results**: Within the first three months of using the tool, animal diseases reported by volunteers surpassed the entire previous year's data. Between 2014 and 2021 the system received 377,000 reports from trained volunteers, with 10,000 reports identifying abnormal health events; 75 incidents were verified as zoonosis of public health importance. One incident of foot and mouth disease in domestic livestock was reported and rapidly contained, preventing ban of the milk and estimated to have saved the local economy the equivalent of $4 million U.S. dollars. Of confirmed poultry outbreaks, 73% were contained within the community of origin; the remaining 27% were contained within neighboring communities without further spread. **Conclusions:** Direct community engagement for disease reporting can lead to efficient and

effective surveillance to stop outbreaks faster and prevent spillover events. These flexible participatory surveillance tools can be adapted in real time to fit local needs, enabling the community to expand use beyond the early detection of disease.

## J3. Epidemiology and Analytical Tools

**3:15 PM – 4:45 PM**

**Centennial Ballroom III**

### Assessing the Uganda Viral Hemorrhagic Fever Surveillance Suspect Case Definition, 2010-2018

**A.N. Whitesell**[1], L. Nyakarahuka[2], J. Baluku[2], S. Balinandi[2], A. Tumusiime[2], and T.R. Shoemaker[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uganda Virus Research Institute, Entebbe, Uganda

**Background:** The suspect viral hemorrhagic fever (VHF) case definition used by the Uganda VHF Surveillance Program is currently defined as a patient with acute illness, fever >38 C°, no alternative diagnosis, and at least four of the following signs and symptoms: vomiting/nausea, diarrhea, muscle or joint pain, chills/rigors, intense fatigue, abdominal pain, skin rash, difficulty swallowing, headache, unexplained bleeding, and/or or jaundice. To determine whether modifications should be made to improve reporting and case identification, 8 years of VHF surveillance data was used to evaluate the efficacy of the current case definition. **Methods:** VHF surveillance data from August 2010-July 2018 was used to calculate sensitivity and specificity estimates for the current case definition. Frequencies of signs and symptoms were compared between cases and non-cases and estimates for sensitivity and specificity were re-calculated using signs and symptoms that were significantly more frequent among cases than non-cases. All sensitivity and specificity estimates were stratified by virus. **Results:** The current suspect case definition had a sensitivity of 51.2% and a specificity of 67.9%. When stratifying by virus, the case definition had the lowest sensitivity when detecting filovirus cases (11.1%) and the highest sensitivity when detecting Crimean-Congo Hemorrhagic Fever cases (72.7%). The presence of at least three signs or symptoms that were significantly more frequent in cases yielded an increased sensitivity of 72.1% and specificity of 60.0% across all VHF cases. When stratified by virus, filovirus cases still had the lowest sensitivity (44.4%), and Rift Valley Fever cases had the highest (82.6%). **Conclusions:** The current VHF surveillance suspect case definition captures approximately half of all confirmed VHF cases from August 2010-July 2018. When evaluated by virus, the sensitivities ranged from 11.1% to 72.7%, indicating the combined VHF case definition may not impact case identification the same for all pathogens. Detecting cases based on three or more significant symptoms rather than the current case definition resulted in improved sensitivity without severely reducing specificity. However, sensitivities still varied across pathogens, further demonstrating that differences across VHFs may need to be considered to improve case detection.

### A Novel Analytics Tool to Estimate Epidemiological Parameter for Communicable Disease Using Contact Tracing Data

**S. Bernard Chawo**[1], C. Verset[3], B.B. Kaburi[1,2], O. Leuci[3], S. Ghozzi[1], C.Duboudin[3], G. Krause[1,2,4]
[1]Department of Epidemiology, Helmholtz Centre for Infection Research, Braunschweig, Germany, [2]Hannover Medical School, Hannover, Germany, [3]Agence Regionale de Sante de Bourgogne Franche-Comte, Dijon, France, [4]German Cener for Infection Research, Braunschweig, Germany

**Background:** The digital surveillance outbreak response management and analysis system (SORMAS) contains a management module to support countries in epidemic response. It consists of documentation, linkage and follow-up of cases, contacts, events, travel returnees, and immunizations. To allow SORMAS users to compute key surveillance indicators and estimate epidemiological parameters from such a complex data set in real time, we developed the SORMAS Statistics (SORMAS-Stats) app based on R-Shiny framework. **Methods:** Based on review and users' requests, we included the following visualization and estimation of parameters in SORMAS-Stats: transmission network diagram, serial interval (*SI*), time-varying reproduction number ($R_t$), dispersion parameter ($K$) and additional surveillance indicators presented in graphs and tables. We estimated *SI* by fitting a Lognormal distribution to the observed serial interval data, computed as the number of days between symptoms onset dates of infector-infectee pairs. We estimated $K$ by fitting a negative binomial distribution to the observed number of infectees per infector. We applied the Markov Chain Monte Carlo approach using the observed serial interval and incidence data to estimate $R_t$. **Results:** Using COVID-19 contact tracing data of confirmed cases reported between February 18, 2021, and May 5, 2021, in Bourgogne-Franche-Comté, France, we constructed a network diagram containing 7542 people, 4724 infector-infectee pairs, 3091 transmission chains with 273 (8.83%) resulting from

events. We estimated mean *SI* of 4.73 days (95% CI, 4.61–4.84) and *K* of 0.62 (95% CI, 0.61–0.63). The weekly estimated $R_t$ values ranged from 0.8 to 1.5. **Conclusions:** We provide a tool for real-time estimation of epidemiological parameters which are essential to monitor an outbreak. These estimates are commensurate with findings from previous studies. SORMAS-Stats would greatly assist public health authorities in the regions using SORMAS or similar tools by providing extensive visualizations and computation of surveillance indicators.

### Using a *Cyclospora cayetanensis* Genotyping Tool To Detect Clusters of Cyclosporiasis – United States, 2020

**L. Ahart**
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Cyclosporiasis is an intestinal illness caused by infection with the parasite *Cyclospora cayetanensis*. Local and multi-state outbreaks of cyclosporiasis are detected every year in the United States when common exposures are identified through epidemiologic investigations. With the development of a *Cyclospora* genotyping tool, cases can also be linked through molecular methods. We used a Centers for Disease Control and Prevention (CDC)-developed genotyping tool to help define clusters of cyclosporiasis in the U.S. from May – August 2020. **Methods:** We applied the CDC Cyclospora genotyping algorithm to identify genetically related case-specimens and examine their temporal-genetic relationship. A temporal-genetic cluster (TGC) was defined as genetically related specimens collected within a sliding two-week timeframe. We compared epidemiologically defined clusters to TGCs to find commonalities in reported food exposures associated with cases in each TGC. Findings were summarized and shared with state and local health department and U.S. Food and Drug Administration partners to inform further epidemiological and traceback investigations. **Results:** During May – August 2020, nine epidemiologic clusters were identified, eight of which had genotyped specimens. The largest epidemiologic cluster identified was a multi-state outbreak of 705 laboratory-confirmed cases linked to a bagged salad mix product; 209 case-specimens linked to the outbreak were genotyped and the majority (90%) were associated with two TGCs. Of the remaining epidemiologically defined clusters with genotyped specimens, two were associated with multiple TGCs and four were each associated with one TGC. One epidemiologic cluster was not associated with any TGC and four TGCs could not be epidemiologically linked to a common source. **Conclusion:** The CDC *Cyclospora* genotyping tool can be used to support epidemiological investigations, but additional work to better understand the discriminatory power of genotyping is needed. Examination of temporal-genetic linkages may be more sensitive than epidemiological methods; more complete epidemiological data could potentially refine an epidemiological cluster when it is associated with multiple TGCs..

### Household Transmission of Acute Gastroenteritis within an Integrated Healthcare Delivery System, 2014–16

**N. Balachandran**[1,2], C.P. Mattison[1,2], L. Calderwood[1,2], R.M. Burke[1], S.B. Salas[3], M.A. Schmidt[3], J. Donald[3], S.A. Mirza[1]
[1]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Cherokee Nation Assurance, Arlington, VA, contracting agency to the Division of Viral Diseases, Centers for Diseases Control and Prevention, Atlanta, GA, USA, [3]Center for Health Research, Kaiser Permanente Northwest, Portland, OR, USA
**Background:** Acute gastroenteritis (AGE) causes over 179 million illnesses annually in the United States, and viral pathogens account for a large proportion of this burden. In this study, we identified factors associated with household AGE transmission. **Methods:** From April 2014–September 2016, we enrolled persons with AGE who sought care at Kaiser Permanente Northwest. Demographic and exposure information was gathered from primary cases and symptomatic household members via standardized telephone interviews. Individuals with the earliest symptom onset were defined as primary cases; secondary cases had symptom onset between 1-7 days after the primary case. Stool samples from participants with AGE were tested for norovirus, rotavirus, sapovirus, and astrovirus. Poisson regression using generalized estimating equations was used to generate incidence rate ratios (IRR). **Results:** We included 2,433 households with 2,491 primary cases and 5,477 household members in our analysis. The secondary attack rate of AGE was 11% and was highest among children <5 years (21%). The median duration between primary and secondary case symptom onset was 3 days (IQR: 2-5 days). Among all primary cases, 633 (25%) had one or more viral pathogens detected. Household members had a higher rate of AGE if <5 years of age (aIRR=1.41, 95% CI: 1.12–1.76), had >3 members in the household (aIRR=1.58, 95% CI: 1.28–1.95) or belonged to households where primary cases were <5 years (aIRR=1.32, 95% CI: 1.06-1.64), positive for norovirus (aIRR=4.00, 95% CI: 3.28-4.89), sapovirus (aIRR=2.06, 95% CI: 1.52-2.79) or rotavirus (aIRR=1.92, 95% CI: 1.29-2.87). **Conclusion:** Our study found that larger household size, presence of children <5 years in the household and infection with enteric viral pathogens, most notably norovirus and sapovirus, were associated with household AGE

transmission. Prevention messaging around frequent hand washing, isolation of sick persons, cleaning and disinfection of surfaces, and proper disposal of diapers may be beneficial in reducing AGE transmission.

### Better Data for Action: Framing an Initiative to Strengthen the Evidence Base on Public Health and Social Measures during Health Emergencies

**R. Ludolph,** J. Lamichhane, T. Nguyen, S. Briand
Global Infectious Hazard Preparedness Department, World Health Organization, Geneva, Switzerland
**Background:** Public health and social measures (PHSM) are vital to curb the spread of viruses with pandemic potential such as SARS-CoV-2. Yet, PHSM such as physical distancing, travel restrictions, school and business closures have a profound impact on health, societies and economies. During the COVID-19 pandemic, most PHSM were implemented following a policy-informed science logic based on the best, yet sometimes scares, available evidence. To improve future decision-making on PHSM by making more nuanced choices and mitigating intervention burden, WHO has launched a global initiative to promote data for action on PHSM. **Methods:** The initiative's strategy to improve the measurement of the effectiveness and impact of PHSM was developed using a mixed-methods approach. The team first conducted a mapping of existing evidence and recommendations on PHSM, followed by key informant interviews. From 31 August to 2 September 2021, the team convened 101 global experts from over 30 countries representing research and policy. Experts reviewed evidence and experiences on PHSM during the COVID-19 pandemic, discussed implementation challenges and solutions, and identified guidance, tools and mechanisms needed to improve the PHSM evidence base. **Results:** Discussions highlighted the need for interdisciplinary collaboration to improve the quality and comparability of data for PHSM decision-making. Based on lessons learnt during the pandemic, experts suggested the following priority activities for the initiative: (i) develop a research agenda, (ii) conduct a global evidence review, (iii) develop a living systematic review database, (iv) standardize the language and measurement of PHSM. Experts further called for the development of a global monitoring system including a network of "PHSM labs" ready for timely data collection and sharing during an emergency. **Discussion:** PHSM decision-making needs to include societal, economic and broader health outcomes in addition to the direct effect of interventions on reducing virus transmission. This requires an interdisciplinary and multi-methods approach to measure their effectiveness and impact. The consultation on priority activities for the WHO initiative was the first step to provide a framework for research collaboration.

### Progress in Immunization Safety Monitoring — Worldwide, 2010–2019

**O. Salman**[1], K. Topf[1], R. Chandler[2], L. Conklin[1]
[1]Global Immunization Division, Center for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uppsala Monitoring Centre, WHO Collaborating Centre for International Drug Monitoring, Uppsala, Sweden
**Background:** Since 2015, the World Health Organization (WHO) has tracked country capacity for vaccine safety monitoring through two main indicators: presence of a national adverse events following immunization (AEFI) causality assessment committee and ≥10 AEFI reports per 100,000 surviving infants annually. National Expanded Programs on Immunization (EPI) and National Regulatory Authorities (NRA) are expected to report aggregate AEFI data through the WHO-UNICEF Joint reporting form (JRF) and case-based AEFI data through VigiBase (maintained by Uppsala Monitoring Center), respectively. This report describes global progress toward meeting these indicators. **Methods:** We used publicly available data on both WHO indicators through the JRF during 2010 and 2015-2019, by region. To assess degree of coordination between EPI and NRA, we compared AEFI data reported to JRF and VigiBase in 2019. To characterize reporting trends, countries were grouped based on World Bank income classifications. **Results:** In 2019, 129 (66.5%) of 194 member states reported having an operational national AEFI causality review committee, compared with 94 (48.5%) in 2010. The proportion of countries reporting ≥10 AEFI per 100,000 surviving infants increased by 15%, from 41.2% in 2010 to 56.2% in 2019. The highest percentage of countries achieving this indicator in 2019 was in the Region of the Americas (71.4%); the largest increase compared to 2010 occurred in the African Region (42.5%). In 2019, 46 (23.7%) of 194 countries reporting to JRF cited a joint EPI and NRA data source. Higher income countries reported more frequently to VigiBase (72.1%) than to JRF (65.5%). **Conclusions:** Over the last decade, global progress has been made toward reaching minimum capacity for vaccine safety monitoring, particularly in the African region. New indicators are needed to better reflect program functionality. Continued global efforts will be vital to address barriers to routine reporting, build national capacity for investigation and data management and sharing between key vaccine safety stakeholders.

## J4. Late-breakers II: Human, Animal, and Environmental Factors Affecting Disease Emergence and Control

**3:15 PM – 4:45 PM**

**Centennial Ballroom IV**

### Genomic Epidemiology of *Candida auris* Suggests Transmission of Echinocandin-Resistant Strains in the United States

**L.A. Parnell**[1], E. Misas[1], S. Hurst[1], M.L. Bentz[1], B. Min[1], N. Le[1], L. Gade[1], K. Forsberg[1], A.P. Litvintseva[1], M.M. Lyman[1], E. Merengwa[2], T. Dang[2], N.A. Chow[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Texas Department of State Health Services, Austin, TX, USA

**Background:** *Candida auris* is an emerging fungus that can cause invasive infection and is associated with high mortality. In addition to its high transmissibility in healthcare settings, it is highly resistant to antifungal drugs, making it challenging to treat infections. Echinocandins are the recommended first-line treatment in the United States, as *C. auris* is commonly resistant to two other major antifungal drug classes. Echinocandin resistance is concerning, but echinocandin-resistant (ech-R) strains have been uncommon in the United States and not historically transmitted between patients. From January to April 2021, seven ech-R isolates were collected from nearby Texas facilities within the same patient transfer network. Epidemiologic findings suggested transmission rather than strains having developed resistance independently. Whole genome sequencing was performed to further characterize these strains and explore the possibility of transmission. **Methods:** *C. auris* isolates (n=7), confirmed as ech-R or pan-resistant, were sequenced using Illumina NovaSeq. Analysis included the newly sequenced isolates and sequences generated previously. MycoSNP was used to assess read quality and identify single-nucleotide polymorphisms (SNPs). A neighbor-joining tree displaying SNPs was constructed using Molecular Evolutionary Genetics Analysis software. Microreact was used for tree visualizations. **Results:** Of the five known *C. auris* clades, all ech-R isolates were within Clade I. The tree topology showed ech-R isolates clustering separately from non-ech-R strains from the same state. The genetic distance within the ech-R cluster ranged from 1-8 SNPs. **Conclusions:** When paired with epidemiologic findings, results demonstrated that the ech-R strains were highly related—supporting that this was one of the first documented instances of transmission of ech-R *C. auris* seen in the United States. Health departments and healthcare facilities should be aware that transmission of ech-R *C. auris* is possible and should ensure that infection prevention and control measures are taken around such cases to prevent transmission.

### Multidrug-resistant *Salmonella* Newport—United States, 2021–2022

**I. Griffin**[1], Z. Ellison[1], M. Birhane[1], H.E. Webb[1], A. McCullough[1], F. Medalla[1], R. Tierney[1], L. Ford[1], J. Collins[1], S.T. Hoang[1], D.C. Payne[1], L.C. Ray[1], C. Schwensohn[1], J. Queen[2], S. Tecle[3], A. Morrison[4], G. Langley[1], M. Leeper[1], L. Francois-Watkins[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Colorado Department of Public Health & Environment, Glendale, CO, USA, [3]California Department of Public Health, Richmond, CA, USA, [4]Texas Department of State Health Services, Austin, TX, USA

**Background:** Surveillance identified a nationwide increase of multidrug-resistant *Salmonella* Newport ("MDR Newport") cases in 2021. Most isolates are resistant to all oral treatment antibiotics. A 2018–2019 outbreak investigation linked MDR Newport to travel to Mexico and consumption of soft cheese from Mexico and beef in the United States. We describe cases reported during June 1, 2021–March 1, 2022, including demographics, possible sources, and antibiotic resistance. **Methods:** Public health laboratories performed whole genome sequencing (WGS) on *Salmonella* isolates. Sequences were uploaded to the PulseNet national bacterial isolate database and analyzed using core genome multi-locus sequence typing. We included 567 isolates related to the MDR Newport strain (within 0–21 allele differences) with records uploaded to PulseNet. We predicted resistance based on resistance genes and mutations present in isolate genomes. Health officials interviewed patients about demographics and exposures. **Results:** Reports of isolates related to MDR Newport increased 122% during the study period compared with the prior year. Among 567 patients from 42 states, 45% bordering Mexico, median age was 34 years (range, <1─88), 280/550 (51%) were male, 154/244 (65%) were Hispanic, and 95/249 (39%) were hospitalized. Overall, 41/116 (35%) reported international travel, 40/41 (98%) to Mexico. Among 72 non-travelers, 41/63 (65%) reported consuming any type of beef, 23/64 (36%) ground beef, 14/52 (27%) carne seca or jerky, and 16/64 (25%) Mexican-style cheese in the 7 days before illness began. Carne seca samples from a commonly reported Mexican brand

yielded several *Salmonella* serotypes but not the outbreak strain. WGS identified 506/565 (90%) patient isolates as resistant to ≥3 antibiotic classes. **Conclusions:** The number of MDR Newport infections that may be difficult to treat has increased. Data continue to suggest that beef consumed in the USA and exposures during travel to Mexico may be sources.

### Fatal Melioidosis in a Child — Georgia, 2021

**J. Pavlick**[1], S. Brennan[1], C. Drenzek[1], J. Gabel[1], J. Gettings[1], M. Hunter[2]
[1]Georgia Department of Public Health, Atlanta, GA, USA, [2] Georgia Department of Public Health - Rome District, Rome, GA, USA

**Background:** In July 2021, Georgia Department of Public Health (DPH) was notified of a fatal case of melioidosis, a disease caused by the bacteria *Burkholderia pseudomallei*. Melioidosis is rare in the United States and typically among international travelers. However, the patient was aged 5 years with no history of travel. Whole-genome sequencing (WGS) results were clonal to 3 other recent nontravel-related melioidosis cases in the U.S. No epidemiologic links were identified. Lack of travel history and infection with the same bacterial strain among cases necessitated further investigation by DPH, with a focus on imported products, since *B. pseudomallei* is not endemic in the continental U.S. **Methods:** DPH interviewed the patient's family to obtain product use history and locations visited by the patient within 30 days of onset. Samples of soil, water, and multiple products were obtained from the patient's home in August and October. Samples were sent to CDC for polymerase chain reaction (PCR) assays, WGS, and culture. Serologic specimens were collected from 3 family members to assess their exposure to *B. pseudomallei.* **Results:** No commonalities in products or locations were identified among the patients. Thirty-eight environmental and 55 product samples were collected during the initial visit; none tested positive for *B. pseudomallei*. Serology collected identified 2 household members with *B. pseudomallei* antibodies, suggesting exposure to this bacterium. During the second visit, an additional 9 environmental and 14 product samples were obtained. One product, an imported aromatherapy room spray, was positive for *B. pseudomallei* by PCR and culture; the sequence was clonal to the patient isolate. **Conclusions:** The cause of melioidosis in this patient was exposure to an imported aromatherapy spray contaminated with *B. pseudomallei*. When this rare and potentially fatal infection is identified, travel history should be obtained; if travel was inconsistent with exposure, the possibility of contaminated imported products should be considered.

### Intercontinental Movement of H5 2.3.4.4 Highly Pathogenic Avian Influenza (H5N1) to the United States, 2021

**S. Bevins**[1], J. Cumbee[2], K. Dilione3, K. Douglass[2], J. Ellis[1], M.L. Killian[4], J. Lenoch[3], S. Shriner[1], M. Torchetti[4]
[1]USDA National Wildlife Research Center, Fort Collins, CO, USA, [2]WS South Carolina, SC, USA, [3]USDA National Wildlife Disease Program, Fort Collins, CO, USA, [4]USDA National Veterinary Services Laboratory, Ames, IA, USA

**Background**: Influenza A viruses have a worldwide distribution and wild birds are the primary wild reservoir. Highly pathogenic lineage viruses identified in 1996 (A/goose/Guangdong/1/1996, [Gs/GD]) have repeatedly spilled over from poultry to wild birds. The eventual emergence of Gs/GD clade 2.3.4.4 has led to more persistent circulation of these high pathogenic viruses in wild birds and high morbidity and mortality outbreaks in poultry on multiple continents. Here, we document a new introduction of HP AIV viruses belonging to the Gs/GD lineage, clade 2.3.4.4b, into wild waterfowl into the United States in the winter of 2022. **Methods**: Genetic analyses reveal these viruses are similar to viruses circulating in Europe in spring of 2021 and in Canada in late 2021. The potential introduction pathway likely includes wild bird migratory routes from Northern Europe that overlap Arctic regions of North America, and then dispersal farther south into Canada and the US. Combining this information with bird band recovery data, we predicted likely routes of continued dispersal, which are currently playing out in real-time. **Results**: These high pathogenic viruses have now been found in more than 500 wild birds, representing the largest high pathogenic outbreak in US wild birds ever documented. The viruses have also spilled over into domestic poultry leading to the loss of more than 20 million chickens and turkeys. One zoonotic infection has been documented. **Conclusion**: These late breaking outbreak data demonstrate how wildlife surveillance can be successfully designed to act as an early warning system for virus introduction, how genetic analyses can be used to better understand spillover events, and how wildlife movement data can be used to predict pathogen dispersal.

### Seroprevalence of SARS-CoV-2 among Working Dogs in Arizona, 2021

**G. Hecht**[1], H.D. Yaglom[2], W. Svoboda[3], N. Sarbo[2], J. Ely[2], D. Jasso-Selles[2], M. Sprenkle[2], H. Mead[2], I. Ruberto[1], D.M. Engelthaler[2], H. Venkat[1,4]

[1]Arizona Department of Health Services, Phoenix, AZ, USA, [2]Translational Genomics Research Institute, Flagstaff, AZ, USA; [3]Hayden Road Animal Hospital, Scottsdale, AZ, USA, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** SARS-CoV-2 (SC2) surveillance is being conducted globally for animals in various settings to better understand One Health transmission. However, surveillance in working dogs has not been implemented. Many public safety organizations employ working dogs trained for specific roles including tracking, scent detection, patrol, crisis response, and search and rescue. These important functions make understanding SC2 transmission in working dogs a top priority. We aimed to conduct a serosurvey of working dogs in Arizona to determine prevalence of SC2 antibodies in this population. **Methods:** We collaborated with a veterinary clinic in Arizona with a high working dog patient volume. Canines were enrolled at clinic visits where handler consent was obtained and a short questionnaire was administered to collect canine demographics, COVID-19 exposure status, and reported symptoms. Serum was collected for SC2 neutralizing antibody testing. Nasal and rectal swabs were collected for PCR testing on dogs with recent SC2 compatible symptoms or COVID-19 exposure. **Results:** During November 30–December 17, 2021, we enrolled 44 working dogs ranging in age from 1.5–10 years (mean = 4.5 years). The majority were of the Belgian Malinois breed (64%) and male (77%). Their roles mostly included hospital patrol (27%), and dual-purpose police patrol and narcotic detection (32%). Of the dogs sampled, 20 had a known prior exposure to COVID-19: six <3 months prior to collection, eight 3–6 months prior, and six >6 months prior. Swabs from three dogs tested PCR negative for SC2. Seven serum samples (16%) had evidence of SC2 neutralizing antibodies. 25% of canines with a known COVID-19 exposure had positive SC2 serology compared with 8% of canines with no known exposure. Among the seven antibody-positive canines, five had known COVID-19 exposure (four to their handler, one to a household member) and two had no known exposure. **Conclusions:** To our knowledge, this is the first seroprevalence study developed to detect zoonotic SC2 events in working dogs. We found evidence of SC2 antibodies in dogs with known and unknown COVID-19 exposures. This highlights the risk for SC2 exposure in working dogs in both their home and duty environments. The potential impacts of SC2 on the abilities of working dogs have strong implications for public safety and public health.

### SARS-CoV-2 at the Zoo: A One Health Approach to Characterize the Clinical, Epidemiologic, and Genomic Presentation of SARS-CoV-2 in Zoo, Sanctuary, and Aquarium Outbreaks in the United States

**R.R. Ghai**[1], K.E. Varela[1], J.M. Ritter[1], K. Terio[2], T. Shrader[3], M. Drozd[4], L. Wright[5], J. Yoshicedo[6], A.Y. Liew[1], A. Carpenter[1], T.A. Moore[1], S. Rekant[7], M.K. Torchetti[7], J. Sleeman[8], C. Barton Behravesh[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]University of Illinois, Brookfield, IL, USA, [3]Lincoln Children's Zoo, Lincoln, NE, USA, [4]University of Nebraska-Lincoln, Lincoln, NE, USA, [5]Great Plains Zoo, Sioux Falls, SD, USA, [6]Honolulu Zoo, Honolulu, HI, USA, [7]U.S. Department of Agriculture, Washington, DC, USA, [8]US Geological Survey National Wildlife Health Center, Madison, WI, USA
**Background:** SARS-CoV-2 infection has been reported in 16 species across the globe to-date – cats, dogs, a binturong, a coati, ferrets, a fishing cat, gorillas, lions, a lynx, mink, otters, a puma, snow leopards, spotted hyenas, tigers, and white-tailed deer. Eleven (69%) of these susceptible species were discovered in zoos, sanctuaries, and aquaria (hereafter zoos). In the US, outbreaks of SARS-CoV-2 in zoos have become increasingly frequent, despite widespread implementation of enhanced biosecurity protocols. Here, we present the findings gathered through SARS-CoV-2 surveillance at the zoo human-animal interface. **Methods:** SARS-CoV-2 positive zoo animals were primarily discovered through passive surveillance after clinical signs consistent with SARS-CoV-2 infection were detected in zoo animals. Samples from cases included here were confirmed at USDA's National Veterinary Services Laboratories. Clinical and epidemiologic data on animal cases were collected in collaboration with state, tribal, local, and territorial health officials and reported to CDC through standardized data collection tools. **Results:** To-date, 130 zoo animals (38% of all positive animals) in 45 outbreaks were confirmed positive for SARS-CoV-2. Commonly infected species included lions (n=40) and tigers (n=50). In 51% (n=23) of outbreaks, a human source of exposure, often a caretaker, was identified. Like people, clinical presentation varied from mild to severe, but often included cough (32%), lethargy (16%), inappetence (15%), nasal discharge (14%), and sneezing (12%). In addition to wildtype strains, zoo animals have been infected with SARS-CoV-2 variants, including Alpha (B.1.1.7) and Delta (B.1.617.2). Notably, 5 big cats in 3 zoos that died within two weeks of SARS-CoV-2 detection were infected with Delta. In each, pathological investigation concluded SARS-CoV-2 likely contributed to the animal's illness and death. **Conclusions:** One Health surveillance and investigation of SARS-CoV-2 outbreaks in zoos has helped to reveal the range of mammalian hosts susceptible to SARS-CoV-2. While the main driver of COVID-19 spread is person-person transmission, zoonotic spread, especially in zoos, underscores the importance of a One Health approach to address the human and animal health and conservation implications of SARS-CoV-2.

## Poster Session 4 Abstracts

**5:00 PM – 6:00 PM**

**Grand Hall**

## COVID-19 and SARS-CoV-2

### Poster 257. Comorbid Conditions Associated with COVID-19 Mortality in a Tertiary Care Hospital in Semi Urban Bangladesh

**K.M. Islam**[1], M.Z. Hossain[1], M.S. Ahmed[1], K. Lee[2], M.M. Rahman[3], M.S. Rahman[3], S. Arifeen[1], E.S. Gurley[2]
[1]International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Johns Hopkins University, Baltimore, MD, USA, [3] Bangabandhu Sheikh Mujib Medical College and Hospital, Faridpur, Bangladesh

**Background**: People with comorbidities are at increased risk of severe COVID-19 disease and mortality. But we do not know how covid-19 infection affects comorbidity in low- and middle-income countries due to large data gap. We aim to estimate the association of comorbidity and death among hospitalized patient in semi urban Bangladesh. **Methods**: We collected demographic information, age, sex, covid-19 testing results and death outcomes from the COVID-19 ward and ICU patient registry books for patients admitted from 25th March 2020 to 30th September 2021 in BSMMC (Bangabandhu Sheikh Mujib Medical College), Faridpur, a tertiary care and dedicated regional COVID-19 hospital. We used multiple logistic regression to estimate the association between COVID-19 mortality and preexisting comorbidities like diabetes, hypertension, heart disease, kidney disease, preexisting respiratory disease, cerebrovascular disease, after adjusting for age and sex. **Result:** A total of 5067 patients were admitted with suspected or confirmed SARS-CoV-2 infections in the two units; 1942 (35%) were female and 929 died (18.3%). The mean age of patients who died with COVID-19 was 59.5 years and 50 years for survivors. Among all the patient with comorbidity 36% died. Patients with any comorbidity listed in their register notes were 7.1 (95% CI 5.9-8.6) times more likely to die than patients without a comorbidity and age was also associated. The odds were 1.8 times higher for patients of 41-60 years and 3.7 times for above 60 years than patients below 40 years of age. The associations were similar for each comorbidity (OR 5.7 to 1.7). Eleven pregnant women were hospitalized with COVID-19 and 6 died, including one with anemic heart failure. **Conclusion:** The associations we estimated may be underestimated given that many people may have undiagnosed chronic conditions in this context. Patients admitted with covid-19 having comorbidity were more vulnerable to die than other developed countries.

### Poster 258. Assessing the Loss of Taste and Loss of Smell Incidence during the Early Phase of COVID-19 Pandemic in Nigeria

**M.D. Adebayo**[1,2], A.F. Adejumo[3], D.S. Akintunde[4], A.B. Adebayo[5], O.O. Adejumo
[1]Epidemiological Section, Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, South Africa, [2]Department of Animal Health, Federal College of Animal Health and Production Technology, Ibadan, Nigeria, [3]School of Community Health & Policy, Morgan State University, Baltimore MD, USA, [4]Durham Region Public Health Department, Whitby, Ontario , Canada, [5]Dofey Veterinary Services, Ibadan, Nigeria

**Background:** At the early phase of COVID-19 pandemic globally, there was a significant rise in symptoms such as loss of taste and/or smell in people who had not experienced such before and these were clinically linked to this novel disease. This study appraised the association between the occurrence of loss of taste and/or loss of smell and Covid-19 testing in Nigeria between January and June 2020. **Method:** A total of 303 participants who fulfilled the inclusion criteria of being ≥18 years and who reported experiencing loss of taste and/or smell between January and June 2020 were drawn from Nigeria's largest online community, Nairaland Forum, using a self-reported questionnaire. Descriptive statistics such as mean, standard deviation and percentages were used to summarize quantitative variables. Chi-square, odds ratio, and logistic regression were used to assess associations using 95% confidence interval (CI). **Results:** Most of the respondents (48.84%) were between age group 26-34 years. 53.47% of the respondents reported loss of taste and smell whereas 13.53% reported loss of taste only and 5.94% reported to have gone for COVID-19 testing. There was significant association between COVID-19 testing and testing for other conditions like malaria ($p=0.005$); blood sugar ($p=0.005$); high blood pressure (HBP) ($p<0.001$); and use of air conditioner ($p=0.005$). Similarly, in bivariate analysis, covariates such as use of air conditioners, malaria testing and HBP testing were significantly associated with COVID-19 Testing ($p<0.05$) while symptoms of loss of taste and/or

smell, alcohol use, typhoid testing and sex were not. Overall, the presence of loss of taste and/or smell was associated with lesser odds of getting tested for COVID-19 (aOR= 0.64, p=0.282). This relationship remained not significant with use of air conditioner as a mediator (aOR=0.68, p=0.303). **Conclusion:** This study showed that given the unique environment like Nigeria with high incidence of common diseases like Malaria, HBP and Diabetes, there were stronger association of people who experienced loss of taste and/or loss of smell going for testing for these diseases than testing for COVID-19. Therefore, more public health promotion needs to be done to get people to test for COVID-19.

### Poster 259. Relationship between Acute Respiratory Illness and Work Attendance during the COVID-19 Pandemic in a Prospective Multi-Center Study, March-November 2020

**O. Shafer**[1,2], F. Ahmed[1], S. Kim[3], J. Chung[3], A. Uzicanin[1], the US Flu Vaccine Effectiveness Network[2,4,5,6,7]
[1]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [3]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4] University of Pittsburgh, Pittsburgh, PA, USA, [5] Texas A&M University, Temple, TX, USA, [6]Kaiser Permanente Washington Health Research Institute, Seattle, WA, USA, [7]University of Michigan, Ann Arbor, MI, USA
**Background:** Persons with COVID-19-like illness are advised to stay home to prevent the spread of the SARS-Cov-2 (SC2) virus. We assessed relationships between symptomatic laboratory-confirmed COVID-19, access to telework, and work attendance during the period March 2020 through November 2020**. Methods:** Employed adults seeking care or presenting at SC2 testing sites with acute illness (<10 days' duration) with fever or cough were enrolled at sites in Michigan, Pennsylvania, Texas, and Washington affiliated with the US Influenza Vaccine Effectiveness Network. Participants were asked to fill out a follow-up survey 1-2 weeks after enrollment to collect information on access to telework prior to their illness and whether they worked onsite, teleworked, or did not work during their illness. SC2 molecular testing of respiratory specimens from nasal or nasopharyngeal swabs were done. Multi-level logistic regression models were used to assess associations between laboratory-confirmed COVID-19, access to telework, and working onsite during illness. Working during illness (i.e., working onsite or teleworking) was also assessed to ascertain productivity. The dependent variable was COVID-19 status (negative, positive) and the independent variables included work attendance, telework access, age, sex, race, education, health status, and site. **Results:** Among 233 SC2-positive and 726 SC2-negative adults who completed the survey within 4 weeks of illness onset, those with COVID-19 were less likely to report working onsite (adjusted odds ratio, $OR_a$: 0.46, 95% CI: 0.33, 0.65) or to work during their illness ($OR_a$: 0.41, 95% CI: 0.30, 0.55). However, among the subset of 207 persons with access to telework, the likelihood of working during illness was similar between the two groups ($OR_a$: 0.96, 95% CI: 0.30, 3.05). **Conclusions:** Adults with laboratory-confirmed COVID-19 were less likely to report working onsite than persons with non-COVID-19 respiratory illness. Access to telework augmented work attendance during the illness.

### Poster 260. CLIA in my SC2 Bioinformatics: Developing the SC2CLIA Cecret Bioinformatics Pipeline for a CLIA-Compliant SARS-CoV-2 NGS Workflow

**A. Huang**[1], E.L. Young[2], A.J. Williams-Newkirk[1], R. Jin[3], M. Thakur[4], S. Lucking[3], J. Rowell[3], G. Williams[1], E. Vidyaprakash[1], T. Griswold[1], P. Smith[1], C. Lane[1], D. Stoneburg[1], M. Turnsek[1], C. Lee[1], H. Martin[1], M. Martinez-Smith[1], S. Rogers[1], J. Folster[1], S. Tong[1], P. Fields[1], H. Carleton[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Utah Public Health Laboratory, Taylorsville, UT, USA, [3]Weems Design Studio, Decatur, GA, USA, [4]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA
**Background:** Diagnostic sequencing of SARS-CoV-2 (SC2) for variant characterization provides an important tool for public health response. Standardized bioinformatics approaches are needed for compliance with Clinical Laboratory Improvement Amendments (CLIA). We describe the SC2CLIA Cecret bioinformatics pipeline for lineage and spike protein substitution calling, determine the cycle threshold (Ct) required to produce appropriate sequence quality for our workflow, and validate this workflow under CLIA. **Methods:** SC2CLIA Cecret was built on the Cecret pipeline for the analysis of SARS-CoV-2 Illumina sequencing data from ARTIC V3/Illumina library preparations. Cecret was written in Nextflow, using Singularity and Docker software containers, for cleaning, reference alignment, variant calling, quality control (QC), lineage classification, and phylogenetics. SC2CLIA Cecret added more QC, spike protein substitution calling, upload to NCBI GenBank capability, PDF and HTML reports, and additional data management using Nextflow, Python, and R. Moreover, GitHub Flow and DevOps-style practices ensured that analyses were traceable, shareable, and repeatable in separated production and development spaces. A total of113 previously sequenced SARS-CoV-2 specimens were used in the validation. Nucleic acid was

extracted, quantified using the CDC Influenza SARS-CoV-2 Multiplex Assay, and sequenced on an Illumina MiSeq using an ARTIC nCoV-2019 V3 and Illumina DNA Prep protocol. To determine a threshold Ct value, 8 specimens were serially diluted, quantified by quantitative RT-PCR, and sequenced. **Results:** The use of containers and Github allows the entire Cecret or SC2CLIA Cecret pipeline to be installed in a Linux environment in an hour. SC2CLIA Cecret analyzed 48 specimens in under an hour. In addition to the validation of SC2 lineage and spike protein substitution calling, we also determined that specimens with SC2 Ct values < 30 yielded acceptable coverage depth, genome coverage, and S-gene coverage for analysis. **Conclusions:** SC2CLIA Cecret quickly and accurately reported lineage and spike protein substitution data from SC2 sequences under a CLIA-compliant workflow. The need for flexible yet traceable bioinformatics analysis for CLIA highlights the advantages of adopting GitHub Flow version control and DevOps-style practices.

### Poster 261. Infection and Case Fatality Rate of Healthcare Workers from COVID-19: A Cross-Sectional Study in Azad Kashmir

**M.A. Khan**
Department of Microbiology, Abbas Institute of Medical Sciences, Muzaffarabad, Azad Kashmir, Pakistan
**Background:** The pandemic COVID-19 disease caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has become a significant health problem globally. In the wake of ongoing pandemic (COVID-19), services of healthcare workers are noteworthy. Health-care workers (HCWs) warrant special attention because of their substantial task of diagnosing and treating critically ill patients putting themselves at the risk for exposure to patients or infectious materials. The aim of this study was to estimate the number of COVID-19 infections and case fatality rate of HCWs in Azad Kashmir during the pandemic period. **Methods:** A Descriptive, cross-sectional was carried out in the COVID 19 Sentinel Unit, in Directorate General Health Office Muzaffarabad from March 15, 2020 to October 12, 2021. The study population included HCWs of different ranks working in either public or private hospitals in Azad Kashmir. Non-probability, consecutive sampling technique was used for sample collection. Both symptomatic and asymptomatic HCWs were tested for COVID-19 with a Real-time reverse transcriptase-polymerase chain reaction (RT-PCR) following the standard protocol. COVID-19 positivity was correlated with demographic characteristics, working location, and medical history. **Results**: A total of 962 laboratory-confirmed infections and 9 deaths were documented in HCWs with a mean age of 38.37 years, ranging 18 to 70 years. Infections were mainly observed in doctors (63.4%, n=610), followed by paramedical staff (28.7%, n=276) and nurses (7.9%, n=76). A significant number of infected HCWs were asymptomatic (38%), while in symptomatic patients, the most prevalent symptoms were fever 44%, myalgia (42%) and cough (38%). Case fatality rate was found higher in nurses (1.31%) despite being the least infected group as compared to doctors (0.98%) and paramedical staff (0.72%). The overall case fatality rate was 0.93%. **Conclusion:** A significant number of HCW were reported to be infected with COVID-19 during COVID-19 pandemic, with overall case fatality rate of 0.93%.

### Poster 262. Assessment of Anxiety and Psychological Distress among Pakistani People during COVID-19 Pandemic, 2020

Moved to Poster Session 1, Monday, August 8, 12:30 PM – 1:30 PM (at end of COVID-19 and SARS-CoV-2 section, after poster 33)

### Poster 263. A Contact Tracing-Health Information Exchange Partnership: An Effective Collaboration for a Data-Driven Response to COVID-19 in Maryland

**C. Babcock**[1], K. Feldman[1], A. Hanks[2], S. Dowling[3], M. Pearlowitz[1]
[1]Maryland Department of Health, Baltimore, MD, USA, [2]Chesapeake Regional Information System for our Patients, Columbia, MD, USA, [3]Slalom, McLean, VA, USA
**Background:** Maryland Department of Health (MDH) relies on accurate and timely data to conduct contact tracing for COVID-19. Maryland's health information exchange, CRISP, houses healthcare data organized through a master patient index (MPI). We describe a robust collaboration between MDH and CRISP that provides the foundation for effective, data-driven contact tracing. **Methods:** MDH and CRISP collaboratively developed data processing infrastructure and meet regularly to review data quality. Hourly, electronic laboratory reports are routed through CRISP to the contact tracing data platform (covidLINK). Additionally, CRISP developed a portal for providers to directly report rapid antigen test results. All positive results are matched with the CRISP MPI to enhance the record with demographic, locating, fatality, vaccination, and hospitalization data. CRISP flags records associated with congregate settings (nursing homes, correctional facilities) and universities. **Results:** For June 15, 2020-September 1, 2021, CRISP pushed 530,000 positive results to covidLINK for contact tracing within an hour of receipt, 99% with a phone number. CRISP found a unique patient identifier for 520,000 (98%) records which allowed for deduplication and data enrichment (e.g., confirmation or addition of race for 383,000 records and ethnicity for

385,000 records). CRISP flagged nearly 2,000 records with a negative polymerase chain reaction (PCR) collected within 48 hours of a positive antigen test. To facilitate investigations in high-risk settings, 18,000 cases in congregate settings were flagged. CRISP geo-coded 99.6% of addresses to route cases for investigation by patient county of residence. **Conclusion:** The robust collaboration between CRISP and MDH has allowed for timely, data-informed case investigations and contact tracing. Data integration has translated into greater success locating cases, more efficient routing of records, enhanced ability to assess disparities and inequities, and rapid investigation of post-vaccination infections. This infrastructure provides a strong foundation for data modernization and public health efforts beyond COVID-19.

### Poster 264. Effect of the COVID-19 Pandemic on PulseNet Submissions and Outbreak Detection

**K. Hise**, H. Carleton, J. Huffman, J. Lavin, M. Schroeder, B. Tolar
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** PulseNet, the national laboratory network for foodborne disease surveillance, has been using DNA fingerprint data to identify outbreaks of foodborne illness since 1996. Over 60 state and local public health laboratory partners upload over 75,000 DNA fingerprints annually to the PulseNet national databases. The number of uploads to the PulseNet national databases had increased until 2015 and had plateaued from 2015 to 2019. We assessed the number of uploads and outbreaks as compared to the previous five years' data to see if the COVID-19 pandemic was potentially impacting submissions and outbreak detection. **Methods:** We examined the weekly, monthly, and cumulative numbers of DNA fingerprint uploads from human cases for Listeria monocytogenes, Shiga-toxin producing Escherichia coli (STEC), Salmonella, and Campylobacter in the PulseNet national databases during the COVID-19 pandemic (March 2020-August 2021) and compared them to the previous five years' uploads. We also compared the trends of the uploads over time. We similarly looked at the number of outbreaks detected by PulseNet. **Results:** Overall, across all organisms, PulseNet saw a decrease in uploads from March 2020 to August 2021 as compared with the uploads during 2015 to 2019. From March 2020 to August 2021, Salmonella and STEC uploads consistently remained below the 5-year average, with an average decrease of 25% and 26%, respectively. Listeria monocytogenes uploads had an average decrease of 9% and returned to the 5-year average since March 2021. Campylobacter uploads decreased on average 15% compared with the 5-year average. All organism uploads, except for Listeria, have increased in 2021 but have not yet returned to 5-year averages. Outbreaks detected by PulseNet were 50% fewer from April 2020 to March 2021 compared with the same time period over the previous five years. **Conclusions:** The number of uploads to the PulseNet national databases and the number of outbreaks detected by PulseNet decreased from March 2020 to August 2021. This decrease correlates with the COVID-19 pandemic. During this time, PulseNet participants reported lower submissions of foodborne bacterial isolates to their labs as a major contributor to the decrease in uploads to the PulseNet national databases.

### Poster 265. Lessons Learned about the Accuracy and Precision of COVID-19 Incident Case Forecasts for the United States from July 2020 through March 2021

**V.K. Lopez**[1], E.Y. Cramer[2], N.G. Reich[2], M. Biggerstaff[1], M.A. Johansson[1]
[1]COVID-19 Response Team, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]University of Massachusetts, Amherst, MA, USA
**Background:** Forecasting within the United States COVID-19 response encompassed a broad collation of modeling efforts via the US COVID-19 Forecast Hub. Information from probabilistic COVID-19 cases forecasts was leveraged to provide situational awareness for the response and inform resource allocation. Retrospective evaluation of forecast skill can inform the appropriate use of forecasts in outbreak response. **Methods:** 960,336 forecasts of weekly incident COVID-19 cases at the national, state, and county level, submitted by 9 to 13 teams from July 2020 to March 2021, were included in the evaluation. Model performance was assessed via the weighted interval score (WIS), a metric that reflects precision and accuracy, by comparing the probabilistic distribution of each forecast to the corresponding observed outcome of reported incident cases. Average WIS and relative WIS, a comparison of scores across teams and scaled to a naïve model, were computed. **Results:** Performance was highly variable between models. Three models consistently outperformed a naïve baseline model at the non-county levels and the county level; yet when comparing 1 week ahead forecasts to those 4 weeks ahead, even these models were unreliable longer horizons. Five teams had worse relative WIS during periods of stability relative to phases of increasing and decreasing growth rates. When forecasting across multiple geospatial scales, models that accounted for spatial correlation had better average WIS relative to models that did not. **Conclusions:** Ideally, forecasts of incident cases serve as an early warning for changes in transmission dynamics. Here, we show that current COVID-19 case forecasts cannot reliably predict key phases of epidemic transitions and therefore should be used with caution for

decision making. Further research is needed to improve predictions from individual models in a changing landscape of mitigation policies, personal behaviors, and transmission.

### Poster 266. Withdrawn

### Poster 267. SARS-CoV-2 Global and Regional Seroprevalence: A Systematic Review and Meta-analysis of Population-based Sero-epidemiological Studies Aligned with the WHO Unity Protocol

**I. Bergeri**[1], M. Whelan[2], H. Ware[2], L. Subissi[1], H.C. Lewis[1], Z. Li[3], X. Ma[4], A. Nardone[1,2], M. Valenciano[1,2], B. Cheng[1], A. Vicari[3], L. Al Ariqi[6], E. Aly[6], J. Okeibunor[8], T. Azim[7], P. Wijesinghe[5], L.V. Li[9], A. Vaughan[10], R. Pebody[10], SeroTracker Consortium, WHO Unity Studies Collaborators, D. Buckeridge[11], N. Bobrovitz[12], R. Arora[2,13], M.D. van Kerkhove[1]

[1]World Health Organization, Headquarters, Geneva, Switzerland, [2]Centre for Health Informatics, Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada, [3]Faculty of Engineering, University of Waterloo, Waterloo, Ontario, Canada, [4]Institute of Health Policy Management and Evaluation, University of Toronto, Toronto, Ontario, Canada, [5]Epiconcept, Paris, France, [6]World Health Organization for the Eastern Mediterranean, Cairo, Egypt, [7]World Health Organization, Regional Office for South-East Asia, New Delhi, India, [8]World Health Organization, Regional Office for Africa, Brazzaville, Congo, [9]World Health Organization, Regional Office for the Western Pacific, Manila, Philippines, [10]World Health Organization Regional Office for Europe, Copenhagen, Denmark, [11]Department of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, Quebec, Canada, [12]Temerty School of Medicine, University of Toronto, Toronto, Canada, [13]Institute of Biomedical Engineering, University of Oxford, Oxford, UK

**Background:** Serological testing is crucial for monitoring the extent of SARS-CoV-2 infection and population-level humoral immunity. However, there is limited standardization of serosurveys, and disproportionately fewer in low-middle income countries. The WHO 'Unity' protocol for population-based sero-epidemiological studies provides a standardized framework for robust and comparable serosurveys of the general population, and applicable in LMICs. We conducted a meta-analysis of studies aligned with the aforementioned 'Unity' protocol, examining differences over time in seroprevalence by age and sex, WHO region, and study design factors. **Methods:** We included serosurveys aligned with the WHO Unity protocol described above, published from 01-01-2020 to 03-09-2021. Our search spanned Medline, Embase, Web of Science, preprint databases, grey literature, and yet unpublished results through the WHO Unity Studies Initiative. We conducted descriptive analysis of seroprevalence, meta-analyzed seroprevalence differences between groups, used meta-regression to identify study factors affecting seroprevalence, and estimated changes in seroprevalence over time. **Results:** We included 604 studies in our analysis from 91 countries. The majority of studies were from the WHO Europe and Americas regions (n=215 and 178 respectively). While we found significantly lower seroprevalence in children and youth 0-19 (PR: 0.79 [0.68-0.92]) and older adults 60+ (PR: 0.78 [0.70-0.87]) compared to adults 20-29, we found no difference in seroprevalence between males and females. The highest median seroprevalence estimates were in the African and South-East Asian regions (16.7% and 24.6%, respectively). Median (IQR) ratio of seroprevalence to cumulative incidence from 2020 Q1 to 2021 Q2 ranged from 4.0 (2.4, 8.3) in the Americas (HIC) to 386.5 (268.5, 684.6) in Africa. **Conclusion:** We present the most comprehensive and comparable analysis of seroprevalence data in the general population to date. Results indicate that seroprevalence varies significantly by region, emphasizing the need for serosurveys in data-scarce regions. Large increases in seroprevalence in predominantly high-income countries reflect increasing vaccination rates, highlighting the continued need for equity in global vaccine distribution.

### Poster 268. SARS-CoV-2 Sewage Surveillance in Guatemala City

**L.F. Santos**[1], B.M. Ramay[1,2], M.R. Lopez[1], C. Cordon-Rosales[1,2], M.F. Ning[3], D.R. Call[2]

[1]Centro de Estudios en salud, Universidad del Valle de Guatemala, Guatemala City, Guatemala, [2]Paul G. Allen School for Global Health, Washington State University, Pullman, USA, [3]Centers for Disease Control and Prevention-Central American Office, Guatemala City, Guatemala

**Background:** Detection of SARS-CoV-2 RNA in sewage may be a useful surveillance tool, particularly in low-resource settings where large-scale human testing is not feasible. Such detection can be implemented over multiple spatial and temporal scales to understand how SARS-CoV-2 is spreading in a population, particularly if data are linked to quantitative results. We carried out a pilot of SARS-CoV-2 detection by RT-PCR in sewage samples by longitudinal sampling at six neighborhood wastewater treatment plants (WTP) and two street discharges in Guatemala City from April to August 2021, when an increase in COVID-19 cases was experienced in the country. **Methods:** There is one dedicated COVID-19 hospital in Guatemala City that was included as a positive control. Sites were selected by convenience according to accessibility and to reflect a range of population densities in the catchment area. One sample was collected every month from each site. Aliquots (50-ml) were heat neutralized,

concentrated using a PEG procedure, and tested by RT-PCR for the presence of nucleoside markers (N1 and N2). Pearson's correlation was used to determine the relationship between the number of patients in the COVID-19 hospital at the time of sample collection and the $2^{Ct}$ values in each sample. **Results:** A total of 36 samples were collected from nine sites over 4 months, and 75% (n=27/36) were positive for SARS-CoV-2 by N1, and/or N2, or both. One of the positive samples (4%, n=1/27) was positive for only for N2. We detected SARS-CoV-2 at every site one to four times with positive detection for all samples from the hospital and two neighborhoods. On average, the N1 marker was more sensitive than the N2 markers [average cycle threshold (Ct) 32.90 and 33.98, respectively]. The $2^{Ct}$ values ranged over three-orders-of-magnitude (from 14 to 15,921). Values were correlated with the size of the patient population at the hospital (r=0.61). We observed a longitudinal increase in the number of positive sites [baseline (27-29 April 2021) 55%, n=5/9; peak (29 June-1 July 2021) 89%, n=8/9]. **Conclusions:** Viral detection from collected sewage samples paralleled an increase in COVID-19 cases in Guatemala City. A correlation identifying the number of infected hospitalized patients and $2^{Ct}$ values may be useful to understand the utility of wastewater SARS-CoV-2 surveillance for use during future surveillance efforts.

### Poster 269. Geospatial Variability in Excess Death Rates during the COVID-19 Pandemic in Mexico: Examining Socio Demographic, Climate, and Population Health Characteristics

**S. Dahal**[1], R. Luo[1], M.H. Swahn[1,2], G. Chowell[1]
[1]Department of Population Health Sciences, School of Public Health, Georgia State University, Atlanta, GA, USA, [2]WellStar College of Health and Human Services, Kennesaw State University, Kennesaw, GA, USA
**Background:** Mexico is one of the countries in Latin America that is bearing the brunt of the COVID-19 pandemic with one of the highest numbers of COVID-19 deaths in the world. Additionally, Mexico was identified as one of the countries with highest excess deaths both in terms of absolute numbers and excess deaths rate per 100 000 population. This study examined how socio-demographic, climate and population health characteristics shape the geospatial variability in excess mortality patterns during the COVID-19 pandemic in Mexico. **Methods:** We used Serfling regression models to estimate all-cause excess mortality rates for all 31 Mexican states and Mexico City. The association between socio-demographic, climate, health indicators and excess mortality rates were determined using multiple linear regression analyses. Functional data analysis characterized clusters of states with distinct excess mortality growth rate curves. **Results:** The overall all-cause excess deaths rate during the COVID-19 pandemic in Mexico until April 10, 2021 was estimated at 39.66 per 10 000 population. The lowest excess death rates were observed in southeastern states including Chiapas (12.72) and Oaxaca (13.42), whereas Mexico City had the highest rate (106.17), followed by Tlaxcala (51.99). We found a positive association of excess mortality rates with aging index, marginalization index, and average household size ($P < 0.001$) in the final adjusted model (Model R2=77%). We identified four distinct clusters with qualitatively similar excess mortality curves. **Conclusions:** Central states exhibited the highest excess mortality rates whereas the distribution of aging index, marginalization index, and average household size explained the variability in excess mortality rates across Mexico. Our excess mortality estimates can help tailor state specific medical and public health interventions to prevent excess mortality in vulnerable areas by targeting specific regions and socio-economic indicators.

### Poster 270. "*They've lost over a year of normal childhood experiences*": Perceptions of Physical and Mental Health Benefits of COVID-19 Vaccines for Children in San Francisco

**A. Nickerson**[1], L. Gutierrez-Mock[1], L. Buback[1], S. Welty[1], L. Anicete[1], W. Enanoria[2,3], M. Reid[1,4,5]
[1]Institute for Global Health Sciences, University of California, San Francisco, CA, USA, [2]Department of Epidemiology and Biostatistics, University of California, San Francisco, CA, USA, [3]San Francisco Department of Public Health, San Francisco, CA, USA, [4]Division of HIV, Infectious Diseases and Global Medicine, University of California, San Francisco, CA, USA, [5]School of Medicine, University of California, San Francisco, CA, USA
**Background:** The Pfizer-BioNTech COVID-19 vaccine was granted Emergency Use Authorization (EUA) by the US FDA in December 2020 and full FDA approval for people aged 16 and over in August 2021. Youth aged 16 to 18 years old were eligible to receive the Pfizer vaccine under the original EUA. In May 2021, the EUA was extended to 12- to 15-year-olds. The Moderna and J&J vaccines are only available to people 18 and over. Our study aimed to understand the landscape of vaccine opinions among San Francisco parents and eligible youth, including parental perspectives on vaccinating children under 12 years of age when eligible. **Methods**: From July 20 - August 31, 2021, semi-structured telephone interviews were conducted in English and Spanish with San Francisco residents (ages 13+) who had recently been tested for COVID-19 (N=83). Adult parents/guardians responded on behalf of minor children (<18 years, N=28). Of the remaining 55 adult participants in this sampling frame, 12 had children under 18. Interviews were audio recorded, transcribed, translated into English when necessary and rapidly analyzed according to matrix analysis methodology. **Results**: Parent/guardian views on youth vaccinations highlighted two

primary themes: COVID-19-related mental health/anxiety issues and returning to school in-person. Parents discussed various mental health issues related to the COVID-19 pandemic in children and often cited these as motivation for sending their children back to school. However, some parents worried about COVID-19 risk at school, and some children had increased anxiety about contracting or spreading COVID-19. Still, a small minority of parents/guardians, often not vaccinated themselves, remained hesitant about vaccinating their children primarily because of concerns about vaccine safety. **Conclusions:** Results suggest that vaccination is perceived as protective for children against COVID-19 risk at school. Many parents believe expanding vaccine eligibility to children <12 years, contingent on robust scientific data, will benefit children's mental and physical health. Effective messaging about youth vaccination should emphasize that vaccine uptake may ameliorate anxiety and improve child wellbeing over and above protecting against COVID-19.

### Poster 271. Epidemiological Assessment of COVID-19 Cluster among Attendees of a Church Activity in Omoro District, Northern Uganda, October 2020

**P.O. Thiwe**[1], D. Emong[1], D. Kadobera[1], B.A. Omoda[1], J. Namayanja[1], I. Akusekera[1], A.R. Ario[1,2], J.R. Harris[3]
[1]Uganda Public Health Fellowship Program, Kampala, Uganda, [2]Ministry of Health, Kampala, Uganda, [3]Division of Global Health Protection, Centers for Disease Control and Prevention, Kampala, Uganda
**Background:** On 2 October 2020, a cluster of COVID-19 infections was reported in Omoro District in northern Uganda. Despite government directives banning public gatherings, many infected persons had reportedly attended a farewell party at Church X on 5 September. We investigated to determine infection source, understand outbreak magnitude, and identify risk factors to inform COVID-19 control measures. **Methods:** We defined a case as a positive PCR for SARS-CoV-2 virus in a respiratory sample from an Omoro District resident, taken from 4 September-5 October 2020. We reviewed records to make a line list and interviewed the index case-patient, church farewell party attendees, and several community members to ascertain possible exposures. We conducted a retrospective cohort study among 62 farewell party attendees. **Results:** Among 23 case-patients (74% male; median age 36 years), 21 (91%) had exposure to a single index case-patient (Case A) before their illness onsets. Fifteen attended the farewell party (party attack rate=24%) and six lived in Case A's village (different from the church village). Case A had onset on 23 August. Case A had no travel history but had multiple traveller contacts through work. Case A was a highly active Church X member, attended multiple Church X services in August and attended the farewell party while ill. A second case-patient, Case B, had onset on 1 September. Case B was also an active Church X member, frequently interacted with Case A, and attended the farewell party. All other case-patients associated with the party had onsets from 8-29 September. Close contact with Cases A (RR=2.4; 95% CI=1.1-5.8) or B (RR=2.6; 95% CI; 1.2-6.7) at the farewell party was associated with infection. **Conclusion:** A social event at a church and lack of adherence to government directives provided an opportunity for spread of COVID-19 to at least 13 persons. We suggested improved adherence to national guidelines and government directives for COVID-19.

### Poster 272. Monitoring Outbreaks of Vaccine Breakthrough Infections in Nursing Homes (MOVIN) COVID-19 Evaluation

**W. Hottel**[1], C. Calabrese[2], K. Sompallae[1,3], V. Reeb[1], M. Pentella[1], A. Hennenfent[2]
[1]State Hygienic Laboratory at the University of Iowa, Coralville, IA, USA, [2]Iowa Department of Public Health, Des Moines, IA, USA, [3]Association of Public Health Laboratories, Silver Spring, MD, USA
**Background:** Current evidence for COVID-19 vaccine effectiveness among residents of long-term care facilities suggests high protection against symptomatic and asymptomatic disease, hospitalization, and death for the COVID-19 strains currently circulating in the US and Iowa. To continually monitor vaccine effectiveness as strains naturally change over time the Iowa Department of Public Health (IDPH), State Hygienic Laboratory at the University of Iowa (SHL), and Centers for Disease Control and Prevention (CDC) partnered to conduct targeted surveillance at select long-term care facilities in Iowa. COVID-19 strains circulating in the community can potentially be introduced into long-term care facilities in a variety of ways, including by unvaccinated persons entering the facility. A facility experiencing positive cases in fully vaccinated residents could be an early indicator of a change in circulating strains. **Methods:** Eight sentinel long-term care sites in Iowa were enrolled for this study. PCR positive samples with cycle threshold (CT) values below 28 were sequenced on a ClearLabs DX instrument utilizing the ARTIC v3 protocol. SARS-CoV-2 genome assemblies were analyzed using an in-house bioinformatics pipeline for lineage assignment using Pangolin version 3.1.8 and pangoLEARN version 2021-07-28. B.1.617.2 and all AY.* sublineages were considered to be the WHO designated "Delta" variant. Phylogenies were generated using a locally maintained Nextstrain build. **Results:** In this study 78 samples were sequenced with 72 assigned a Pangolin lineage. All 72 had lineage assignments included as part of the Delta Variant of Concern (VOC). Only two of the sentinel sites had a positive sequence from a resident. In facility A, 23 staff and 11 residents had positive sequences, whereas

facility B had 9 staff and 17 residents with positive sequences. In these two facilities there was a single inferred introduction of SARS-CoV-2 among the resident population, despite there being multiple distinct introductions among the staff at these facilities. **Conclusions:** Similar to international, national, and state trends, the Delta VOC is the dominant variant present in the long-term care sentinel sites in Iowa during the first quarter of this study. Multiple community introductions in facility staff with rare outbreak propagation among residents indicates that high vaccination rates and other prevention measures may limit transmission in long-term care facilities.

### Poster 273. Waiting or Going Back Home? Healthcare Workers' and Patients' Opinions Regarding the Use of a Decision-Making Tool for Patients with Respiratory Symptoms in Emergency Rooms

**E. Dubé**[1,2], A. Lorcy[2]
[1]Quebec National Institute of Public Health, Quebec City, QC, Canada, [2]CHU de Québec-Laval University Research Center, Quebec City, QC, Canada

**Background:** To deal with the rising volume of consultations and long waiting time at the emergency rooms (ER) in Quebec hospitals, an electronic decision-making tool was developed to assist patients or parents of children consulting in ER for respiratory symptoms. The tool uses ~20 questions tailored to age groups (children aged 5 months-5 years old, children aged 5-12 years old, teens/adults aged 12 years and older) to assess symptoms and risk of complications. Based on their answers, three options are proposed to patients: 1) return at home and watch symptoms; 2) return at home and consult a primary care provider; 3) stay at ER. This qualitative study aims were: 1) to describe the opinions of ER healthcare workers (HCWs) and patients regarding the use of the decision-making tool and 2) to identify barriers and enabling conditions of its implementation in ER. **Methods**: Data were collected in one ER in Quebec City (Canada) during the COVID-19 pandemic (summer and fall 2020). More than 45 hours of observation (i.e., a research technique used to gain insights on the hospital organization and culture) was done at triage and at the minor emergencies sector. Semi-directed interviews were conducted with 17 participants (HCWs=10, patients=7). The participants were all volunteers and signed informed consent forms. **Results:** The format and content of the decision-making tool were generally well appreciated by the participants. The decision-making tool was developed to be used by patients and parents once at the ER. But most of the patients would prefer to use it online, before consultation, and go to the ER as a last resort, even more during the COVID-19 pandemic. HCWs noted that use of the decision-making tool at the ER implies more work: it would require to be used according to a specific protocol that defines the users' selection criteria and when to use the tool in the patient management process. Both HCWs and patients agreed to say that patients and parents of sick children would not leave the ER, except under specific conditions: if they are reassured, if they get the information they need and some practical advice to manage the symptoms at home. **Conclusion**: The decision-aid was well-received and perceived as easy to understand and use. The implementation of such tool appears to be more beneficial if used online before consultation, especially in the pandemic context where non-urgent visits in the ER should be limited.

### Poster 274. Outdoor Recreational Activities Not Associated with SARS-CoV-2 Acquisition: A Case-Control Study

**M.J.A. Reid**[1,2,3]*, T.C. Bulfone[3,4]*, C. Blat [1,5], Y.-H. Chen[5], L. Gutierrez-Mock[1], A. Nickerson[1], L. Buback[1], S. Welty[1], W.T.A. Enanoria[5,6]
*Shared first author, [1]Institute for Global Health Sciences, University of California, San Francisco, CA, USA, [2]Division of HIV, Infectious Diseases and Global Medicine, University of California, San Francisco, CA, USA, [3]School of Medicine, University of California, San Francisco, CA, USA, [4]UC Berkeley-UCSF Joint Medical Program, CA, USA, [5]Department of Epidemiology and Biostatistics, University of California, San Francisco, CA, USA, [6]San Francisco Department of Public Health, San Francisco, CA, USA

**Background:** Access to recreational physical activities, particularly in outdoor spaces, has been a crucial outlet for physical and mental health during the COVID-19 pandemic. There is a need to understand if these activities are associated with increased risk of SARS-CoV-2 infection. This study aimed to examine risk factors for SARS-CoV-2 transmission related to recreational physical activities in San Francisco, California. **Methods:** This study utilized an unmatched case-control design, in which cases were individuals ≥12 years of age who tested positive for SARS-CoV-2 infection and controls were those who tested negative in San Francisco-between April 7th and June 8th, 2021. Telephone surveys were used to collect information about exposures and activities during the two weeks before testing. Analysis included unvaccinated individuals only. **Results:** Among 139 cases and 35 controls, participants who conducted any recreational physical activity were at lower odds of testing positive (adjusted OR: 0.23, 95% CI: 0.09, 0.57), as were those who participated in recreational activities in outdoor spaces (aOR: 0.19, 95% CI: 0.07, 0.51), compared to those who did not conduct any activity. Those who visited outdoor parks, beaches or playgrounds were also at lower odds of testing positive (aOR: 0.33, 95% CI: 0.14, 0.75). There was no

association between testing positive and indoor recreational activities, frequency of the activity or group size, mask use, or social distancing during the activity. **Conclusions:** In this case-control study, the odds of SARS-CoV-2 infection was 81% lower among unvaccinated individuals who conducted outdoor recreational physical activity in the two weeks prior to testing than those who conducted no activity. While this analysis supports pre-existing research that activity in outdoor spaces pose negligible COVID-19 risk, additional future analyses of these results will include a mediation analysis to further understand this relationship.

### Poster 275. First Two Waves of COVID-19 Pandemic in Djibouti: Epidemiology and the Vaccination Strategy Developed for the Response

**M. Elhakim**[1], S.B. Tourab[2], F. Salem[1], R. Van De Weerdt[1]
[1]World Health Organization, Djibouti Country Office, Djibouti-ville, Djibouti, [2]Ministry of Health of Djibouti, Djibouti-ville, Djibouti

**Background:** Since the first reported case of COVID-19 in Djibouti in March 2020 up to the end of May 2021, the country faced two major waves of the pandemic. Although the first wave that occurred last year, 2020, progressed more slowly in Djibouti compared to the majority of the countries in the WHO Eastern Mediterranean Region, the second wave, this year 2021, appeared to be much more aggressive in terms of number and severity of cases, as well as the fatality rate. **Methods:** All data used in this article is collected by the Ministry of Health (MoH) of Djibouti and retrieved by WHO team through the daily communiqué developed and published by the MoH. **Results:** Since 17 March 2020 up to 31 May 2021, Djibouti reported officially 11,533 confirmed cases of COVID-19 with 154 related deaths (CFR: 1.3%) and an attack rate of 1.2%. During the study period, the country faced two major waves of COVID-19 pandemic. The first one started in the epidemiological week 16/ 2020 (12-18 April) and ended in epidemiological week 25/ 2020 (14-20 June) with 4,274 reported cases including 46 deaths (CFR: 1.1%). While the second wave started in epidemiological week 11/ 2021 (14-20 March) and ended in epidemiological week 18/ 2021 (2-8 May) with 5,082 reported cases including 86 deaths (CFR: 1.7%). During the period from December 2020 to February 2021, a high committee has been formed in Djibouti, through a presidential decree, in order to develop the National Strategy for Vaccine Deployment in the country to respond to the COVID-19 pandemic in the most effective way, with the support of WHO, UNICEF and Gavi. The country received three different vaccines during the period from March to May 2021. The first lot of vaccines arrived to Djibouti, in March 2021, through the COVAX facility, and the two other types were received through bilateral agreements with other governments. **Conclusions:** The government in Djibouti spent huge effort to respond to the COVID-19 pandemic and its waves in the most adequate way, within the available resources in the country. The study is describing the epidemiology of the two waves of COVID-19 that attacked the country and is explaining the national vaccination strategy that the MoH follows for response.

### Poster 276. Perception and Acceptability of Vaccination against COVID-19 among Health Professionals in the City of Kinshasa

**S. Mbala**[1], N. Taty[2,3], T. Vita[3], N. Meschnet de Richmond[2], D. Bompangue[3]
[1]Master 1 in Ecology of Infectious Diseases, University of Kinshasa, Kinshasa, Democratic Republic of Congo, [2]Montpellier Geography and Planning Laboratory, University of Paul Valéry, Montpellier, France, [3]Research and Training Unit on Ecology and Control of Infectious Diseases, University of Kinshasa, Kinshasa, Democratic Republic of the Congo

**Background:** Health workers are on the front line of managing the COVID-19 pandemic. They are therefore at high risk of exposure and occupational transmission of SARS-CoV-2, which gives them priority for early vaccination against COVID-19. In the Democratic Republic of the Congo, vaccination began on April 19, 2021, but there are cases of hesitation among the general population and health professionals in particular. This study aims to assess the level of perception and acceptability of vaccination against COVID-19 among health professionals in Kinshasa (pandemic epicenter in the Democratic Republic of the Congo) in order to identify the factors linked to vaccine hesitation. **Method:** A cross-sectional analytical study was carried out from August 8 to September 8, 2021. A total of 479 questionnaires were administered to health professionals in 17 health structures in the city of Kinshasa. Univariate and multivariate analyzes were carried out by the Excel software and the R 3.4.4 software. **Results:** A total of 479 healthcare professionals participated in the study, of which 59.5% were between 25 and 34 years old and 79% were men. All the respondents were familiar with the COVID-19 and its vaccine, 46.8% of the respondents did not intend to be vaccinated the most mentioned reasons for non-vaccination are the lack of sufficient information on this vaccine ( 20.3%), fear of long-term side effects (19.2%) and contradictions in vaccine information (15.5%). %). Reluctance to get vaccinated was significantly associated with insufficient information (moderately informed or poorly informed) about the COVID-19 vaccine, i.e., for moderately informed respondents (OR = 2, 95% CI, 1 , 04

to 4018) and those who are poorly informed (0R = 5.46, 95% CI, 1.85 to 20.5). **Conclusion:** For better acceptance of the vaccine against COVID-19 by the general population and health professionals in particular, it is important to strengthen communication on vaccines, especially interpersonal communication.

### Poster 277. Harvest Variants: Enhancing the Harvest Suite for Rapid Characterization of SARS-CoV-2 within-Host and between-Host Variation

**Y. Liu**[1], R.M. Barnett[1], B. Kille[1], J. Kearney[1], A. Balaji[1], N. Sapoval[1], M. Nute[1], G. Godbold[2], K. Ternus[3], T.J. Treangen[1]
[1]Rice University, Houston, TX, USA, [2]Signature Science, Charlottesville, VA, USA, [3]Signature Science, Austin, TX, USA
**Background:** Real-time monitoring of viral mutations of circulating SARS-CoV-2 lineages is a key step in understanding changes to SARS-CoV-2 replicative fitness and transmissibility within and between human hosts. While consensus level mutations can reveal patterns of adaptive evolution of SARS-CoV-2, solely focusing on consensus level mutations will miss emerging variants of concern that lay hidden at low frequencies. However, extracting high quality low frequency information at the scale of presents numerous challenges. We have developed Harvest Variants to overcome these challenges, capable of tracking both consensus level mutations and low frequency intrahost variants of SARS-CoV-2. **Methods:** Harvest Variants first retrieves SARS-CoV-2 raw short read sequencing datasets and existing assembled genomes from the NCBI Sequence Read Archive (SRA). The datasets go through quality control, read mapping, variant and consensus calling, multiple genome alignment, and phylogenetic analysis. Next, a customized biocuration database connects the identified variants with their functional significance. The data within our custom biocuration database was populated through expert human review of credible scientific literature, noting mutations that have been experimentally verified to have an impact on specific functions. To help with the expert curation, we developed a Deep Learning based Named-Entity Recognition pipeline. The pipeline was trained on the CORD-19 database that was able to accurately annotate SARS-CoV-2 mutations from articles to reduce the search space for efficient verification by experts. Finally, information about per sample variation, sample metadata, and related biocurations are packaged into a web-based searchable database. **Results:** Harvest Variants was tested and validated on thousands of SRA datasets and nucleotide records of SARS-CoV-2. Our results have shown that the Harvest Variants pipeline is able to efficiently and accurately process large volumes of genomic data while providing insightful phylogenetic details based on both consensus level and low frequency mutations in the given samples. **Conclusions:** Harvest Variants is an end-to-end SARS-CoV-2 variant tracking pipeline that is capable of large-scale identification and curation of within and between host variation.

### Poster 278. Individual Factors associated with Early Uptake of COVID-19 Vaccination among Health Workers in Georgia, 2021

Moved to Poster Session 3, Tuesday, August 9, 12:30 PM – 1:30 PM (at end of COVID-19 and SARS-CoV-2 section, after poster 199)

### Poster 279. Substance Use Disorders and Concurrent Bacterial and COVID-19 Infection: A Descriptive Analysis of a Sample in Metropolitan Atlanta

**I.L. Zambrano-Acosta**[1,2], S. Thomas[1,2], A. Tunali[1,2], M.M. Farley[1,2]
[1]Georgia Emerging Infections Program (GA EIP) Atlanta, GA, USA, [2]Emory University School of Medicine, Atlanta, GA, USA
**Background**: Previous studies suggest that certain populations with substance use disorders (SUDs) and alcohol use disorders (AUDs) are disproportionately affected by COVID-19 and invasive bacterial infections. However, little is known about the risk of concurrent invasive bacterial infection and COVID-19 infection in people with SUDs and AUDs. A preliminary analysis was performed using statal data to provide a foundation for additional research. **Methods:** Clinical and epidemiologic data were collected as part of the CDC funded GA EIP Active Bacterial Core surveillance (ABCs) in 2020. Medical records were reviewed for ABCs cases occurring in residents of the twenty-county Atlanta Metropolitan Statistical area. ABCs cases of invasive bacterial pathogens Group B *Streptococcus* (GBS), Group A *Streptococcus* (GAS), *Haemophilus influenzae* (Hi), and *Streptococcus pneumoniae* (SPN) were included. COVID-19 test results were collected from the State reporting system. Concurrent disease was defined as a positive COVID test within 30 days of ABCs infection. SUD was defined as addiction to marijuana (not smoking marijuana), opioids, cocaine, or methamphetamine. A bivariate analysis was conducted to obtain descriptive statistics. **Results:** A total of 962 ABCs cases (50% GBS, 19% GAS, 5% Hi, and 26% SPN) were identified in 2020. Concurrent COVID infection was present in 15% (N=145) of ABCs cases; the proportion was similar for each pathogen. SUD was noted in 6% (n=55) of all ABCs cases (7% for Hi/SPN; 5% for GAS/GBS, p=0.36). However, among ABCs cases with concurrent COVID-19, SUD was more common among Hi/SPN cases (9%) vs GAS/GBS

cases (2%); p=0.01. AUD was noted in 6% of Hi/SPN cases and 4% of GAS/GBS cases, p=0.18; no difference (p=0.17) in AUD was noted among ABCs pathogens with concurrent COVID-19. **Conclusion:** Fifteen percent of patients with ABCs invasive bacterial infections had concurrent COVID-19 in 2020. SUD was more common among patients with concurrent COVID-19 and invasive Hi and SPN infections, known respiratory pathogens. Further research is needed to better define risk of concurrent COVID-19 and invasive bacterial infections, particularly among individuals with SUD/AUD.

### Poster 280. COVID-19 Vaccine Hesitancy in the Dominican Republic: Findings from a National Household Survey

**S. Garnier**[1,2], C. Then[3], M. de St Aubin[2,4], A. Cadavid Restrepo[5], H. Mayfield[5], L. Iselin[6], D. Dumas[2,4], W. Duke[7], F. Peña[3], A. Kucharski[8], R. Skewes[3], E. Zielinski-Gutiérrez[9], C. Lau[5], E. Nilles[2,3], M. Vázquez[10]
[1]Harvard University, Cambridge, MA, USA, [2]Harvard Humanitarian Initiative, Cambridge, MA, USA, [3]Dirección General de Epidemiología, Santo Domingo, Dominican Republic, [4]Brigham & Womens Hospital, Boston, MA, USA, [5]University of Queensland, Brisbane, Australia, [6]University of Oxford, Oxford, UK, [7] Universidad Nacional Pedro Henríquez Ureña, Santo Domingo, Dominican Republic, [8]London School of Hygiene & Tropical Medicine, London, UK, [9]Centers for Disease Control and Prevention, Central America Regional Office, Guatemala City, Guatemala, [10]Yale School of Medicine, New Haven, CT, USA
**Background:** There is little data about vaccine hesitancy in the Dominican Republic (DR)—a source of concern during the COVID-19 pandemic. Administration of COVID-19 vaccines in the DR started in March 2021; by mid-June, vaccines were available for all persons ≥ 16 yrs. We aimed to characterize COVID-19 vaccine hesitancy (CVH) in the DR to inform and guide public health policy. **Methods:** This study is part of an ongoing population-representative, cross-sectional household survey that aims to enroll 7,000 healthy individuals across the DR to understand the epidemiology of SARS-CoV-2. CVH was defined as would not, probably would not, or unsure of accepting a COVID-19 vaccine. Questions were developed based on the validated Vaccine Hesitancy Scale (VHS) and examined demographic, social, and behavioral correlates of CVH. Descriptive and multiple logistic regression analyses were performed. **Results:** From April 15 to August 13, 2021, 3,131 participants ≥16 years of age were enrolled. Overall, CVH was low (7.8%), but higher in younger age groups (13.3% among 16–24 years). Multivariate odds ratios for CVH were 0.64 (95% CI 0.43–0.96), 0.45 (0.29–0.70) and 0.24 (0.13–0.46) for 25-45, 45-65, and >65 years compared to the 16-24-year age group. Reasons for CVH were believing COVID-19 vaccines were not necessary (57.6%), not effective (33.3%), or not safe (16.3%). CVH individuals reported high levels of trust in local doctors (trusted by 91%) and religious leaders (82%); trust in social media was high among the 16-24-year age group (78%). **Conclusions:** We report data from a national survey in the DR, the country's first extensive household survey of CVH. Communication campaigns should consider developing strategies to reach younger age groups. Country-specific data are essential to guide strategic communication and vaccination policy during the pandemic.

### Poster 281. Emergence and Growth of the SARS-CoV-2 Delta Variant of Concern in British Columbia, Canada

**Y.L.E. Chan**[1,2], N. Prystajecky[1,3], M. Chong[1], Y. Joffres[1], M. Taylor[1], H. Sbihi[1,3], E. Galanis[1,3]
[1]BC Centre for Disease Control, Vancouver, BC, Canada, [2]Public Health Agency of Canada, Ottawa, ON, Canada, [3]University of British Columbia, Vancouver, BC, Canada
**Background:** The SARS-CoV-2 Delta variant of concern (VOC) is more transmissible than non-VOC and other VOC strains and has rapidly become dominant worldwide. For example, in the UK, the Delta VOC grew to 80% of sequenced cases 10 weeks after detection of its fifth case. In contrast, the Delta VOC took 17 weeks to reach 80% prevalence following its fifth case in British Columbia (BC), Canada (2020 population = 5.1 million). We summarize the characteristics of the earliest Delta VOC cases in BC and describe its emergence and growth. **Methods:** COVID-19 testing and public health follow-up data from the BC Centre for Disease Control (BCCDC) were matched to quantitative PCR and whole genome sequencing data from the BCCDC Public Health Laboratory. We described the epidemiologic and phylogenetic characteristics of the earliest Delta VOC COVID-19 cases reported in BC with collection dates between Mar 1 and Jun 30, 2021. We examined the growth of the Delta VOC by measuring its proportion over time among all incident COVID-19 cases in BC with collection dates up to Aug 28, 2021. **Results:** The first known Delta VOC case in BC was detected during epiweek 12 (Mar 21, 2021). From Mar 1 to Jun 30, 2021, 1,178 Delta VOC cases were reported in BC, with 13% having travelled internationally during their incubation period. The majority were unvaccinated (83.2%), while 2.5% were fully vaccinated. The proportion of Delta VOC cases remained ≤15% of weekly incident COVID-19 cases until 14 weeks after first detection. On Jul 1, 2021 (epiweek 26), when 78% of BC's eligible population were partially vaccinated and 33% were fully vaccinated, public health restrictions were lifted, allowing increased indoor capacities, recreational

country-wide travel, and removal of mandatory mask use in public indoor spaces. The Delta VOC then rapidly grew to dominance, reaching >70% of weekly incident cases by epiweek 29 and >85% by epiweek 30, and drove a fourth wave of COVID-19 cases in BC. **Conclusions:** Delta VOC cases and prevalence remained low in BC while public health restrictions were in place. Lifting of these measures while two-dose vaccine coverage was low facilitated the rapid growth and dominance of Delta VOC in BC. Maximising COVID-19 vaccine coverage is needed to minimize Delta VOC transmission without strict public health measures in place.

### Poster 282. Country-wide Ethno-Anthropological Evaluation to Understand COVID-19 Vaccine Hesitancy in Guatemala

**M. Berger**[1], I. Fortin[2], D. Da'Costa[1], D. Ochaita[1], L. Álvarez[4], E. Mazariegos[3], D. Sierra[3], E. Montúfar[3], M. Guzmán[4], C. Jarquin[4], M. Rondy[4]
[1]Universidad del Valle de Guatemala, [2]LabEtnográfico, Guatemala, [3]Ministerio de Salud Pública y Asistencia Social, Guatemala, [4]Pan American Health Organization, Guatemala
**Background:** By August 2021 32% of Guatemala's adult population had received at least one dose of a COVID-19 vaccine. Differences in vaccine coverage by department showed inequities in access between poorly vaccinated rural and well vaccinated urban settings. We report preliminary findings of a country-wide ethno-anthropological evaluation to understand differences in vaccine coverage and reasons behind vaccine hesitancy in Guatemala, to be used in designing a culturally pertinent communication campaign in a plurilingual country setting. **Methods:** Quantitative and mixed qualitative methods were employed to understand vaccination barriers, behavior tendencies and unravel explanatory models. Interviews were conducted with healthcare personnel in local health areas to understand service provider perspectives; and with community leaders, traditional healers and midwives to understand demand perspectives, preferences and recommendations. Surveys were implemented in households to understand vaccine end-users' perspectives. Analysis and consultation groups with target population representatives validated key communication messages, delivery mechanisms and local allies. **Results:** During August-September 2021, we conducted 643 household surveys, 369 interviews, and 15 analysis and consultation groups in 7 health areas in Guatemala. Vaccine willingness ranged from 52-75% among household representatives. End users have limited confidence in local health authorities (25-65%) and COVID-19 vaccine safety (20-33%). A total of 38% of household representatives reported community and religious leaders play an important role in recommending vaccination. Perceptions on preferred effective delivery mechanisms differ between end users and health personnel. **Conclusions:** Communication messages, delivery mechanisms, and strategic local allies must be diversified for effective message delivery in COVID-19 vaccination campaigns. Focusing on local dialects (beyond 24 root languages), including religious and ethnographic aspects pertinent to individual cultures is key to increasing message uptake and addressing myths about vaccine safety. Generating mechanisms to involve community and religious leaders in message delivery is essential to support national vaccination campaigns against COVID-19 in Guatemala.

### Poster 283. SARS-CoV-2 Transmission Potential and Rural-Urban Disease Burden Disparities across Alabama, Louisiana, and Mississippi

**S.K. Ofori**, C.A. Ogwara, S. Kwon, X. Hua, K.M. Martin, A.K. Mallhi, I.C.-H. Fung
Jiann-Ping Hsu College of Public Health, Georgia Southern University, Statesboro, GA, USA
**Background:** To quantify SARS-CoV-2 transmission potential across three US states and test if statistically significant differences exist across counties in the 50th, 75th, and 100th percentile per capita cumulative case count. **Methods:** To determine the time-varying reproduction number, $R_t$ of SARS-CoV-2 in Alabama, Louisiana, and Mississippi, we applied the R package 'EpiEstim' to the time series of daily incidence of confirmed cases, March 9, 2020 – May 17, 2021. The epidemic curve was shifted backward by nine days to account for the incubation period and reporting delay. Linear regression was performed between $\log_{10}$-transformed cumulative incidence and $\log_{10}$-transformed population size at four time points: June 17, 2020, October 17, 2020, February 17, 2021, and May 17, 2021. Median $R_t$ percentage change when policies changed was determined. **Results:** Rural Alabama counties experienced higher per capita cumulative case counts than urban ones on June 17 [slope= -0.32, 95%CI (-0.50, -0.15)] and October 17, 2020 [slope=-0.08, 95%CI (-0.14, -0.02)]. Whereas Louisiana and Mississippi saw the disproportionate impact of SARS-CoV-2 in rural counties compared to urban ones throughout 2020 and 2021. These were seen with negative slopes across all four time points for Louisiana and Mississippi. $R_t$ across the three states decreased significantly with a record of 20% decrease following the implementation of the stay-at-home order. We observed decreases in $R_t$ at different levels across states following other policies, including initial vaccination rollouts in mid-December 2020 for Alabama and late March 2021 for Louisiana and Mississippi. **Conclusion:** We found extensive community transmission of SARS-CoV-2 across all three states and selected counties with median

7-day-sliding window Rt estimates between 1 and 1.3 after March 2020. $R_t$ decreased significantly across all three states to below 1 following the first vaccination roll-out.

### Poster 284. Utilizing GIS to Inform Microplanning of Canvassing Team Deployments To Increase COVID-19 Vaccination Rates in Wake County, North Carolina

**B. Shroyer**[1], S. Soneja[2], A. Gall[2], M. Smelyanskaya[2], N. Mushonga[3], P. Bennett[3]
[1]Wake County Long Range Planning Department, Raleigh, NC, USA, [2]Resolve to Save Lives, New York, NY, USA, [3]Wake County Health & Human Services Division, Raleigh, NC, USA
**Background:** To increase vaccination rates in Wake County, NC, Wake County Human Services Division (WCHS), which is responsible for COVID-19 operations and public health broadly in the county, began a series of campaigns in May 2021 to address vaccine access and hesitancy issues in four county census tracts prioritized due to low vaccination rates. WCHS deployed door-to-door canvassing teams to raise awareness around getting vaccinated. To maximize the potential of reaching unvaccinated citizens, we developed a metric that quantified the number of unvaccinated people in each subdivision and apartment complex. This metric informed operational planning on a weekly basis. **Methods:** WCHS maintains a record of all individuals vaccinated in Wake County, NC, which includes a geocoded address. Wake County Emergency 911 Services maintains an index of every household, apartment complex and mobile home unit address within the county. Using this index, we determined the number of household units within each census tract of the county. Utilizing 2019 census tract population estimates, we then estimated the average number of people in each household. Based upon the geocoded vaccination data, we then estimated the percentage vaccinated per household and aggregated this estimate up to each subdivision and apartment complex. Using this information, we calculated the estimated remaining number of unvaccinated people per subdivision and apartment complex. To mask this information, we categorized them into quintiles, effectively creating five categories representing tiers of increasing range of number of people unvaccinated. **Results:** Maps classifying estimates of unvaccinated people per subdivision and apartment complex were used to direct canvassing teams to the areas with the highest concentration of unvaccinated people, with the intent that they could use their time as effectively and efficiently as possible. **Conclusions:** Using a data-driven approach to human resource deployment can save time and increase efficiency while increasing vaccination rates.

### Poster 285. Impact of Vaccination on Hospital Admission for COVID-19 in Islamabad Capital Territory (ICT)

**N. Noreen**[1], I. Naveed[2], N.U. Khan[3]
Directorate of Central Health Establishments, Islamabad, Pakistan, [2]PIMS, Islamabad, Pakistan, [3]FGPC, Islamabad, Pakistan
**Background:** Pakistan as national policy began vaccination drive against Covid-19 by targeting front-line healthcare workers and high-risk groups w.e.f 2nd February through Adult vaccination centers across Pakistan. As a part of the countrywide campaign, senior citizens above 60 years of age and other age quarters were registered and vaccinated through a computerized database. Since 30th May Pakistan is vaccinating all eligible age groups from 18 years of age. This study aimed to evaluate the impact of a 2-dose COVID-19 vaccination campaign on Covid-19 hospitalizations in Islamabad (ICT). **Methods:** It was a retrospective descriptive study done from June 2021 to September 2021 on the daily hospital admissions and deaths in Covid-19 wards of Public sector hospitals in Islamabad (ICT). Data were abstracted from the hospital admission database. The analysis was done as descriptive statistics calculating the percentages and frequencies using Epi info version 7 and Microsoft Excel 10 statistical components. **Results:** A total of 3,485 patients with covid-19 were admitted to hospitals of ICT from June 2021 to September 2021, out of which 2,701 (77.5%) were unvaccinated. It found that 502 (14.4%) of the patients had received their first dose (partially vaccinated) and 252 (7.2%) had their second dose (fully vaccinated). Out of total admitted cases, 147(0.5%) deaths were recorded and the majority (74.8%) of the deaths were among unvaccinated individuals (n=110). A total of 242 patients with previous covid-19 (reinfection) were not included in the analysis. **Conclusion:** Results of the study indicate that vaccination has a significant effect on reducing the COVID-19 infection, hospital admissions, and deaths. Ramped up vaccination campaign has helped to significantly push down the daily infection rates and hospital admissions during the fourth wave of the covid pandemic. Nonetheless, extended compliance with non-pharmaceutical interventions is essential to achieve and sustain this impact.

### Poster 286. Public Health Implications of COVID-19 Vaccine Attitude among a Predominantly Minority Race/Ethnicity Sample in the Southern US

**W. Huang**[1], E. Dove-Medows[2], J. Shealey[3], K. Sanchez[3], L. Benson[3], D.D. Seymore[3], P.S. Sullivan[4], H.M. Bradley[5], A.J. Siegler[1,4]

[1]Department of Behavioral, Social, and Health Education Sciences, Rollins School of Public Health, Emory University, Atlanta, GA, USA, [2]Center for Sexuality and Health Disparities, School of Nursing, University of Michigan, Ann Arbor, MI, USA, [3]Department of Population Health Sciences, School of Public Health, Georgia State University, Atlanta, GA, USA, [4]Department of Epidemiology, Rollins School of Public Health, Emory University, Atlanta, GA, [5]Department of Epidemiology, Georgia State University, Atlanta, GA, USA
**Background:** Quantitative survey data have established disparities in willingness to take COVID-19 vaccine. To understand the context surrounding the vaccine attitudes among a predominantly minority race/ethnicity population sample in the Southern US. **Methods:** We conducted 29 in-depth interviews with a sample of households selected from an address-based sampling frame in Atlanta, GA, between February 6 to June 27, 2021. The interview explored COVID-19 and vaccine knowledge, perceived benefits and consequences of vaccination, trust, social influences, and vaccination intention through open-ended questions. Interview guide was accommodated for those interviews conducted during a time in which not all participants were eligible for a COVID-19 vaccine. Thematic analysis was used to explore barriers and facilitators of COVID-19 vaccination. **Results:** Decision-making about vaccination was consistently described as a dynamic process, with information largely gained from news and social media. Participants reported being scared by rare adverse events, disproportionate to the risk. Moreover, a few participants described COVID-19 vaccine as safe, instead many participants worried about their safety. Other identified barriers included limited trust in the government and believing in conspiracy theories. Facilitators included positive promotion of vaccine from trusted members within the community, mobilization of vaccine effort through work communities, protecting other people, and provision of vaccine access at local and familiar sites at convenient times. **Conclusion:** The powerful influence of social media should be leveraged to facilitate pro-vaccination norms with accurate information, and positive narratives. Employers should be mobilized to promote vaccination by facilitating a supportive culture and offering vaccines on-site. To optimize vaccine uptake and vaccine equity, future efforts to support vaccine uptake must continue to be grounded in community-based approaches and actively seek to address concerns arising from each community with effective health communications.

## Epidemiologic Studies

### Poster 287. Epidemiology of Acute Flaccid Myelitis in The Netherlands

**J. Helfferich**[1], M. de Lange[2], K. Benschop[2], B.C. Jacobs[3], C. van Leer-Buter[1], A. Meijer[2], D. Bakker[4], E. de Bie[4], H.M.H. Braakman[5], R. Brandsma[6], R. Neuteboom[3], E.H. Niks[7], J.M. Niermeijer[8], V. Roelfsema[9], N. Schoenmaker[10], L. Sie[11], H.G.M. Niesters[1], O.F. Brouwer[1]*, M.J.M. te Wierik[2]*
[1]The University of Groningen, University Medical Center Groningen, Groningen, the Netherlands, [2]National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands, [3]Erasmus University Medical Center, Rotterdam, the Netherlands, [4]Amsterdam University Medical Center, Amsterdam, the Netherlands, [5]Amalia Children's Hospital, Radboud University Medical Center, Nijmegen, the Netherlands, [6]University Medical Center Utrecht, Utrecht, the Netherlands, [7]Leiden University Medical Center, Leiden, the Netherlands, [8]Elisabeth-Tweesteden Hospital, Tilburg, the Netherlands, [9]Martini Hospital, Groningen, the Netherlands, [10]Isala Hospital, Zwolle, the Netherlands, [11]Haga Hospital, the Hague, the Netherlands; *Shared last authors
**Background:** Acute flaccid myelitis (AFM) is a polio-like syndrome recognized since 2012 which mainly affects children. AFM has been associated with different viruses, in particular enterovirus D68 (EV-D68). Reported incidence rates in the USA vary between 0.01-0.07/100.000 persons/yr (based on numbers of the CDC), but reliable incidence rates in European countries including the Netherlands are not available. **Methods:** A retrospective review of electronic health records was done in six university hospitals and four large general hospitals in the Netherlands. Patients <18 years were selected based on diagnostic codes related to clinical syndromes with weakness and/or infection between January 2014 and December 2019. A structured scoring list was applied to the selected health records. Potential cases of AFM listed by clinicians in the participating hospitals were also included, if not part of the initial selection. Cases were classified into five categories by applying current diagnostic criteria of AFM: uncertain, possible, probable, definite or no AFM. Seasonal occurrence of AFM was correlated to laboratory surveillance-based incidence rates of EV-D68 in the Netherlands. **Results:** The selection procedure yielded 143 patients. Seven of them were classified as definite AFM, 8 as probable AFM, 3 as possible AFM and 14 were classified as uncertain. EV-D68 was identified in 3 definite and 1 probable case. One EV-D68 positive case did not fulfil AFM criteria. Of the 15 cases classified as definite or probable AFM, 6 had initially been diagnosed with AFM and 7 with transverse myelitis. The calculated incidence rate of AFM in the Netherlands was 0.07/100.000 children/year. AFM cases clustered in periods with an increased incidence of EV-D68. **Conclusions:** AFM is a rare disease with only few cases diagnosed in the Netherlands. In almost half of them transverse myelitis had been initially diagnosed. The real incidence of AFM is probably higher than we estimated for various reasons. The

temporal correlation with EV-D68 incidence further supports its association with AFM. Introduction of a national surveillance program might help in determining the real burden of this often disabling disease.

### Poster 288. Epidemiology and Risk Factors Related to Severity of Clinical Manifestations of COVID-19 in Outpatients in Haiti

**M.A.B. Lucien**[1¶], K. Pierre[2¶], G. Jean-Denis[3¶], J. Rigodon[4¶], C.M. Worrell[5], M.C. Calderon[3], A. Couture[6], A. Flynn[6], L.F. Codina[3], A.S. Vicari[7], S. Marseille[2], T.J.B. Koama[4], B. Fouche[8], G. Joseph[1], I. Journel[1], K. Rendel[2], Y. Grant-Greene[4], N.P. Jean-Charles[4], D. Lafontant[2], S. Amouzou[2], W. Pierre[2], M.G.R. Clement[9], S. Juin[4], J. Boncy[1], P. Dely[2]

[1]National Public Health Laboratory (LNSP)/ Ministry of Public Health and Population (MSPP), Port-au-Prince, Haiti, [2]Directorate of Epidemiology, Laboratories and Research (DELR)/MSPP, Port-au-Prince, Haiti, [3]Pan American Health Organization, World Health Organization (PAHO/WHO), Port-au-Prince, Haiti, [4]US Centers for Disease Control and Prevention, Port-au-Prince, Haiti, [5]Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]COVID-19 International Task Force Emergency Response Capacity Team, Centers for Disease Control and Prevention, Atlanta, GA, USA, [7]Pan American Health Organization, World Health Organization (PAHO/WHO), Washington DC, USA, [8]Quisqueya University, Port-au-Prince, Haiti, [9]Ministry of Public Health and Population (MSPP), Port-au-Prince, Haiti

[¶]These authors contributed equally to this work

**Background**: Haiti's first COVID-19 cases were confirmed on March 18, 2020, and subsequently spread throughout the country. The objective of this study is to describe outpatient clinical manifestations of COVID-19 and to identify risk factors for the severity of clinical manifestations in Haiti. **Methods**: We conducted a retrospective study of COVID-19 outpatients diagnosed from March 18-August 4, 2020, using demographic, epidemiological, and clinical data reported to the Ministry of Health (MoH). We used univariate and multivariate analysis, including multivariable logistic regression, to explore the risk factors and specific symptoms related to persons with symptomatic COVID-19 and the severity of symptomatic COVID-19 disease. **Results**: Of 5,389 cases reported to MOH during the study period, 1,754 (32.5%) were asymptomatic. Amongst symptomatic persons, 2,747 (75.6%) had mild COVID-19, and 888 (24.4%) had moderate-to-severe disease; the most common symptoms were fever (69.6%), cough (51.9%), and myalgia (45.8%). The odds of having moderate-to-severe disease were highest among persons with hypertension (OR = 1.72, 95% Confidence Interval [CI] (1.34, 2.20)), chronic pulmonary disease (OR = 3.93, 95% CI (1.93, 8.17)) and tuberculosis (OR = 3.44, 95% CI (1.35, 9.14)) compared to persons without those conditions. The odds of having moderate-to-severe disease increased with age but was also seen among children aged 0-4 years (OR=4.10, 95% CI (1.03,27.47)), when using 10-14 years old as the reference group. All older age groups, 50-64 years, 65-74 years, 75-84 years, and 85+ years, had significantly higher odds of having moderate-to-severe COVID-19 compared with ages 10-14 years. **Conclusions**: These findings from a resource-constrained country highlight the importance of surveillance systems to track emerging infections and risk factors. In addition to co-morbidities described elsewhere, tuberculosis was a risk factor for moderate-to-severe COVID-19 disease.

### Poster 289. Viral Causes and Epidemiology of Severe Acute Respiratory Illness at Three Large Tertiary Hospitals in Egypt: Results from Acute Respiratory Sentinel Surveillance January 2020-May 2021

**N. Fawzy**[1], F. Osman[2], H. BahaaEldin[3], S. Samy[3], S. Afifi[2], A. AbdElbasset[1], E.M. Haroun[1], M. Shawky[1], H. AbuElsood[2], A. Eid[4]

[1]Cairo Directorate of Health, Ministry of Health and Population, Cairo, Egypt, [2]Department of Epidemiology and Surveillance, Ministry of Health and Population, Cairo, Egypt, [3]Field Epidemiology Training Program, Ministry of Health and Population, Cairo, Egypt, [4]Preventive Sector, Ministry of Health and Population, Cairo, Egypt

**Background:** Severe Acute Respiratory Infection (SARI) is a leading cause of morbidity and mortality worldwide where viral causes play a major role. To-date SARS-CoV-2 caused more than 244 million cases and 4.9 million deaths worldwide, while influenza yearly results in one billion cases and 650,000 deaths. Egypt has established SARI surveillance in a network of 12 hospitals all over the country to identify disease causes and burden. This study aims at describing causes and epidemiology of SARI in Egypt during COVID-19 pandemic using surveillance results. **Methods:** Study conducted in the largest three referral tertiary hospitals in Egypt. WHO case definition is used to identify patients admitted with SARI. Patients are interviewed using standardized data collection form and provide Nasopharyngeal/Oropharyngeal swabs for SARS-CoV-2, influenza, and RSV PCR testing. Data of 17 months between January 2020 and May 2021 obtained and descriptive data analysis for demographic, clinical, and epidemiologic characteristics performed. **Results:** Overall 1,500 patients were enrolled, their mean age was 48±20.7

years, (758) 50.5% were males and 138 (9.2%) were diabetics. Of all patients 546 (36.4%) tested positive for SARS-CoV-2, 13 (0.9%) Influenza and 12 (0.8%) *RSV*. *SARS-CoV-2* peaked in spring (week 15, 2020), tended to infect older ages (mean age 51.3±17 years), resulted in 47 (8.6%) deaths, 53% of them >65 years while influenza peaked in winter (week 6, 2020), infected young ages (mean age 16.9± 16 years) and *RSV* infected children (mean age 8.2±6.6 months), with no fatalities reported among influenza or *RSV* patients. SARS-CoV-2 was more severe than the other viral causes, with higher rates of pneumonia, ICU admission and mechanical ventilation than patients with influenza and RSV (47.7% vs 0.7% vs 0.12%, 26.2% vs 0% vs 0.4% and 15.6% vs 0% vs 0% respectively). Influenza subtypes identified included A/H1N1 (38.4%), Flu-B (38.4%) and A/H3 (23%). **Conclusions:** Egypt sentinel surveillance better described causes, epidemiology, and burden of SARI in Cairo. Surveillance indicated that SARS-CoV-2 caused severe course and higher fatality than influenza and RSV, with higher fatality in older ages. Diabetes could increase risk of hospitalization from SARI. Surveillance should be maintained to describe changes in SARI impact, and trends over time.

### Poster 290. The Changing Causes and Epidemiology of Acute Infectious Neurological Diseases over the Last Two Decades, Egypt, 1998-2020

**M. Abdelshafy**, B. Mostafa, H. Abu elsoud, S. Samy, H. Abd Elraouf, E. Abbas, S. Afifi, A. Eid
Ministry of Health and Population, Cairo, Egypt

**Background:** Acute Infectious Neurological Diseases (AIND) remains a major cause of mortality and morbidity worldwide. Case fatality rate from AIND reaches 25%, in addition survivors could develop permanent disabling neurologic sequelae such as epilepsy, mental retardation, or deafness. Vaccination against N. Meningitis with A-C vaccine for school children and Hib for infants are compulsory in Egypt. Egypt has established sentinel surveillance 1998-2004 to better describe bacterial causes and epidemiology of the disease. It was re-established in 2016 to describe the current epidemiology and disease trends. This study aims at describing the change in causes and epidemiology of AIND in the last two decades. **Methods:** Surveillance established in eight sentinel sites distributed all over the country. All patients admitted to the participating hospitals with signs and symptoms of AIND are eligible. Lumbar puncture is performed routinely for suspected patients. Patients are confirmed using CSF culture and/or PCR. Descriptive data analysis was performed for patients confirmed with bacterial meningitis 2016-2020. AIND causes and patients' epidemiologic characteristics were compared between1998-2004 and 2016-2020 to identify changes occurred in last two decades. **Results:** During study period, 9,712 patients, out of them 3,501 had CSF specimens tested. Out of tested patients 782 (22.5%) were positive for bacterial cause including 429 (12.2%) by culture and 353 (10.3%) by PCR. The main bacterial cause identified was S. pneumonia representing 90.4%, followed by N. Meningitides 5.2%, Hi non-b 2.2% and Hib 1.0%. N. Meningitis B represents 80% and W135 16%. The most common S. pneumonia serotypes were 19F (9.9%), 1 (8.2%), 6A/6B (8.2%), 18A/18B/18C/18F (5.9%), and 14 (5.2%). Compared to 1998-2004, proportion of S. pneumonia as a cause of AIND significantly increased, while Hib, N. Meningitis. Hi non-b, N. Meningitis W135 and S. pneumonia 19F had emerged. **Conclusions:** Egypt sentinel surveillance succeed to describe the change in causes and epidemiology of AIND. Proportion of patient infected with S. pneumonia had increased, while Hib and N. Meningitis dramatically decreased, which could be result of successful vaccination programs. Vaccination policy should be revised based on emergence of Hi non-b and N. Meningitis W135.

## Waterborne Diseases and Hand Hygiene

### Poster 291. Spatiotemporal Trends in US Rotavirus Laboratory Detections after Rotavirus Vaccine Introduction -- 2009-2021

**E. Burnett**, U.D. Parashar, A. Winn, A.T. Curns, J.E. Tate
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Since rotavirus vaccines were introduced in the United States in 2006, there has been a decline in rotavirus laboratory detections, shortened winter seasons, and the emergence of a pattern of alternating years of high and low rotavirus activity. Before vaccine introduction, annual US rotavirus activity showed a consistent and characteristic spatiotemporal pattern, starting in the Southwest in the fall and migrating across the country to peak in Northeast in spring. In this analysis, we evaluate spatiotemporal trends in rotavirus laboratory detections during the 2009-2021 surveillance years. **Methods:** Laboratories reporting to the National Respiratory and Enteric Virus Surveillance System were eligible for inclusion in a given surveillance year (July to June) if ≥1 PCR or EIA rotavirus test per week was reported during ≥26 weeks and totaling ≥100 annual tests. For each laboratory, the season peak was the week with the highest 7-week moving average of the number of rotavirus positive tests during the national season, which we defined as 3-week moving average of percent positivity >10% lasting ≥2 consecutive

weeks. Laboratories were excluded if the peak 7-week moving average was ≤0.15 tests. We input peak week as a continuous variable and the geospatial coordinates of each laboratory into a spherical variogram model for Kriging spatial interpolation to determine patterns across the US. **Results:** Following the established biennial trend, the 2010-2011, 2012-2013, 2014-2015, 2016-2017, and 2018-2019 surveillance years had >10% rotavirus positivity for ≥2 weeks and were included in the geospatial analysis. Over time, there was a lower number of rotavirus positive tests and percent positivity during the national peak week, as well as a shorter season duration. During all 5 seasons, the earliest peak week occurred in Texas, Arkansas, and the western Gulf coast, with some other early activity in the Midwest and intermountain west. **Conclusions:** Changes to spatial patterns in the peak week of rotavirus activity emerged across the US following rotavirus vaccine introduction. The earliest peak week activity has shifted from the Southwest in the prevaccine era to Texas, Arkansas, and Louisiana since 2010. Further analyses are needed to understand the contribution of factors like vaccine coverage to these patterns.

### Poster 292. Economic Impact of Norovirus Disease Burden in Two Community Cohorts in Peru

**C. Romero**[1], J. Neyra[1], I.R. Ortega-Sanchez[2], L.E. Calderwood[2,3], G. Soto[1], A.K. Kambhampati[2], W.R. Campbell[4], A.J. Hall[2], Y. Tinoco[1], S.A. Mirza[2]
[1]US Naval Medical Research Unit No. 6, Lima, Peru, [2]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Cherokee Nation Assurances, Arlington, VA, USA, [4]Division of Infectious Diseases, Department of Internal Medicine, Walter Reed National Military Medical Center, Bethesda, MD, USA
**Background:** Costs of norovirus-related illness have been documented in developed countries; however, little is known about the costs incurred by cases and/or caregivers due to norovirus illness in Peru and Latin America. We assessed the financial impact of indirect and out-of-pocket (medical and non-medical) costs of laboratory-confirmed norovirus illness on families of peri- urban communities in Peru. **Methods:** Using a standard cost-of-illness approach from patient and caregiver perspectives, we evaluated the norovirus-related economic impact in families from two peri-urban communities in Peru: (1) Puerto Maldonado (Madre de Dios) from October 2012 to August 2015 and (2) San Jeronimo (Cusco) from April 2015 to April 2019. Acute gastroenteritis (AGE) cases were identified through active surveillance, and economic data were prospectively collected in follow-up interviews with cases or family members. Stool samples were collected and tested for norovirus, and laboratory-confirmed norovirus cases were included in this analysis. Economic data included direct medical (e.g., medications) and non-medical (e.g., transport) out-of-pocket costs associated with seeking medical care, as well as indirect costs (i.e., income lost from work time missed). **Results**: In 3,438 participants from 685 households, we identified 330 norovirus-associated AGE episodes during the surveillance periods. Economic data was reported for 69% (226/330) of norovirus episodes. A norovirus episode cost a median of US $5 (IQR $2 - $13) in direct costs and US $22 (IQR $11 - $44) in indirect costs. Medication expenses accounted for 63% of direct costs, followed by healthcare consultation (24%). Productivity losses accounted for 72% of the total financial burden on households. **Conclusions**: Out-of-pocket and indirect costs of laboratory-confirmed norovirus episodes in peri-urban communities in Peru are substantial and may support the potential benefits of prevention strategies including prospective vaccines.

### Poster 293. Norovirus GII.4 Evolution since Emergence of GII.4 Sydney Variant

**L. Barclay**[1], J.L. Cannon[1,2], A. Montmayeur[1], M.L. Ward[1], J. Vinjé[1], P. Chhabra[1]
[1]Divsion of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]CDC Foundation, Atlanta, GA, USA
**Background:** Norovirus GII.4 viruses are the most prevalent strain causing acute gastroenteritis worldwide. Until 2012, new GII.4 variants emerged every 2-3 years, but since then, GII.4 Sydney viruses have been the dominant strain with only a novel polymerase, P16, replacing the P31 polymerase in 2015. To better understand the changing evolutionary pattern of GII.4 noroviruses, we aimed to characterize GII.4 viruses causing outbreaks in the US over the past 9 years. **Methods:** We analyzed 831 GII.4 Sydney 5'-end capsid sequences from outbreak and sporadic cases between September 2011 to August 2020 that were reported to CaliciNet. Of these samples, 212 full VP1 sequences were obtained using amplicon NGS. Maximum-likelihood phylogeny was performed on the complete VP1 sequences. New GII.4 variants were assigned by comparing the average phylogenetic distance and standard deviation (sd) values between all sequences within and between phylogenetic GII.4 sub-cluster(s), using pair-wise distance matrices of VP1. We reconstructed the evolutionary dynamics using BEAST including all GII.4 variant sequences from GenBank. **Results:** A total of 28 GII.4 sub-clusters based on 5'-end ORF2 nucleotide sequences had >2% sequence divergence. In most years, 2-4 sub-clusters circulated with up to 9 during the 2014/15 season when the new GII.4 Sydney[P16] recombinant emerged. Complete VP1 phylogenetic analysis demonstrated most of these >2% sub-clusters grouped with GII.4 Sydney or into 4 tentative new GII.4 variants, which diverged from GII.4 Sydney or GII.4 New Orleans. **Conclusions:** Between 2011 and 2020, GII.4 Sydney viruses showed substantial

genetic diversity with certain sub-clusters circulating at low levels a few years prior to becoming predominant. We also detected several GII.4 viruses that could potentially become new pandemic GII.4 variants. Early detection and characterization of new variants will assist in determining the pandemic potential and will inform future vaccine formulations to control norovirus illness.

### Poster 294. Norovirus in the Caribbean, 2010-2020

**L. Indar**, M. Frank,[1] G. Gonzalez-Escobar, J. St John
Caribbean Public Health Agency, Port of Spain, Trinidad & Tobago
**Background:** Norovirus (NoV) is highly transmissible and is one of the leading causes of epidemic gastroenteritis globally. It is a significant cause for the burden of diarrhea illness across all age groups. Travel related norovirus outbreaks in the Caribbean threaten tourism sustainability. **Methods:** CARPHA collects monthly laboratory reports from its 26 Member states that include Norovirus. Countries also send samples to CARPHA for testing or isolates for further subtyping. Norovirus testing is conducted in the Caribbean using Norovirus Antigen Elisa or PCR Assay Subtyping by genogroups is done at CARPHA and sequencing is done at the CDC. **Results:** From 2010-2020 over 280 outbreaks of gastroenteritis (GI) were reported to CARPHA, and cases increased by 43%, one third of which were travel-related. Norovirus, first introduced to the Caribbean via visitors, is now the most frequent cause of GI outbreaks in visitor populations and the 2$^{nd}$ common cause of GI outbreaks in local populations after *Salmonella*. One hotel outbreak in a popular tourism destination in 2012 caused 1,256 illnesses, closure, travel advisories and a 30% decline in arrivals. Since 2015, there were 11 hotel outbreaks, impacting almost 2000 persons and several community outbreaks. Norovirus is also the most common illnesses reported in Caribbean cruises, with 3 such outbreaks occurring in 2019. One outbreak in January 2019 resulted in 277 guests and crew members reporting illness, passengers were made to stay onboard and massive refunds were paid. Of 338 NoV isolates submitted to CARPHA, 20% were GI genogroup and 80% were the GII genogroup. A new Norovirus strain, (GII.4 Sydney) originating in Australia, has already been reported in CMS. **Conclusions:** NoV poses a threat to national and regional health, tourism, and economic sustainability. Early detection and enhanced public health interventions for NoV are necessary for CMS. COVID-19 hygiene measures can also control Norovirus spread.

### Poster 295. Norovirus Infection among All Ages in Bangladesh: A Case-Control Study, 2018-2021

**Z. Abdullah**[1], M.E. Hossain[1], N. Balachandran[2], S. Mirza[2], M. Rahman[1], J. Vinjé[2], U.D. Parashar[2], S.M. Satter[1]
[1]icddr, b, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Norovirus is a well-recognized cause of acute gastroenteritis (AGE) worldwide. Better understanding of epidemiology and risk factors of norovirus infection among people of all ages in Bangladesh will be essential for improved control measures including future vaccines. This study aimed to estimate the prevalence of norovirus among patients hospitalized with and without AGE, circulating genotypes, and risk factors in Bangladesh. **Methods:** From March 2018- August 2021, every 20$^{th}$ AGE patient and an age-sex matched non-AGE control were enrolled from 10 tertiary care hospitals. Demographic and clinical information and stool samples were collected. Specimens were tested for norovirus using real-time RT-PCR. Norovirus positive samples were genotyped and tested for co-infections using FastTrack multiplex PCR assays. **Results:** A total of 1397 AGE cases and 1225 non-AGE controls were enrolled and norovirus was detected in 9% of AGE cases and 15% of controls. Among norovirus positive patients, highest prevalence was among children <5 years (case vs. control, 95% vs. 87%). Norovirus GII viruses were predominant both in cases (80%) and controls (77%), and the most prevalent genotype was GII.3[P16] (25% vs. 24%). Norovirus positive patients were frequently co-infected with rotavirus (case vs. control, 53% vs. 50%) or adenovirus (case vs. control, 25% vs. 32%) while other pathogens were infrequently detected. From conditional logistic regression analysis, compared to cases; controls reported a higher proportion of exposure (36% vs. 84%) to an AGE patient in last 10 days ($p < 0.001$, adjusted OR = .1, 95% CI = .07-.17) and have a longer median duration between admission and sample collection ($p<.001$, adjusted OR = .3, OR = .24, 95% CI = .20-.29). **Conclusions:** Norovirus was frequently detected in tertiary care hospitals in Bangladesh especially among children <5 years with GII.3 viruses being most prevalent. The higher positivity rate among controls may be due to exposures prior to enrolment or nosocomial infection and requires further investigation.

### Poster 296. Hand Hygiene Infrastructure and Practices among Healthcare Staff in Belize during the COVID-19 Pandemic

**A. Ly**[1], R.I. Manzanero[2], N. Bivens[1], C. Craig[3], E. Hawes[1], T. Erickson[1], F. Morey[2], A. Medley[3], M.J. Lozier[3], K.O. Murray[1]
[1]Baylor College of Medicine and Texas Children's Hospital, Houston, TX, USA, [2]Belize Ministry of Health and Wellness, Belmopan, Belize, [3]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Healthcare workers are among the highest risk for infection with SARS-CoV-2 due to their close interaction with patients. Hand hygiene is an important method to mitigate COVID-19 transmission, but implementation of best practices for hand hygiene can be limited in low- and middle-income countries. **Methods:** We conducted a baseline assessment at 11 public healthcare facilities in Belize in July 2021 to better understand hand hygiene practices and available resources. We assessed handwashing stations (HWS) and alcohol-based hand rub (ABHR) dispensers in patient and non-patient contact areas. We also observed hand hygiene practices among staff, with proper hand hygiene defined as either handwashing with soap or using ABHR before and after patient contact. Descriptive statistics and logistic regression using generalized estimating equations to account for clustering within health facilities were used to analyze the data. **Results:** Of the 363 rooms assessed, 278 (77%) had either a functional HWS with soap or an ABHR dispenser. Among the 228 of 363 rooms (63%) with a functional HWS with soap, 187 (82%) had drying materials. Specifically, within the 313 patient contact rooms, 209 (67%) had a functional HWS with soap, of which 174 (83%) had drying materials. Among 306 ABHR dispensers evaluated, 244 (80%) were functional. Proper hand hygiene occurred during 363 of 742 (49%) opportunities observed for hand hygiene before or after patient contact. Proper hand hygiene was less likely to be performed by lab technicians (AOR = 0.22; 95% CI = 0.11, 0.42) and patient care assistants (AOR = 0.07; 95% CI = 0.02, 0.26) compared with physicians. Proper hand hygiene was more than twice as likely to occur after patient contact, compared with before contact (AOR = 2.52; 95% CI = 1.84, 3.46). **Conclusion:** Proper hand hygiene practice is critical to disease control and prevention efforts, and our study identified multiple opportunities for improvement. Based on WHO guidelines, we will assist with implementing measures to improve access to ABHR and hand hygiene practices, such as providing additional ABHR dispensers, hand hygiene education, and recommendations for ABHR production and management. These interventions will protect healthcare workers and patients during the COVID-19 pandemic and beyond.

### Poster 297. Evaluation of Hand Hygiene Resources and Their Use in Guatemalan Health Facilities

**A.P. Garzaro**[1], N. Fahsen[1], C.Q. Pratt[2], C. Cordon-Rosales[1], M.J. Lozier[2], D. Call[3], B.M. Ramay[1,3]
[1]Universidad del Valle de Guatemala, Guatemala City, Guatemala, [2]U .S. Centers for Disease Control and Prevention, Atlanta, GA, USA [3] Paul G. Allen School for Global Health, Washington State University, Pullman, WA, USA

**Background:** Poor hand hygiene practices (HH) in healthcare facilities (HCF) pose substantial health risks to patients and healthcare workers (HCW), particularly in low- and middle-income countries, especially due to the COVID-19 pandemic. One potential evidence-based approach to overcome barriers to HH is through wide scale distribution of alcohol-based hand rub (ABHR). **Methods:** We conducted a baseline assessment of water supply, ABHR supply and access at patient care areas, and HH practices of HCW before and after patient contact in HCFs located in the department of Quetzaltenango, Guatemala during May–June 2021. HCFs with access to basic water service were selected by convenience sampling. Appropriate HH practice was defined as the use of ABHR or handwashing with soap and water. **Results:** Approximately 45% (19/42) of health facilities in the District Health Area were included in this survey (1 permanent healthcare center, 4 health centers, and 14 health posts). Most facilities (95%, 18/19) reported periodic interruptions in water supply with some interruptions (58%, 11/19) due to general water shortages in the community. All HCFs received ABHR from District Health Area, but 53% (10/19) reported an insufficient supply, and 30% (6/19) reported periodic interruptions of ABHR supply. Of 80 patient care areas, 71 (89%) had ABHR readily available, 31 (39%) had functional handwashing stations with water and soap, and 9 (11%) had no HH resources. Health centers had a larger proportion of patient care areas with ABHR than health posts, (97% vs 83%; p=0.04). Sixty-eight of 98 HCWs (69%) were approached and agreed to be observed. An average of four observations were made per HCW totaling 247 observations before and after patient interactions. Appropriate HH was exercised in 19% (n=47) and 44% (n=109) of observations before and after patient contact, respectively. ABHR use accounted for 83% (39/47) and 85% (93/109) of appropriate HH before and after patient contact, respectively. **Conclusions:** ABHR is an important HH resource in Guatemalan HCFs; Universidad de Valle de Guatemala, with the support of CDC, is supplementing ABHR supply to HCFs. To address noted adherence gaps, HCWs could benefit from HH information, education, and communication support for improving hand hygiene practices during patient care.

### Poster 298. Assessment of Hand Hygiene Facilities, Water Fetching Distance, and Hand Hygiene Compliance among Healthcare Workers in Rural Healthcare Facilities-Uganda

**F. Tusabe**[1], M. Kesande[1], J. Nanyondo[1], S. Nabatyanga[1], H. Isabirye[1], A. Medley[2], S. Yapswale[1], C. Pratt[2], M. Lamorde[1], M. Daud[3], D. Berendes [2]

[1]Infectious Diseases Institute, Makerere University, Kampala, Uganda, [2]Waterborne Disease Prevention Branch, Division of Foodborne, Waterborne, and Environmental Diseases, Centres for Disease Control and Prevention, [3]Kenya Field Epidemiology and Laboratory Training Program, Kisumu, Kenya
**Background**: Continuous access to resources is essential for effective hand hygiene (HH) in healthcare facilities (HCF) to prevent infections, but behavior change may also be necessary. We assessed the availability of water and HH materials and adherence in 40 HCFs in two Ugandan districts (21 HCFs in Kotido; 19 HCFs in Moroto). **Methods:** A WASH assessment tool was used to collect data on HH materials and access to water. Hand hygiene observations were conducted before and after patient contact among a random sample of staff present at the time of the survey chosen using the Random UX phone application. **Results:** Most HCF assessed (37/40) were small (level II or III). Almost all HCF (98%) reported ever having alcohol-based hand rub (ABHR) on-site, though 64% of HCF said ABHR was not enough for the facility needs. About half of HCFs (45%) reported that in the last year there was insufficient water for handwashing, and 70% reported at least one interruption in water supply (median: 3 months/year with at least one disruption to water supply). Twenty-three HCF (58%) accessed their water source within the facility premises while 25% had a water source located more than 500 meters away. Of the 312 patient encounters observed, 77% had ABHR present and 22% had water and soap. Appropriate HH was performed in 128 of 624 patient contacts (21%). Clinical officers (31%) were most likely to perform appropriate HH followed by midwives (25%), nurses (21%), laboratory technicians (11%), and doctors (9%). HH adherence was 16% before patient contact and 24% after patient contact. **Conclusion**: HH adherence is challenging with intermittent access to hand hygiene resources. While distance to water sources may affect water availability for handwashing, behavioural interventions when supplies are present must complement access to HH infrastructure at HCFs.

### Poster 299. Hand Hygiene Practices and Perceptions among Healthcare Workers in the Dominican Republic in the Context of COVID-19: A Qualitative Assessment

**C.E. Craig**[1], C.D. Schnorr[2], C.J. Then Paulino[3], P. Martinez,[4] C. Ripkey[1], M.J. de St. Aubin[2,5], D. Dumas[2,5], K. Roberts[2], W. Duke[6], E. Zielinski Gutiérrez[7], R. Skewes-Ramm[3], M. Lozier[1], E.J. Nilles[2,5,8]
[1]National Center for Emerging Zoonotic and Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Brigham and Women's Hospital, Boston, MA, USA, [3]Dirección General de Epidemiología, Santo Domingo, Dominican Republic, [4]Dr. Toribio Bencosme Hospital, Ministry of Public Health and Social Assistance, Moca, Espaillat, Dominican Republic, [5]Harvard Humanitarian Initiative, Cambridge, MA, USA, [6]Universidad Nacional Pedro Henríquez Ureña, Santo Domingo, Dominican Republic, [7]Central America Regional Office, Centers for Disease Control and Prevention, Guatemala City, Guatemala, [8]Harvard Medical School, Boston, MA, USA
**Background**: Practicing proper hand hygiene (HH), which includes washing hands with soap and water or sanitizing with alcohol-based hand rub (ABHR), is a key method for preventing healthcare-associated infections. In the context of the COVID-19 pandemic, health care facilities (HCFs) in low- and middle-income countries that lack resources to practice proper hand hygiene are at increased risk of transmission. **Methods**: To better understand perceptions of, experiences with, and barriers to practicing proper HH among healthcare workers (HCWs) in the Dominican Republic, we conducted 20 in-depth interviews with clinical, administrative, and facilities staff at two large hospitals in Moca and San Pedro de Macorís in September 2021. Interviews were conducted in Spanish, transcribed, translated to English, coded in NVivo, and analyzed using a thematic approach. **Results**: In preliminary analyses, both handwashing with soap and water and sanitizing with ABHR were common practices in HCFs, though washing hands with soap and water was preferred by most HCWs. Participants felt motivated to practice HH by a desire to protect themselves, their families, and patients from infection. Some stated that they were prompted to practice HH by posters or the presence of HH stations; others described a lack of external cues. Shortage of HH supplies was a concern for some HCWs, and lack of time for HH was a commonly reported barrier. Participants had mixed perceptions of colleagues' practices; some felt that all staff practiced HH, while others described other staff as not adhering to proper HH. Recommendations for improving HH in HCFs included installing more ABHR dispensers, providing training materials or messaging, and providing staff supervision to monitor HH practices. **Conclusions**: Understanding the experiences and perceptions of HH among HCWs provides insights into what interventions may be most effective to improve adherence and decrease nosocomial transmission during the COVID-19 pandemic. Our findings suggest that increasing access to ABHR, combined with appropriate messaging and supervision, may increase HCWs' capacity for practicing HH and improve adherence rates. Recommendations will be shared with the HCFs to encourage implementation of appropriate behavior change interventions.

### Poster 300. Approach for Sustainable District–led Production and Distribution of Alcohol-based Hand Rub in Uganda

**M.S. Kesande**[1], J. Nanyondo[1], F. Tusabe[1], S. Yapswale[1], D. Berendes[2], M. Lozier[2], A. Medley[2], C. Pratt[2], C. Craig[2], F. Ociti[1], H. Isabirye[1], M. Lamorde[1]
[1]Infectious Diseases Institute, Makerere University, Kampala, Uganda, [2]Waterborne Disease Prevention Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: A sustainable, continuous supply of alcohol-based hand rub (ABHR) is essential for healthcare workers in health facilities. World Health Organisation provides guidance for production in individual health facilities. In Uganda, using this guidance, an innovative approach was implemented at the district local government level to produce and subsequently distribute ABHR to primary level health facilities that have limited capacity for local facility-level production. This project targets governmental/district engagement with local partners to ensure sustainability. **Methods**: District stakeholders were engaged to obtain buy-in and define roles and responsibilities. Four staff members in each of 6 supported districts were nominated by District Health Officers for training (2 staff members were trained to produce ABHR and conduct internal quality control; 2 were trained on external quality control). Districts provided ABHR production unit facilities and facilitated integration within the government essential supplies delivery system - National Medical Stores in Uganda, which supports last-mile delivery to facilities. An implementing partner purchased initial raw materials necessary for production. The cost of materials for local production was compared to the price of commercial ABHR available in Uganda. **Results**: Between January-August 2021, 23 staff members were trained, and 380 batches of quality-assured ABHR (17,820 L) were produced and distributed to 278 health facilities. Consumption of ABHR in the first distribution was used to benchmark predicted ABHR consumption per targeted facility in subsequent months. Increased demand for ABHR due to the COVID-19 pandemic was addressed through emergency requests on a case-by-case basis. ABHR local production costs $3/L for materials, less than half of commercial ABHR ($8). **Conclusion**: Early results suggest that this approach is potentially sustainable but requires national advocacy as well. Leveraging existing distribution systems while building local capacity for ABHR production and distribution may improve longevity of such innovations in similar resource limited settings.

### Poster 301. Qualitative Analysis of Hand Hygiene Practices of Belizean Healthcare Workers

**N. Bivens**[1], R. Manzanero[2], A. Ly[1], C. Craig[3], E. Hawes[1], F. Morey[2], A. Medley[3], M.J. Lozier[3], K.O. Murray[1]
[1]Baylor College of Medicine and Texas Children's Hospital, Houston, TX, USA, [2]Belize Ministry of Health and Wellness, Belmopan, Belize, [3]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Proper hand hygiene, which includes handwashing with soap and water and sanitizing with alcohol-based hand rub (ABHR), continues to be one of the most effective ways to prevent infections in healthcare facilities. During the COVID-19 pandemic, healthcare workers (HCWs) in low- and middle-income countries (LMIC) are at a heightened risk of infection due to limited supplies and constrained infrastructure. **Methods:** A qualitative assessment was conducted to explore methods, perceptions, and barriers to hand hygiene practices from the perspective of HCWs in Belize to address needs and provide recommendations. Focus group discussions were conducted with administrative and clinical staff at 11 public hospitals and clinics in all six administrative districts of Belize. The discussions were recorded, transcribed, coded using MaxQDA, and analyzed using a thematic analysis approach. **Results:** HCWs felt motivated to practice hand hygiene by a desire to protect family and patients from disease and by the sense of comfort it offers, as well as by external cues such as posters, presence of ABHR, and media coverage of COVID-19. When identifying priority situations for practicing hand hygiene, HCWs emphasized using hand hygiene between patient contacts, especially in invasive procedures. A common barrier to proper hand hygiene was a lack of ABHR or hand drying materials. Due to these shortages and high patient volume during the pandemic, many HCWs preferred using personal ABHR bottles to sanitize their hands. Additionally, HCWs expressed concerns about facility ABHR and soap drying their skin; many HCWs brought personal hand hygiene products or moisturizer to reduce these effects. Focus group participants identified the need for regular hand hygiene education, higher quality products, and increased hand hygiene supplies for patients to address these concerns. **Conclusions:** This study found that HCWs were motivated to perform hand hygiene but expressed concerns about product availability and quality. These perspectives will inform recommendations to help support hand hygiene efforts in Belize during the COVID-19 pandemic and beyond. Author recommendations include improving ABHR supply chain and management at each facility and launching an educational campaign to improve hand hygiene knowledge and practices.

### Poster 302. Hand Hygiene Resources and Hand Hygiene Adherence among Healthcare Workers at Two Large Healthcare Facilities in the Dominican Republic

Moved to Poster Session 3, Tuesday, August 9, 12:30 PM – 1:30 PM (following Special Populations section, after poster 256)

## Respiratory Diseases and Influenza

### Poster 303. Risk of Acute Lower Respiratory Infection among Community Dwelling Older Adults (≥60 Years) based on Their Frailty Status: Preliminary Results from INSPIRE Cohort

**S. Saha**[1], R. Amarchand[2], R. Kumar[2], A.O. Prabhakaran[1], G. Gopal[2], P. Rajkumar[3], S.D. Bhardwaj[4], S. Kanungo[5], B. Manna[5], K.E. Lafond[6], E. Azziz-Baumgartner[6], A. Krishnan[2]
[1]US Centers for Disease Control and Prevention, New Delhi, India, [2]All India Institute of Medical Sciences, New Delhi, India, [3]National Institute of Epidemiology, Chennai, Tamil Nadu, India, [4]National Institute of Virology, Pune, Maharashtra, India, [5]National Institute of Cholera and Enteric Diseases, Kolkata, West Bengal, India, [6]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: Frailty among older adults because of decline in physiological reserve and functional status is often associated with poor health outcomes. However, role of frailty as a risk factor for acute lower respiratory infection (ALRI) is not well understood, especially in low resource settings. We evaluated the risk of ALRI because of frailty in a multi-site cohort of community-dwelling adults aged ≥60 years in India. **Methods**: During July 2018-March 2020, we assessed frailty among participants at enrolment then quarterly using Edmonton Frailty Scale (EFS) at four sites - rural area of Ballabgarh, peri-urban site of Chennai and urban slums of Pune and Kolkata. We categorized frailty based on total EFS score as: no (0-4), vulnerable (5-6), mild (7-8), moderate (9-10), and severe frailty (≥11 points). Project nurses visited participants weekly to check if anyone had developed ALRI within the last 7 days defined as new or worsening of cough, difficulty breathing, dyspnea, chest pain, respiratory rate >20 breaths/minute, measured fever, or a symptom complex of fever, sweating, headache, and myalgia. We estimated hazards ratio (aHR) of developing ALRI within 90 days from their last frailty assessment, using cox proportional hazards model adjusted for age group, gender, BMI, current or past history of smoking, wealth quintile, self-reported co-morbidity, disability and site. **Results**: We followed 6016 participants during the study period with mean age of 67 years (SD: 7) and comprised 2494 (42%) males. At enrolment 2478 (41%) were non-frail, 2003 (33%) vulnerable, 1151 (19%) mildly, 338 (6%) moderately and 46 (1%) were severely frail. Proportion of non-frail adults was most in Ballabgarh (62%) and least in Kolkata (25%). Some form of disability (vision/hearing/physical movement) was reported by 75% and 70% had a self-reported co-morbidity. We detected 1033 episodes of ALRI in 811 (13%) participants. The aHR were 1.0 (95% CI: 0.8-1.2) in vulnerable, 1.3 (95% CI: 1.0-1.8) in mildly, 1.5 (95% CI: 0.9-2.3) in moderately and 1.1 (95% CI: 0.4-3.5) in severely frail compared to non-frail participants. **Conclusion**: Half of the older adults in the cohort were frail, but only those with mild frailty seemed to be at significantly higher risk for ALRI. Further research would be useful to understand the dynamics between frailty and ALRI.

### Poster 304. Strengthening National Capacities to Prepare for and Respond to Acute Respiratory Infections (ARIs)

**S. Goldin**
World Health Organization, Geneva, Switzerland
**Background:** Current and past pandemics demonstrate that a holistic focus on acute respiratory infection (ARI) programme development and strengthening is paramount. To support countries in developing a holistic approach to ARI preparedness and response, WHO created a multisectoral virtual course focused on strengthening the relevant national core capacities under the International Health Regulations (2005). This course was designed by a Steering Committee which included all three levels of WHO and was one of the first WHO Academy courses to launch. **Methods:** WHO regional offices nominated eight country teams to participate in this pilot. Each team included 2-5 Ministry of Health, National Influenza Centre, and Country Office staff. From June – October 2021, participants completed four practical modules on the key components of a holistic, national strategy to prepare for and respond to ARIs. In each module, learners gained knowledge through self-study videos, readings, and case studies before, as a group, analyzing their national strengths, weaknesses, opportunities, and threats (SWOT) and drafting the relevant strategy component and recommendations for action. Global and regional experts provided detailed feedback throughout, and five 'Live Talk' sessions enabled further expert-led and peer learning. **Results:** Of the eight pilot countries, six countries (75%) from four WHO regions developed a policy brief that highlighted the rationale and value of a holistic approach to ARI program strengthening. Key themes the countries identified included: the need to avoid creation of duplicate systems for different ARIs, the cost-effectiveness of leveraging influenza systems and

processes for surveillance of other ARIs, and the benefits of having a multi-sectoral approach to ARI preparedness and response. In addition, five countries (63%) from four WHO regions are anticipated to conclude the course with a draft national ARI strategy. These countries will receive additional assistance to finalize and implement their strategies, including through stakeholder workshops to ensure multisectoral engagement and simulation exercises to test and enhance national systems and processes. To improve future iterations of this course, the countries will provide summaries of their experience developing and implementing their strategy. **Conclusions:** Countries gained experience and competencies in developing an ARI strategy to enhance national preparedness and response. A key outcome was the development of 35 national champions who can advocate for holistic approaches to prevention, control, and preparedness for ARIs through national capacity-building.

### Poster 305. High Genetic Diversity of *Legionella pneumophila* within a Hospital Water System – Implications for Nosocomial Legionellosis Investigations

**V. Reeb**[1], D. Diekema[2], N. Hall[1], W. Hottel[1], E. Twait[1], L. Boyken[2], L. Herwaldt[2]
[1]State Hygienic Laboratory at the University of Iowa, Coralville, IA, USA, [2]University of Iowa Hospitals and Clinics, Iowa City, IA, USA

**Background:** *Legionella pneumophila*, which can colonize man-made water systems, is known to cause hospital-acquired pneumonia via inhalation of contaminated aerosols. A better understanding of the genomic diversity of *L. pneumophila* present in a hospital water system is critical during Legionnaires' disease outbreak investigations to understand the association between a water source and clinical cases. **Methods:** Since 1981, the University of Iowa Hospitals and Clinics (UIHC) has archived clinical and environmental *Legionella* isolates collected from the facility's buildings, providing an ideal data set for studying *L. pneumophila* evolution within a complex hospital water system over time. Whole genome sequencing (WGS) was performed on 48 clinical and 73 environmental isolates, which included isolates from several nosocomial outbreak investigations that took place between 1981 and 1993. **Results:** Genome data analyses showed that several populations of *L. pneumophila* coexisted within this hospital water system. Known sequence types (e.g., ST1, ST36, ST39, ST68, ST224, and ST1983) as well as novel STs were identified. The globally widespread ST36 and ST1 were the most prominent at UIHC while ST68 and ST1983 have not yet been reported in the US. High quality SNP analyses revealed that some *Legionella* strains persisted in the water system for long periods of time and some were transient. Moreover, strains were either localized (e.g., ST68) or widespread (e.g., ST36) throughout several buildings. Genome comparison of clinical isolates from the 1988 nosocomial outbreak at UIHC showed that multiple, distinct strains (with > 100 core SNP differences) were recovered, indicating that several outbreaks may have occurred at the same time. Furthermore, more recent clinical and environmental isolates collected at times several decades after the outbreaks were closely related, indicate bacterial persistence and continued risk of illness. **Conclusions:** The delimitation of outbreaks in this hospital was redefined by WGS, demonstrating that genomic evaluation of clinical and environmental isolates is necessary to guide *Legionella* outbreak investigations.

### Poster 306. Whole Genome Sequencing Provides More Discriminatory Power for Determining *Legionella* Clusters in New York State

**M.C. Rowlinson**, D. Wroblewski, W. Haas, E. Nazarian, K. Musser, L. Mingle
Wadsworth Center, New York State Department of Health, Albany, NY, USA

**Background:** In 2016 Centers for Disease Control and Prevention reported an increase in the incidence of legionellosis from 0.42 to 1.62 cases per 100,000 persons between 2000-2014 in the United States. New York State has experienced similar increases since 2000 with a high of 1,426 clinical cases reported in 2018. The Wadsworth Center (WC) public health laboratory collaborates with epidemiology and environmental partners to identify cases and investigate outbreaks. In 2015, a large outbreak of *Legionella pneumophila* (Lp) occurred in New York City with 138 cases and 16 deaths. The environmental and epidemiologic investigation, along with laboratory testing including the use of Whole Genome Sequencing (WGS) played a key role. There has been a subsequent increase in regulation and surveillance and in the number of environmental and clinical samples WC receives. Any resulting isolates are sequenced by WGS and analyzed for relatedness. **Methods:** Water samples from environmental sources, primary clinical samples and *Legionella* isolates derived from environmental and clinical sources were received at WC. Isolates were confirmed as Lp by real-time PCR and WGS was performed according to established protocols. Data were analyzed using an in-house developed pipeline to determine relatedness. **Results:** WC analyzed 484 samples (317 environmental, 167 clinical) since 2019. Lp DNA was detected in 54/219 primary environmental samples and was isolated from 35/54 (65%). Lp was identified in 90/98 (91%) submitted environmental isolates. WC received 130 clinical isolates and 37 primary samples. Lp was identified in 122/130 (94%) of the clinical isolates, 5/130 were other *Legionella* species and 3/130 were not *Legionella.* Lp DNA was detected in 25/37 (67%)

primary samples and isolated from 18/25 (72%). Phylogenetic analysis by WGS was performed on all isolates. In 2021, WGS linked a clinical case and hot tub isolate to a 2019 cooling tower isolate that was implicated in a previous outbreak. **Conclusions:** Investigations for Lp have increased over the last several years, WGS being essential to epidemiologic analysis. WGS is more discriminatory than prior methods, enables the laboratory to determine relatedness between samples over longer timeframes, and can establish unexpected associations that would have previously been missed.

### Poster 307. Withdrawn

### Poster 308. Status of Pneumococcal Meningitis in Burkina Faso after 13-Valent Pneumococcal Conjugate Vaccine Introduction and Before a Schedule Change, 2018 -2020

**L. Childs**[1], G. Sawadogo[2], R. Ouédraogo-Traoré[3], I. Medah[4], I. Yaméogo[4], I. Ouedraogo[4], A. Sidibe[4], L. Sangaré[5], A.S. Ouédraogo[6], S. Ouangraoua[7], I. Tonde[3], M. Tamboura[3], K. Gnada[7], H. Kafando[5], K. Ouattara[5], F Tarbangdo[2], R.L. Zoma[2], H.F. Aké[2], M. Kobayashi[8], L. McGee[8], T. Pilishvili[8]
[1]National Foundation for the Centers for Disease Control and Prevention, Inc., Atlanta, GA, USA, [2]Davycas International, Ouagadougou, Burkina Faso, [3]Centre Hospitalier Universitaire Pédiatrique Charles De Gaulle, Ouagadougou, Burkina Faso, [4]Ministère de la Santé, Ouagadougou, Burkina Faso, [5]Centre Hospitalier Universitaire-Yalgado Ouédraogo, Ouagadougou, Burkina Faso, [6]Centre Hospitalier Universitaire Sourou Sanou, Bobo-Dioulasso, Burkina Faso, [7]Centre Muraz, Bobo-Dioulasso, Burkina Faso, [8]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Introduction of 13-valent pneumococcal conjugate vaccine (PCV13) in the immunization schedule in Burkina Faso in 2013 reduced meningitis caused by vaccine serotypes (VT) in young children. Despite these declines, VTs continued to cause infections in all ages with serotype 1 being the predominant disease-causing serotype in 2016 - 2017. In June 2021, Burkina Faso changed the PCV13 schedule from three primary doses (3+0) to two primary doses with one booster dose (2+1), as evidence suggests a 2+1 schedule may provide better protection against VT strain colonization and stronger indirect effects. We evaluated nationwide meningitis data in 2018 – 2020 to establish a baseline disease burden to document the potential impact of the PCV13 schedule change. **Methods:** Nationwide meningitis surveillance collects demographic and clinical information and cerebrospinal fluid (CSF) laboratory testing results from meningitis cases. We defined a suspected meningitis case as sudden fever onset with neck stiffness or other meningeal signs and a pneumococcal case as a suspected case with *Streptococcus pneumoniae* isolated from CSF by culture or detected by real-time polymerase chain reaction (PCR). Pneumococcal serotypes were identified using PCR. We estimated the annual incidence and adjusted the incidence for proportion of cases with CSF tested at a national laboratory. **Results:** In 2018 – 2020, there were 6,207 suspected meningitis cases of which 527 were confirmed pneumococcal meningitis. The proportion of pneumococcal cases was higher in children 5-14 years (43%) compared to children <5 years (30%) and adults (28%, $p<0.0001$) in 2018 – 2020. When comparing the adjusted pneumococcal meningitis incidence by year, it did not differ for persons <5 years (1.8 – 2.2 cases per 100,000) or persons ≥5 years (0.7 – 1.2 cases per 100,000). Serotype results were available for 82% (432) of pneumococcal meningitis cases in 2018 – 2020, and 65% (279) of these were caused by VTs. The most common VTs in 2018 – 2020 were serotypes 1 (n=226/279, 81%) and 5 (n=23/279, 8%). **Conclusion:** PCV13 serotypes, specifically serotype 1, continue to be the predominant cause of pneumococcal meningitis. Continued monitoring of strains causing meningitis is needed to document additional impact of the PCV13 schedule change on pneumococcal meningitis.

### Poster 309. Pneumonia-associated Mortality among Community Dwelling Cohort of Adults Aged ≥60 Years in India: Before and during COVID-19 Comparison

**S.D. Bhardwaj**[1], V. Potdar[1], R. Ghuge[1], R. Kumar[2], R. Amarchand[2], A.O. Prabhakaran[3], G. Gopal[2], P. Rajkumar[4], S. Kanungo[5], B. Manna[5], K.E. Lafond[6], E. Azziz-Baumgartner[6], S. Saha[3], A. Krishnan[2]
[1]Indian Council of Medical Research-National Institute of Virology, Pune, India, [2]All India Institute of Medical Sciences, Delhi, India, [3]Centers for Disease Control and Prevention, New Delhi, India, [4]Indian Council of Medical Research-National Institute of Epidemiology, Chennai, India, [5]Indian Council of Medical Research-National Institute of Cholera and Enteric Diseases, Kolkata, India, [6]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** As of 2011, India had approximately 100 million persons aged ≥60 years. Little is known about pneumonia-associated mortality in this population. **Methods:** We followed a cohort of community dwelling adults aged ≥60 years weekly in district of Ballabgarh (North), Kolkata (East), Chennai (South) and Pune (West India) from July 2018 to June 2021. Consenting adults aged ≥60 years in field practice area were enrolled in the study. Decedents in the cohort were assessed using a standardized verbal autopsy (VA) tool by trained staff within four

weeks of death. Staff interviewed the family members of decedents and analysed the medical records, when available. We calculated the annual cause specific mortality rate attributable to pneumonia (ICD-10 Code J18-J22 & U07.2) in the cohort per 100 person-years (100py). To assess the impact of the COVID-19 pandemic, we describe the proportion of deaths attributable to pneumonia before COVID-19 (July 2018-March 2020) and during COVID-19 (April 2020-June 2021) as testing for SARS CoV-2 among persons who died was unavailable. **Results**: We followed 6,016 older adults and identified 720 (12%) deaths. Teams completed 665 VA (341 before COVID-19 and 324 during COVID-19). The median age of the deceased was 68 years (IQR 63 – 75 years) and 50.6% were female. At-least one co-morbid condition was present in 65.4%, hypertension being the most common among 41.5%. Only four (0.5%) were vaccinated against influenza. All-cause mortality was 3.7/100py (95% CI 3.3-4.1) before COVID-19 and 4.9/100py (95% CI 4.4-5.4) during COVID-19. Out of 665 deaths,7% were attributed to pneumonia in the before COVID-19 period and 16% during COVID-19. The pneumonia-associated mortality rate was 0.2/100py (95% CI 0.1-0.3) before COVID-19 and to 0.7/100py (95% CI 0.4-0.9) during COVID-19. **Conclusion:** In our study, both all-cause and pneumonia-associated mortality increased during COVID-19 period, this highlights the importance of COVID-19 vaccination in this vulnerable population. Low influenza vaccination coverage emphasizes on strengthening the Influenza vaccination program in this group.

### Poster 310. Cost and Resource Utilization Among Older Adults Hospitalized with Pneumonia in India

**A.O. Prabhakaran**[1], R. Amarchand[2], R. Kumar[2], G. Gopal[2], P. Rajkumar[3], G. Kumar[3], S.D. Bhardwaj[4],V. Potdar[4], S. Kanungo[5], B. Manna[5], A. Chakraborti[5],K.E. Lafond[6], E. Azziz-Baumgartner[6], S. Saha[1], I.R. Ortega-Sanchez[6], A. Krishnan[2]

[1]US Centers for Disease Control and Prevention-India Office, New Delhi, India, [2]All India Institute of Medical Sciences, New Delhi, India, [3]National Institute of Epidemiology, Chennai, India, [4]National Institute of Virology, Pune, India, [5]National Institute of Cholera and Enteric Diseases, Kolkata, India, [6]US Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Community-acquired pneumonia (CAP) is an important cause of hospitalization of older adults. Assessing cost of CAP hospitalization aids in economic evaluation of preventive interventions and guides policy decisions. **Methods:** We estimated cost from a societal perspective and resource utilization among adults aged ≥60 years admitted with CAP in 8 public and 8 private hospitals in 4 Indian cities (i.e., Delhi, Kolkata, Pune, and Chennai) from December 2018 to March 2020. We interviewed participants, reviewed case record and follow-up bills to estimate the direct medical cost of diagnosis, treatment, and follow-up; direct nonmedical cost of travel, lodging and food; and indirect cost of caregivers' lost income from admission to 7 days post discharge. Resources used in investigation, medication, procedures, and days of admission in ward or intensive care unit (ICU) were recorded. We used WHO methods to estimate public hospital bed-day cost. Median and interquartile range (IQR) cost is presented in US Dollars ($) (for the study 1$=70.5 Indian rupees) and by hospital type, age-group, chronic condition, and influenza infection. **Results**: We identified 1,109 CAPs in private (63%) and public (37%) hospitals; participants were aged a median of 68 years (IQR:63-75) and 38% were female. Median duration of hospitalization was 5 day (IQR: 3-8); 43% required ICU admission and 10% mechanical ventilation. Influenza was detected in 134 (12.3%). Antibiotics and antivirals were used in 96% and 23% of admissions. Median total cost of CAP hospitalization $191 (IQR: 98-495) in public and $937 (IQR: 355-1618) in private hospitals; influenza CAP had a similar cost (i.e., $181 (IQR:105-327) in public and $1118 (IQR:376-1775) in private hospitals). Cost of CAP care was greater among persons aged ≥75 years ($887) vs. those aged 60-74 years ($466, P<0.001), with chronic conditions ($605) vs. without chronic conditions ($378, P<0.001) and among those admitted to ICU ($1445) vs. treated in the wards ($585, P<0.001). **Conclusion:** Cost of CAP is approximately 6-times higher in private vs. public hospitals and among older adults with chronic disease and requiring ICU care; influenza CAP were as costly as other CAP hospitalization. These findings could aid in cost-benefit analyses of influenza vaccination in the older adults.

### Poster 311. Ventilator-associated Pneumonia (VAP) Prevention Bundle in the Neurosurgical Intensive Care Unit, Cho Ray Hospital, Vietnam

**P.M. Thang**[1], V.T.H. Thoa[1], L.T.A. Thu[1], N.V. Nhieu[2], T.Q. Vinh[2], N.T. Thuc[3], H.T.K. Phuong[4], T.T.T. Ha[5], N.T.P. Lan[6], A.M. Vasquez[6]

[1]Department of Infection Control, Cho Ray Hospital, Ho Chi Minh City, Vietnam, [2]Department of Neurosurgical ICU, Cho Ray Hospital, Ho Chi Minh City, Vietnam, [3]Department of Arrhythmia, Cho Ray Hospital, Ho Chi Minh City, Vietnam, [4]Medical Services Administration, Vietnam Ministry of Health, Hanoi, Vietnam, [5]PATH, Seattle, WA, USA, [6]U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Ventilator-associated pneumonia (VAP) is the most common healthcare-associated infection (HAI) at Cho Ray Hospital (CRH). However, there has been limited success improving VAP rates at CRH despite multiple interventions. In Vietnam, use of a systematic approach to improving infection prevention and control has not been common. We introduced a quality improvement (QI) approach with a VAP prevention bundle in the Neurosurgical ICU (NICU) at CRH to improve VAP rates. **Methods:** A VAP care bundle, including weaning and sedation protocol, was implemented in the NICU from April 2019 to April 2021. Baseline VAP rate per 1,000 ventilator-days and ratio of ventilator days to patient-days (device utilization ratio; DUR) were captured for 12 months preceding the intervention (2018). Independent two-sample t-test analysis was conducted to quantify the difference in the mean baseline VAP rate and one and two years after the intervention. Process measures to monitor staff adherence to bundle elements were recorded. **Results:** Mean baseline VAP rate reduced significantly from 21.3 pre-intervention to 15.0 after first year post-intervention ($p<0.05$) and 14.5 after second year post-intervention ($p<0.05$). The mean DUR was relatively unchanged from 0.82 pre-intervention to 0.89 after first year and 0.85 after second year post-intervention. Mean bundle adherence for physician elements increased from the first to second year (ventilator weaning protocol from 48% to 62%, daily sedation reduction from 53% to 66%, and early ordering of physical therapy from 39% to 48%, respectively). Bundle adherence for nursing elements (i.e., head of bed elevation, endotracheal tube cuff pressure, oral care, and changing of heat and moisture exchanger) was high throughout the intervention period (range 84-100%). **Conclusion:** Use of a QI approach to implementing a VAP care bundle intervention significantly decreased the VAP rate in the NICU at CRH over time as adherence to bundle elements improved. Continued reductions in the VAP rate will focus on improving adherence to physician bundle elements, and the intervention will be expanded to additional units.

### Poster 312. Machine Learning Models for Predicting Decreased Susceptibility to Ceftriaxone in *Neisseria gonorrhoeae*

Moved to Poster Session 3, Tuesday, August 9, 12:30 PM – 1:30 PM (at end of Antimicrobial Resistance section, after poster 240)

### Poster 313. Characterization of the *Neisseria meningitidis* Serogroup C ST-10217 Outbreak in Burkina Faso, 2019

**J.L. Kibler**[1], H.E. Reese[1], S. Ouattara[2], H.F. Ake[3], T.F. Tarbangdo[3], I. Yameogo[3], R. Ouedraogo[4], R. Zoma[3], E. Seini[5], I. Tonde[4], M. Sanou[4], N. Topaz[1], A.C. Retchless[1], X. Wang[1], R. Novak[1]
[1]Division of Bacterial Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Direction de la Protection de la Santé de la Population, Ouagadougou, Burkina Faso, [3]Davycas International, Ouagadougou, Burkina Faso, [4]Centre Hospitalier Universitaire Pédiatrique Charles De Gaulle, Ouagadougou, Burkina Faso, [5]West African Health Organization, Ouagadougou, Burkina Faso
**Background:** Burkina Faso, positioned within the meningitis belt of Africa, experiences hyperendemic meningococcal meningitis in the dry season (November to June) annually. In January of 2019, a cluster of deaths was reported near Burkina Faso's border with Niger and triggered an outbreak investigation. The objective of this analysis was to describe the outbreak and response and the microbiologic features of the strain. **Methods:** Demographic and laboratory data for meningitis cases were collected through national case-based surveillance. Cerebrospinal fluid specimens were collected from suspected meningitis patients. Meningitis pathogens and serogroups were determined using direct real time-PCR. Whole genome sequencing was performed on a subset of confirmed meningococcal isolates. Descriptive analysis was used to characterize the spatial distribution, demographic features, and response efforts of the outbreak. **Results:** 295 total suspect cases were recorded from epidemic weeks 5 to 18 of 2019 in this outbreak, which began in the Diapaga district and expanded into three neighboring districts in the Est and Sahel Regions (Gayeri, Sebba, and Dori). 94 cases were confirmed to be *Neisseria meningitidis* serogroup C (NmC). Three districts crossed the alert threshold and Diapaga and Sebba were most impacted with cumulative incidences of 31 and 27 cases per 100,000 persons, respectively. 80% of confirmed cases were between 5-29 years and 56% were male. Sequencing of twelve samples from the outbreak revealed that they belonged to NmC sequence type 10217 (ST-10217) with identical PorA and FetA types. Three reactive vaccination campaigns using meningococcal serogroup ACYW vaccines were conducted in 7 sites from February–June to control outbreak spread. **Conclusions:** *Neisseria meningitidis* serogroup C (NmC) ST-10217 is the same strain responsible for previous large-scale epidemics in Niger and Nigeria. Although resulting in a relatively small outbreak across two regions in 2019, the expansion of this strain into Burkina Faso could cause similarly large outbreaks over the next several years. This report highlights the importance of a responsive national surveillance system and laboratory network in providing timely and spatially explicit case-level data to aid in outbreak monitoring, response efforts (i.e., vaccination), and strain tracking across the region.

### Poster 314. Fluoroquinolone Resistance in a Global Compendium of *Mycobacterium tuberculosis* Isolates

**A. Brankin**[1], K.M. Malone[2], The CRyPTIC Consortium
[1]University of Oxford, Oxford, UK, [2]EMBL-EBI, Hinxton, UK
**Background:** The spread of multi-drug resistant (MDR) tuberculosis (TB) poses a serious threat to TB treatment success. Fluoroquinolones are recommended second-line antibiotics that form the backbone of MDR treatment regimens, however there is limited global data on fluoroquinolone resistance from the past 15 years and diagnostic testing remains low. **Methods:** The Comprehensive Resistance Prediction for Tuberculosis: an International Consortium (CRyPTIC) has collected 15,211 *M. tuberculosis* clinical isolates. The isolates have undergone whole genome sequencing and have measured minimum inhibitory concentrations to 13 antitubercular drugs, including the fluoroquinolones levofloxacin and moxifloxacin. **Results:** The compendium comprises 5 TB lineages originating from 23 countries across 4 continents. 6,814 isolates were resistant to at least one drug, including 2,146 samples resistant to levofloxacin and 1,724 samples resistant to moxifloxacin. We show the most common fluoroquinolone resistance conferring mutations observed in a range of phenotypic backgrounds and how several mutations have evolved within the population homoplastically. Using previously established mutation catalogues, we found that 89.5% of moxifloxacin resistant and 90.2% of levofloxacin resistant isolates could be correctly predicted from their genetics. Concerningly, resistance to either fluoroquinolone was more common than resistance to the mycobacterial specific drug ethambutol in an isoniazid and rifampicin susceptible background, suggesting a level of pre-existing second line resistance. **Conclusions:** We suggest that careful surveillance of resistance and stewardship of fluoroquinolones, both in TB and other infectious diseases, will be paramount for treatment success in future. Ultimately, we hope that this matched genotypic-phenotypic dataset will accelerate resistance diagnostic development for TB, by enrichment of mutation catalogues and identification of diagnostic gaps and resistance patterns.

### Poster 315. How Much Evidence is Enough to Justify Empirical Treatment for Tuberculosis in Patients with AIDS and Fever of Unknown Origin?

**S.J. Hentosh**, M.D. Antonioli, G.M. Aisenberg
McGovern Medical School, Houston, TX, USA
**Background:** Fever of unknown origin (FUO) in people living with *human immunodeficiency virus* (PLHIV) has a broad differential diagnosis. These patients provide a unique challenge to clinicians, requiring a balance of the harms of empirical treatment with those of not treating a potentially lethal infection. **Methods:** We summarize the evidence supporting empirical therapy for TB in PLHIV. **Results:** Current cough, fever, night sweats, and unintentional weight loss can be used in resource limited settings to identify PLHIV who need further diagnostic testing (sensitivity 78% specificity 49%). >2 weeks of cough AND world health organization defined “danger signs” (tachycardia >120 beats/minute, fever >39C, or tachypnea >30 breath/minute) has shown to have increased survival (44% reduction in 8-week mortality). Moderate to severe anemia (Hb<10.9 g/dL in men and Hb<9.9 g/dL in women) is associated with improved sensitivity of screening tests (Urine lipoarabinomannan (LAM): 54% vs. 0%, sputum microscopy and urine LAM: 71% vs. 15%, and sputum Xpert: 74% vs. 41%). CD4 < 200 cells/ml chest radiograph findings are predominately non-cavitary infiltrates and consolidation. Miliary shadows and pericardial effusion significantly are increased among patients with CD4 <200 cells/ml. Typical TB pulmonary lesions are seen only in about 33%. Computed tomography commonly shows lymphadenopathy and nodular opacities with an increased prevalence of military disease. Consolidation and cavitation are seen with less frequency. Pooled sensitivity and specificity of LF-LAM in patients with CD4 thresholds <100 cells/μL were 61% and 89% respectively. Positive smear in addition to the Nucleic Acid Amplification (NAAT) is 98% sensitive. Smear negative sensitivities are 72%, 85%, and 90% for one, two or three specimens, respectively. Positive NAAT results in a smear-negative patient can be valuable for the early detection of TB in approximately 50% to 80% of cases. Tuberculin Skin Test (TST) sensitivity is 64.3% (10 mm) and 71.2% (5 mm). Interferon Gamma Release Assay (IGRA) sensitivity is not increased when used in conjunction with the TST. Sensitivity is decreased in PLHIV: 63% in HIV positive and 84% in HIV negative. **Conclusions:** Choosing not to treat empirically has its risks given that many PLHIV may not show typical signs such as radiographic findings of TB.

### Poster 316. Withdrawn

### Poster 317. Predictors of Treatment Outcomes in Tuberculosis Prisons Patients in Bangladesh: A Retrospective Cohort Study

**M.J. Sujan**[1], M.A. Taleb[2], F. Banu[3], A.A. Clara[4]

International Vaccine Institute, CAPTURA, Dhaka, Bangladesh, [2]The Medicines, Technologies, and Pharmaceutical Services, USAID, Dhaka, Bangladesh, [3]JBRSOFT, Dhaka, Bangladesh, [4]North South University, Dhaka, Bangladesh
**Background:** For decades, tuberculosis (TB) has been one of the leading causes of death around the world. Controlling it is the most pressing concern in global public health. Because health problems within and outside prisons are interconnected, jail health is an important element of public health. Bangladesh is a high-burden country for tuberculosis, according to the World Health Organization. The goal of this study was to determine the risk factors for successful and poor treatment outcomes among prison detainees in Bangladesh. **Methods:** From 2015 to 2020, a retrospective cohort study was conducted in five divisions across the country. Data was taken from an electronic case-based surveillance system run by the national TB control programme (NTP), which supports the Directorate General of Health Services. The statistical data analysis software Stata Version-16.0 and Python 3.0 were used to enter, clean, and analyze the data. **Results:** A total of 230 inmates were chosen for this study. Of these, males were 91.74 percent (n=211) and females were 8.26 percent (n=19). The cohort's average age and standard deviation were 38.49 ± 14.44. The majority of the patients, 96.96 percent (n=223), were newly registered, with only 3.04 percent (n=7) having previously received treatment. Our findings demonstrated that the majority of the patient's treatment outcomes were successful (66.96 percent, n=154), whereas 33.04 percent (n=76) were unsuccessful. Treatment outcomes were determined by the site of disease, initial and current treatment regimens, bacteriologically confirmed and clinically diagnosed cases, gender, body mass index, and age. **Conclusions**: Younger age and male gender may be independent risk factors for tuberculosis in jails, according to the findings. The NTP may target to improve screening of all new convicts before to admiration, service scope, laboratory capacity, and quality in health centers, as well as putting in place relevant interventions as soon as possible.

### Poster 318. More Avian Influenza Outbreaks Reported during 2013-2021 than the Previous 8 Years

**C.M. Szablewski**, C. Iwamoto, S.J. Olsen, C.M. Greene, L.M. Duca, C.T. Davis, K.C. Coggeshall, W.W. Davis, P.L. Gould, J.C. Kile, E. Azziz-Baumgartner
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Avian influenza (AI) is a health, economic, and food security risk, and while many outbreaks have been reported globally in the past year, it is unclear whether outbreaks are occurring more frequently or in more places. We analyzed AI reports submitted to animal and public health authorities January 2013–June 2021, and compared them to 2005–2012 reports, to assess changes in AI global spread. **Methods:** We abstracted information about AI from the World Organization for Animal Health (OIE) World Animal Health Information System for animal outbreaks and from the World Health Organization (WHO) Event Information Site for human infections with AI. We described the subtypes and pathotypes of influenza A virus identified in birds by year and in which countries the outbreaks and viruses were identified. For human infections, we summarized subtype and pathotype, geographic location, bird exposure, age, reported case fatality proportion, and evidence of human-to-human transmission (HTH) with AI virus. Data was compared to published data from 2005-2012. **Results:** From 2013-2021, 51% (92/182) of OIE member states identified 34 AI virus subtypes (15 high pathogenic [HPAI] and 19 low pathogenic) during 14,561 bird outbreaks; 16 (47%) subtypes were reported for the first-time and 91% of outbreaks were HPAI. The most frequently reported subtype was HPAI H5N8 (6465, 44%) followed by HPAI H5N1 (3832, 26%). One in four countries (24/92) reported AI outbreaks in birds for the first time. Of 194 WHO member states, 17 (9%) reported 1,927 AI infections of 9 virus subtypes among humans. Only one country with human infections, Oman, had never reported an AI outbreak among animals. Of cases with no missing values, 74% of infected humans (1393/1880) had a known animal exposure, 62% (1184/1916) were among working age adults (i.e., 18-64 years), 22% (432/1927) died, and 3% (53/1927) were possible or confirmed HTH transmission events. **Conclusions:** AI outbreaks in birds occurred in more countries than previously reported with 24 countries reporting their first outbreak; 16 new virus subtypes were identified representing a two-fold increase compared to 2005-2012. Most human infections were associated with animal exposure. Continued monitoring for AI outbreaks in birds and human infections with AI will be essential for pandemic preparedness.

### Poster 319. The Burden of Influenza-associated Respiratory Hospitalizations in Vietnam, 2014–2016

**N.C. Khanh**[1], A.L. Fowlkes[2], N.D. Nghia[1], T.N. Duong[1], N.H. Tu[1], T.A. Tu[1], J.W. McFarland[2], T.T.M. Nguyen[3], N.T. Ha[3], P.L. Gould[3], P.N. Thanh[4], N.T.H. Trang[5], V.Q. Mai[6], P.N. Thi[7], S. Otsu[7], E. Azziz-Baumgartner[2], D.D. Anh[1], A.D. Iuliano[2]
[1]National Institute of Hygiene and Epidemiology, Hanoi, Vietnam, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Influenza Division, US Centers for Disease Control and Prevention, Hanoi,

Vietnam, [4]Tay Nguyen Institute of Hygiene and Epidemiology, Buon Ma Thuot, Dak Lak, Vietnam, [5]Pasteur Institute Ho Chi Minh, Ho Chi Minh City, Vietnam, [6]Pasteur Institute Nha Trang, Nha Trang, Khanh Hoa, Vietnam, [7]World Health Organization Vietnam Country Office, Hanoi, Vietnam
**Background:** To provide an estimate of the of influenza-associated respiratory hospitalizations to guide prevention and control policies to complement influenza vaccine production capacity in Vietnam. **Methods:** We conducted a hospital admission survey (HAS) in four provinces representing Vietnam's major regions with at least one hospital participating in severe acute respiratory infection (SARI) surveillance. All hospitals within the provinces reported acute respiratory infection (ARI) hospitalizations retrospectively from 2014–2016 with ICD-10 admission codes J06 and J09–J22. The proportion of ARI admissions meeting WHO's SARI case definition was determined through medical record review. We calculated provincial influenza-associated ARI and SARI hospitalization rates by attributing the age- and month-specific influenza percent positive and dividing by the provincial population; provincial influenza-associated ARI and SARI rates were pooled and extrapolated to the national population. We used Monte Carlo simulation to calculate the 95% uncertainty intervals (UI). **Results:** Of 3,626 medical chart reviews, 61% met SARI criteria. Twenty-two percent of 6,647 SARI surveillance specimens tested positive for influenza. From 220,217 reported ARI hospitalizations, the mean influenza-associated hospitalization rates per 100,000 were 218 (95% UI 197–238) for ARI and 134 (95% UI 119–149) for SARI. Influenza-associated SARI hospitalization rates per 100,000 were highest among children <5 (1,123; 95% UI 946–1301 and adults ≥65 years 207; 95% UI 186–227). **Conclusions:** Influenza-associated hospitalizations disproportionately occurred among the youngest and oldest in Vietnam, underscoring the need for prevention and control measures, such as vaccination in these at-risk populations.

### Poster 320. Detection of Influenza A Viruses in Humans and Poultry through an Integrated One Health Surveillance Platform in Bangladesh

**S. Chowdhury**[1], A. Aleem[1], Z. Akhtar[1], A. Islam[1], E. Azziz-Baumgartner[2], J.A. Mott[2], J.C. Kile[2], T.C. Davis[2], S. Ghosh[1], P.K. Gosh[1], M.E. Hossain[1], M.Z. Rahman[1], M. Rahman[1], M. Rahman[1], A. Islam[1], F. Chowdhury[1]
[1]International Centre for Diarrheal Diseases Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Avian influenza A viruses (AIV) continue to circulate in domestic poultry in Bangladesh, with >550 reported outbreaks. As of 30 September 2021, 8 human infections reported. Since 2007, icddr,b has been conducting influenza virus surveillance in humans and poultry to support government efforts to detect and control influenza outbreaks. This abstract highlights the findings of integrated one health surveillance from January to December 2018. **Methods:** The animal surveillance teams visited 10 live bird markets (LBMs) each monthly to collect cloacal and tracheal samples from backyard, commercial poultry and environment. Environmental samples were prepared by mixing swabs from different environmental surfaces. The human surveillance team enrolled severe acute respiratory infection (SARI) patients from intensive care units (ICU), coronary care units (CCU), medicine and pediatric wards of eight tertiary care hospitals to collect nasopharyngeal and throat swabs. All samples were tested to detect influenza A viruses using real time RT-PCR. **Results:** We collected 3,320 poultry, 484 environment and 2,681 SARI samples (ICU: 20, CCU: 518, medicine ward:1413, pediatric wards:730). Influenza A viruses were detected in 837 (25%) poultry, 259 (54%) environmental samples and 337 (13%) SARI patients. H5 subtype was detected in 270 (8%, 95% CI: 7-9%) poultry, 142 (29%, 95% CI: 25-33%) environmental, and 0 (0%, 95% CI: 0-13%) human samples. H9 subtype was identified in 422 (13%) poultry, 71 (15%) environmental sample, and 0 (0%, 95% CI: 0-13%). No poultry, environment, or human samples were positive for H7 subtype. Among the influenza A positive human samples, 270 (80%) were positive for H1N1 (pdm09) and 67 (20%) for H3. Approximately half 441 (53%) of influenza in poultry was detected November-March; most influenza in human 336 (99%) was detected June-September. **Conclusions:** Avian influenza H5 and H9 subtypes remain enzootic in domestic poultry. The endemic situation of avian influenza viruses in domestic poultry raises the concerns for possible genetic reassortment between human and avian viruses. Findings of this report are useful to the veterinary and public health authorities to target peak influenza season for enhanced surveillance, LBM decontamination and vaccination campaign in humans and poultry.

### Poster 321. Cost-effectiveness of Seasonal Influenza Vaccination in Pregnant Women, Healthcare Workers and Adults ≥ 60 Years of Age in Lao People's Democratic Republic

**I.R. Ortega-Sanchez**[1], J.A. Mott[2], W. Kittikraisak[2], V. Khanthamaly[3], M. McCarron[4], S. Keokhonenang[5], P. Ounaphom[6], C. Pathammavong[5], K. Phounphenghak[5], P. Sayamoungkhoun[5], P. Chanthavilay[8], J. Bresee[7], C. Tengbriacheu[5]

[1]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Influenza Division, Centers for Disease Control and Prevention, Nonthaburi, Thailand, [3]Influenza Division, Centers for Disease Control and Prevention, Vientiane, Lao PDR, [4]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Maternal and Child Health Center, Ministry of Public Health, Vientiane, Lao PDR, [6]Department of Hygiene and Health Promotion, Vientiane, Lao PDR, [7]Task Force for Global Health and Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]University of Health Sciences, Ministry of Health, Vientiane, Lao PDR

**Background**: Pregnant women, healthcare workers (HW), and adults ≥60 years have shown an increased vulnerability to seasonal influenza virus infections and complications. In 2012, the Lao People's Democratic Republic (Lao PDR) initiated a national influenza vaccination program for these target groups. A cost-effectiveness analysis is required to inform program sustainability. **Methods***:* We designed a decision-analytical model and collected influenza-related medical resource utilization and cost data, including indirect costs. Input data were obtained from medical record abstraction, interviews of patients and staff at hospitals in the national influenza sentinel surveillance system and/or from literature reviews. We compared the annual disease and economic impact of influenza illnesses in each target group in Lao PDR under no vaccination and vaccination scenarios, and then estimated the cost-effectiveness of the vaccination. We also performed multivariate sensitivity analyses. **Results***:* Overall, the vaccination of pregnant women, HWs, and adults ≥60 years could annually save 10,367 doctor visits, 1706 days of hospitalizations, 38,000 days of work, and 1280 life-years lost due to laboratory-confirmed influenza illness. After vaccination costs of 23.7 billion Kip (2,526,711 USD) for the three target groups, the vaccination program would cost to Lao PDR 6.8 billion Kip (724,964 USD) annually. The incremental cost per life-year saved was 35 million Kip (3,733 USD) and 8.2 million Kip (875 USD) for pregnant women and adults ≥60 years, respectively. However, vaccinating HWs provided societal cost-savings to Lao PDR, returning 2.55Kip for every single Kip invested. Vaccine effectiveness, attack rate and illness duration were the most influential. **Conclusion**: Influenza vaccination of HWs in Lao PDR would be cost-saving while targeting vaccination to pregnant women and adults ≥60 would range from cost-effective to highly cost-effective per WHO standards.

### Poster 322. Prevalence and Distribution of Avian Influenza A(H5) Virus Clades in Live Bird Markets of Vietnam, 2019-2021

**D.T. Nguyen**[1], L.V. Nguyen[1], M.Q. Phan[1], J. Jones[2], E. Pusch[2], Y. Jang[2], G. Yang[2], S. Thor[2], T.D. Nguyen[3], P.T. Nguyen[4], P.T.T. Tran[1], A.Q. Nguyen[1], C.D. Vo[1], J. Barnes[2], P.L. Gould[4,5], T.T.M. Nguyen[5], N.T. Ha[5], L.T.P. Nguyen[5], T.H. Nguyen[1], T.M. Hoang[1], C.T. Davis[2]

[1]Department of Animal Health, Ministry of Agriculture and Rural Development of Vietnam, Hanoi, Vietnam, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]National Center for Veterinary Diagnostics, Department of Animal Health, Hanoi, Vietnam, [4]Regional Animal Health Office No.6, Department of Animal Health, Hanoi, Vietnam, [5]Office of the US Centers for Disease Control and Prevention, Hanoi, Vietnam

**Backgrounds:** Highly pathogenic avian influenza (HPAI) A(H5) viruses continue to circulate in Vietnamese poultry. Active surveillance for HPAI viruses in poultry sold at live bird markets (LBMs) was conducted in 13 of 63 provinces throughout Vietnam from January 2019 to August 2021. The study objectives were to assess the prevalence of avian influenza type A virus and H5, H5N1, H5N6 and H5N8 subtype viruses and characterize the geographical and temporal distribution of A/H5 virus clades across the country. **Methods:** Monthly sampling was conducted in 100 LBMs with high poultry consumption located in 72 communes in 13 high-risk provinces with a history of AI outbreaks or borders with China. A total of 11,130 oropharyngeal pooled swab samples (five individual birds per pool) were screened for influenza A virus; all influenza A positives were then tested for A/H5, and A/H5 positive samples were then tested for N1, N6 and N8 parallelly by real-time RT-PCR. The Hemagglutinin of each individual A/H5 virus-positive swab was sequenced. Phylogenetic analysis was conducted to identify the clade and overall genetic diversity of the viruses. **Results:** LBM prevalence of influenza A virus, A/H5, A/H5N1, A/H5N6 and A/H5N8 subtype virus was 38.54% (4,290), 3.54% (394), 1.47% (164), 1.63% (181), 0.02% (2), respectively, over the cumulative 32 months of surveillance. The positive samples were detected all year round, so there does not appear to have a clear seasonal pattern. Phylogenetic analyses indicated that A/H5N1 viruses belonged to clade 2.3.2.1c and persisted only in the south, whereas A/H5N6 viruses belonged to clade 2.3.4.4h and 2.3.4.4g and were found simultaneously in northern, central and southern Vietnam. Additionally, A/H5N8 viruses belonging to clade 2.3.4.4b were recently detected in both this LBMs surveillance and poultry outbreaks in the northern and central regions of Vietnam. **Conclusions:** Given the overlapping temporal and geographic distribution of genetically diverse HPAI A(H5) clades and the antigenic divergence described for these clades, current HPAI A(H5) poultry vaccines used in Vietnam may require multivalent formulations containing representatives of clade 2.3.2.1c and one or more clade 2.3.4.4 viruses.

### Poster 323. Effect of COVID-19 Pandemic on Reporting of Routine Influenza Surveillance Data to the Global Platform FluNet

**A. Hammond**, B. Maharjan, S. Hirve, D. Pereyaslov, M. Medina, V. Cozza, W. Zhang
Global Influenza Programme, World Health Organization, Geneva, Switzerland

**Background:** FluNet is a web-based tool for influenza virological surveillance existing since 1997. National Influenza Centres and other national influenza reference laboratories provide critical data to FluNet for tracking global influenza transmission in combination with epidemiological data. Aggregated surveillance data on samples tested and positive (including subtype information) are reported weekly, either directly or indirectly through regional platforms. Visualizations of influenza surveillance data are available on WHO's website. The COVID-19 pandemic has disrupted health systems including routine influenza surveillance systems, including reporting to FluNet. WHO's Global Influenza Programme has made multiple efforts to emphasize the importance of continued influenza surveillance including the reporting of data to global platforms. **Methods:** To assess the effect of the COVID-19 pandemic on the reporting of routine influenza surveillance data to FluNet, data on the number of countries reporting data to FluNet for each week of 2019, 2020 and 2021 was extracted on 20 September 2021. **Results:** In the five years, a gradual increase in the number of countries reporting over time is observed until early 2020. Each year, a decrease in the number of countries reporting is observed during part of the year. In all years except 2020, the decrease occurred from week 20 until week 40. In 2020, the decrease began earlier around week 5. Reporting in late 2020 reached levels seen in previous years. In early 2021, the number of countries reporting was at or lower compared to all previous years except 2017 but was above levels seen in 2020 after week 5. **Conclusions:** A decrease in the number of countries reporting to FluNet occurring between week 20 and 40 is likely due to the seasonal surveillance and reporting taking place in countries in the temperate northern hemisphere. A decrease in reporting occurred earlier than usual in 2020 and likely reflects disruptions due to the COVID-19 pandemic. Reporting increased to usual levels at the end of 2020. In the first half 2021, reporting remains at or above levels seen in 2020 but remained less than that seen in the first part of 2019.

### Poster 324. Safety and Immunogenicity of Trivalent Inactivated Influenza Vaccine in Healthy Thai Adults Aged 18 – 64 Years: A Double-blinded, Three-arm, Randomized, Controlled Trial

**K. Prasert**[1], P. Praphasiri[2], S. Nukphook[3], D. Ditsungnoen[2] S. Chawalchitiporn[1], K. Poopipatpol[4], P. Wirachwong[4], S. Prangpratarnporn[4], P. Narakorn[4], S. Surichan[4], N. Suthepakul[4], N. Thangsupanimitchai[4], P. Puthavathana[5], J. Patuanond[6], J.A. Mott[2,7]
[1]Nakhon Phanom Provincial Hospital, Nakhon Phanom, Thailand, [2]Influenza Program, Thailand Ministry of Public Health-US Centers for Disease Control and Prevention Collaboration, Nonthaburi, Thailand, [3]Institute of Preventive Medicine, Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand, [4]The Government Pharmaceutical Organization, Bangkok, Thailand, [5]Center for Research and Innovation, Faculty of Medical Technology, Mahidol University, Salaya, Nakhon Pathom, Thailand, [6]Clinical Epidemiology Unit, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand, [7]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** To obtain data for dossier submission of trivalent inactivated vaccine produced by the Government Pharmaceutical Organization (GPO), we evaluated safety and immunogenicity of locally produced vaccine, in healthy Thai adults. **Methods:** We conducted a double-blinded, three-arm, randomized, controlled trial in Thailand during September 2019-October 2020. Participants aged 18-64 years were assigned 3:3:1 to a single intramuscular injection of GPO-Tri Fluvac seasonal trivalent split virion inactivated influenza vaccine; a saline placebo; or an active comparator licensed vaccine. Antibody titers were assessed of three vaccine antigens by HAI assay before and four weeks after vaccination. Non-inferiority of GPO-Tri Fluvac compared to comparator vaccine was assessed by post vaccination geometric mean titer (GMT) ratios and differences in seroconversion rates at day 28 (proportion with antibody titer < 1:10 at baseline and with post-vaccination titer of ≥ 1:40; or pre-vaccination titer of ≥ 1:10 and a ≥ 4-fold post-vaccination increase). Safety data were collected for 12 months. Solicited adverse events were recorded by participants on diary cards for seven days after vaccination and unsolicited adverse events were assessed at healthcare facility or self-reported at any time. **Results:** 4,284 participants were assigned to GPO-Tri Fluvac (n=1,836), placebo (n=1,836) and active comparator (n=612). 1,832 were analyzed for immunogenicity endpoints (611 for GPO Tri Fluvac, 612 for Placebo and 609 for comparator). GMT ratios at day 28 were 1.09 (95%CI: 0.89, 1.34), 1.12 (0.86, 1.45) and 0.98 (0.81, 1.19), seroconversion difference rates were 1.74 (95%CI: -2.77, 6.25), 2.22 (-2.40, 6.84) and -0.57 (-5.41, 4.27) for influenza A(H1N1), A(H3N) and Flu B. Adverse events were not different across vaccination groups. Unsolicited adverse events were 9.5%[75/1836] and 10.8%[66/612], and Solicited adverse events were 25.5% and 29.4% for GPO Tri Fluvac and comparator. **Conclusions:** GPO Tri Fluvac was well-tolerated, immunogenicity was non-inferior and met criteria for adult vaccine licensure.

### Poster 325. Active Surveillance for Avian Influenza Viruses in Lao PDR, 2019-2021

**P. Phommachanh**[1], V. Asana[1], V. Khanthamaly[2], S. Na Nan[3], J. Mott[4], C. T. Davis[5], B. Kounnavong[6], B. Khamphaphongphane[7], O. Prasarnphanich[3]
[1]The National Animal Health Laboratory, Vientiane Capital, Lao PDR, [2]Influenza Division, Centers for Disease Control and Prevention, Vientiane Capital, Lao PDR, [3]Division of Global Health Protection, Centers for Disease Control and Prevention, Bangkok, Thailand, [4]Influenza Division, Centers for Disease Control and Prevention, Bangkok, Thailand, [5]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]Defense Threat Reduction Agency, Vientiane Capital, Lao PDR, [7]Center for Laboratory and Epidemiology, Vientiane Capital Lao PDR

**Background:** Live bird markets have been implicated in the zoonotic transmission of avian influenza viruses from poultry to humans throughout Southeast Asia. Sustained active surveillance for avian influenza virus in animal populations at potential sources of exposure, with appropriate linkages to human surveillance and response activities, is critical for early detection and response. **Methods**: The National Animal Health Laboratory (NAHL) of the Lao PDR, with technical and financial assistance from the U.S. Centers for Disease Control and Prevention, conducted active surveillance for avian influenza viruses in live bird markets in Bokeo, Luang Namtha, Oudomxay, Vientiane Capital, and Xiangkhouang provinces from January 2019 to June 2021. Oropharyngeal and cloacal specimens were collected monthly from ducks and chickens. Environmental samples were also collected. NAHL tests specimens for Influenza A(H5, H7 and H9) by RT-PCR. **Results**: In 2019, 250 (6.8%) of 3,691 total animal and environmental specimens tested positive for influenza A viruses. Of the 250 specimens positive for influenza A viral RNA (vRNA), 2 were positive for highly pathogenic avian influenza (HPAI) A(H5N1), 3 were positive for HPAI A(H5N6), and 216 were positive for influenza A(H9) vRNA. In 2020, 305 (8.5%) of 3,598 total animal and environmental specimens tested positive for influenza A viruses. Of these specimens, 33 were positive for HPAI A(H5N1), 2 were positive for HPAI A(H5N6), and 216 were positive for influenza A(H9) vRNA. From January to June 2021, 119 (6.8%) of 1,755 total animal and environmental specimens tested positive for influenza A viruses. Of the 119 specimens positive for influenza A viruses, 15 were positive for HPAI A(H5N6), and 104 were positive for influenza A(H9) vRNA. **Conclusion**: Avian influenza viruses were commonly found in live bird markets in Lao PDR. Conducting active surveillance facilitates rapid detection of circulating avian influenza strains and outbreak response.

### Poster 326. Seasonal Influenza Vaccination in Kenya: What Determines Healthcare Workers' Willingness to Accept and Recommend Vaccination?

**N.A. Otieno**[1], R. Kalani[2], J. Ayugi[1], E. Osoro[3], P. Muturi[3], L. Ndegwa[4], M.S. Ebama[5], G.O. Emukule[4]
[1]Kenya Medical Research Institute, Center for Global Health Research, Kisumu, Kenya, [2]Kenya Ministry of Health, Disease Surveillance and Response Unit, Nairobi, Kenya, [3]Washington State University Global Health – Kenya, Nairobi, Kenya, [4]US Centers for Disease Control and Prevention, Influenza Program, Nairobi, Kenya, [5]The Task Force for Global Health, Center for Vaccine Equity, Decatur, GA, USA

**Background:** Data on healthcare workers' (HCW) willingness to accept or recommend seasonal influenza vaccination in countries without influenza vaccination programs are limited. **Methods:** We conducted a cross-sectional survey in 7 of the 47 counties in Kenya, where we conduct surveillance for severe acute respiratory illness, to examine knowledge, attitudes, and perceptions of HCWs towards seasonal influenza disease and vaccination. We enrolled a convenient sample of HCWs (professionals delivering clinical services directly/peripherally to patients) from 5 health facilities in each county: a county referral hospital, a health center, a dispensary, a private health facility and a faith-based health facility. We used chi square tests and logistic regression models to identify variables that were associated with HCW's willingness to accept or recommend seasonal influenza vaccination. **Results:** From May-June 2018, we enrolled 2,035 HCWs from 35 facilities. Most of the HCWs (82%) were from public health facilities and 64% were female. Of the HCWs who had heard of seasonal influenza (1,671/2,012, 83%), 87% believed that seasonal influenza could cause severe illness. Most (1,076/1,209, 89%) of the HCWs were willing to receive the seasonal influenza vaccine if it was recommended for HCWs and provided for free, and 91% (1,441/1,576,) would vaccinate their patients or recommend vaccination if the vaccine was available. Only 18% (213/1212) had received the vaccine before. HCWs who believed that influenza could cause severe illness (adjusted odds ratio [aOR] 2.2; 95% CI 1.3-3.5) and that people around them were better protected if they were vaccinated (aOR 3.1; 95% CI 2.0-4.6) were more willing to get vaccinated, while females (aOR 0.6; 95% CI 0.4-0.9) were less willing to get vaccinated compared to their male counterparts. Willingness to recommend seasonal influenza vaccination to patients was higher among HCWs who had seen patients with influenza (aOR 1.7; 95% CI 1.2-2.5), believed it could cause severe illness (aOR 2.0; 95% CI 1.3-3.2) and HCWs who believed that people around them are better protected if the HCW is vaccinated (aOR 3.6; 95% CI 2.3-5.7). **Conclusion:** Our findings suggest

favorable attitudes among HCWs towards seasonal influenza vaccination, many of whom are motivated by the desire to protect others around them.

### Poster 327. The Assessment of an Updated Standardized Approach for Risk Associated with Zoonotic or Animal Influenza Viruses – TIPRA

**M.D. Samaan**[1], R.J. Webby[2], T.P. Fabrizio[2], D. Pereyaslov[1], W. Zhang[1]
[1]Global Influenza Programme, Global Infectious Hazards Preparedness, WHO Emergency Programme, WHO, Geneva, Switzerland, [2]Department of Infectious Diseases, St. Jude Children's Research Hospital, Memphis, TN, USA

**Introduction:** Multiple incidences of human infection by zoonotic *influenza A* viruses highlighted the importance of monitoring the pandemic potential associated with these viruses. *Influenza* virus evolution is dynamic and constant with limited understanding of its pandemic risk. To better prepare for the next pandemic and to prioritize preparedness activities, it is important to conduct risk assessment. In 2020 WHO updated and published the 2nd release of the Tool for *Influenza* Pandemic Risk Assessment (TIPRA). Version 2 was used to assess nine *influenza* subtypes including rescoring of previous runs performed using first released version. **Method:** Using a multi-attribute additive model, the tool assesses two components: the pandemic likelihood (potential) of acquiring the capacity for sustained human to human transmission and the public health impact if human to human transmission started to occur. A broad spectrum of experts scored ten risk elements, based on knowledge available at the time of assessment. TIPRA version 2 was used to re-evaluate the risk of TIPRA version 1 results and to run additional exercises. **Result:** All exercises performed were on H5N6 (2x), H7N9 (2x), H9N2 (2x), and H1N1 virus possessing triple reassortment internal gene cassette (H1N1 TRIG) (2017), H5 clade 2.3.2.1c (2020) and H5 clade 2.3.4.4b (2021). H1N1 TRIG showed the highest likelihood among the nine assessment exercises. H5N6 and H7N9 subtypes had a moderate-high impact. During risk assessment exercises performed using TIPRA 2 in 2020 and 2021, risk elements scoring was more consistant among experts, in comparison to version 1. Risk results of TIPRA version 1 and 2 were comparable.**Conclusion:** Timely risk assessment using TIPRA to generate comparable results – a risk map is a scientific approach to prioritize the risks of subtype/clade viruses for preparedness activities and relevant policy making. Updated TIPRA is more robust in comparison to previous version.

## Zoonotic and Vector-borne Diseases

### Poster 328. Knowledge of Frontline Healthcare Workers on Arboviral Diseases in Armenia

**L. Paronyan**, K. Gevorgyan, M. Sargsyan, L. Avetisyan, A. Vanyan
National Center of Disease Control and Prevention, State Noncommercial Organization, MOH, Yerevan, Republic of Armenia

**Background:** In Armenia, the only case of Crimean-Congo hemorrhagic fever (CCHF) was registered in 1974, even though CCHF virus has been detected in ticks during entomological surveys in 1986-1996 and 2016. In 2006, a large entomological survey identified 125 distinct strains of arboviruses, including West Nile virus. Continued entomological studies show the expansion of relevant vectors of emerging diseases. Currently, healthcare facilities don’t report suspect cases of arboviral diseases nor send specimens for laboratory investigations. Our objective was to determine the knowledge of arboviruses among Armenian health care workers to evaluate their ability to report disease occurrence. **Methods:** We administered a structured pre-tested questionnaire on epidemiology, distribution, etiology, and signs and symptoms of arboviral diseases. The questionnaire was administered to epidemiologists and clinicians of different specialties (family doctors/therapists, surgeons, otorhinolaryngologists, oculists, dermatologists, and infection-disease specialists) in all 10 regions and capital city. Each question was assessed by scores with the index of right answers showing the level of knowledge on arboviral diseases. **Results**: Of 449 health-care workers who participated in the assessment: 15% (n=67) were male, 67% (n=301) were ≥50 age group, 46.1% (n=207) from distant (more than 100km) regions**.** There were 42 epidemiologists and infectious diseases specialists, 135 clinicians of other specialties and 272 family doctors/therapists. No association was noted in the age/sex or distance from the capital on the knowledge on arboviral diseases. Epidemiologists, infectious diseases specialists and family doctors/therapists were more aware of arboviral diseases scoring on average 33.4 (index interval: 29.7-37.1) with other specialists scoring much lower on average 11.4 (index interval: 0.3-22.5). **Conclusion**: Overall knowledge on arboviral diseases is very low among doctors in all regions. A surveillance system for arboviral diseases in Armenia should be strengthened through training programs to rationalize the collection and analysis of data, estimate the burden of diseases, and contribute to conducting effective public health policy for prevention and timely treatment of cases.

### Poster 329. Incidence of Lyme Disease Diagnoses among Medicare Beneficiaries, 2016-2019

**A.M. Schwartz**, C. Nelson, A.F. Hinckley
Centers for Disease Control and Prevention Division of Vector-Borne Diseases, Fort Collins, CO, USA
**Background:** Lyme disease (LD) is the most commonly reported vector-borne disease in the United States, with the majority of cases reported among children and older adults. Past efforts to estimate the burden of LD diagnoses in the United States have relied upon commercial insurance claims data, which generally lack information on older adults. To better enumerate and characterize LD diagnoses among adults aged ≥65 years, we analyzed data from Medicare, the federal health insurance program. **Methods:** LD diagnoses were identified among Medicare fee-for-service (FFS) beneficiaries aged 65 and older who were enrolled in Medicare Parts A, B and D for 12 months or until death during 2016-2019. Clinician-diagnosed LD was identified among inpatient claims data using ICD-10-CM codes for LD or LD-related conditions and among outpatients using ICD-10 codes for LD in combination with Part D claims for antibiotics used to treat LD. **Results:** During 2016-2019, 88,573 LD diagnoses were identified; a small proportion of diagnoses (<2%) were identified among inpatient records. Annual incidence ranged from 112-137 diagnoses/100,000 beneficiaries. For all study years, median age was 73, incidence was higher in males (129-157/100,000) compared to females (101-123/100,000), and 81-83% of diagnoses occurred among residents of states with historically high LD incidence. Most diagnoses (55-59%) occurred during the summer months (May-August). **Conclusions:** Using LD-specific ICD codes and treatment data, we identified a high incidence of clinician-diagnosed LD among the Medicare FFS population. Characteristics of patients with LD diagnoses were comparable to those of cases identified through national surveillance; more diagnoses occurred among males and in the summer months. LD incidence among beneficiaries 65 and older was comparable to that of older age groups in past claims analyses. Older adults, a group more likely to have comorbidities and a complicated clinical course, represent a large number of LD diagnoses in the US; additional analysis is needed to better understand risk factors and clinical manifestations in this high-risk group. Next steps include additional refinement and validation of methods and expansion of analysis to include more years and Medicare Advantage participants.

### Poster 330. Evaluating Public Acceptability of a Potential Lyme Disease Vaccine Using a Population-Based, Cross-Sectional Survey in High Incidence Areas of the United States

**S.A. Hook**[1], A.J. Hansen[2], S. Niesobecki[2], J. Meek[2], J. Bjork[3], E. Kough[3], M. Peterson[3], E. Schiffman[3], H. Rutz[4], A. Rowe[5], J. White[5], J.L. Peel[6], B.J. Biggerstaff[1], A.F. Hinckley[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Connecticut Emerging Infections Program, Yale School of Public Health, New Haven, CT, USA, [3]Minnesota Department of Health, St Paul, MN, USA, [4]Maryland Department of Health, Baltimore, MD, USA, [5]New York State Department of Health, Albany, NY, USA, [6]Colorado State University, Fort Collins, CO, USA
**Background:** Lyme disease incidence is increasing, despite current prevention options. New Lyme disease vaccine candidates are in development, however, investigation of the acceptability of a Lyme disease vaccine among potential consumers is needed prior to any vaccine coming to market. We conducted a population-based, cross-sectional study to estimate willingness to receive a potential Lyme disease vaccine and factors associated with willingness. **Methods:** The web-based survey was administered to a random sample of Connecticut, Maryland, Minnesota, and New York residents June – July 2018. Survey-weighted descriptive statistics were conducted to estimate the proportion willing to receive a potential Lyme disease vaccine. Multivariable, multinomial logistic regression models were used to quantify the association of sociodemographic characteristics and LD vaccine attitudes with willingness to be vaccinated. **Results:** Surveys were completed by 3,313 respondents (6% response rate). We estimated that 64% of residents were willing to receive a Lyme disease vaccine, while 30% were uncertain and 7% were unwilling. Compared to those who were willing, those who were uncertain were more likely to be parents, adults 45 – 65 years old, non-white, have less than a bachelor's degree, or have safety concerns about a potential Lyme disease vaccine. Those who were unwilling were also more likely to be non-white, have less than a bachelor's degree, or have safety concerns about a potential Lyme disease vaccine. In addition, the unwilling had low confidence in vaccines in general, had low perceived risk of contracting Lyme disease, and said they would not be influenced by a positive recommendation from a healthcare provider. **Discussion:** Overall, willingness to receive a Lyme disease vaccine was high. Effective communication by clinicians and public health practitioners regarding safety and other vaccine parameters to those groups who are uncertain about Lyme disease vaccination will be critical for increasing vaccine uptake and reducing Lyme disease incidence.

### Poster 331. Racial Differences in Lyme Disease Diagnoses in a Large Midwestern Healthcare System

**A. Schotthoefer**[1], K. Kugeler[2], K. Cooley[2], E. Scotty[1], J. Mayer[1], J. Meece[1], A. Schwartz[2], A. Hinckley[2]

[1]Marshfield Clinic Research Institute, Marshfield, WI, USA, [2]Centers for Disease Control and Prevention, Fort Collins, CO, USA
**Background:** Lyme disease (LD) is one of the most common notifiable diseases in the northeastern, mid-Atlantic, and upper Midwest United States. Nearly 90% of cases are reported among people who are non-Hispanic White. People of other races and ethnicities may be at lower risk for LD or there may be differences related to healthcare access, delivery, and recognition that disproportionately affect non-White persons. We explored data from electronic medical records (EMR) at one large healthcare system in an area with high LD incidence in the Midwest to better understand patterns of possible LD diagnoses according to patient race and ethnicity. **Methods:** A retrospective cohort of 62,103 persons evaluated for LD during 2016–2019 was created from patients with at least one of: an ICD-10 code for LD; diagnostic tests performed for LD; prescriptions for an antibiotic used for treatment of LD. We compared characteristics associated with possible LD diagnoses by patient race and ethnicity using chi-square tests. **Results:** Race and ethnicity were available for 55,862 (90%) of patients in the cohort. Only 1,728 (3.1%) identified as non-White, of those 1,644 (2.9%) identified as non-White, non-Hispanic. The percentage of non-White patients who were female was higher than that among White patients (57% vs 52%, $p<0.0001$); patient age distributions were similar among races. White persons evaluated for possible LD were more likely to have an ICD-10 code for LD associated with their encounter (7% vs 5%, $p<0.0001$), and have a test ordered (60% vs 54%, $p<0.0001$) than non-White persons. Compared to all other non-White patients, Black persons were least likely to have an ICD code for LD (1% vs 5%) and Asian persons were most likely to have LD tests ordered (58% vs 49%). Test positivity and frequency of treatment were similar among races. **Conclusions:** Examining patterns associated with patient race and ethnicity in EMR data for persons with possible Lyme disease suggests non-White people may have different experiences in relation to clinical evaluation for possible LD than White persons. Further study is needed to determine if there are underlying differences in clinical presentation, healthcare-seeking behaviors, or provider practices that may explain these differences.

### Poster 332. Geostatistical Modelling and Prediction of Rift Valley Fever Seroprevalence among Livestock in Uganda

**C.T. Telford**[1], T. Shoemaker[1], L. Nyakarahuka[2], C. Cossaboom[1], L. Waller[3], U. Kitron[3]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uganda Virus Research Institute, Entebbe, Uganda, [3]Emory University Rollins School of Public Health, Atlanta, GA, USA
**Background**: Rift Valley Fever (RVF), caused by Rift Valley Fever virus (RVFV), is an arboviral hemorrhagic fever endemic to countries in Africa and the Middle East. Recent outbreak investigations in Uganda indicate undetected RVFV circulation among both humans and livestock. **Methods**: A RVFV serosurvey was carried out among livestock in 28 Uganda districts. A geostatistical model of RVF was used to quantify the relationship between RVF seropositivity and key environmental predictors of viral transmission using model-based geostatistics. Model parameters were used to estimate RVF seroprevalence on a map of the country for 2017, and a map was generated showing the probability that RVF seroprevalence exceeded 10% in each prediction location. Model parameters were then fit to the covariate values for the year 2020 to identify geographic regions at risk of RVFV circulation according to the most recently measured environmental conditions. **Results**: Variables resulting in the best fit to RVF seroprevalence sampling data included precipitation seasonality, enhanced vegetation index (EVI) seasonality, distance to the nearest river, and change in population density. Predicted RVF seroprevalence for 2017 was highest in the Northwestern quadrant of the country, surrounding Lake Victoria, and along the Southern Cattle Corridor, where there was a high probability that RVF seroprevalence exceeded 10%. Predicted seroprevalence was lowest in the Northeastern region. Fitting the model to the most recently available covariate data for the year 2020, we identified areas with potential risk of recent viral circulation in Northwestern Uganda surrounding several National Parks, and in Northeastern Uganda, an area which has low documented RVF seroprevalence among livestock. **Conclusions**: RVF seroprevalence among livestock in Uganda was spatially heterogeneous, and specific regions were identified with high probability of seroprevalence greater than 10%. Elevated RVF seroprevalence was most significantly associated with moderate seasonality in precipitation and increases in population density. Fitting model parameters to covariate data for the year 2020, we identified locations where RVFV circulation may exceed that which was predicted for 2017 and which should be prioritized for disease surveillance efforts.

### Poster 333. Rift Valley Fever Infection among Patients with Severe Febrile Illness, Northern Tanzania, 2016-19

**C. Costales**[1,2], J.D. Klena[3], K. Patel[3], A. Gibbons[3], A.G. Leach[3], R.B. Martines[4], A.R. Mremi[5], P. Amsi[5], N.H. Kalengo[6], B.T. Mmbaga[7,8], S.R. Zaki[4], J.M. Montgomery[3], V.P. Maro[6,8], M.P. Rubach[1,2], J.A. Crump[1,2,8,9]

[1]Division of Infectious Diseases and International Health, Department of Medicine, Duke University Medical Center, Durham, NC, USA, [2]Duke Global Health Institute, Duke University, Durham, NC, USA, [3]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Infectious Diseases Pathology Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Department of Pathology, Kilimanjaro Christian Medical Centre, Moshi, Tanzania, [6]Department of Medicine, Kilimanjaro Christian Medical Centre, Moshi, Tanzania, [7]Kilimanjaro Clinical Research Institute, Kilimanjaro Christian Medical Centre, Moshi, Tanzania, [8]Kilimanjaro Christian Medical University College, Tumaini University, Moshi, Tanzania, [9]Centre for International Health, University of Otago, Dunedin, New Zealand
**Background:** The inter-epidemic behavior of Rift Valley Fever Virus (RVFV) is incompletely understood. We studied severe and fatal febrile illness in northern Tanzania during a period that included a small outbreak of RVFV-associated livestock abortions in the hospital catchment in May through August 2018. **Methods:** From November 2016 through May 2019 patients presenting with fever to Kilimanjaro Christian Medical Centre and Mawenzi Regional Referral Hospital, Moshi, Tanzania were screened within 24 hours of admission and enrolled. Acute plasma or post-mortem blood was collected and tested for RVFV by PCR. Decedents underwent autopsy, including histopathology with immunohistochemistry (IHC). Next generation sequencing and phylogenetic analysis was performed for RVFV PCR positive plasma specimens. **Results:** Of 1,039 febrile patients and 153 febrile decedents enrolled between November 2017 through May 2019, RVFV was detected by PCR in plasma from one (0.1%) febrile patient and one (0.7%) febrile decedent each enrolled in July 2018 and each reporting close livestock contact. Participant 1 was a 28-year-old male admitted with fever for 7 days associated with night sweats, headache, photophobia, and myalgias. He was discharged after two days of hospitalization with a provisional diagnosis of enteric fever and recovered. Participant 2 was a 24-year-old female admitted with a 5-day history of subjective fever, abdominal pain and distention, vomiting, and oliguria, subsequently developing jaundice. She had experienced a spontaneous abortion one month before enrollment. She developed renal failure and suffered a fatal cardiac arrest on hospital day 7. Autopsy revealed acute fulminant hepatitis with positive IHC staining for RVFV in liver and kidney. By phylogenetic analysis, sequences from both participants belong to Clade I, Kenya-2 sublineage, and were highly similar to sequences from a 2017 outbreak in southwestern Uganda. **Conclusions:** Through surveillance of severe and fatal febrile illness hospitalizations in northern Tanzania, we confirmed that a small RVFV livestock abortion outbreak was associated with contemporaneous human infections that might otherwise have been undetected. Sequence similarities to a 2017 Uganda outbreak suggest a complex epidemiology of RVFV during inter-epidemic periods.

### Poster 334. Nipah Virus Detection at Bat Roosts following Spillover Events in Bangladesh, 2012–2019

**C.D. McKee**[1], A.U. Islam[2], M.Z. Rahman[2], S.U. Khan[2], M. Rahman[2,3,4], S.M. Satter[2], A.R. Islam[5,6], C.K. Yinda[7], J.H. Epstein[5], P. Daszak[5], V.J. Munster[7], P.J. Hudson[8], R.K. Plowright[9], S.P. Luby[10], E.S. Gurley[1,2]
[1]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [2]icddr,b, Dhaka, Bangladesh, [3]Institute of Epidemiology, Disease Control and Research, Dhaka, Bangladesh, [4]Global Health Development/Eastern Mediterranean Public Health Network, Amman, Jordan, [5]EcoHealth Alliance, New York, NY, USA, [6]Deakin University, Geelong, Australia, [7]National Institute of Allergy and Infectious Diseases, Hamilton, MT, USA, [8]Pennsylvania State University, State College, PA, USA, [9]Montana State University, Bozeman, MT, USA, [10]Stanford University, Stanford, CA, USA
**Background:** Nipah virus is a zoonotic virus in bats that produces cases of fatal encephalitis in humans almost every year in Bangladesh. However, knowledge of the dynamics and genetic diversity of Nipah virus circulating in bats and at the human-animal interface is limited by current sampling efforts, which produce few detections of viral RNA. We report on a series of investigations at bat roosts identified near human Nipah cases in Bangladesh between 2012 and 2019. **Methods:** Pooled roost urine was collected from bat roosts within a 20 km radius of case households by placing plastic tarps under the bat roost in the early morning. Urine was divided into aliquots and tested for Nipah RNA via real-time PCR. Positive roosts were visited repeatedly until Nipah RNA was no longer detected. The detection rate on a per-visit and per-aliquot basis were compared with previous published surveys of Nipah shedding in bats. **Results:** Pooled bat urine samples were collected from 23 roosts; seven roosts (30%) had at least one sample with Nipah RNA detected from the first visit. In subsequent visits to these seven roosts, RNA was detected in bat urine up to 52 days after the presumed exposure of the human case, although the probability of detection declined rapidly with time. Compared to previous surveys, the Nipah detection rates were similar on a per-visit basis (23% vs. 28%), but the per-aliquot rate was significantly higher in our study than in previous reports (4.7% vs. 0.48%). **Conclusions:** These results suggest that rapidly deployed investigations of Nipah virus shedding

from bat roosts near to human cases could increase the success of viral sequencing and lead to better knowledge of Nipah virus ecology and genetic diversity.

### Poster 335. Knowledge, Attitudes, and Practices on Rocky Mountain Spotted Fever among Physicians in a Highly Endemic Region — Mexicali, Mexico

**N. Bestul**[1,2], R. Padilla[3], T. Montaño[4], A. Márquez[3], M. Fierro[4], O.E. Zazueta[3], P.A. Armstrong[1]
[1]Rickettsial Zoonoses Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [3]Secretaría de Salud de Baja California, Mexicali, Baja California, México, [4]Imperial County Health Department, El Centro, CA, USA
**Background:** Rocky Mountain spotted fever (RMSF) is a potentially fatal tickborne disease caused by the bacterium, *Rickettsia rickettsii*, and transmitted primarily by the brown dog tick (*Rhipicephalus sanguineus*) in the Southwestern United States and Mexico. RMSF can be rapidly fatal if not treated early with doxycycline, making healthcare worker awareness and education critical to reduce morbidity and mortality. Mexicali has been experiencing an epidemic of RMSF, with 779 confirmed cases reported, and a case-fatality rate of 16% during 2008–2019. **Methods:** A cross-sectional study was conducted with 290 physicians and physicians in-training across 12 medical facilities in Mexicali. A 23-item questionnaire was administered to assess knowledge, attitudes, and practices for clinical, epidemiologic, and preventive aspects of RMSF. **Results:** Half of participants were female, the largest age group was 25–44 (47%), and the median time in practice of 6 years (IQR: 1–21.5). Less than half (48%) surveyed were confident where diagnostic testing could be performed, and two-thirds did not regularly order serology (67%) or molecular diagnostic (66%) tests for RMSF when a patient presented with fever. Sixty-four percent were aware doxycycline is the recommended first-line treatment for children < 8 years with suspected RMSF. When comparing healthcare workers with < 6 years of experience to those with ≥ 6 years, more experience was associated with greater confidence in where to have diagnostic testing performed (pOR = 2.3; p-value = 0.004), and frequency of ordering laboratory tests (serology, pOR = 3.3; p-value = 0.002; PCR, pOR = 3.9; p-value = 0.001). **Conclusions:** This study's findings show an overall appreciation by Mexicali physicians of the importance of tickborne diseases and their public health impact. However, gaps in knowledge, especially regarding pediatric treatment and diagnostics, were also identified. Continued RMSF education, including information on diagnostic testing, is key to improving patient outcomes.

### Poster 336. Individual, Household, and Community Characteristics Associated with Toxoplasmosis Infection in Southern Chile using Hierarchical Data Structures

**S.S. Berg**[1], C. Munoz-Zanzi[2], A.G. Rivera Juarez[1]
[1]University of St. Thomas, St. Paul, MN, USA, [2]University of Minnesota, Minneapolis, MN, USA
**Background:** Toxoplasmosis is a globally prevalent zoonotic infection caused by the parasite *Toxoplasma gondii* with a wide range of clinical symptoms in humans. *T. gondii* has a complex lifecycle with many opportunities for human infection, including direct contact with contaminated soil through gardening and consumption of contaminated food. Both the behavior of the individual and of those living in their household may increase risk of infection, suggesting that an explicitly hierarchical approach is needed. This study aims to describe the seroepidemiology of toxoplasmosis by considering the interactions between risk factors occurring at the individual, household, and community level. **Methods:** We conducted a cross-sectional serosurvey of 616 individuals in 223 households from 8 rural village and farm communities in the Los Rios Region of Chile. This survey included blood samples to test for *Toxoplasma* antibodies and questions on suspected sociodemographic and behavioral risk factors for each individual and household. We used exploratory factor analysis to identify latent variables and hierarchical structural equation modeling to identify risk factors associated with toxoplasmosis infection at each level. **Results:** 378 participants tested positive for *T. gondii* antibodies, resulting in an overall seroprevalence of 61.4%. After accounting for age, sex, and socioeconomic variables, seropositivity was primarily associated with occupational risk factors at the individual level, such as cleaning barns and working in agriculture, and food-related factors at the household level, such as the source and preparation of meat, fruits, and water. **Conclusions:** Seroprevalence was high in both rural and farm communities, with unique risk profiles at the individual and household level. These findings highlight the benefits of employing a hierarchical approach to studying the epidemiology of infections and encourage investigation into less-studied mechanisms for toxoplasmosis transmission.

### Poster 337. Emergence of a Distinct Picobirnavirus Genotype Circulating in Patients Hospitalized with Acute Respiratory Illness

**M.G. Berg**, K. Forberg, L.J. Perez, K.C. Luk, T.V. Meyer, G.A. Cloherty
Infectious Diseases Research, Abbott Diagnostics, Abbott Park, IL, USA

**Introduction:** Picobirnaviruses (PBV) are genetically diverse, double stranded RNA viruses with bi-segmented genomes, found globally in a wide species range. PBV are typically associated with gastrointestinal infections in immunocompromised individuals, having only recently been connected to acute respiratory illness (ARI). **Methods:** Metagenomic next-generation sequencing (mNGS) was deployed to identify new viruses involved in ARI. Nextera libraries were sequenced on an Illumina MiSeq. SURPI was used to catalog known pathogens while RAPsearch and psiBLAST were used to identify divergent viral reads. Extractions and qPCR were performed on Abbott m2000 instruments. Maximum likelihood was used for phylogenetic tree reconstruction and Bayesian inference for trait analysis. **Results:** A divergent PBV genome was assembled *de novo* from the sputum of Colombian (South America) patient ABT3406 hospitalized for ARI. The RdRp protein branched with rare sequences previously reported in respiratory patients from Cambodia (2009) and China (2018). Hospitalized individuals (n=130) were screened with a novel qPCR assay for capsid and RdRp that enabled detection and characterization of 25 additional PBV infections circulating in Colombia and US. Phylogenetic analysis of RdRp highlighted the emergence of two lineages linked to ABT3406 and Asian strains, which together clustered as a distinct genotype. Bayesian inference further established capsid and RdRp sequences as both significantly associated with ARI. While mNGS indicated various viral and bacterial co-infections were common, four individuals devoid of other pathogens suggest PBV is not exclusively opportunistic. **Conclusions:** The novel lineage we characterize here, along with additional variants having high identity to strains reported in Asia, all cluster together phylogenetically and represent the dominant PBV strains identified in ARI patients. As with influenza, PBV possesses the capacity to cross species and rapidly evolve by reassortment. The high prevalence and genetic features linking it to ARI indicate this PBV genotype has the potential to become a global threat.

### Poster 338. Alaskapox: Recent Cases of an Emerging Viral Infection and Investigation of Zoonotic Sources — Alaska, 2020—2021

**F.M. Whitehill**[1,2], E.Q. Mooring[3,4], K.G. Newell[2,4], A. Kunkel[1,2], F.S. Minhaj[1,2], C.N. Morgan[1], Z.R. Werle[5], L.E. Olson[6], K. Wilkins[1], C.M. Gigante[1], W. Davidson[1], A.M. Matheny[1], B.W. Petersen[1], Y. Nakazawa[1], Y. Li[1], V.A. Olson[1], J.B. McLaughlin[4], A. McCollum[1], J.B. Doty[1]
[1]Division of High Consequence Pathogens and Pathology, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Division of Scientific Education and Professional Development, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Division of Preparedness and Emerging Infections, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Alaska Division of Public Health, Anchorage, AK, USA, [5]Tanana Valley Clinic, Fairbanks, AK, USA, [6]University of Alaska Museum, Fairbanks, AK, USA
**Background:** In 2015, the first case of *Alaskapox virus* (AKPV) infection was confirmed near Fairbanks, Alaska. In 2020, a second case was confirmed in another Fairbanks resident. In 2021, two additional probable cases of AKPV were identified in the same area. Many orthopoxviruses (OPXV) are known to infect small mammals. OPXV infections in humans and domestic or agricultural animals may occur via contact with infected wild animals. In 2020 and 2021, small mammals were sampled near the case patients' homes to search for evidence of AKPV infection. **Methods:** Patient lesion samples were tested by OPXV-generic real-time polymerase chain reaction (rt-PCR), virus isolation, and whole genome sequencing. Patient sera were tested for anti-OPXV IgG and IgM antibodies by enzyme-linked immunosorbent assay (ELISA). Small mammal samples were tested with OPXV-generic and AKPV-specific rt-PCR assays and for anti-OPXV IgG. Serum was collected from dogs and cats that lived on the same property as one case patient and were tested for anti-OPXV IgG. **Results:** Lesion samples from the 2020 and 2021 patients were positive for OPXV DNA and yielded viable virus. The viral genome from the 2020 isolate differed from the 2015 isolate, which was 210,797 bp in size, by 177 SNPs (>99% identical). The 2020 patient's serum was positive for anti-OPXV IgM and negative for IgG. In 2020 and 2021 combined, 385 small mammals were collected representing shrews (*Sorex* sp.) and 7 genera of rodents. Among 176 animals collected in 2020, 34 (20%) had evidence of past or current infection with an OPXV by ELISA or PCR. Viable virus was isolated from 2 (1%) animals, a vole (*Myodes* sp.) and a shrew, and confirmed as AKPV via sequencing. Genome sequencing of the 2021 patients' isolates, testing of the small mammals collected in 2021, and serology for close contacts and domestic animals are underway. **Conclusions:** AKPV, an emerging zoonotic virus, may be spread by wild small mammals living in peri-domestic areas. Public health communication is focused on increasing awareness of the illness and reinforcing standard messages about wildlife and animal contact precautions. Additional studies are needed to examine the host range, geographic distribution, and viral circulation of AKPV among potential animal reservoirs.

### Poster 339. Enhanced Surveillance of West Nile Virus in Slovenia

**M. Korva**[1], N. Knap [1], V. Ivović [2], K. Kalan[2], J. Šušnjar[2], T. Knapič[3], T. Trilar[3], T. Avšič-Županc[1]

[1]Institute of Microbiology and Immunology, Faculty of Medicine, University of Ljubljana, Slovenia, [2]Department of Biodiversity, Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Koper, Slovenia, [3]Slovenian Museum of Natural History, Ljubljana, Slovenia
**Background:** West Nile virus (WNV) is a flavivirus transmitted by mosquitoes. Infections in humans vary from asymptomatic to West Nile fever (WNF) or West Nile neuroinvasive disease (WNND). In 1995, a serosurvey on forest workers confirmed the presence WNV IgG antibodies in screened samples, indicating, circulation of WNV in Slovenia. WNV infection in humans are retrospectively investigated in all patients with meningitis/meningoencephalitis, negative for tick-borne encephalitis and >65 years of age. The first case of WNV infection was confirmed retrospectively in 2013 in a 79-year-old man with meningitis. A network for surveillance of mosquito-borne diseases was established in 2017 in Slovenia. Mosquitoes are sampled monthly in 36 areas with 165 locations from April to October and on 21 control locations from November to March. **Methods:** The mosquitoes were sampled using BG-Sentinel traps and CDC traps baited with CO2, which operated for 24 h. The mosquitoes were identified to the species level, pooled and tested for flavivirus presence by real-time RT-PCR. Patients' serum and cerebrospinal fluid were tested with ELISA for the presence of specific IgM/IgG antibodies. The detected virus was isolated and whole genome was obtained with next generation sequencing. **Results:** The number of captured and screened mosquitoes increased annually: 199 (2017), 3054 (2018), 7900 (2019), 28173 (2020) and 33720 (2021). The captured mosquitoes belonged to the genera: *Aedes*, *Ochlerotatus*, *Culex*, *Anopheles*, *Culiseta* and *Coquillettidia*. WNV was detected only in 2018 in a pool of *Culex* sp. mosquitoes. The same year, 3 patients with WNND were confirmed by detection of IgM antibodies in the CSF. In one of the patients, WNV RNA was detected in the urine sample. The whole genome of the WNV was sequenced from the patient's urine sample. The genome sequences confirmed that the Slovenian isolates from both mosquitoes and patient belong to WNV lineage 2 and are most similar to the Austrian isolates. **Conclusions:** Slovenia is not highly endemic for WNV, but the enhanced surveillance enabled us to recognize the virus circulation very early in 2018. The monitoring of mosquitoes as well as the knowledge of clinicians and public health officials regarding the virus' presence in our environment are necessary to introduce the preventive measures, for example screening of blood donations and real-time diagnosis of patients.

### Poster 340. A Risk Assessment of Human Brucellosis Infection in Shirak, Armenia

**A. Andryan**
National Center for Disease Control and Prevention, SNCO of the RA Ministry of Health, Shirak Marz, Armenia
**Background:** Brucellosis has been on the rise in Armenia for the last six years. It is endemic to Shirak marz and incurring a heavy economic burden. Within the last ten years outbreaks of brucellosis were recorded among animals in all 119 communities of Shirak with several cases among humans as well. We sought to evaluate the causes and epidemiological patterns of brucellosis in humans. Epidemiological, geographic, and clinical specifics of brucellosis will help to develop effective countermeasures. **Methods:** Between 2014 and 2020, we collected blood samples from 2,192 randomly selected residents of 121 communities in Shirak. We used Wright-Huddleston assays to test the samples against brucellosis. Participants with lab-confirmed brucellosis completed retrospective epidemiological questionnaires to determine associated risk factors; as a control, 1,992 healthy individuals also completed the questionnaire. We used ArcGIS 10.1 to develop risk maps. **Results:** During the study, 199 (9.1%) out of 2,192 cases in humans were confirmed to have brucellosis. Out of 199 positive cases, 112 reported direct contact with animals, with laboratory-confirmed brucellosis, and 34 reported consumption of unprocessed dairy products. Among respondents exposed to sick animals, the infection risk odds ratio was 4.6 times higher than that of those who did not have contact with agricultural animals. In 2014, 26 cases were diagnosed in 7 communities and in 2020, 96 cases in 23 communities. Most patients (74%) are 48-68 years old, 69% male, 31% female with 53.3% of patients suffering from severe articulations and high fever. **Conclusion:** In the last six years, there has been a growth trend in brucellosis due to increased nutritional factors from milk in the region (nutritional risk: RO=4.6). The number of cases increased by 27.1% and the number of communities by 30.4% in 2014-2020 compared to the increase in rearing of farm animals. These findings indicate that until effective brucellosis control measures are implemented in the Shirak Marz, the risk of infection will remain high, both inside and outside of known disease foci.

### Poster 341. Applying One Health Approach to Outbreak Investigation and Control in Human Brucellosis, Nakhon Ratchasima, Thailand, 2019

**C. Jitpeera**[1], K. Ekgatat[2]
[1]Division of Communicable Diseases, Department of Disease Control, Ministry of Public Health, Nonthaburi, Thailand, [2]National Institute of Animal Health, Nonthaburi, Thailand

**Background:** Brucellosis is a neglected zoonosis disease that affects humans, animals, and economics. There was a notification of two human brucellosis cases in two neighborhood sub-districts in Nakhon Ratchasima province in April 2019. An interdisciplinary team was conducted to control and give the recommendation to prevent the other event. **Methods:** Active case finding was performed among people who live in the same village of confirmed cases. Suspected human cases were defined as any person who had a history of exposure to animal farming, ingestion of undercooked meat or unpasteurized dairy products, and had fever with one of these following symptoms: headache, joint pain or back pain, fatigue, weight loss, and swelling or redness of testis, during January 1 to April 30, 2019. Blood from suspected cases was collected for Rose Bengal Test (RBT), Complement Fixation Test (CFT), and Indirect Enzyme-Linked Immunosorbent Assay (I-ELISA). Probable cases were defined as suspected cases that had positive RBT. Confirmed cases were defined as suspected cases that had hemoculture reported as *Brucella* spp. Serum from brucellosis susceptible animals was collected. The confirmed animal was an animal with either I-ELISA or CFT test positive. **Results:** There were 3-confirmed cases, 2-probable cases, and 1-suspected case among 113-screened people. All patients had a history of farm practice before illness and had close contact with goats and animal secretion without gloves. Most cases (66.7%) did not know brucellosis before the disease. We found positive animals in Bun Lung Subdistrict. The overall attack rate among screened cows and goats was 12.5% and 8%, respectively. **Conclusions:** The overall attack rate was 5%. We recommended educating healthcare and animal farmworkers about brucellosis to improve their awareness. Screening tests such as RBT should be applied for the suspected human case. Multi-sectoral collaboration, mainly information exchange, should be strengthened.

## Late-breakers

### Poster LB-65. A Sneak Peek into the Field Infodemiology Manual: Harnessing Real-Time Data for Infodemic Management

**N.M. Konne**[1], A. Ishizumi[2], E. Wilhelm[1], J. Kolis[1], H. Chiou[1], C. Voegeli[1], S. Machiri[3], C. Czerniak[2], R. Ludolph[2], T. Nguyen[2], D. Prybylski[1], T. Purnat[2]
[1]Global Immunization Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]World Health Organization (WHO) Department for Epidemic and Pandemic Preparedness and Prevention (EPP), Geneva, Switzerland, [3]African Field Epidemiology Network (AFENET), Kampala, Uganda
**Background:** An effective response to a pandemic like COVID-19 can be challenged by an infodemic, defined as an overabundance of information, including both accurate and inaccurate information that spreads rapidly. As the infodemic influences people's health beliefs and behaviors, it can pose a serious threat to vaccination and other pandemic mitigation efforts. Infodemics, including mis- and dis-information, fuel public health concerns and undermine outbreak responses, but public health capacity for their management has been limited. The Field Infodemiology Manual (FIM) addresses this urgent need by providing a framework and guide to monitor, detect, and manage infodemics. **Methods:** The FIM was developed by vaccine safety and demand experts convened by CDC in partnership with WHO**.** It is designed to meet the urgent needs of infodemic managers, health communicators, epidemiologists, and other key public health stakeholders at national and subnational levels – providing critical guidance for the design and implementation of field investigations about infodemics. **Results** The FIM provides the groundwork for infodemic management through several key concepts and methodologies. First, social listening is examined as a public health surveillance system and function of field investigation to help determine when to respond to public health threats. Second, methodologies for conducting social listening are described, starting with guiding principles for data collection and analysis to inform public health intervention, policies, and programs. Key challenges and evolving intervention approaches, as well as limitations and ethical considerations are then discussed. Finally, the FIM provides guidance on developing more effective communication strategies for broader public health impact. **Conclusions:** The FIM provides guidance for rapidly identifying and responding to information signals to help mitigate the impact of health mis- and dis-information. The FIM should be field-tested to assess its feasibility, usability, and adaptability in different types of public health events and emergencies.

### Poster LB-66. Assessment of the Adverse Events following Immunization (AEFI) Surveillance and Response System in Liberia

**K.S. Sadigh**[1,2], Z. Gilani[2], T. Yeabah[3], M. Dahlke[2], M. Kromah[4], M. Baysah[5], T. Kanter[6], R. Idowu[6], J. Gidudu[2], A. Clarke[4]
[1]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]African Field Epidemiology Network, Monrovia, Liberia, [4]Ministry of Health, Monrovia, Liberia, [5]World Health Organization, Monrovia, Liberia, [6]Centers for Disease Control and Prevention, Monrovia, Liberia

**Background:** Prompt identification, reporting, management, and investigation of adverse events following immunization (AEFI) are important to maintain public confidence in vaccination programs. In Liberia, a secretariat coordinates AEFI activities between the national regulatory authority, the Ministry of Health (MOH) and partners. Surveillance officers and clinicians collect data about reported AEFI. A causality assessment committee evaluates vaccine relatedness of serious AEFI or those posing a potential risk to the health of the recipient. We assessed the AEFI surveillance and response system in Liberia where four vaccines, including two COVID-19 vaccines, were recently introduced. **Methods:** The National AEFI Surveillance System Gap Identification questionnaire, a standardized assessment tool, was administered to MOH personnel and consultants in Liberia in September 2021 specifically for COVID-19 vaccines. We attended national AEFI data harmonization and causality assessment committee meetings. Consultations took place with key individuals from the CDC-Liberia country office, MOH, national regulatory authority, and World Health Organization. **Results:** As of September 8, 2021, a total of 58,481 adults had been vaccinated with either the Janssen or AstraZeneca COVID-19 vaccines, and 115 AEFI, including two serious AEFI, were reported to the MOH. Staffing and reporting mechanisms were effective at most levels, including national, county, district, and health facility, but weaknesses were identified at the community level. All AEFIs were investigated though causality was often deemed inconclusive because of lack of clinical information obtained by clinicians. Several electronic data systems exist for AEFI reporting, although no system fulfills all needs and interoperability between systems is limited. **Conclusions:** The existing infrastructure of Liberia's AEFI surveillance and response system allows for adequate investigation of reported AEFI. The system could be strengthened by augmenting community level reporting through direct involvement of community health assistants; optimizing the role of clinicians in acquiring clinical data; and improving the efficiency of electronic safety data systems.

### Poster LB-67. Clinical Outcomes of Previously Admitted COVID-19 Confirmed Patients in Ospital ng Makati: A 1-year Follow-Up Study

**C.A. Dorado**, Y.S.D. Gatchalian, M.L.G.V. David, C.R. Cipriano
Ospital ng Makati, Makati City, Philippines

**Background:** The long-term health consequences of COVID-19 remain largely unclear. Although there have been a number of cardiovascular events and persistent pulmonary symptoms observed in COVID-19, the long-term significance of it remains unknown. The aim of this study was to determine the clinical outcomes occurring within 1 year among previously admitted COVID-19 confirmed patients at Ospital ng Makati from July to September 2020. **Methods:** This prospective cross-sectional study was conducted from July 2021 to September 2021 at Ospital ng Makati. We enrolled adult patients who were previously admitted for confirmed COVID-19 regardless of severity. Eligible patients were contacted via telemedicine a year after their discharge. Information regarding events after COVID-19 admission were collected and confirmed with the hospital's electronic medical records. **Results:** Seventy-seven (77) previously admitted patients from July to September 2020 were successfully contacted. Fifty-nine (76.62%) consulted at the ER after discharge, while 23.3% did not have any ER consults or readmission. Patients seen at the ER were readmitted due to Acute Coronary Syndrome (7), Acute Stroke (6) and Pneumonia (27). Logistic regression was done to determine the probability of incidence of getting pneumonia after one year among patients previously admitted for COVID-19. Results revealed among those previously admitted for COVID confirmed, mild had a 23.07% probability of getting pneumonia within one year after discharge and those admitted for COVID severe had a 33.33% probability of contracting pneumonia. Results showed that only re-admissions for pneumonia within one-year post discharge had a significant association with previous admission for COVID-19 infection. There was no noted association between admission for Acute coronary syndrome and stroke. **Conclusion:** There is an association between previous COVID infection and readmission for pneumonia within one year of discharge. Patients previously admitted for COVID 19 infection classified as moderate to severe have a greater likelihood of getting readmitted for pneumonia one-year post discharge. There is no association between previous COVID infection and being readmitted for ACS and ischemic stroke within one year from discharge.

### Poster LB-68. Comparison of Clinical Presentation of Laboratory Confirmed Hospitalized Pediatric COVID-19 Cases Between Delta and Omicron Predominant Periods in Atlanta, Georgia

**G. Kallas**[1,2,3], A. Joseph[1,2,3], A. Patterson[1,3,4], J. Manning[1,2,3], C. Surell[1,2,3], W. Rich[1,2,3], K. Openo[1,2,3], E. Anderson[1,2,3]
[1]Georgia Emerging Infections Program, Decatur GA, USA, [2]Division of Infections Disease, School of Medicine, Emory University, Atlanta, GA, USA, [3]Atlanta Veterans Affairs Medical Center, Atlanta, GA, USA, [4]Foundation for Atlanta Veterans Education and Research, Decatur, GA, USA

**Background:** The Georgia Emerging Infections Program, funded by the Centers for Disease Control and Prevention, performs population-based surveillance of COVID-19 hospitalizations. We sought to describe the differences between children 0-17 years of age for COVID-related illness during the Delta (June 27- December 18, 2021) and Omicron (December 19, 2021 - February 28, 2022) predominant periods. **Methods:** Analysis was conducted using surveillance data of children residing in an eight-county catchment area hospitalized with a laboratory-confirmed SARS-CoV-2 infection within 14 days of admission. A COVID-related hospitalization was defined as a patient admitted to a hospital with acute respiratory symptoms or underlying pre-existing conditions exacerbated by COVID-19. Prevalence rates and disease severity (ICU admission, oxygen support) were compared between those who were admitted for a COVID-related versus a non-COVID-related reason during Delta and Omicron. **Results**: Out of 898 total pediatric hospitalizations, 594 were sampled for this study. The percentages of COVID-related hospitalizations among those admitted with a SARS-CoV-2 positive test was higher during Delta (71.7%) than the Omicron periods (61.1%) (RR: 1.17; 95% CI: 1.04, 1.32). This difference was not statistically significant in children 0-4 years (Delta = 82.8%; Omicron = 72.7%) (RR: 1.14, 95% CI: 0.99, 1.30) but was in children 5-17 years (Delta = 66.2%; Omicron = 45.7%) (RR: 1.45; 95% CI: 1.15, 1.82). Among patients with COVID-related hospitalization, the prevalence of ICU admission was 1.83 (95% CI: 1.21, 2.76) times greater and oxygen support was 2.13 (95% CI: 1.39, 3.27) times greater during Delta than Omicron. In comparison, among patients with non-COVID related hospitalization, the prevalence of ICU admission was not different (1.09; 95% CI: 0.66, 1.80) and oxygen support did not differ (0.58; 95% CI: 0.26, 1.25) between the two periods. **Conclusions:** The Delta period consisted of 388 admits and Omicron included 510 admits. Although the total number of hospitalizations increased, the percentage of children hospitalized with COVID-related symptoms decreased. Additional data are needed to understand how COVID-related admissions impact the economic burden felt by hospital systems as they change practices to combat new and emerging variants.

### Poster LB-69. Continued Low Circulation of Influenza in the 2021–22 Season in Temperate Northern India: Implications for Future

**P. Koul**, H. Mir
Sher-i-Kashmir Institute of Medical Sciences, Srinagar, J&K India
**Background:** We have previously demonstrated a Northern hemispherical (NH) pattern of seasonal influenza viral circulation in Kashmir, north India as against the predominantly Southern hemispherical (SH) circulation in the rest of the country. Since April 2020, concurrent with SARS CoV2 viral circulation, most countries have seen historically low seasonal influenza virus circulation but a resurgence was noted globally in the NH circulation regions in the 2021-22 season. Since data are scant from developing countries, we set out to study the contribution of influenza viral infection among cases of Severe Acute Respiratory Illness (SARI) in the flu seasons of 2020-21 and 2021-22 in Kashmir, India. **Methods:** Consenting patients hospitalized with SARI to a North Indian tertiary care hospital from November to March 2020-21 and 2021-22 were recruited and nasopharyngeal swabs tested for influenza viruses and their subtypes by real time RT PCR. **Results:** In both the flu seasons of 2020-21 and 2021-22, a negligible circulation of influenza virus was demonstrated. In 2020-21, 3 cases of influenza ((A/H3N2 = 2, B/Yamagata = 1) were detected among 1102 patient with SARI whereas in the 2021-22 season, 3 cases (all A/H3) were detected among 1041 patients. All the 3 in 2021-22 were admitted with an exacerbation of underlying COPD and other comorbidities included cardiovascular disease (n=2) and diabetes (n=1). Patients received standard of care and oseltamivir and had an uneventful recovery. None of the influenza positive patients had received prior influenza vaccination. **Conclusion:** In contrast to the previous influenza seasons, influenza viral circulation in temperate North India, continued to remain low in the 2020-21 and 2021-22 influenza seasons. These could be attributed to non-pharmaceutical interventions like travel restrictions, quarantine, social distancing, school/workplace closures, mask wearing and enhanced hand hygiene and would argue for routine adoption of those measures in future. Lack of exposure to influenza could, however, lower population immunity and increase the severity of large outbreaks upon a future global resurgence.

### Poster LB-70. COVID-19 Variant Dynamics among Individuals with Repeat Whole Genome Sequencing Tests in South Carolina

**S. Sarkar**, J. Scott, D. Drociuk, A. Smith, R. Radcliffe, L. Mitchell
South Carolina Department of Health and Environmental Control, Columbia, SC, USA
**Background:** With the rapid development of whole genome sequencing (WGS) for COVID-19 variant identification, use of WGS results by public health is also in development. To explore the ability of using WGS results, an analysis of a public health surveillance system, the South Carolina Infectious Disease and Outbreak Reporting Network (SCION), was performed. This assessed WGS reporting dynamics, including repeat WGS

testing, time between WGS testing, and proportion of individuals with results indicating multiple COVID-19 variants. **Methods:** WGS results with specimen collection dates between 27 Mar 2020, and 18 Mar 2022, were obtained. Lineages and sub-lineages of all variants were identified and classified by the main variant classification. Invalid and duplicate results were removed from analysis. Microsoft Access/Excel and SAS were used for descriptive analysis. **Results:** A total of 22,341 unique individuals (1.5% of total confirmed and probable cases reported to public health) yielded 22,671 WGS results; 293 (1.3%) individuals had multiple WGS results. Most variants were Delta (60.1%) and Omicron (33.6%). Among 293 individuals with multiple WGS results, the average time between specimen collection dates was 17.8 days, with most (95.6%) individuals having 2 WGS results and the remainder having up to 5 results. Differing variants were reported among 23 (7.3%) individuals, with an average time between collection dates of 153.3 days. Among these, 18 (78.3%) had prior infection with Delta, and subsequent infection with Omicron, and 2 (8.7%) had Alpha followed by Omicron infections. **Conclusion:** This analysis assessed the current state of variant dynamics among South Carolina COVID-19 cases with WGS results. A small percentage of confirmed and probable cases had WGS results. Although most individuals with multiple WGS results indicated the same variant, there is evidence that some were infected with different variants. A limitation to this analysis includes data potentially not being representative, due to sequencing performed on a limited number of specimens. Also, the Omicron surge may have contributed to the larger number of Omicron results and proportion of previous Delta results with subsequent Omicron results. These findings prompt further investigation into variant and time dynamics using surveillance data.

### Poster LB-71. Detection of NDM-producing *E. coli* from a Dog through Veterinary-Public Health Surveillance Partnership — Minnesota, 2022

**A.L. Beaudoin**[1], A. Gross[2], M. Anacker[2], J. Kaiyalethe[2], L. Kollmann[1], K. Little[3], J. Bender[3], M. Boyd[3], J. Granick[3], K. Olsen[4], K. Smith[1], R. Lynfield[1], P.M. Snippes Vagnone[2]
[1]Minnesota Department of Health, St. Paul, MN, USA, [2]Minnesota Department of Health Public Health Laboratory, St. Paul, MN, USA, [3]University of Minnesota Veterinary Medical Center, St. Paul, MN, USA, [4]University of Minnesota Veterinary Diagnostic Laboratory, St. Paul, MN, USA
**Background:** Carbapenemase-producing Enterobacterales (CPE) are of urgent public health concern, with resistance to most antibiotics, including carbapenems. Major U.S. risk factors for human CPE colonization or infection include exposure to antibiotics and healthcare, especially hospitalization abroad. Detection of infection, colonization, and transmission in veterinary settings is challenging. Awareness is low and, when conducted, antibiotic susceptibility testing panels are often too narrow for detection. **Methods:** In 2020, the Minnesota Department of Health (MDH) and University of Minnesota Veterinary Medical Center (VMC) initiated collaborative surveillance to detect CPE in companion animal patients. In February 2022, imipenem-resistant *E. coli* isolated from a canine post-surgical wound specimen at VMC was submitted to MDH for phenotypic (modified carbapenem inactivation method, mCIM) and molecular (polymerase chain reaction, PCR) carbapenemase testing. Animal CPE screening was conducted by PCR (Cepheid GeneXpert Carba-R) on rectal swab specimens. Positive specimens underwent culture and isolation. Genetic sequencing (Illumina MiSeq), multi-locus sequence typing, resistance gene identification, and single nucleotide polymorphism relatedness assessment followed. **Results:** The clinical *E. coli* isolate was mCIM-positive, with $bla_{\text{NDM-5}}$ detected. The dog lived in a congregate animal facility in a Midwest state, where screening of 27/72 (38%) dogs and 0/6 cats recovered $bla_{\text{NDM-5}}$. From 26 isolates, 3 *E. coli* sequence types (ST), ST361 (n=20), ST167 (n=5), and ST1136 (n=1) were identified, with high intra-type relatedness. Two dogs harbored ≥1 ST. $bla_{\text{NDM}}$ was detected in 3/8 (38%) staff-owned dogs screened offsite. In June 2021, the index dog arrived from the Middle East after trauma-related surgical implant failure, with ensuing surgery and continuous antibiotic exposure in the U.S. Other imported dogs live in the congregate animal facility. **Conclusions:** Canine CPE prevalence was high in a congregate animal facility, posing exposure risk to other animals and humans. Veterinary-public health collaboration is essential for CPE detection. Risk factors for dog colonization and transmission of CPE, including importation, healthcare, and antibiotic exposures, require investigation.

### Poster LB-72. Development of Multi-antigen Microspot Arrays Based Immunoassay for Differential and Definitive Diagnosis of Typhoid Fever

**K.A.L. Khan**, Z.S.A. Kader
Advanced Medical and Dental Institute, Universiti Sains Malaysia, MY
Typhoid fever is a food-borne and water-borne disease caused by *Salmonella* Typhi. It is a global, multi-organ infectious disease that is highly endemic in developing countries. Alarming reports of cases associated with travellers and domestic source have been reported in industrial countries. Therefore, typhoid fever is currently

a neglected re-emerging infectious disease as it does not discriminate developing or industrial countries. The symptoms are broad and often overlap with other infectious disease. Culture isolation is the gold standard diagnosis for typhoid. However, culture isolation such as blood culture takes 4 to 5 days and the results were affected by antibiotic treatment. On the other hand, currently available diagnostic kits are confined to detection of antibodies against limited antigens and hampered by significant degree of cross reactivity. Therefore, the available diagnostic kits lack sensitivity and specificity. Typhoid fever is treatable with antibiotics but there has been dismaying increase in antibiotic-resistance strains especially in developing countries such as Pakistan. Hence, accurate and timely diagnosis is necessary for early life saving treatment. The purpose of this research is to develop a simple, rapid and highly reliable, antigen microspot arrays-based immunoassay for detection of IgM, IgG and IgA antibody isotypes. The assay is developed by using differentially extracted antigens from *S.typhi* and *S.spp.* In this research, antigen microspot arrays-based immunoassay comprised of whole cell protein (WCP), cell surface protein(CSP) and surface depleted-whole cell protein(sdWCP) were derived from whole cell bacterial proteins of *S.typhi* and *S.spp*. The optimized concentration of antigens were used to develop immunoassay and was subjected to standard immunoassay procedure for detection of IgM, IgG and IgA antibody isotypes. The sensitivity, specificity, positive predictive value(PPV) and negative predictive value(NPV) of antigen microspot arrays-based immunoassay was determined by testing against panel of sera consisting of typhoid patient, vaccinated subject, healthy subject and other diseases. Antigen microspot arrays-based immunoassay produced very promising results for IgM, IgG and IgA antibody isotypes. The performance of the test was very encouraging with sensitivity of 100% for WCP and sdWCP and 92% for CSP. The specificity of the assay were 100% for all three antigens. The PPV of the assay for all three antigens were also 100%. The NPV varies against the antigen which include 100% for WCP and sdWCP and 91% for CSP. The antigen microspot arrays-based immunoassay produce accurate, reliable results with high sensitivity, specificity, PPV and NPV when tested against panel of sera consisting of typhoid patient, vaccinated subject, healthy subject and other diseases. Therefore, this assay is proven to be an important diagnostic tool for differential diagnosis of typhoid fever, vaccinated subjects, possible carriers, and subjects with febrile illness. To our knowledge, this is the first report to discuss the applications of antigen microspot arrays-based immunoassay for differential and definitive diagnosis of typhoid fever. The development of this novel antigen microspot arrays-based immunoassay serves as simple, rapid diagnostic tool for early detection of typhoid fever in endemic and non-endemic areas. On the other hand, this assay can also be used as a tool in vaccine evaluation study and seroepidemiological survey for typhoid prevalence study. Patent has also been filed for this assay (Application number/MyIPO: PI2021004913).

### Poster LB-73. Distribution Expansion of Dengue Vectors and Climate Change in India

**S.S.A. Hussain, R.C. Dhiman**
ICMR-National Institute of Malaria Research, Dwarka, New Delhi, India
**Background:** India has witnessed a five-fold increase in dengue incidence in the past decade. However, the nation-wide distribution of dengue vectors, and the impacts of climate change are not known. In this study, species distribution modelling was used to predict the baseline and future distribution of Aedine vectors in India on the basis of biologically relevant climatic indicators. **Methods:** Known occurrences of Aedes aegypti and Aedes albopictus were obtained from the Global Biodiversity Information Facility database and previous literature. Bio-climatic variables were used as the potential predictors of vector distribution. After eliminating collinear and low contributing predictors, the baseline and future prevalence of Aedes aegypti and Aedes albopictus was determined, under three Representative Concentration Pathway scenarios (RCP 2.6, RCP 4.5 and RCP 8.5), using the MaxEnt species distribution model. **Results:** *Aedes aegypti* was found prevalent in most parts of the southern peninsula, the eastern coastline, northeastern states and the northern plains. In contrast, Aedes albopictus has localized distribution along the eastern and western coastlines, northeastern states and in the lower Himalayas. Under future scenarios of climate change, *Aedes aegypti* is projected to expand into unsuitable regions of the Thar desert, whereas *Aedes albopictus* is projected to expand to the upper and trans Himalaya regions of the north. **Conclusions:** Overall, the results provide a reliable assessment of vectors prevalence in most parts of the country that can be used to guide surveillance efforts, despite minor disagreements with dengue incidence in Rajasthan and the northeast, possibly due to behavioural practices and differences in sampling efforts.

### Poster LB-74. Early Implementation of Truenat™ MTB and MTB-RIF Dx Assays at the Peripheral Level in Zimbabwe: Challenges and Lessons Learned

**E. Reisdorf**[1], P. Nzombe[2], H. Mutunzi[2], T. Sakubani[3], R. Simbi[3], C. Sandy[3], G. Kahenya[1], L. Cobb[1], W. Van Gemert[4], M. Moore[1]

[1]Infectious Disease Detection and Surveillance (IDDS), Rockville, MD, USA, [2]Infectious Disease Detection and Surveillance (IDDS), Harare, Zimbabwe, [3]Zimbabwe Ministry of Health and Child Care, Harare, Zimbabwe, [4]Stop TB Partnership, Geneva, Switzerland
**Background:** Truenat™ MTB and MTB-RIF Dx assays are being implemented for the first time in Zimbabwe and placed in peripheral laboratories to decentralize and provide rapid molecular diagnostic testing near the point of care. End-users at each of 20 sites were trained and completed a verification panel to demonstrate proficiency. **Methods**: Implementation of Truenat™ testing started in December 2021. Feedback on implementation was solicited from the end users at a refresher Truenat™ training workshop in March 2022. Nineteen of twenty (95%) end users participated and provided feedback. In addition, key performance indicator (KPI) data was collected monthly from all sites to monitor usage and performance. **Results:** The most frequent challenges identified by the end users included poor sample quality, need for additional hands-on training, inability to attend external quality assessment (EQA) training due to sporadic internet connection, prolonged power outages, and low number of samples received. A key observation from site visits was a gap in quality management system awareness as there was no evidence of standard operating procedures, maintenance logs, or quality improvement records. KPI data showed that despite the key challenges, sites reported testing data monthly. Performance improved over time as demonstrated by decreasing error/invalid rates from 12.5% in December to 3.1% in February while the number of tests performed steadily increased. **Conclusions**: Implementation of Truenat™ at the peripheral level in Zimbabwe has been successful despite the key challenges. KPI data demonstrated performance improvement over time. Lessons learned included having: (1) a trained group of "superusers" is essential to support implementation of a quality management system assist with EQA reporting; and (2) end-user in-person refresher training including good laboratory practices, EQA and quality management system sensitization; and (3) solar charging solutions; and (4) demand creation workshops and sample collection training to local health care workers and the community to increase awareness, utilization and improve sample quality.

### Poster LB-75. Evaluation of COVID-19 Cases by Vaccination Status and Lineage, New York, March 2021-January 2022

**K. Engesser**[1], R. Hoelzl[1], K. Burzlaff[1], A. Russell[2], A. Muse[1]
[1]New York State Department of Health (NYSDOH) Emerging Infections Program, Albany, NY, USA, [2]NYSDOH Wadsworth Center Virology Laboratory, Albany, NY, USA
**Background**: A sentinel surveillance system allowed for epidemiologic and molecular characterization of SARS-CoV-2 infection among vaccinated and unvaccinated individuals. **Methods**: Eligible COVID-19 cases were selected from a random sample of positive specimens that had been tested by real-time polymerase chain reaction (RT-PCR) from 3/1/2021-1/31/2022 at a New York State academic medical center with a 25-county service area and had been submitted to the state public health lab for SARS-CoV-2 whole genome sequencing. Using the statewide immunization information system, fully-vaccinated cases were defined as adults aged ≥18 years who completed an FDA-authorized COVID-19 primary vaccine series ≥ 14 days before a positive RT-PCR. Partially vaccinated or previously infected COVID-19 cases were excluded. Vaccinated cases were matched to at least 1 unvaccinated case (control) by week of positive specimen collection. Relative risk (RR) and odds ratios (OR) with 95% CIs were calculated to compare patient demographics, underlying conditions, symptomatic status, disease severity and outcome by vaccination status and lineage. **Results**: Of 1,332 SARS-CoV-2 positive patients sampled during the study period, 956 (72%) met inclusion criteria with 356 cases matched to 391 controls. Lineage data are currently available for 666 (89%) enrolled cases and controls with the majority attributed to Delta (71.5%) and Omicron (19.1%). Compared to controls, vaccinated cases were more likely to be residents of long-term care facilities (RR=1.61, 1.28-2.02), and less likely to have underlying conditions (RR=0.80, 0.69-0.92) and identify as non-Hispanic Black when compared to non-Hispanic White (RR=0.68, 0.53-0.87). Cases had a decreased likelihood of COVID-19 symptoms (OR=0.65, 0.44-0.95), inpatient admission (OR=0.39, 0.29-0.52), and mortality (OR=0.51, 0.29-0.86) when compared to controls, irrespective of lineage. **Conclusions:** The study findings demonstrate continued vaccination protection against hospitalization and other severe outcomes, which persisted regardless of lineage. Communication about vaccine benefits continues to be critical to reducing COVID-19-related morbidity and mortality.

### Poster LB-76. Formative Evaluation of Hand Hygiene in Public Guatemalan Elementary Schools in the Context of the COVID-19 Pandemic

**M. Pieters**[1], N. Fahsen[1], C. Cordon-Rosales[1], R. Quezada[1], J. Paniagua[1], C. Pratt[2], C. Craig[2], T. Brown[2], K. McDavid[2], E. Zielinski-Gutierrez[3], M. Lozier[2], A. Gomez[1]

[1]Center for Health Studies, Universidad del Valle de Guatemala, Guatemala City, Guatemala, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Centers for Disease Control and Prevention, Guatemala City, Guatemala
**Background:** Hand hygiene is important to prevent the spread of infectious diseases, including COVID-19. Our study evaluates the conditions for hand hygiene practices in elementary schools to inform the design of an intervention and ensure a safe return to classes in the context of COVID-19. **Methods:** We conducted a formative evaluation of hand hygiene in six public elementary schools in three municipalities of Quetzaltenango, Guatemala from October 13 – November 15, 2021. Baseline assessments evaluated the infrastructure for hand hygiene practices (HHP). In-depth interviews with 12 teachers explored HHP, perceptions during COVID-19, and challenges for improvement. Water quality was assessed by measuring chlorine, and when no chlorine was found, a sample was taken to look for total coliforms and *E.coli*. **Results:** All six schools had access to water from a municipal source, but four schools reported water was not always available due to mechanical problems or shortages. Although all schools had handwashing stations, only 43.1% of the stations had soap available; one school lacked soap at all stations. All schools had hand sanitizer and two reported insufficient sanitizer. During interviews, respondents described insufficient hand hygiene stations with many located in a single area. Some respondents preferred using soap and water over hand sanitizer, while others were comfortable using both. Lack of soap and hand sanitizer supply due to budgetary constraints were mentioned as main challenges to HHP. Free chlorine residual was not detected in any school. One school's water tested positive for *E.coli*. **Conclusions:** Based on these data, an intervention to improve hand hygiene to mitigate the risk of COVID-19 transmission to support a safe return to school would include: (1) increasing the number of handwashing stations and distributing them throughout the school (2) establishing steady supplies of soap and hand sanitizer, and (3) use of chlorinated water for handwashing.

### Poster LB-77. Immune Responses to Group 2 Seasonal and Pandemic Influenzas

**H.J. Klim**[1,2], J.S. Bolton[3,4], L. Stolle[4], C.P. Thompson[4]
[1]Wellcome Centre for Human Genetics and Pandemic Sciences Institute, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK, [2]The Future of Humanity Institute, University of Oxford, Oxford, UK, [3]The Jenner Institute, University of Oxford, Oxford, UK, [4]Warwick Medical School, University of Warwick, Coventry, UK
**Background:** Influenza A viruses (IAV) pose a threat to global health due to often ineffective seasonal vaccines and the emergence of pandemic strains from non-human animals. To address these concerns, there has been a substantial push towards vaccines which will confer protection against a broader number of IAV strains than current seasonal vaccines. **Methods:** This study presents an evolutionary analysis of two influenza subtypes (H3 and H7) and identifies epitopes which may be useful as broadly protective vaccine targets. Sequence variability was compared with an analysis of antibody binding sites through mean hamming distance to define so-called epitopes of limited variability (ELVs). This analysis was followed by pseudotyped microneutralization assays involving six H3N2 viruses on 672 donor samples. **Results:** The structural analysis yielded four novel epitopes of limited variability, including a potentially shared antibody binding site between in H3 and H7 HAs. These epitopes may prove useful as vaccine targets for a broadly protective Group 2 IAV vaccine. The microneutralization assays demonstrate that there is an association between the year of primary IAV exposure and neutralizing ability, which may be caused by the phenomenon of immune imprinting. **Conclusions:** The proposed method of computationally defining ELVs can highlight previously unnoticed evolutionary patterns in IAV. When paired with serological studies, this in silico method will improve our ability to identify cross-reactivity between IAV subtypes and design more broadly protective vaccines.

### Poster LB-78. Introducing Foresight for Strengthening Pandemic and Epidemic Preparedness: Future Scenario Development Process and Methodology

**N. Shindo**[1], M.M. Mathis[1], A. Alexiou[2], J. Hargrave[2], Z. Loncar[1], M.L. Lim[1], S. Briand[1]
[1]World Health Organization, Geneva, GE, Switzerland, [2]Arup, London, United Kingdom
**Background:** The COVID-19 pandemic has shown the complex nature of pandemics and epidemics that humanity collectively face in the 21st century. Foresight thinking and methodologies are increasingly used in the business world, contributing to better performance of "future-ready" firms. This novel approach augments the prevailing retrospective approach by creating space for scenario-based strategic dialogue. **Methods:** The first step in the scenario building process involved investigation of the key components of the system of change, to identify critical determinants of epidemics and pandemics. The second step involved agreeing on the time horizon within which to explore the future. To contribute to immediately actionable practical ways forward, a relatively short time horizon (3-5 years) was set. For the third step of the process, the Social, Technological Economic, Environmental, Political

(STEEP) framework was applied to identify high-impact trends. Next, a comprehensive desk analysis of the trends was conducted, coupled with brainstorming and expert review sessions to agree on and refine key factors. Key factors are drivers that actively impact the future shape of the system under investigation, and they provided the baseline structure for the development of the 'morphological box,' which is a Foresight method to produce scenarios based on combinations of key factor projections. Logic-based consistency analysis and decisions are made across all combinations of projections using a software tool. **Results:** Critical determinants of epidemic and pandemics were identified and grouped into three categories: Pathogen and host characteristics, Public health and social measures, and Contextual factors. Using the STEEP framework, 25 high-impact trends were identified. Analysis of the key components of the system and a review of the trends resulted in an initial set of key factors across the three categories. The key factors were validated and refined in two workshop sessions across and beyond WHO involving multi-disciplinary expertise. A final set of 20 key factors was obtained. A morphological box was populated with plausible, mutually exclusive projections under each key factor. Among the numerous plausible combinations resulting from the software-based analysis, four combinations were chosen which best reflect the research, expert conversations, and outcomes to date. **Conclusions**: The four scenarios, the final combinations of projections that were selected, provided a set of alternative, consistent, and plausible pathways into the future that could be used as a tool for strategic dialogue.

### Poster LB-79. Isepamicin: Re-evaluation of Older but "Forgotten" Antimicrobial Agents

**H. Gautam**
Department of Microbiology, All India Institute of Medical Sciences (AIIMS) New Delhi, India
**Background:** Isepamicin is a semisynthetic derivative of gentamicin B and has the advantage that it is less affected by aminoglycoside-inactivating enzymes. Isepamicin has been introduced in clinical practice in 1988 in Japan. It has been available in only a limited number of countries. However, its interpretative criteria are not included in CLSI/EUCAST/FDA. Breakpoints for isepamicin have been proposed by the Comité de l'Antibiogramme de la Société Française de Microbiologie (CA-SFM). **Methods:** The antimicrobial activity of isepamicin was compared to other aminoglycoside antibiotics in 42 MDR *Acinetobacter baumannii* clinical isolates. The susceptibility was determined using broth microdilution and interpreted as per CLSI guidelines for amikacin and gentamicin while the guidelines from CA-SFM were used to interpret isepamicin susceptibility. Aminoglycoside modifying enzyme (AME) genes, aminoglycoside acetyltransferases (AACs), aminoglycoside phosphotransferases (APHs), and aminoglycoside nucleotidyltransferases (ANTs) were investigated by multiplex PCR method. **Results:** The antimicrobial susceptibility to isepamicin, gentamicin, and amikacin was found to be 50%, 35.7% and 30.9%, respectively. Amongst the 21 strains susceptible to isepamicin, only 8 were susceptible to gentamicin and 7 were susceptible to amikacin. AME genes were possessed by 22 (52.4%) of the total 42 strains. The most prevalent aminoglycoside modifying mechanism was AACs (12/42) {aac(6')1b in 10 strains and aac(3)-I in two strains} followed by ANTs ( 11/42) {ant(3')-I} and APHs (4/42) {aph(3')-I}. Out of 21 isepamicin susceptible strains, 9 were positive for AME genes, otherwise being susceptible phenotypically. **Conclusion:** In the present era of emerging antimicrobial resistance, isepamicin could be a preferable therapeutic option for the infections caused by MDR and XDR strains. Although the clinical use of aminoglycosides comes with significant issues but in the scenario of increased drug resistance, the older alternative like isepamicin could come to a rescue, more so, literature says that its less nephrotoxic and ototoxic than other aminoglycosides.

### Poster LB-80. One Health Genomic Surveillance and Response to a University-based Outbreak of the Delta AY.25 Lineage, Arizona, September – December 2021

**H.D. Yaglom**[1+], M. Maurer[2,+], B. Collins[2], J. Hojnacki[2], J. Monroy-Nieto[1], T. Martins[3], S. Packard[2], J.R. Bowers[1], D. Erickson[4], K. Simmons[4], B. Brock[4], J. Cocking[4], S. Smith[4], C. Hepp[4], D.M. Engelthaler[1]
[1]Translational Genomics Research Institute, Flagstaff, AZ, USA, [2]Coconino County Health and Human Services, Flagstaff, AZ, USA, [3]Arizona Department of Health Services, Phoenix, AZ, USA, [4]Northern Arizona University, Flagstaff, AZ, USA, [+]co-first authors
**Background:** Large scale outbreaks of the SARS-CoV-2 (SCV2) Delta variant have occurred in numerous settings. Delta was the predominate variant circulating in Arizona throughout the latter half of 2021, with AY.25 (a well-established Delta sub-lineage) comprising approximately 10% of sequenced genomes. An outbreak of an AY.25 clone, associated with a university campus, was initially identified through routine phylogenetic analyses. Sequencing of wastewater surveillance samples, which had been in place across the university to provide an early warning for COVID19 outbreaks, provided retrospective evidence of the presence of the outbreak strain prior to the initial identified cases. **Methods:** Genomic sequencing of SCV2 PCR positive samples were performed by several laboratories and genomes uploaded to GISAID were utilized to build phylogenies. Genomic data for the distinct

outbreak subclade was shared with local public health partners. Epidemiologic and exposure information routinely gathered through contact tracing was collated and matched with the available genomes. Wastewater collected twice weekly from sites across campus was tested for SCV2 by RT-qPCR, and subsequently sequenced to identify variants. **Results:** The earliest case for which a genome was produced was September 2nd (10 days after the fall semester began). Majority of cases (70%) occurred among first-year undergraduate students living on and off campus, with on-campus students residing largely in three freshman dormitories. The AY.25 outbreak strain was detected in nine wastewater samples collected between August 19th through September 23rd; SCV22 in these samples contained a cladedefining mutation (C18840T), which was identified in multiple wastewater samples prior to and following the identification of the cluster. Several large on and off campus gatherings, including Greek life parties during September were identified as a common source of exposure. **Conclusions**: This AY.25 outbreak was likely seeded by the extensive interactions of students on and offcampus and congregation in dormitories, followed by secondary transmission to the community. The university and public health department worked together to facilitate timely reporting of cases, identification of close contacts, and other necessary response strategies. The university implemented mitigation testing strategies, driven by wastewater surveillance results and when cases in any given dormitory reached >1% of the population living in that building. The emergence of new SCV22 variants and the potential threat of other infectious disease outbreaks on university campuses presents the need for One Health data driven, targeted interventions.

### Poster LB-81. Qatar's National Response to COVID-19 Pandemic – A Retrospective Study

**S. Jaffrey**[1], D. Bansal[1], M. Nour[1], H. Al-Romaihi[1], M.H.J. Al-Thani[1], E.A.B. Abd Farag[1], A.M. Al Khal[2]
[1]Health Protection & Communicable Diseases Division, Ministry of Public Health, Doha, Qatar, [2]Hamad Medical Corporation, Doha, Qatar

**Background**: The alarming rate at which the COVID-19 spread across the world had a palpable impact upon all countries, including Qatar. The rapid transmission of the disease called for a decisive and practical response to successfully manage and control its spread given that it caused economic stagnation, increased burden on health care, and impeded global travel. **Methods**: This study utilized mixed methods design, using retrospective internal data along with qualitative interviews from healthcare professionals from Ministry of Public Health of Qatar from different sectors and profession tiers. **Results**: Qatar was quick to enact viable measures against COVID-19 using epidemiological data and followed WHO recommendations on top of instituting protocols specific to the locale to curb the spread of the disease. The country restricted nonessential travel and implemented strict face-masks policy, and hygiene practices. Qatar government developed Etheraz, a health status monitoring mobile application to control movements of those who were COVID-19 positive, SAVES, an electronic surveillance system, was setup in record time to track COVID-19 cases. Laboratory and hospital capacities were increased to accommodate the increasing number of cases. Staff recruitment across all sectors saw exponential increase to address high number of calls and cases, along with getting additional support from volunteers. Qatar Red Crescent and QFFD along with other partners sent aid to over 182 countries to help their local efforts to control the spread of COVID-19. **Conclusions**: Qatar performed with exceptional capacity given the immediacy of the COVID-19 pandemic across the globe. This adverse event served to galvanize the country into strengthening health defenses and enhance quality of life for its residents. Due to COVID-19, Qatar is well equipped to tackle any future instances of communicable disease pandemic.

### Poster LB-82. Rapid Detection of SARS-CoV-2 Mutations of Interest with a High-throughput and Cost-efficient Workflow

**M. Veling**[1], P. Xie[1], G. Filippov[1], E. Dougherty[1], Y. Sun[1], T. Perroud[1], Y. Tong[1]
[1]PerkinElmer Health Science Inc., Waltham, MA, USA

**Background:** Tracking the emergences of SARS-CoV-2 variants is critical for public health decision making. While many of the mutations have little clinical impact on the virus, some mutations can change disease progression. In particular, mutations in the Spike (S) protein have been found to impact viral transmissibility, susceptibility to immune response, and potential treatments. The variants can be identified by the presence of certain mutations of interest (MOIs), which have known or potential clinical relevance. Here, we present a series of PerkinElmer's PKamp™ VariantDetect™ assays/kits to detect mutations which have been identified in certain SARS-CoV-2 variants with high sensitivity and specificity in around 2 hrs. **Method:** More than eleven multiplexed qualitative real-time RT-PCR assays/kits were developed and evaluated with quantified synthetic SARS-CoV-2 variant RNAs using the same PCR run program with FAM/VIC/ROX/Cy5 as detectors. Each assay, based on mutation-specific TaqMan probes, provides combination detection of up to 3 MOIs together with *N* and *ORF1ab* genes as reference in a single reaction. Total twelve MOIs (69-70Del, K417N/T, L452R/Q, E484K/A/Q, Q493R, N501Y, P681H/R) in

the *S* gene were evaluated. **Results:** All evaluated combinations/kits showed high specificity (no cross-talking with 5E5 copies/reaction for wild type or other variant types) and high sensitivity (ranging from 40 to 1000 copies/reaction, respectively). Some kits can detect certain mutations with presence/absence difference in Delta and Omicron variant. Example kits are L452R/E484K/E484Q, L452R/P681H/P681R, K417N/K417T/69-70Del, K417T/K417N/P681R, L452R/E484K/Q493R, L452R/E484K/69-70Del, E484K/E484Q/E484A. The robust performance of the kits has been demonstrated in three publications from investigators. 104 samples from clinical settings were evaluated with kit L452R/E484K/E484Q and K417T/K417N/P681R and showed >98.5% agreement with NGS results. **Conclusions:** PKamp™ VariantDetect™ SARS-CoV-2 real-time RT-PCR assay is a cost-efficient fast solution with high sensitivity and flexibility for the establishment of a surveillance panel to monitor circulating variants with clinically relevant mutations in a certain region and period. For research use only. Not for use in diagnostic procedures.

### Poster LB-83. Seroprevalence of Toxocariasis in Kuwait and Its Association with Eosinophilia

**M.A. Al-Awadhi**[1], W. Jamal[1,2]
[1]Research Core Facility, Faculty of Medicine, Kuwait University, Kuwait City, Kuwait, [2]Department of Microbiology, Faculty of Medicine, Kuwait University, Kuwait City, Kuwait

**Background:** Toxocariasis is a worldwide helminthic infection which is transmitted from infected dogs and cats and has been associated with peripheral blood eosinophilia. The CDC placed toxocariasis among the top 6 parasitic diseases in the USA which are prioritized for public health action. To our knowledge, there are no reports on human toxocariasis in Kuwait or other GCC countries. This study aims at investigating the seroprevalence of toxocariasis among allergy patients in Kuwait and its association with eosinophilia, age, gender, nationality, and history of direct contact with dogs or cats. **Methods:** From September to December 2021, the laboratory records of allergy patients referred to Al-Rashed Allergy Hospital, Kuwait were reviewed and a total of 400 serum samples were selected: 200 samples from patients with normal eosinophil count (<500 cells/µl) and 200 samples from patients with eosinophilia (>500 cells/µl). The sera were screened for anti-*Toxocara canis* IgG antibodies via antibody enzyme-linked immunosorbent assay (Ab-ELISA). The seropositive patients were asked about their history of direct contact with dogs or cats. Statistical analyses were performed using Microsoft Excel® Analysis ToolPak software. **Results:** Toxocariasis seropositivity was detected in 10 out of 400 (2.5%) allergy patients. Five patients had eosinophilia while 5 had normal eosinophil count. There was no difference in mean age or gender between *Toxocara*-seropositive and seronegative patients ($P>0.05$). The seroprevalence rate was lower-than-expected among Kuwaiti patients (2/307, 0.7%) in comparison with non-Kuwaiti patients (8/57, 14.0%) ($\chi 2 = 33.603$, $df = 1$, $P<0.001$) who originated from endemic South/Southeast Asian countries. Seven out of 8 (87.5%) seropositive patients had a history of direct contact with cats, dogs, or both. **Conclusions:** The seroprevalence rate of toxocariasis in Kuwait was 2.5%. Raising awareness and routine deworming of domestic dogs and cats remain crucial for toxocariasis prevention.

### Poster LB-84. Towards Global Equity in Accessing Scarce Medical Products in the Event of Epidemics or Pandemics

**I. Ghiga**, S. Briand
Epidemic and Pandemic Preparedness and Prevention Preparedness Division, WHO Emergency Programme, Geneva, Switzerland

**Background:** Crisis's advantage is that they make you think afresh and forsake preconceptions. The one we are currently living highlighted major global inequities in accessing scarce medical products. Past solutions to access vaccines, therapeutics and diagnostics during a pandemic included donation-based approaches and proved deficient in ensuring sufficient quantities or timeliness in access for beneficiaries. Furthermore, other non-COVID-19 pandemic preparedness access and benefits sharing mechanisms were not readily transferable due to their pathogen-specific applicability. With the stark reminder that no country can unilaterally end the acute phase of a pandemic and that past global mechanisms are not yet fully effective, it has become an urgent imperative for WHO and partners to develop novel solutions in this space. **Methods:** Scoping review including examination of existing access mechanisms such as PIP and COVAX, to create a typology matrix to help design access to scarce medical products mechanisms and articulate a set of core criterions for related evaluation frameworks. **Results:** A typology matrix to create different access and benefits sharing mechanisms is developed. This is anchored in interventions to overcome sources of inequity along major blocks of the health research and innovation pathway for medical products from basic research up to delivery. Considering these, a three-dimensional typology matrix to help design access mechanisms is articulated along the following pillars: *i) access* (type and reach /beneficiaries), *ii) benefits* (type and source), and *iii) funding mechanism*. Different models for access mechanisms can be designed by combining the proposed features, each with different merits. To tailor evaluation frameworks, core criterion questions are

proposed. **Conclusions:** This typology matrix represents foundational work to meet the urgency of finding mechanisms adapted to the 21st century challenges, and the growing risk of more pandemics. In addition, this endeavor facilitates related discussion on addressing perennial challenges such as mechanisms' financing, resolving tensions between different solutions and minimizing power asymmetries that may lead to inequalities. However, solutions need to be not only built but also be constantly tendered to in the interpandemic period.

### Poster LB-85. Universal COVID-19 Vaccines: Buccal Films and Microneedle Patch based Novel Subunit Polymer-Matrix Vaccine

**S.R. Patil**, S. Vijayanand, D.J. Joshi, I.J. Menon, M.J. D'Souza
Mercer University, Vaccine Nanotechnology Laboratory, Center of Drug Delivery Research, College of Pharmacy, Atlanta, GA, USA
**Background:** COVID-19 remains a global threat, reflecting importance of frequent vaccination. Our vaccine approaches address the need for globally available, non-invasive universal vaccine against COVID-19. We utilized critical regions of non-infectious proteins (spike and nucleoprotein) conserved in mutating strains of SARS-CoV-2 as antigens. Polymer-based microparticles avoid cold chain storage, a major drawback of current vaccines limiting their availability worldwide. Moreover, buccal dissolving film (BDFs) and microneedles (MNs) overcome vaccine hesitancy by eliminating painful intramuscular route. Additionally, they induce systemic and mucosal immunity using specialized immune cells. **Methods:** Antigens and adjuvants (Alum + MF59+CpG) were formulated as MPs using poly-(lactic-co-glycolic acid) and incorporated in polymers to formulate BDFs and MNs. MPs were characterized and assessed for induction of nitrite, autophagosomes, and co-expression of antigen-presenting molecules with co-stimulatory molecules (MHC I-CD86, MHC II-CD-40) in antigen-presenting cells. Mice were immunized with prime and booster doses. Mice sera were assessed using ELISA for presence of spike and nucleoprotein specific IgG, IgG subtypes, and IgA. Post-sacrifice secondary lymphoid organs were isolated and evaluated for presence of helper, cytotoxic T cells with cytokine secreting cells using flow cytometer. **Results:** We successfully formulated and characterized BDFs and MNs with MPs. In vitro, MPs significantly (**$p<0.001$) induced nitrite, autophagosomes, MHC I-CD86, MHC II-CD-40 indicating presence of innate and adaptive immune markers. Immunization induced significantly higher (****$p<0.0001$) humoral, mucosal responses demonstrated by serum antibody titers of IgG, IgG subtypes, and IgA. Cellular immune response was demonstrated by presence of significantly (*$p<0.05$) higher levels of helper, cytotoxic T cells, IL-4 and IFN- γ secreting cells providing viral clearance. **Conclusion:** Buccal film and microneedle-based vaccines were able to induce balanced Th1 and Th2 systemic and mucosal immune responses. These highly patient-compliant vaccines could enhance the feasibility of vaccine roll-out and mass immunization worldwide, protecting against mutating strains of SARS-CoV-2.

## Wednesday, August 10, 2022

## Poster Session 1 Abstracts

**12:30 PM – 1:30 PM**

**Grand Hall**

## COVID-19 and SARS-CoV-2

### Poster 342. Pattern of Antibiotic Dispensing at Pharmacies during the COVID-19 Pandemic in Bangladesh according to the WHO Access, Watch, Reserve (AWaRe) classification

**M.A. Islam**[1], Z. Akhtar[1], M.Z. Hassan[1,2], S. Chowdhury[1], M.M. Rashid[1], M.A. Aleem[1,3], P.K. Ghosh[1], S. Mah-E-Muneer [1], S. Parveen[1], M.K. Ahmmed[1], M.S. Ahmed[1], A.K. Basher[1], A. Palit[1], M.A.A.J. Biswas[1], Z. Khan[4], K. Islam[4], N. Debnath[4], M. Rahman[1,5], F. Chowdhury[1]
[1]International Centre for Diarrhoeal Disease Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]University of Oxford, Oxford, UK, [3]University of New South Wales, Sydney, Australia, [4]Fleming Fund Country Grant to Bangladesh, Dhaka, Bangladesh, [5]Global Health Development, EMPHNET, Dhaka, Bangladesh
**Background:** Antibiotic usage surged globally during the COVID-19 pandemic. We described the pattern of antibiotic dispensing at pharmacies in Bangladesh according to the 2019 WHO Access, Watch, Reserve (AWaRe) antibiotic classification to aid pharmacy-targeted national antibiotic stewardship interventions. **Methods:** From January 27 – July 10, 2021, we conducted a point prevalence survey at randomly selected 112 urban and 16 rural pharmacies across Bangladesh. We conducted interviews among randomly selected customers aged >18 years who

purchased medicines from the participating pharmacies during 10 AM to 10 PM on the day of the survey. We collected data on customer's demographics and medicines dispensed by the drug sellers; and performed descriptive analysis to describe the pattern of antibiotic dispensing. **Results:** We interviewed a total of 2,686 customers; of them, 79% were male, and their median age was 38 years (IQR: 29 – 50 years). Of all customers, 22% (580) purchased a total of 642 courses of antibiotics. Twenty percent (481/2,351) customers in urban and 30% (99/335) in rural pharmacies purchased antibiotics. Over half of the customers (52%; 304/580) purchased antibiotics without registered physicians' prescription. Of the 642 purchased antibiotics, Watch-group accounted for the majority (54%; 344), followed by Access-group (36%; 234) and Reserve-group (10%; 64) as per the WHO AWaRe classification. Those who purchased Access-group antibiotics, 59% of them purchased without a registered physician's prescription, and the proportion was 47% for Watch-group and 44% for Reserve-group. Access-group, Watch-group and Reserve-group antibiotics dispensing accounted for 36%, 53% and 11% in urban pharmacies and 41%, 54% and 5% in rural pharmacies respectively. **Conclusions:** Watch-group antibiotics accounted for majority of the dispensed antibiotics, and nearly half of the antibiotics were dispensed without a registered physician's prescription. Our study findings underscore the need for implementing strict policy and pharmacy-targeted antibiotic stewardship interventions in Bangladesh. Integration of the WHO AWaRe classification into the national action plan on antimicrobial resistance (AMR) in Bangladesh and emphasizing mass awareness might contribute to mitigate AMR in the country.

### Poster 343. Healthcare Utilization and Diagnoses in COVID-19 Patients Followed for Up to One Year

**A.L. Fitzpatrick**[1], A.E. Fohner[1], T.E. West[1], N. Sotoodehnia[1], N. Gentile[1], C. Senter[1], S. Yarborough[1], J. Bertolli[2], J.M.S. Lin[2], E. Unger[2], Q. Vu[2]
[1]University of Washington, Seattle, WA, USA, [2] Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: The burden of persisting symptoms in COVID-19 patients has been reported to range from 22 to 51% depending on time since onset. Understanding patterns of healthcare utilization following acute SARS-CoV-2 infection is needed to inform clinical practice and healthcare resource planning. Our objective was to describe the post-COVID utilization of healthcare services and associated diagnoses of patients followed for up to one year. **Methods:** Data from the electronic health records of all patients tested for COVID-19 by PCR from March 1, 2020, through February 28, 2021, were extracted from University of Washington Medicine patient records. Information on patient demographics, type and frequency of healthcare encounters, and diagnoses based on ICD codes were compared between patients with positive versus negative SARS-CoV-2 PCR test results. **Results:** A total of 4,480 patients tested positive and 103,000 persons tested negative for COVID-19 over the one-year period. Age was similar between both groups (mean 47 years). The proportions of African-Americans (15%) and Hispanics (20%), among those who tested positive and reported race/ethnicity, were higher than the proportions among those who tested negative (9% and 8%, respectively). Over 23,100 healthcare encounters were identified among the 3,838 patients who sought care after their positive COVID-19 test. Of these patients, 28% had at least one hospitalization and 72% received only outpatient care. A median of 4 (IQR 2-11) and 2 (IQR 1-6) healthcare encounters occurred in initially hospitalized patients and outpatients, respectively. Among all 2,294 patients with ≥6 months follow-up, 17% were diagnosed with a code recognized as potentially related to post-COVID-19 conditions representing 92% of patients seeking care after 6 months. Diagnoses occurring within these post-COVID visits after 6 months included mood/anxiety disorders (31% of patients), myalgia/arthralgia (23%), arrythmias (14%), sleep disorders (13%), fatigue/malaise (10%), ear/nose/throat conditions (9%), abdominal pain (7%) and dyspnea (6%). **Conclusions:** Patients with positive COVID-19 tests continue to require medical care months after infection. Identification of those at greatest risk and mechanisms underlying these conditions is greatly needed.

### Poster 344. Antibiotic Usage in COVID-19 Patients Admitted at Selected Tertiary Care Hospitals of Bangladesh (June- July 2021)

**Z.H. Habib**[1], M. Murshed[2], S.B.G. Rasul[1], M. Rahman[1], N. Afreen[1], S. Islam[2], K. Heitz[2], T. Shirin[1]
[1]Institute of Epidemiology, Disease Control & Research (IEDCR), Dhaka, Bangladesh, [2]American Society for Microbiology, Washington, DC, USA
**Background**: COVID-19 is a viral disease caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), with variable clinical presentations. Physicians use different medications with a wide range of antibiotics to treat COVID patients both in wards and Intensive Care Units (ICUs) of hospitals in a desperate attempt to save the life of the patients. As antibiotic use is the main driver of antibiotic resistance, the overuse and misuse of antibiotics are to be identified to carb the problem. **Methods:** It was a cross-sectional study conducted in selected ten public and private tertiary care hospitals throughout the country to find out the antibiotic used to treat the COVID-19

patients. All the patients admitted in the COVID ward and COVID ICU in the designated hospitals from June 1 to July 31 were included in the study and their antibiotic use and outcome were recorded from the bed head ticket using a case report form. **Results**: In this study, data was collected from 870 patients from COVID wards and 121 patients from COVID ICU who have received 1168 and 157 antibiotics respectively during their treatment. Ceftriaxone (47%) and Meropenem (30%) were the most used antibiotics in COVID ward and COVID ICU respectively. Meropenem (17%), Co-amoxiclav (12%), Moxifloxacin (09%) and Remdesivir (04%) were the other four frequently used antimicrobials in COVID ward whereas Doripenem (11%), Clarithromycin (11%) Tigecycline (10%), Ceftriaxone (06%), Piperacillin plus Tazobactam (6%) were the other four frequently used antibiotics in COVID ICU. Only 3% patients were not advised for antibiotic in COVID ward whereas no patient in COVID ICU were treated without antibiotics. During the period of admission most of the patients were treated with single antibiotic both in COVID ward (65%) and ICU (74%). Use of multiple antibiotics at the same time during hospital stay were higher in COVID ward (26.49%) than COVID ICU (20.86%). Up to four antibiotics were used at a time in COVID ward (0.23%) and three antibiotics were used in COVID ICU (0.86%). **Conclusion**: It was a small-scale study conducted for understanding of antimicrobial use in COVID-19 patients for evidence-based actions to promote prudent use of antibiotics. This study showed frequent use of advanced generation of antibiotics in COVID-19 patients in all the hospitals which is quite alarming.

### Poster 345. The Importance of Food and Food Systems in A Novel, Infectious Respiratory Disease Outbreak: Role of CDC's Food Systems Working Group in the COVID-19 Response

**B.L. Dumas**, D.J. Sharp, S. McGarry, S.D. Wiley, A. Liang
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** The Centers for Disease Control and Prevention (CDC) COVID-19 response activated the Food Systems Working Group (FSWG) to address concerns about outbreaks among workers in food processing plants, disruptions in the food supply chain and food access, and early uncertainties related to the safety of food during the COVID-19 pandemic. FSWG goals were to: 1) provide coordination of food-related subject matter expertise, 2) engage partners on COVID-19 topics related to food and nutrition security, and 3) prevent the spread of COVID-19 among essential workers in food service, production, and processing. **Methods:** From April 2020-July 2021, over 100 CDC staff from a variety of disciplines formally rostered to FSWG or served as a liaison to FSWG from other COVID-19 response taskforces and units. Intra-agency coordination connected multisectoral expertise from multiple disciplines, such as One Health, environmental health, worker-safety, health equity, vaccines, and support to state and local agencies. Activities included participating in interagency groups, liaising with federal food regulatory agencies, outreach and technical assistance, and data analytics. **Results:** FSWG members reviewed over 800 federal COVID-19 materials and served as primary developers or substantial contributors to over 25 food and food worker-related federal guidance and communication materials and scientific publications; hosted over 100 partner calls; participated in over 20 webinars; and provided technical assistance to federal and non-federal partners on a broad range of topics, including agriculture and food processing worker outbreaks and community food security. **Discussion:** Traditionally, a public health emergency response to a respiratory infectious disease does not bring attention to risks associated with food and disruptions to the food supply chain. While no COVID-19 cases were reported to CDC related to consuming or handling food, the COVID-19 pandemic highlighted the interdependent aspects of food systems and public health. Given the contributions of FSWG, early activation of this capability could improve federal and non-federal coordination to protect the nation's critical food infrastructure and public health during future emergencies.

### Poster 346. Risk Factors for COVID-19 among Persons with Substance Use Disorder with Hospital Visits – United States, April 2020 – December 2020

**AR Board**[1,2,3], S Kim[1,4], J Park[1,5], L Schieber[1,3], GF Miller[1,6], J Pike[1,7], L Cremer[1,3], A Asher[1,8]
[1]COVID-19 Response, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Division of Overdose Prevention, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Division of Foodborne, Waterborne, and Environmental Diseases, Atlanta, GA, USA, [5]Division of Diabetes Translation, Centers for Disease Control and Prevention, Atlanta, GA, USA, [6]Division of Injury Prevention, Centers for Disease Control and Prevention, Atlanta, GA, USA, [7]Immunization Services Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [8]Division of Viral Hepatitis, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Factors associated with coronavirus disease 2019 (COVID-19) among persons with substance use disorder (PWSUD) are not well understood. We aimed to identify risk factors associated with COVID-19 in this population. **Methods:** Using the Premier Healthcare Database Special COVID-19 Release, we conducted a case-

control study using ICD-10-CM codes to identify PWSUD aged 12 and older with hospital visits during April–December 2020. Multivariable logistic regression was used to calculate adjusted odds ratios (aOR) and 95% confidence intervals (CI) to identify factors associated with COVID-19 diagnosis among PWSUD (e.g., age, sex, race/ethnicity, U.S. Census Region, urban/rural classification, insurance payor type, comorbidities, and substance use disorder [SUD] type), and then stratified by SUD type. **Results:** From April-December 2020, 18,298 (1.3%) of 1,429,154 persons with SUD in the database had a COVID-19 diagnosis. Among PWSUD, opioid use disorder (OUD; aOR=1.24, 95% CI=1.18-1.32), alcohol use disorder (AUD; aOR=1.16, 95%CI=1.11-1.22), cocaine or other stimulant use disorder (COUD; aOR=1.28, 95% CI=1.22-1.34), multiple SUDs (aOR=1.20, 95%CI=1.15-1.26) chronic lower respiratory disease (aOR=1.32, 95% CI=1.26-1.37), chronic hepatitis (aOR=1.45, 95% CI=1.34-1.57), and diabetes (aOR=1.78, 95% CI=1.71-1.86) were associated with higher odds of COVID-19. Older age was also a significant risk factor. **Conclusions:** Among a sample of PWSUD, OUD, AUD, COUD, multiple SUDs, and associated comorbidities were associated with increased odds of COVID-19 diagnosis. Integration of COVID-related care, care of other comorbidities, and SUD treatment may benefit PWSUD. Future studies are needed to understand the effectiveness of COVID-19 prevention in this population and to reduce disparities among subpopulations at increased risk.

### Poster 347. A Rapid Survey of State and Territorial Public Health Partnerships with Faith-Based Organizations to Promote COVID-19 Vaccination

**S. Santibanez**[1], A. Ottewell[2], P. Harper-Hardy[2], M. Lewis[2], J. Blumenstock[2], E. McGowan[2], M. Allen[2], M.A. Cooney[2], E. Ryan[1,3], J. Donovan[1], H. Christensen[4], J. Harris[4], C. Wilkins[1], N. Smith[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]The Association of State and Territorial Health Officials, Arlington, VA, USA, [3]Tanaq Support Services, St. George Island, AK, USA, [4]U.S. Department of Health and Human Services, Center for Faith-Based and Neighborhood Partnerships, Washington DC, USA
**Background**: During the COVID-19 pandemic, media accounts emerged describing faith-based organizations (FBOs) working alongside health departments to support the COVID-19 response. While these anecdotal reports were encouraging, the extent and characteristics of such partnerships were unknown. HHS, CDC, and ASTHO sought to determine: (1) the frequency of health department partnerships with FBOs, and (2) factors supporting and hindering such partnerships. **Methods**: We developed a 13-question electronic survey to assess levels and types of state, local and territorial engagement with FBOs, partnership facilitators and barriers, funding awarded to FBOs, accomplishments, and health collaboration beyond COVID-19. In May 2021, ASTHO sent the survey to directors of public health preparedness in the 59 ASTHO member jurisdictions and four major U.S. cities (N=63). Directors were encouraged to enlist colleagues, such as immunization managers and minority or health equity directors, to complete the questionnaire. Twenty-six of 63 jurisdictions surveyed responded, for a response rate of 41%. **Results**: Twenty-four of 26 respondents (92%) reported their department or agency engaged with FBOs to promote COVID-19 vaccination. All 24 viewed these partnerships as valuable in reaching racial and ethnic minority groups, and 21 of 24 (88%) said FBOs served as actual vaccination sites. Other funded COVID-19 response activities included community engagement, personal protective equipment or hand sanitizer distribution, COVID-19 testing, assistance being able to safely quarantine or isolate, trainings for FBOs on responding to a pandemic, public health emergency messaging and assistance with translation of materials and public service announcements. Of the 24 respondents, 23 said they collaborated with churches, 18 with mosques, 14 with synagogues, and 14 with temples. Respondents described success in engaging with diverse religious communities around COVID-19 vaccination, such as “vaccine clinics at three mosques, which helped with vaccine rates in immigrant communities.” **Conclusions**: Our findings suggest that public health officials in many jurisdictions were able to work effectively with FBOs during the COVID-19 pandemic to provide essential education and mitigation tools to diverse communities. Future preparedness and response efforts may benefit from building upon these partnerships.

### Poster 348. Colonization with Multidrug Resistant Bacteria in Russian COVID Intensive Care Units

**I. Morozova**, O. Ni, A. Kruglov, N. Matushkov, V. Petrova, A. Bykov, D. Protsenko
Moscow City Hospital №40, Moscow Healthcare Department, Moscow, Russia
**Background:** The problem of hospital acquired multidrug resistant (MDR) bacteria is one of the most important in hospitals. During the COVID-19 pandemic, it is more urgent due to a high staff workload, patient transfer between hospitals, and the increased outpatient antibiotic prescription in Russia. **Methods:** We analyzed the dynamics of colonization with MDR bacteria among Moscow COVID ICU patients. The samples from upper respiratory tracts and from gastrointestinal tracts were studied; for ventilator-dependent patients, lower respiratory tract samples were also analyzed. **Results:** In our study, among ICU patients, 40 percent of those previously hospitalized or transferred from other hospitals already carried multi-resistant microorganisms. All mechanically ventilated (MV) patients

staying in ICU for more than four days were colonized by MDR bacteria on days 4-17. The spectrum includes extensively drug resistant strains *Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa,* and *Stenotrophomonas maltophilia*. Only one patient was MRSA colonized. In contrast, among non-MV ICU patients, the cases of bacterial colonization were quite rare. Therefore, the stay in ICU itself is not the risk factor for colonization. The level of COVID-associated lung involvement did not correlate with the dynamics of colonization. **Conclusions**: Our results suggest that extensively drug resistant gram-negative bacteria colonization may be common in MV COVID-19 patients in Russia. At present, MRSA is rather uncommon for these patients. The most important risk factor for the colonization with multi-resistant bacteria is mechanical ventilation during more than 4 days. Further research using molecular genetic methods is planned to reveal the resistance mechanisms of the bacteria and the ways of their transmission inside and between hospitals.

### Poster 349. COVID-19 Testing of U.S.-Bound Agricultural Workers in Mexico

**J. Teleaga**[1,2], Z.A. White[1], J. Cervantes[3], R. Assael[3], G. Berrera[3], S. Toney[1], N. Marano[1], A. Rodriquez-Lainz[1], C. Assael[3], A. Ortega[4], C.G. Chappelle[1], N. Bustamante[1], K. Moser[1], D.L. Posey[1]
[1]Division of Global Migration and Quarantine, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education Fellowship Program, Oak Ridge Associated Universities, Oak Ridge, TN, USA, [3]Clínica Médica Internacional, Monterrey, Nuevo León, Mexico and Tijuana, Baja California, Mexico, [4]International Panel Physicians Association, El Paso, TX, USA
**Background:** The COVID-19 pandemic has presented major public health concerns to populations worldwide. One risk for the United States is the potential for importation and spread of COVID-19 from populations who cross the border for work, such as the H-2A temporary agricultural workers. H-2A workers are seasonal agricultural workers who temporarily migrate to the United States to supplement the U.S. agricultural workforce. Approximately 300,000 workers enter each year; over 90.0% are from Mexico. **Methods:** A voluntary screening pilot was performed with Clínica Médica Internacional (CMI), a clinic that performs medical exams for US-bound immigrants in Mexico, to determine the H-2A workers' SARS-CoV-2 infection status before U.S. entry. The CERTEST Viasure Real Time PCR Detection Kit for SARS-CoV-2 was used at two pilot sites. We collected participants' demographics, test results, and turnaround times for testing from February 2021 to May 2021. CMI shared data with CDC weekly. Workers who tested positive and their close contacts were managed by local authorities in Mexico and completed isolation or quarantine before U.S. entry. **Results:** During this pilot, a total of 1,195 workers were tested for SARS-CoV-2; 1,175 (98.0%) were male. Only 15 (1.3%) tested positive. Mean reported time of test results was 31 hours (minimum: 6 hours; maximum: 59 hours) after specimen collection. **Conclusions:** This pilot demonstrated that there is interest in the H-2A workers' community to receive SARS-CoV-2 testing prior to U.S. entry and using the immigration clinic is a viable strategy to help reduce the spread of COVID-19. Moreover, testing for SARS-CoV-2 can be done without slowing entry into the United States.

### Poster 350. Reduction in COVID-19 Incidence following Implementation of Control Measures, Mombasa, Kenya, 2020

**F. Ouma**[1,2], B. Okotu[2,3], F. Mugo[2,4], R. Mwanyamawi[5], F. Odhiambo[2]
[1]Department of Health, Kisumu County, Kisumu, Kenya, [2]Field Epidemiology and Laboratory Training Program, Kisumu, Kenya, [3]Department of Health, Marsabit County, Marsabit, Kenya, [4]Nutrition and Dietetics Unit - Ministry of Health, Nairobi, Kenya, [5]Department of Health, Mombasa County, Mombasa, Kenya
**Background**: By 31st August 2020, about 25 million people had contracted COVID-19 with nearly 800,000 deaths reported globally. Kenya recorded 34,315 cases. Mombasa County had been classified as a hotspot and witnessed sustained control efforts leading to a reduction in incidence in August 2020. We described the epidemiology, knowledge, attitude, and practices associated with this decline. **Methods**: We reviewed health records on socio-demographics, exposure, and clinical characteristics and compared proportions in June and August 2020. We conducted key informant interviews and focused group discussions using a structured questionnaire to assess the county's COVID-19 control strategies and to assess community knowledge, attitude, and practices. The study population was health management teams and community members. We obtained informed consent before interviews and omitted personal identifying information. Descriptive statistics were used to analyze the data. **Results**: We reviewed 2,405 records. Incidence in June was 39.7% (955/2405) and in August 13.8% (332/2405), a reduction of 74%. There was 3.1% decrease among individuals aged 15 to 24 years, 1.27% among females, 5.24% among symptomatic cases, 5.1% in Mvita Sub-County and1.8% among prisoners. However, there was a 3.5% increase in transport sector players. The county government and partners developed a response structure, procured health commodities in April 2020 and distributed face masks, sensitized Community Health Assistants and Volunteers, conducted community social behavior change communication (SBCC) in May 2020. In June 2020, they

initiated community dialogue, installed handwashing stations, distributed bicycles for active surveillance and contact tracing, and donated food and toiletries to households, and disseminated community SBCC materials. Local radio stations offered free airtime for SBCC. Community members could identify COVID-19 symptoms, modes of transmission, and prevention methods. **Conclusion**: Strategic fund allocation and disbursement, aggressive stakeholder participation, and rigorous SBCC could have helped reduce COVID-19 incidence. There was need to strengthen SBCC among transport operators.

### Poster 351. Adjusting National Border Health COVID-19 Response Strategies using Cross-border Informal Movement Patterns–Uganda, 2021

**D. Eurien**[1], K. Mehta[2], E. Mayoki[1], H. Itiakorit[1], F. Ayesiga[1], H. Sekabira[1], G. Ssentogo[1], E. McIntyre[2], J. Ojwang[2], A. Boos[2], S. Ward[2], D. Matwire[3], M. Luzinda[3], H. Mayinja[3], I. Makumbi[3], A. Muruta[3], A. Ario[3], P. Elyanu[1], R. Merrill[2]
[1]Baylor, Kampala, Uganda, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Uganda Ministry of Health, Kampala, Uganda
**Background:** Global population movement continues to play a critical role in the spread of COVID-19. Public health preparedness and response benefit from adjusting border health and surveillance strategies to unique sociocultural and economic contexts associated with movement patterns. This project was designed to understand cross-border population movement between Uganda and neighboring countries to strengthen border health interventions to mitigate the spread of COVID-19 by land travel in Uganda. **Methods:** Between December 2020 and July 2021, the Ugandan Ministry of Health (MOH), Baylor-Uganda, and the U.S. Centers for Disease Control and Prevention (CDC) conducted community-engagement activities to characterize informal cross-border movement using the Population Connectivity across Borders (PopCAB) toolkit in three districts of Kasese, Ntoroko and Bundibugyo. The team conducted 30 focus group discussions and key informant interviews with 141 participants including healthcare providers, traditional healers, traders, security and transportation officials, and district and community leaders. **Results**: During the COVID-19 lockdown, from March to December 2020, cross-border movement between Uganda and the Democratic Republic of the Congo decreased but continued driven by activities concerning asylum, healthcare, trade, and social occasions. People seeking healthcare and crossing for family reasons identified alternative routes with minimal security to avoid quarantine early in the pandemic and COVID-19 test costs. Additionally, the Congolese visited healthcare facilities providing Ebola treatment in Uganda believing the facilities also provided COVID-19 treatment. **Conclusion**: The Ugandan MOH used information about cross-border movement to update national border health and COVID-19 response strategies. Additionally, they aimed to tailor district-level strategies by identifying healthcare facilities for improved infection prevention and control, identify geographic areas for refresher surveillance training for village health teams, and border areas for enhanced traveler screening. This project provides an example of using a better understanding of informal cross-border population movement patterns to adjust public health programming for pandemic response.

### Poster 352. An Increased Public Health Threat of Antimicrobial Resistance Bacteria in the COVID-19 Era

**K. Sargsyan**[1], T Ghalechyan[1], N Stepanyan[1], L Niazyan[2]
[1]National Center for Infectious Diseases “Nork”, Ministry of Health, Republic of Armenia, [2]Yerevan State University, Yerevan, Armenia
**Background:** The novel coronavirus has revealed a bigger issue the world is facing with antimicrobial resistance (AMR). Antibiotic overuse undoubtedly leads to an exacerbation of a slowly progressive pandemic. We hypothesized that uncontrolled use of antibiotics has impacted the emergence of AMR pathogens’ circulation in Armenia. **Methods:** We conducted a prospective observational cohort study among patients with COVID-19 who were hospitalized in the National Center of Infectious Diseases (April 1– November 30, 2020). We describe the microbiological spectrum and antibiotic sensitivity results of sputum obtained from hospitalized patients. **Results:** Of 387 sputum samples from SARS-CoV-2 PCR-positive patients, different bacteria were isolated in 246 samples (63.6%). The prevailing pathogen was *S. pneumoniae* (176 cases, 71.5%), followed by *S. aureus* (38 cases, 15.4%), *Candida* (20 cases, 8.1%), *Pseudomonas aeruginosa* (5 cases, 2%) and *E. coli* (4 cases, 1.6%). A sharp decrease in sensitivity was noted over time to azithromycin (from 55% to 15%), levofloxacin (from 75% to 52%), cefotaxime (from 68% to 49%), augmentin (from 72% to 61%) and meropenem (from 87% to 76%). We discovered 79 pathogens with multidrug resistance to 11-15 of 19 antimicrobials tested. Multidrug resistance was higher in patients who self-administered antibiotics before hospitalisation. In this group, an average hospital stay increased from 9 to 13 days and the mortality rate was 9.1% higher in patients with resistant bacterial co-infections. **Conclusion:** The results of our study confirmed our hypothesis with a defined resistance to a broad spectrum of antimicrobials and

increased trends in the temporal dynamics. An empiric administration of antibiotics with no susceptibility examination prior treatment initiation had negative impact in terms of poor treatment outcomes, prolonged hospital stays and emergence of nosocomial threats. Studies on AMR evolution need to support a stronger antibiotic stewardship, as pathogens do not respect borders.

### Poster 353. The Impact of Vaccination on COVID-19 Outbreak in the Islamabad Capital Territory

**I. Naveed**[1], N. Noreen [2]
[1]PIMS, Islamabad, Pakistan,[2] Directorate of Central Health Establishments, Islamabad, Pakistan
**Background:** Pakistan as national policy began vaccination drive against Covid-19 by targeting front-line healthcare workers and high-risk groups w.e.f 2nd February through Adult vaccination centers across Pakistan. As a part of the countrywide campaign, senior citizens above 60 years of age and other age quarters were registered and vaccinated through a computerized database. Since 30th May Pakistan is vaccinating all eligible age groups from 18 years of age. This study aimed to evaluate the impact of a 2-dose COVID-19 vaccination campaign on reducing incidence and hospitalizations in Islamabad (ICT). **Methods:** An agent-based model of SARS-CoV-2 transmission was developed and parameterized with the ICT demographics and age-specific COVID-19 outcomes. Healthcare workers and high-risk individuals were among the priority group for vaccination. Vaccine efficacy of 79% against the disease was considered following 2 doses administered 21 days apart achieving 50% vaccine coverage of the overall population of Islamabad within 242 days (February 21-September 21). The vaccine efficacy against infection was varied and adjusted as specified 10% pre-existing population immunity for the base-case scenario. The model was calibrated to an effective reproduction number of 1.0 accounting for current non-pharmaceutical interventions in Pakistan. **Results:** The result of the study revealed that vaccination reduced the overall attack rate to 0.5% (95% CI: 0.4- 0.7%) from 1.3% (95% CI: 0.7% -1.5%) without vaccination, over 240 days study period. The highest relative reduction (42%) was observed among individuals aged 65 and older. Vaccination reduced the covid infection risk, hospitalizations, and deaths decreasing by 23.5% (95% CrI: 20.3%-24.7) 74% (CI: 72.4-76.3%) and 42.3% (95% CI: 40.5% – 43.1%), respectively, across the same time period. **Conclusions**: Results of the study indicate that vaccination had a significant brunt on mitigating and reducing the COVID-19 outbreaks, even with limited protection against infection. Ramped up vaccination campaign has helped to significantly push down the daily infection rates and hospital admissions during the fourth wave of the covid pandemic. Nonetheless, extended compliance with non-pharmaceutical interventions is essential to achieve this impact.

### Poster 354. Clinical and Economic Impact of COVID-19 on Plantation Workers: Preliminary Results from the Guatemala Agricultural Workers and Respiratory Illness Impact (AGRI) Study

**D. Olson**[1,2,3], D.M. Calvimontes[3,4], M.M. Lamb[2], G. Guzman[3], E. Barrios[3], A. Chacon[3], N. Rojop[3], K. Arias[3], M. Gomez[3], G.A. Bolanos[3], J. Monzon[5], A.N. Chard[6], C. Iwamoto[6], K. Quicke[7], G. Ebel[7], E. Zielinski Gutierrez[5], E. Azziz-Baumgartner[5], F.G. Hayden[8], H. Mansour[9], K. Edwards[10], L.S. Newman[2,11,12,13], E.J. Asturias[1,2,3,4]
[1]Department of Pediatrics, Division of Infectious Disease, University of Colorado School of Medicine, Aurora, CO, USA, [2]Department of Epidemiology and Center for Global Health, Colorado School of Public Health, Aurora, CO, USA, [3]Center for Human Development, Fundacion para la Salud Integral de los Guatemaltecos, FSIG, Retalhuleu, Guatemala, [4]La Comisión Presidencial de Atención a la Emergencia COVID-19 (Coprecovid), Guatemala, [5]Centers for Disease Control and Prevention, Division for Global Health Protection (CDC-DGHP), Guatemala City, Guatemala, [6]Centers for Disease Control and Prevention, Influenza Division, Atlanta, GA, USA, [7]Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, CO, USA, [8]Department of Medicine, Division of Infectious Diseases and International Health, University of Virginia School of Medicine, Charlottesville, VA, USA, [9]Department of Economics, University of Colorado – Denver, Denver, CO, USA, [10]Department of Pediatrics, Division of Infectious Disease, Vanderbilt University School of Medicine, Nashville, TN, USA, [11]Department of Medicine, University of Colorado School of Medicine, Aurora, CO, USA, [12]Center for Work, Health, and the Environment, Colorado School of Public Health, Aurora, CO, USA, [13]Department of Environmental and Occupational Health, Colorado School of Public Health, Aurora, CO, USA
**Background:** Although agricultural workers are essential in maintaining food security, little is known about their risk of infection during pandemics. We aim to characterize the risk of respiratory infections and the resulting clinical and socioeconomic burden of disease in a cohort of banana plantation workers. **Methods:** We enrolled eligible workers within a large agribusiness in southwest Guatemala from June 15-December 30, 2020 in the AGricultural workers and Respiratory Impact (AGRI) study. Workers were followed for influenza-like illnesses (ILI) through self-reporting symptoms to study nurses, sentinel surveillance at health posts, and active monitoring of absenteeism registry. Nasopharyngeal swabs from workers with ILI were tested for SARS-CoV-2 using Q COVID rapid antigen tests (SD *Biosensor*® Republic of Korea). All workers with ILI and randomly selected asymptomatic controls

underwent epidemiologic, clinical severity, and well-being indexes (Flu-iiQ®), and socioeconomic surveys at diagnosis and at 7- and 28-day follow-up. Absenteeism and productivity data were collected from the agribusiness records. **Results:** Of the 1,431 workers enrolled, 84.1% were male and median individual monthly income was US $337.2 (IQR: $311.3-389.1). By April 25, 2021, workers had developed 58 ILIs (7.1/100 P-Y); of these, 11 (19%) were associated with laboratory-confirmed SARS-CoV-2 (1.4/100 P-Y). At diagnosis, workers with ILI and SARS-CoV-2 positive test results reported more anosmia (63.6% vs 21.1%; p=0.01), dysgeusia (72.7% vs 34.2%; p=0.02), difficulty concentrating (63.6% vs 23.7%, p=0.01), and irritability (90.9% vs 34.2%, p<0.001) than SARS-CoV-2 negative workers with ILI. Workers with SARS-CoV-2 had greater absenteeism (p<0.001) and income losses (median US$ 127.1 vs $0, p<0.001), and reported more severe symptoms and negative impact on well-being than SARS-CoV-2 negative workers with ILI. **Conclusions:** Approximately one in five cases of ILI among plantation workers were attributable to SARS-CoV-2. Compared to SARS-CoV-2 negative workers with ILI, workers with SARS-CoV-2 had more severe disease, absenteeism, and protracted symptoms, and lost approximately one-third of monthly income during recovery. These findings support the prioritization of workers in the agricultural sector for vaccination against COVID-19.

### Poster 355. Withdrawn

### Poster 356. Infection Outcomes in Fully Vaccinated Healthcare Personnel with Known SARS-CoV-2 Exposure before and after Delta Variant Emergence — Minnesota, January–August 2021

**A.J. Ruhland**, P. D'Heilly, B. Friedman, A. Fell, A. Beaudoin, K. Como-Sabetti, R. Lynfield
Minnesota Department of Health Infectious Disease, Epidemiology, Prevention and Control Division, St. Paul, MN, USA

**Background:** Since March 2020, Minnesota Department of Health (MDH) has required healthcare facilities to report healthcare personnel (HCP) exposures to persons with confirmed SARS-CoV-2 infection for exposure risk assessment. SARS-CoV-2 vaccination of HCP started in December 2020. We describe exposures and infection outcomes of vaccinated and unvaccinated HCP and compare outcomes before and after Delta variant emergence. **Methods:** During January 19, 2021–August 16, 2021, exposed HCP from hospitals, clinics, and congregate care were interviewed. HCP with higher-risk (HR) exposures had close contact to someone with COVID-19 in household/social settings or an occupational interaction without all proper personal protective equipment according to CDC risk assessment. HCP with HR exposures were matched to cases reported to MDH to identify positive SARS-CoV-2 test results in 14 days after exposure. Vaccination status at time of exposure was confirmed in the Minnesota Immunization Information Connection. HCP were considered vaccinated ≥2 weeks after the last vaccine series dose. "Delta" period began June 20, when >50% of sequenced specimens were identified as Delta. **Results:** Of 2596 HCP with HR exposures (662 occupational, 1934 household/social), 40% were vaccinated and 12% tested positive within 14 days. Overall, unvaccinated HCP were more likely to test positive than vaccinated HCP (20% vs 6%, p<0.001). The proportion of unvaccinated HCP testing positive did not differ during Delta to pre-Delta (24% vs 20% p=0.323). Vaccinated HCP tested positive more often during Delta than before (12% vs 5%, p<0.001). Both unvaccinated and vaccinated HCP exposed in household/social settings were more likely to test positive during Delta than pre-Delta (32% vs 22%, p=0.049; and 28% vs 6%, p<0.001, respectively). Positivity after occupational exposure only increased during Delta for vaccinated HCP (5% vs 0%, p=0.001). **Conclusions:** Overall, fully vaccinated HCP were less likely to test positive for SARS-CoV-2 after HR exposure than unvaccinated HCP. However, since Delta emergence, vaccinated HCP tested positive more often. HCP household/social exposures result in infection more often than occupational exposures. Ongoing surveillance is important to assess infections in HCP and impact of waning immunity and booster doses.

### Poster 357. Risk Factors of COVID-19 Breakthrough Infections in Pakistan

**A. Hussain**, M.A. Syed
Field Epidemiology Laboratory Training Pakistan, Health Department, Government of Sindh, Karachi, Pakistan

**Background:** Closely, after one year of first COVID-19 case in Wuhan, China, the World Health Organization) approved COVID-19 vaccines for global use in December 2021. Donated Sinopharm was the first vaccine started from February 2021 and till July 2021 about 42 lac individuals claimed to be fully vaccinated in Pakistan. Even with the high efficacy of available COVID-19 RNA vaccine, breakthrough infections (BTIs) have been reported in Pakistan. The objectives were to assess the burden and to explore the risk factors of BTIs to prevent the potential outbreaks. **Methods:** In this cross-sectional study, COVID-19 vaccine breakthrough infectious case was adopted as the detection of SARS-CoV-2 RNA in specimen collected from respiratory tract of individuals, from February 20 to July 20, 2021, after 14 or more days of receipt of all recommended doses of an FDA approved COVID-19 vaccine. The demographical features, immunization status, occurrence of BTI in days, severity of disease, comorbidity,

smoking habit, alcohol usage, opioid overdose and mortality status had collected with the help of 38556 phone calls, utilizing software generated random cell numbers. Statistical analysis was accomplished utilizing Epi Info version-7. **Results:** Overall response-rate was 55.32%. With male preponderance, mean age was 41.8±19 years. Median period was 38.6 days (IQR, 25-63) for contracting BTI. Mostly respondents claimed to be asymptomatic (87.6%). Mild to moderate BTIs were reported among 10.8%, while only 1.3% were developed severe disease. Recovery rate was 99.8% with only 3 deaths. There was significant statistical relation of comorbidity and smoking habits with BTIs ($p<0.05$). **Conclusion:** The BTIs were rare and no vaccine found to be 100% effective. Comorbidity and smoking habits shown the risk factors for BTIs. However, further research is needed to establish the true association. Vaccination should be enhanced to achieve 100% coverage. Strong surveillance system for BTIs should be strengthen as we cannot afford to miss a single case.

### Poster 358. The Impact of COVID 19 on Pregnant and Nonpregnant Females at Reproductive Age, February - July 2020 – Egypt

**H. BahaaEldin**[1], H. Abu El Sood[1], S. Samy[1], Y. Khader[2], M. AbdelFatah[1], M. Hassany[1], S. Afifi[1], A. Eid[1]
[1]Ministry of Health and Population, Cairo, Cairo, Egypt, [2]Jordan University of Science and Technology, Amman, Amman, Jordan

**Background:** Since the beginning of the COVID-19 pandemic, it has been argued that pregnant females are at increased risk of severe infection. Studies suggested that pregnant females with COVID-19 are more likely to develop respiratory complications, require intensive care unit admission and invasive ventilator. Currently no sufficient evidence is available to conclude the definite effect of COVID-19 on pregnant females given the novelty of the virus. This study aimed to describe the epidemiological and clinical characteristics of pregnant females with COVID-19 and identify risk factors for disease unfavorable outcome in pregnant females by comparing them to non-pregnant female COVID-19 patients at reproductive age. **Methods:** A retrospective study conducted for females aged 18-49 with confirmed COVID-19 in Egypt, February-July 2020. Data was obtained from Egypt National Surveillance, bivariate and Multivariate analysis for demographic and clinical characteristics and outcomes of COVID-19 between pregnant and nonpregnant females including ICU admission, need for ventilator and death was performed. **Results:** A total of 23,095 females identified, their mean age was 35.1±8.1 years. Of those, 408 (1.8%) were pregnant, with mean ±SD age of 29.3±8.1 years. Pregnant patients were more likely to have severe course and disease outcome (4.9% vs. 1.7%, $p<0.001$). Rate of hospitalization (54.7% vs. 41.1%, $p<0.001$), ICU admission (2.9% vs. 1.2%, $p<0.01$) and require ventilator (2.7% vs. 0.7%, $p<0.001$) were significantly higher among pregnant compared to nonpregnant females with COVID-19. Factors associated with severe outcomes in females at reproductive age with COVID-19 included: age >30 year, having underling medical condition, and living in rural areas. **Conclusion:** Pregnant females with COVID-19 are at higher risk of severe symptoms and outcome including ICU admission, requiring ventilator and death due to COVID-19. To reduce risk of COVID-19 severe outcome among pregnant females, counseling about importance of seeking medical care and health education should be performed.

## Antimicrobial Resistance

### Poster 359. Carbapenemase-producing *Acinetobacter baumannii* as an Emerging Threat in Wisconsin

**M.R. Lasure**[1], A. Valley[1], A. Dowdell[2]
[1]Wisconsin State Laboratory of Hygiene, Madison, WI, USA, [2]Wisconsin Division of Public Health, Madison, WI, USA

**Background:** In 2019, CDC characterized carbapenem-resistant *Acinetobacter baumannii* (CRAB) as an urgent threat. The Wisconsin Division of Public Health (WDPH) began doing surveillance for CRAB in 2018 in response to an outbreak at a hospital, which was linked to several long-term care facilities (LTCFs). Since then, the Wisconsin State Lab of Hygiene (WSLH) has expanded its testing capabilities in order to detect colonization with CRAB. **Methods:** WSLH performs testing for identification, antimicrobial susceptibility testing (AST), and molecular detection of carbapenemase genes in clinical isolates. Some carbapenemase genes are more common in CRAB, including OXA-23, OXA-24/40, and OXA-58. WSLH began molecular detection for these Class D carbapenemases in August 2019. For detection of colonization with CRAB, WSLH is able to test axilla/groin, rectal, and tracheostomy swabs. **Results:** From mid-2019, when WSLH began molecular detection for carbapenemases that are most commonly found in CRAB, 263 Wisconsin CRAB isolates have been tested. 246 (94%) were positive for a carbapenemase. The most common was OXA-24/40-like, which accounted for 242 (98%) of carbapenemase genes detected, with the remaining 4 testing positive for OXA-23-like carbapenemase. No KPC, IMP, VIM, NDM-1,

OXA-48-like, or OXA-58-like carbapenemases were detected in Wisconsin CRAB isolates. Of the clinical isolates tested, 41 (20%) of 209 isolates were non-susceptible to all antibiotics tested. In the first year of this surveillance, 78 of 87 isolates (90%) were from the Southeastern region of the state, while in the second year 133 of 176 isolates (76%) were from that same region. **Conclusions:** CRAB isolates are highly likely to contain a carbapenemase gene and be resistant. CRAB in Wisconsin is likely to contain the same OXA-24/40 carbapenemase and is being more commonly in regions outside Southeastern Wisconsin. More surveillance to determine the extent of CRAB in Wisconsin is necessary.

### Poster 360. Cryptic Carbapenemase Activity of *bla*$_{OXA-2}$ in *Pseudomonas aeruginosa*

**R.A. Stanton**[1], D. Campbell[1], J.B. Daniels[1], G.A. McAllister[1], A.L. Halpin[1,2]
[1]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Commissioned Corps, US Public Health Service, Rockville, MD

**Background:** While traditionally considered a narrow-spectrum β-lactamase, OXA-2 can confer a carbapenemase-producing phenotype in *Pseudomonas aeruginosa*, as isolates with the gene are often positive by the modified carbapenem inactivation method (mCIM) assay. However, other isolates carrying *bla*$_{OXA-2}$ are consistently mCIM-negative. Here we seek to determine if this contradiction is driven by changes in expression of *bla*$_{OXA-2}$. **Methods:** Whole genome sequencing (WGS) and the mCIM assay were used to identify discrepant pairs of *bla*$_{OXA-2}$-carrying *P. aeruginosa* isolates (one mCIM+ and one mCIM-) from three different sequence types (STs). We then performed antimicrobial susceptibility testing for the isolates against three carbapenems. Reverse transcription-quantitative polymerase chain reaction (RT-qPCR) was used to determine the relative expression of *bla*$_{OXA-2}$ in the presence and absence of meropenem. WGS data were analyzed using a core genome multilocus sequence typing (cgMLST) scheme to identify common gene variations between the isolate pairs. We also re-ran the mCIM assay on a series of five two-fold serial dilutions of the bacteria from normalized initial concentrations on the ST179 *bla*$_{OXA-2}$-carrying isolates as well as isolates with the metallo-β-lactamases (MBLs) *bla*$_{VIM}$ and *bla*$_{IMP}$ from the same ST. **Results:** There was no difference in AST patterns between the mCIM+/mCIM- isolate pairs, nor did the expression of *bla*$_{OXA-2}$ vary. There were also no changes in gene expression in the presence or absence of meropenem. cgMLST analyses identified seven genes that differed for each of the mCIM+/mCIM- pairs, including a component of a multidrug (MDR) efflux pump system, *opmJ*. The isolates with *bla*$_{VIM}$ and *bla*$_{IMP}$ MBLs remained mCIM+ after three dilutions, while the ST179 isolates with *bla*$_{OXA-2}$ became mCIM- after a single dilution. **Conclusion:** The variations in mCIM results between *bla*$_{OXA-2}$-carrying *P. aeruginosa* isolates were not driven by changes in gene expression, but instead by other factors (e.g., variations in MDR efflux pumps). Our results identified a technique to differentiate between isolates with OXA-2 or MBLs, by re-running the mCIM assay with a four-fold dilution. This approach can be used with mCIM+ isolates that are negative by PCR for known MBLs to rapidly eliminate the possibility of a novel MBL.

### Poster 361. High Prevalence of Multidrug-Resistant Organisms in Hospitalized and Healthy Community Individuals in Dhaka City, Bangladesh: Findings from the Antibiotic Resistance in Communities and Hospitals (ARCH) Study

**F. Chowdhury**[1], S. Mah-E-Muneer[1], S. Bollinger[2], A. Sharma[2], D. Ahmed[1], K. Hossain[1], Z. Hassan[1], M. Rahman[1], D. Vanderende[2], D. Sen[1], P. Mozumder[1], R.M. Smith[2], U. Luvsansharav[2]
[1]International Centre for Diarrhoeal Disease and Research, Bangladesh (icddr,b), Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA

**Background:** Measuring the prevalence of multidrug-resistant organism (MDRO) colonization is critical to understanding burden and guiding prevention strategies. We assessed the colonization prevalence of three MDROs in hospitals and the surrounding community: Enterobacterales with resistance to extended-spectrum cephalosporins (ESCrE) or carbapenems (CRE) and methicillin-resistant *Staphylococcus aureus* (MRSA). **Methods:** Stool and nasal samples were collected from adults in three hospitals and from community dwellers within the hospitals' catchment area. Samples were plated on CHROMagar™ ESBL, mSuperCARBA, or MRSA agar plates. Up to three morphotypes per plate underwent identification and antibiotic susceptibility testing using Vitek® 2. Isolates were confirmed as ESCrE when resistant (R) to ceftriaxone and susceptible or intermediate to all tested carbapenems, CRE when R to at least one tested carbapenem, or MRSA when R to oxacillin or positive by cefoxitin screen. **Results:** Of 743 enrolled participants in hospitals, all provided nasal swabs and 719 (97%) provided stool samples. Among 768 community participants, all provided nasal swabs and 714 (93%) provided stool samples. Participants' median age in years was 40 (IQR: 30-55) and 35 (IQR: 25-40), among hospital and community participants, respectively. Three hundred ninety-eight (54%) hospital and 274 (36%) community participants were male. MRSA colonization was similar (p=0.43) in both hospital 21% (154) and community 22% (172) participants. The

prevalence of ESCrE was higher in hospitalized participants compared to community [82% (591) vs. 78% (554); p=0.03] and a similar pattern was observed for CRE colonization [37% (266) vs. 9% (66), respectively; p≤0.001]. The most frequently identified resistant Enterobacterales were *Escherichia coli* and *Klebsiella pneumoniae* for hospital (73% and 22%, respectively) and community (75% and 18%, respectively). Fewer hospitalized participants had no MDRO identified compared to community [7% (50) vs. 16% (117); p≤0.001]. **Conclusion:** Most hospital and community participants were colonized with at least one clinically important MDRO, putting them at risk for developing antibiotic resistant infections and facilitating continued spread of MDROs in both the community and hospital.

### Poster 362. Increases in Percentage of *Campylobacter* Infections Resistant to Antibiotics—United States, 2005–2018

**L. Ford**[1], Z. Cui[1], J. Healy[1], L. Ahart[1], F. Medalla[1], L. Ray[1], J. Reynolds[1], M.E. Laughlin[1], D.J. Vugia[2], S. Hanna[3], C. Bennett[1], J. Chen[1], D.C. Payne[1], L.K. Francois Watkins[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]California Department of Health, Richmond, CA, USA, [3]Tennessee Department of Health, Nashville, TN, USA
**Background**: Antibiotic resistance is a growing problem globally and limits treatment options. Macrolides are recommended for empiric treatment of *Campylobacter* infection; fluoroquinolones are an alternative. We describe the epidemiology of resistant *Campylobacter* infections in the United States. **Methods**: The Foodborne Diseases Active Surveillance Network (FoodNet) population-based surveillance system receives information on laboratory-confirmed *Campylobacter* cases from 10 US sites. The National Antimicrobial Resistance Monitoring System (NARMS) receives a subset of isolates from FoodNet sites for antimicrobial susceptibility testing. We used a Bayesian mixed effects model to estimate trends in *Campylobacter* incidence, adjusting for the use of culture-independent diagnostic testing. We linked FoodNet culture-confirmed cases with NARMS data and used binomial log-linear models to compare the percentage of isolates resistant to erythromycin (a macrolide) or ciprofloxacin (a fluoroquinolone) during 2005–2016 to 2017–2018, stratified by demographics and travel history. We used multivariable logistic regression models to examine the association of international travel with resistance. **Results**: Adjusted *Campylobacter* incidence has decreased an average of -2.9% (95% CrI -4.1%–-1.5%) each year since 2012. Among 14,638 isolates, the percentage of resistant infections increased from 2.6% to 3.3% for erythromycin (p=0.04) and from 24.5% to 29.7% for ciprofloxacin (p<0.001). The increase in erythromycin-resistant infections remained significant when stratified among males, children <5 years, Whites, and Hispanics; the increase in ciprofloxacin-resistant infections also remained significant for these groups. International travelers were more likely than non-travelers to have infections resistant to erythromycin (aOR 1.7, 95% CI 1.4–2.4) or ciprofloxacin (aOR 6.0, 95% CI 5.4–6.7), with risk highest following travel to Asia for both. **Conclusions**: The incidence of *Campylobacter* infections has decreased slightly. However, the percentage of isolates resistant to antibiotics recommended for treatment has increased. International travel increases the risk of a resistant infection. Antibiotic resistance by global region should be considered when treating travelers empirically.

### Poster 363. Characterization of the 15th Vancomycin-Resistant *Staphylococcus aureus* Isolate from the United States — Michigan, 2021

**A.S. Gargis**[1], R. Balbuena[1], D. Campbell[1], T.O. Ewing[1,2], C. Longo[1,2], P. Bumpus-White[1,2], N. Wilmott[1,2], J. Ilutsik[1,2], N. Reese[1], D. Lonsway[1], B. Brennan[3], S. McNamara[3], K. Jones[3], J. Padilla[4,5], M. Sheth[4], J. Lee[4], B.B. Yoo[1], A. Lawsin[2], S.L. McKay[1], G.A. McAllister[1], A.L. Halpin[1], D.C. Ham[1], M. Walters[1], J.D. Lutgring[1], J.K. Rasheed[1], C.A. Elkins.[1] M. Karlsson[1]
[1]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Goldbelt C6, LLC, Chesapeake, VA, USA, [3]Michigan Department of Health and Human Services, Lansing, MI, USA, [4]Biotechnology Core Facilities Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]ASRT Incorporated, Atlanta, GA, USA
**Background:** Vancomycin-resistant *Staphylococcus aureus* (VRSA) are rare but significant organisms of public health concern. Since 2002, there have been 14 cases of VRSA in the United States. In May 2021, cultures from a chronic foot wound of a long-term care facility resident in Michigan yielded a suspect VRSA, which was subsequently confirmed by the Centers for Disease Control and Prevention (CDC). We present the phenotypic and genotypic characterization of the 15th VRSA isolate (VRSA15) in the United States. **Methods:** Antimicrobial susceptibility testing was performed using reference broth microdilution and cefoxitin disk diffusion. *spa* typing was performed by Sanger sequencing and SCC*mec* typing by real-time PCR. Whole genome sequencing (WGS) was also completed (Illumina MiSeq). Assembly and multilocus sequence typing (MLST) were performed using CDC's in-house bioinformatics pipeline, QuAISAR-H. Whole genome MLST (wgMLST) was performed using

BioNumerics (v7.6). **Results:** VRSA15 displayed resistance to oxacillin, cefoxitin, clindamycin, erythromycin, levofloxacin and vancomycin (MIC: 1024 µg/mL). WGS confirmed presence of *mecA* and *vanA*; *spa* and SCC*mec* typing were inconclusive. MLST revealed VRSA15 belonged to ST5, clonal complex (CC) 5. wgMLST grouped VRSA15 with USA100 sequences and previous USA100 VRSA isolates. The *vanA* operon was encoded on transposon Tn*1546*, located on an ~39kb contig that shared ~20kb (99% sequence identity) with the staphylococcal plasmid pLUH02 and contained a putative origin of transfer, and enterotoxin, cadmium resistance, and replication initiation (*repA_N*) genes. **Conclusions:** Like VRSA1-12 and 14, VRSA15 belonged to CC5, a lineage associated with healthcare infections. The *vanA*-carrying Tn*1546* is derived from enterococci and is typical of U.S. VRSA isolates; vancomycin-resistant *Enterococcus faecalis* was also isolated indicating potential interspecies transfer. Furthermore, VRSA11a/11b (Delaware, U.S.) also contained a plasmid with Tn*1546* and a pLUH02 backbone. VRSA15 represents the first confirmed case identified in the United States since 2015. It serves as an important reminder to clinical laboratories and infection control personnel to follow established guidelines to ensure prompt recognition, isolation, and management of future VRSA cases.

### Poster 364. Longitudinal Isolation of VRSA from a New York State Patient in 2004 with Chromosomal Vancomycin Resistance Genes

**W. Haas**[1], N. Singh[1], W. Lainhart[2], L. Mingle[1], E. Nazarian[1], K. Mitchell[1], D. Bopp[1], G. Nattanmai[1], D. Kohlerschmidt[1], M.C. Dickinson[1], K.A. Musser[1]
[1]Wadsworth Center, New York State Department of Health, Albany, New York, USA, [2]Sonora Quest Laboratories, Tucson, AZ, USA
**Background**: Vancomycin-resistant *Staphylococcus aureus* (VRSA), an important multidrug-resistant organism of public health concern, has been identified in 14 cases in the United States since 2002. In 2004, the New York State Department of Health's Wadsworth Center and the Centers for Disease Control and Prevention confirmed the third reported VRSA isolate from a patient in a long-term care facility. The patient had multiple indwelling catheters/tubes and had been treated repeatedly for chronic urinary tract infections with various antibiotics. **Methods**: Specimens were collected in 2004 over a period of 4.5 months from the patient's urine, rectum, and nephrostomy tube. Isolates of vancomycin-resistant enterococci (VRE), methicillin-resistant *Staphylococcus aureus* (MRSA), and vancomycin-resistant *S. aureus* (VRSA) were characterized. To better understand the microbial genetics, we used a combination of long- and short-read sequencing technologies to reconstruct and compare the genomes of 18 of these clinical isolates. **Results**: We determined that the *vanA* locus is present on a plasmid in all 11 VRSA isolates. In addition to vancomycin, the plasmid also confers resistance to macrolides, tetracycline, and various aminoglycosides. Unlike other VRSA isolates described previously, the plasmid is integrated into the chromosome in eight of the isolates due to homologous recombination mediated between two regions derived from transposon Tn*5405*. Two of the VRSA isolates are methicillin-susceptible but differ by only 11 or fewer single-nucleotide polymorphisms (SNP) from all other methicillin-resistant VRSA isolates in this study. By comparison, a MRSA isolate from the patient's roommate differed by 33 SNPs from the closest MRSA isolate from the patient. Our results support the hypothesis that a single isolate of MRSA obtained the *vanA* gene from a co-infecting VRE isolate and then diverged through various recombination events. **Conclusions**: While only a limited number of VRSA isolates have been reported from the US, they are frequently reported in other countries. A better understanding of the genetics underlying the emergence of VRSA strains can positively impact public health in the future.

## Respiratory Diseases and Influenza

### Poster 365. Multi-decade National Cohort Identifies Adverse Pregnancy and Birth Outcomes associated with Acute Respiratory Infection Hospitalisations during the Influenza Season

**J. Duque**[1,2], A.S. Howe[1], H. Petousis-Harris[1]
[1]The University of Auckland, Auckland, New Zealand, [2]Abt Associates, Atlanta, GA, USA
**Background:** Despite the WHO recommendation that pregnant women be prioritised for seasonal influenza vaccination, coverage in the Western Pacific Region remains low. We explored ecological associations between acute respiratory infection hospitalisations and adverse birth outcomes during influenza epidemic and non-epidemic periods to substantiate the value proposition for maternal influenza vaccination. **Methods:** We designed a 16-year retrospective cohort study among all New Zealand residents to evaluate risks associated with maternal acute respiratory infection (ARI) hospitalisation during the influenza season. ARI hospitalisations were identified using select ICD-10-AM primary and secondary discharge codes from chapter J00-J99 (diseases of the respiratory system). Hospitalisations were selected to capture admissions during the influenza season (May-September). Hazard

ratios (HR) and 95% confidence intervals (CI) for maternal ARI hospitalisation and adverse outcomes were estimated using Cox proportional hazards models. Models were adjusted for maternal age, ethnicity, and smoking status. **Results:** We identified 822,391 pregnancies among all New Zealand residents of reproductive age, 5,095 (0.5%) of which had at least one ARI hospitalisation during the influenza season. Pregnant women who were hospitalised with ARI during the influenza season were more at-risk of preterm birth (incidence rate 70.3 per 10,000 person-weeks vs 47.4 per 10,000 person-weeks; HR 1.5, 95% CI 1.4-1.6), and low-birthweight (incidence rate 61.5 vs 33.1 per 10,000 person-weeks; HR 1.7, 95% CI 1.6-1.9) compared to pregnant women who did not experience an ARI hospitalisation during the influenza season. **Conclusion:** In this population-based cohort study of pregnant women, being hospitalised for an ARI during the influenza season increased the risk for delivering preterm and delivering a low-birth-weight infant.

### Poster 366. Adapting an Integrated Acute Respiratory Infections Sentinel Surveillance to the COVID-19 Pandemic Requirements, Egypt, 2020 - 2021

**M. Fahim**[1], B. AbdElGawad[1], H. Abu El Sood[1], E. Ahmed[1] A. Naguib[1], S. Elshaty[1], M. AbdelFatah[1], S. Afifi[2], A. Mohsen[3], A. Eid[1]
[1]Ministry of Health and Population, Cairo, Egypt, [2]Consultant for Ministry of Health and Population, Cairo, Egypt, [3]National Research Center, Cairo, Egypt
**Introduction:** An integrated surveillance for acute respiratory infections (ARIs) involving influenza-like illness (ILI), severe acute respiratory infections (SARI) and pneumonia was established in Egypt 2016 to identify causes of ARIs in Egypt. In response to COVID-19 pandemic, WHO encouraged countries to adapt their ARIs surveillance systems to address the emerging challenges. This report aims at describing Egypt experience in adapting ARI surveillance to COVID-19 pandemic situation. **Methods:** WHO case definitions are used to identify patients, NP/OP swabs collected and tested for influenza and COVID-19 by RT-PCR at the central lab. Patients interviewed using standardized questionnaire, data entered using web-based application. Due to surge of patients with ARI during the pandemic, surveillance methodology was modified to enroll first two ILI patients every day, and every fifth SARI and pneumonia case. Two swabs are collected per patient, one for immediate COVID-19 testing and the other transferred weekly for influenza testing at central lab. **Results:** Between January 2020 - August 2021, 9,734 patients enrolled including 5,539 (56.9%) hospital admitted. Overall, 3,424 (35.2%) were caused by SARS-CoV-2, 357 (3.7%) influenza, 31 (0.3%) co-infection. Compared to influenza, SARS-CoV-2 patients were significantly older (mean age 50.4±17.3 vs 19.0±17, $p<0.001$) and more hospitalized (81.5 vs 5.0%, $p<0.001$). SARS-CoV-2 hospitalized patients have longer time to admission than influenza patients (4.0±3.7 vs 2.6±1.8 days, $p<0.001$) and stay longer at hospital (6.5±6.0 vs 4.9±9.1, $p<0.001$). Influenza patients had higher rates of ICU admission, required ventilator with higher CFR than COVID-19 (33.3% vs 12.0%, $p=0.01$ and 11.1 vs 2.6, $p=0.48$, 13.0 vs 11.2, $p=0.37$ respectively). Influenza subtypes identified were A/H3 56.7%, A/H1pdm 19.3%, FLU-B 23.2% and 0.8% Mixed infection. **Conclusion:** Egypt ARI integrated surveillance better described the epidemiology and virology of influenza and SARS-CoV-2. Surveillance indicated that influenza could cause more severe outcome than SARS-CoV-2. Care should be provided to influenza patients to prevent poor outcomes. Integrated ARI surveillance should be maintained to better describe the epidemiological and virological characteristics of ARIs for decision-making.

### Poster 367. Active Adverse Event Following Immunization (AEFI) Reporting after Administration of Newly Licensed Domestically Produced Influenza Vaccine – Vietnam, 2020-2021

**N.T. Ha**[1], T.T.M. Nguyen[1], T.X. Nguyen[2], H.M. Nguyen[2], V.T.C. Ha[3], T.P. Nguyen[2], J. Bresee[2], M. McKinlay[2], D. Richardson[2], K.E. Lafond[4], A.L. Fowlkes[4], S.Y. Chu[5], P.L. Gould[1]
[1]U.S. Centers for Disease Control and Prevention, Vietnam Country Office, Hanoi, Vietnam, [2]General Department of Preventive Medicine, Ministry of Health of Vietnam, Hanoi, Vietnam, [3]Partnership for Influenza Vaccine Introduction, Task Force for Global Health, Atlanta, GA, USA, [4]Influenza Division, U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA, [5]Global Immunization Division, U.S. Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: In 2019, Vietnam licensed its first locally produced trivalent seasonal inactivated influenza vaccine, IVACFLU-S, manufactured by the Institute for Vaccines and Medical Biologicals (IVAC). For the 2020 season, Task Force for Global Health's Partnership for Influenza Vaccine Introduction (PIVI) purchased 136,000 doses of IVACFLU-S to administer to healthcare workers (HCW) in 24 provinces in Vietnam. Active surveillance for adverse events following immunization (AEFI) was conducted. **Methods**: Vietnam's General Department of Preventive Medicine developed a web-based application for AEFI reporting, with assistance from CDC's Vietnam country office, and encouraged vaccinees to report AEFIs, including mild symptoms or local reactions. At day 7 after vaccination, all vaccinees were contacted via email; local health staff also contacted a proportionate 2% sample

of vaccinees by phone (i.e., one in every 50 vaccinees), using a questionnaire to ask about local or systemic AEFI. In addition, immunization sites and hospitals could also report AEFIs for any vaccinees presenting for care. **Results**: A total of 133,067 (98%) influenza vaccine doses were administered to HCWs. Of these, 20,011 (15%) responded through email to the web-based survey with 17,234 (86%) reporting they had no adverse events and 2,777 (14%) reporting an AEFI. The majority, 2775 (99.93%) reported mild adverse events; 2 (0.07%) reported serious AEFI (anaphylaxis) – 1 was later confirmed. Among vaccinees, 2,388 persons were contacted via phone; 1,805 (76%) stated they tolerated vaccination well without symptoms and 583 (24%) reported mild AEFI. In comparison, providers reported 1,848 (1.4%) among all 133,067 vaccinees to the national traditional AEFI reporting system: all were mild. Reporting AEFI through more than one method was possible, but not documented. **Conclusions**: The vast majority of AEFI reports were mild which is reassuring for the safety of IVACFLU-S vaccine. Compared with the traditional AEFI reporting system, the active AEFI surveillance collected a greater number of AEFIs. Although the phone-based survey resulted in a higher proportion of reported AEFI, the email-based survey, a cost-effective method that can access more people with minimal costs and is feasible for large-scaled vaccination campaigns.

### Poster 368. The Burden of Influenza among Kenyan Pregnant and Postpartum Women and Their Infants, 2015–2020

**N.A. Otieno**[1], B.O. Nyawanda[1], M. McMorrow[2], M. Oneko[1], D. Omollo[1], S. Lidechi[1], M.-A. Widdowson[3], B. Flannery[2], S.S. Chaves[4], E. Azziz-Baumgartner[2], G.O. Emukule[4]
[1]Kenya Medical Research Institute, Center for Global Health Research, Kisumu, Kenya, [2]Centers for Disease Control and Prevention, Atlanta, GA, United States, [3]US Centers for Disease Control and Prevention, Division of Global Health Protection, Nairobi, Kenya, [4]US Centers for Disease Control and Prevention, Influenza Program, Nairobi, Kenya
**Background:** In tropical Africa, data about influenza-associated illness burden are needed to assess potential benefits of influenza vaccination among pregnant women. We estimated the incidence of influenza among pregnant and postpartum women and their infants in Siaya County, Kenya. **Methods:** We enrolled women at <31 weeks gestation and conducted weekly follow-up until 6 months postpartum to identify acute respiratory illnesses (ARI). We defined ARI among mothers as reported cough, rhinorrhoea or sore throat, and among infants as maternal-reported cough, difficulty breathing, rhinorrhoea or clinician diagnosis of respiratory illness. We collected nasal/nasopharyngeal and oropharyngeal swabs from mothers/infant with ARI and tested for influenza A and B using molecular assays. We calculated antenatal incidence of laboratory-confirmed influenza among mothers and postnatal incidence among mothers and infants. **Results:** During June 2015–May 2020, we screened 3,217 pregnant women and enrolled 3,066 who met the criteria for study participation. We analysed data from 3,026 pregnant women at a median gestational age of 16 weeks (interquartile range [IQR], 13, 18) and followed 2,550 infants. Incidence of laboratory-confirmed influenza during pregnancy (10.3 episodes per 1,000 person-months [95% CI 8.6–11.8]) was 2-fold higher than in the postpartum period (4.0 [95% CI 2.6–5.5]; $p<0.01$). Incidence was significantly higher among HIV-infected pregnant women (15.6 [95% CI 11.0–20.6] vs. 9.1 [95% CI 7.5–10.8]; $p<0.01$). Incidence among young infants was 4.4 (95% CI 3.0–5.9) and similar among HIV-exposed and HIV-unexposed infants. **Conclusion:** Our findings suggest a substantial burden of influenza illnesses during pregnancy, with a higher burden among HIV-infected mothers. Kenyan authorities should consider the value of vaccinating pregnant women, especially if HIV-infected.

### Poster 369. Antibody Responses Induced by Trivalent Inactivated Influenza Vaccines among Pregnant and Non-Pregnant Women: A Matched Cohort Study

**S. Nakphook**[1,2], J. Patumanond[3], M. Shresthal[4], K. Prasert[5], M. Chittaganpitch[6], J.A. Mott[7,8], P. Praphasiri[7]
[1]Department of Disease Control, Institute of Preventive Medicine, Ministry of Public Health, Nonthaburi, Thailand, [2]Faculty of Medicine, Thammasat University, Pathum Thani, Bangkok, Thailand, [3]Faculty of Medicine, Center for Clinical Epidemiology and Clinical Statistics, Chiang Mai University, Chiang Mai, Thailand, [4]Faculty of Social Sciences and Humanities, Department of Society and Health, Mahidol University, Nakhon Pathom, Thailand, [5]Department of Primary Care Unit and Family Medicine, Nakhon Phanom Provincial Hospital, Nakhon Phanom, Thailand, [6]National Institute of Health, Ministry of Public Health, Nonthaburi, Thailand, [7]Influenza Program, Thailand Ministry of Public Health - US Centers for Disease Control and Prevention Collaboration, Nonthaburi, Thailand, [8]Influenza Division, US Centers for Disease Control and Prevention, Atlanta, Georgia, United States of America
**Background:** We compared influenza antibody titers among vaccinated and unvaccinated pregnant and non-pregnant women. **Methods:** During June 1– September 30, 2018, four groups of cohort participants—vaccinated pregnant, unvaccinated pregnant, vaccinated non-pregnant, and unvaccinated non-pregnant women were selected by

matching age, gestational age, and the week of vaccination. Serum antibody titers against each strain of 2018 Southern Hemisphere inactivated trivalent influenza vaccine (IIV3) were assessed by hemagglutination inhibition (HI) assay on Day 0 (pre-vaccination) and Day 28 (one-month post-vaccination) serum samples. Geometric mean titer (GMT), GMT ratio (GMR), seroconversion (defined as ≥ 4-fold increase in HI titer), and seroprotection (i.e. HI titer ≥ 1:40) were compared across the study groups using multilevel regression analyses, controlling for previous year vaccination from medical records and baseline antibody levels. **Results:** A total of 132 participants were enrolled in the study (33 in each of the four study groups). The baseline GMTs for influenza A(H1N1), A(H3N2), and B vaccine strains were not significantly different among all four groups (all p-values >0.05). After one month, both vaccinated groups had significantly higher GMT, GMR, seroconversion, and seroprotection than their unvaccinated controls (all p-values <0.05). The seroconversion rate was over 60% for any strain among the vaccinated groups, with the highest (88.8%) observed against A(H1N1) in the vaccinated pregnant group. Similarly, at least 75% of the vaccinated participants developed seroprotective antibody levels against all three strains; the highest seroprotection was found against A(H3N2) at 92.6% among vaccinated non-pregnant participants. Antibody responses (post-vaccination GMT, GMR, seroconversion, and seroprotection) were not significantly different between pregnant and non-pregnant women for all three strains of IIV3 (all p>0.05). **Conclusions:** The 2018 seasonal IIV3 was immunogenic against all three vaccine strains and pregnancy did not seem to alter the immune response to IIV3. These findings support the current influenza vaccination recommendations for pregnant women.

### Poster 370. Risk Factors for Acute Lower Respiratory Tract Infection (ALRI) and Influenza-Associated ALRI among Adults aged ≥60 Years in India: Results from a Two-Year Cohort Study

**K.E. Lafond**[1], P. Rajkumar[2], R. Kumar[3], R. Amarchand[3], A. Prabhakaran[4], A. Choudekar[5], G. Gopal[6], A. Chaudhary[5], G. Kumar[2], V. Potdar[7], S.D. Bhardwaj[7], S. Kanungo[8], B. Manna[8], A.K. Chakrabarti[8], E. Azziz-Baumgartner[1], S. Saha[4], L. Dar[5], A. Krishnan[3]

[1]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]National Institute of Epidemiology, Chennai, India, [3]Centre for Community Medicine, All India Institute of Medical Sciences, New Delhi, India, [4]Influenza Program, US Centers for Disease Control and Prevention, New Delhi, India, [5]Department of Microbiology, All India Institute of Medical Sciences, New Delhi, India, [6]Center for Disease Dynamics, Economics & Policy, New Delhi, India, [7] National Institute of Virology, Pune, India, [8] National Institute of Cholera and Enteric Diseases, Kolkata, India

**Background**: Awareness of risk factors for severe acute respiratory disease among older adults is essential for timely care seeking and interventions such as vaccination and treatment. However, data are limited on risk factors among older adults in lower- and middle-income countries. **Methods:** We established a community-based cohort among adults aged ≥60 years at four diverse sites (urban, peri-urban, and rural) across India. Project nurses visited participants weekly to check if participants had developed acute lower respiratory tract infection (ALRI) within the last seven days (defined as new or worsening of cough, difficulty breathing, dyspnea, chest pain, respiratory rate >20 breaths/minute, measured fever, or a symptom complex of fever, sweating, headache, and myalgia). Nasal and throat samples were collected for each ALRI episode and tested for influenza by RT-PCR. We collected data on individual and household risk factors including comorbidities, smoking, and biomass fuel use by self-report at baseline. We calculated adjusted rate ratios (aRR) for incidence of ALRI and influenza-associated ALRI by key risk factors. **Results:** During July 2018 – March 2020, we followed 6,016 individuals and identified 1085 ALRI episodes, including 99 influenza-associated ALRI episodes. Age was associated with increased risk of ALRI; aRRs for 65-74 years and 75 and older were 1.4 (95% CI: 1.1-1.6) and 1.5 (95% CI: 1.1-1.9), respectively, versus those aged 60-64 years. ALRI risk also increased with number of comorbid conditions, (aRR=3.0, 95% CI: 2.0-4.5 for those with four or more conditions versus those with no conditions) and among current smokers (aRR=1.3, 95% CI: 1.1-1.6). Participants with tuberculosis (TB) or chronic respiratory disease also had elevated risk of ALRI (aRR=2.6, 95% CI: 1.6-4.1 and aRR=3.8, 95% CI 3.2-4.6, respectively). Similar trends were identified among influenza-associated ALRI episodes, though these were not significant because of limited sample size. **Conclusions:** In this cohort, risk of ALRI and influenza-associated ALRI were associated with older age, comorbidities, particularly TB and chronic respiratory diseases, and smoking. Better awareness of these risk factors can be used to target local public health messaging and encourage timely care-seeking among the highest risk older adults.

### Poster 371. Incidence of Influenza-associated Acute Respiratory Infection among Adults Aged ≥60 Years in Multi-site Community Cohort in India

**R. Kumar**[1], R. Amarchand[1], A.O. Prabhakaran[2], A. Choudekar[1], G. Gopal[1], S. Dhakad[1], P. Rajkumar[3], G. Kumar[3], V. Potdar[4], S.D. Bhardwaj[4], S. Kanungo[5], B. Manna[5], A.K. Chakrabarti[5], A. Chaudhary[1], K.E. Lafond[6], E. Azziz-Baumgartner[6], S. Saha[2], L. Dar[1], A. Krishnan[1]

[1]All India Institute of Medical Sciences, New Delhi, India, [2]Influenza Division, CDC India Country Office, New Delhi, India, [3]National Institute of Epidemiology, Chennai, India, [4] National Institute of Virology, Pune, India, [5]National Institute of Cholera and Enteric Diseases, Kolkata, India, [6]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background**: Despite a growing population of persons aged ≥60 years, few data are available on the incidence of influenza among older adults in India. We conducted a prospective multi-site cohort study among community dwelling adults aged ≥60 years to estimate the incidence of influenza-associated acute respiratory infection (ARI). **Methods:** During July 2018-March 2020, trained nurses conducted weekly household surveillance for ARI among cohorts at four sites: Ballabgarh, Chennai, Kolkata, and Pune. We defined ARI as new onset/ worsening of cough or difficulty in breathing in the last seven days and ALRI as ARI along with dyspnea or chest pain, a respiratory rate of >20 breaths/minute, and either measured fever or a reported symptom complex of fever, sweating, headache, and myalgia; those not fulfilling this criterion were categorized as AURI. Nurses collected nasal and throat swabs from all ALRI cases and 20% of randomly selected AURI cases for influenza testing by real time reverse transcriptase polymerase chain reaction (RT-PCR). We also estimated the fraction of AURI cases without respiratory samples that, if sampled, would have tested positive for influenza by assuming unsampled cases had a similar probability of testing positive for influenza as sampled cases identified the same site and epidemic and added thus derived influenza-associated AURI incidence to influenza-associated ALRI to estimate influenza-associated ARI incidence. **Results:** We followed 6,016 older adults for 7,903 person-years. The median age of the cohort was 65 years (IQR 62-70); and 0.2% reported influenza vaccination. The incidence of ARI was 145.1 (CI- 142.5-147.8)/100py and ALRI was 13.1 (CI-12.3-13.9)/100py. Incidence of influenza-associated ARI was 6.8 (CI-6.3-7.4)/100py. The influenza associated ALRI rate was 1.3 (CI-1.0-1.5)/100py. In year 1 (July 2018-June 2019) when influenza A pdm9(H1N1) was the predominant strain 10.1% of ALRI and 4.6% of AURI samples were positive for influenza; in year 2 (July 2019-March 2020) when influenza A(H3N2) and influenza B was predominant strain, 8.0% of ALRI and 3.5% of AURI samples were positive. **Conclusions:** 1-in-77 older adults had influenza detected in a case of ALRI each year in this cohort which has very low coverage of influenza vaccine, suggesting the utility of exploring the value proposition of influenza vaccination among older adults.

### Poster 372. Multi-patient, Multi-species KPC Outbreak in an Iowa Long Term Care Facility

**M. Nelson**[1], W. Hottel[1], V. Reeb[1], W. Aldous[1], M. Pentella[1], A. Hennenfent[2], N. Wilde[2], T. Goss[2]
[1]State Hygienic Laboratory at the University of Iowa, Coralville, IA, USA, [2]Iowa Department of Public Health, Des Moines, IA, USA
**Background:** *Klebsiella pneumoniae* cabapenemase (KPC) is an Ambler class A carbapenemase of critical public health importance. While first described in *Klebsiella pneumoniae*, this plasmid-mediated carbapenemase can be transferred to other members of the Enterobacterales via horizontal gene transfer. In 2017, as part of routine carbapenem resistant Enterobacterales (CRE) surveillance, the State Hygienic Laboratory (SHL) at the University of Iowa (UI) identified an *Escherichia coli* isolate harboring a KPC-3 gene. Within three years, *Providencia stuartii*, *Klebsiella pneumoniae*, and *Proteus mirabilis* were also isolated from the same index patient, all harboring KPC-3. Six months after confirming the *K. pneumoniae*, the bacterium harboring KPC-3 was isolated from a patient who resided down the hall from the index patient. Following a point-prevalence-study (PPS) at the patient's residential facility, five residents of the same unit were confirmed to be colonized with KPC producing bacteria, *E. coli*, *K. pneumoniae*, *P. stuartii*, *P. mirabilis*, and *Citrobacter freundii*. **Methods:** Whole-genome sequencing utilizing the Illumina MiSeq platform and bioinformatics analysis using an in-house pipeline run on the UI Argon High Performance Computing cluster. **Results:** 23 isolates spanning five species, five patients, and four years all harbor a KPC-3 gene variant and IncC plasmid replicon sequence with 100% sequence homology. **Conclusions:** Carbapenemase producing organisms are an urgent public health threat causing hard to treat, often fatal infections. Adherence to infection control policies is essential to prevent the transmission of CRE's in health care settings. Horizontal gene transfer of carbapenemase carrying plasmids increases the risk of ongoing transmission, further highlighting the need for adherence to infection control policies.

### Poster 427. Care for Latent Tuberculosis Infection at Kaiser Permanente Southern California: 2009 – 2018

**H. Chen**[1] , K. Bruxvoort[1,2], Z. Li[1], R. Wei[1], L. Qian[1], H. Fischer[1], S.F. Shaw[1], B. Spence[1], B. Lewin[3], J. Skarbinski[4,5], J.H. Ku[1], S.Y. Tartof[1,6]
[1]Kaiser Permanente Southern California, Department of Research & Evaluations, Pasadena, CA, USA , [2]University of Alabama at Birmingham, Department of Epidemiology, Birmingham, AL, USA, [3]Kaiser Permanente Los Angeles, Department of Family Medicine, Los Angeles, CA, USA, [4]Kaiser Permanente Northern California,

Division of Research, Oakland, CA, USA, [5]Kaiser Permanente Oakland Medical Center, Department of Infectious Diseases, Oakland, CA, USA, [6]Kaiser Permanente Bernard J. Tyson School of Medicine, Department of Health System Science, Pasadena, CA, USA
**Background**: In California, 80% of active tuberculosis (Mycobacterium tuberculosis) arises from latent tuberculosis infection (LTBI), and more than two million Californians are estimated to have LTBI. Successful treatment of LTBI involves multiple steps from comprehensive screening to treatment completion. However, gaps in the LTBI care cascade are not well characterized. This study aimed to assess the steps in the care cascade among patients screened for LTBI at Kaiser Permanente Southern California (KPSC) in order to identify gaps and inform future interventions. **Methods**: We performed a descriptive study within a retrospective cohort of adults from KPSC using electronic health records to identify patients screened for LTBI with a TST (Tuberculin Skin Test) or IGRA (interferon-gamma release assay) from 2008 – 2018. Patients aged <18 years or those with prior active TB were excluded. We described the proportion of individuals completing each step of the LTBI care cascade. LTBI treatments included isoniazid, rifampin, isoniazid and rifampin, or isoniazid and rifapentine, per national LTBI treatment guidelines. **Results**: Overall,1,207,974 patients were screened for LTBI, of which 6% tested positive for LTBI. Of the 73,006 patients testing positive for LTBI, 66% had a chest Xray. Of the 45,412 patients who had a chest X-ray, 68% (N=31,170) were not prescribed LTBI medications, 5.5% (N=2,496) did not initiate medication within 1 year from first prescription, and 23.6% (N=10,745) initiated treatment within 1 year from first prescription. Of patients who initiated medication within one year from first prescription (N=10,745), 49% (N=5,237) completed treatment. **Conclusions**: This study found that a large proportion of patients with LTBI are not prescribed treatment, and many patients who begin treatment do not complete it. Further work is needed to understand reasons for not treating patients with positive tests and to improve screening algorithms. Furthermore, tailored interventions are needed to help patients complete LTBI treatment.

## Zoonotic and Vector-borne Diseases

### Poster 373. A Generalizable One Health Framework for the Control of Zoonotic Diseases

**R.R. Ghai**[1], R.M. Wallace[1], J.C. Kile[1], T.R. Shoemaker[1], A.R. Vieira[1], M.E. Negron[1], S.V. Shadomy[1,2], J.R. Sinclair[1], G.W. Goryoka[1], S.J. Salyer[1], C. Barton Behravesh[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Food and Agriculture Organization of the United Nations, Rome, Italy
**Background:** Effectively preventing and controlling zoonotic diseases requires a One Health approach involving collaboration across sectors responsible for human health, animal health, and the environment. The Generalizable One Health Framework (GOHF), a five-step framework was developed to provide a standardized structure for using a One Health approach at the local, sub-national, national, regional, or international level. The GOHF builds off existing international One Health guidance by providing a framework that initially focuses on capacity building for zoonotic disease programs. **Methods:** The GOHF was developed by subject matter experts in One Health, zoonotic diseases, public health, and animal health. This framework was developed by combining successful existing and idealized processes for implementing zoonotic disease programming globally. **Results:** The GOHF is divided into three components. The first is a visualization that outlines a stepwise approach to managing zoonoses, including: 1) engaging stakeholders; 2) assessing existing capacity; 3) developing plans to address zoonoses; 4) implementing plans; and 5) monitoring and evaluating progress. The second component is a toolkit that compiles existing resources matched to steps of the framework. The final component are schematics of five frequently prioritized zoonoses (anthrax, brucellosis, zoonotic influenza viruses, rabies, and viral hemorrhagic fevers), that illustrate recommended One Health approaches taken to surveillance and response. **Conclusions:** The GOHF highlights that while developing prevention and control programs will require specialized technical expertise, the One Health approach taken is similar irrespective of the zoonoses. Further, rather than build independent programs for priority zoonotic diseases, guidance provided by the GOHF is intended to deepen One Health capacity with the objective of gradually building a comprehensive One Health system that can combat a variety of shared health threats at the human-animal-environment interface.

### Poster 374. Strengthening Anthrax Emergency Preparedness: Evaluation of Rapid Same-Day BSL-3 Whole Genome Sequencing at the New York State Wadsworth Center Biodefense Laboratory

**D. Centurioni**, A. Conley, B. Cherney, L. Rishishwar, V. Chivukula, H. McLaughlin, T. Kongphet-Tran, L. Medina-Cordoba, P. Michel, T. Maxson, T. Aden, J. Villanueva, T. Wolford, J. Bugrysheva, M. Perry, D. Sue
Centers for Disease Control and Prevention, Atlanta, GA, USA; NYS Wadsworth Center Biodefense Laboratory, Albany, NY, USA; Association of Public Health Laboratories, Silver Spring, MD, USA

Following an emergency event involving *Bacillus anthracis*, detection of antimicrobial resistance (AMR) will guide decisions about anthrax treatment and post-exposure prophylaxis to save lives. CDC's BioDefense Research and Development laboratory completed a pilot study of same-day whole genome sequencing for *B. anthracis* in collaboration with the Association of Public Health Laboratories and the New York State Department of Health Wadsworth Center. Eleven *B. anthracis* strains were sequenced using a portable long-read DNA sequencer (MinION) at the Wadsworth Center Biodefense BSL-3 laboratory using BDRD developed protocols. Genomic data sets were analyzed on-site using custom bioinformatics software called PiMA. The software was installed on the same laptop that powered the MinION sequencer, and performed quality control analysis, de novo sequence assembly, identification and characterization of AMR features, including the detection of plasmids, integration sequences and mutations. *B. anthracis* nucleic acid was prepared from culture isolates and sequenced in the same biological safety cabinet, thereby reducing the time to results. For single-plex runs, the chromosome and virulence plasmid(s) were assembled after only 15 minutes of sequencing. Following analysis, chromosomal single nucleotide variants (SNVs) related to fluoroquinolone resistance were interrogated, and correctly identified. However, a SNV located in a homopolymeric region that can confer *B. anthracis* penicillin resistance was not reliably resolved by MinION sequencing alone. In this study, laboratory scientists successfully profiled plasmids, mutations, and genetic signatures associated with AMR in under 5 hours, demonstrating that trained laboratory scientists could rapidly sequence and analyze *B. anthracis* in a BSL-3 using a portable sequencer, strengthening public health preparedness for an emergency anthrax response.

### Poster 375. Epidemiological and Clinical Characteristics of a Chikungunya Outbreak along Thai-Myanmar Border, Thailand, 2019 - 2020

**S. Bhengsri**[1], S. Thamthitiwat[1], S. Uttayamakul[2], P. Sawatwong[1], N. Chuenchom[3], S. Chaoprasert[4], S. Butapun[4], S. Boonlong[4], B. Skaggs[1], E. Bloss[1], C.J. Gregory[1,5]
[1]Division of Global Health Protection, Centers for Disease Control and Prevention, Bangkok, Thailand, [2]Bamrasnaradura Infectious Diseases Institute, Nonthaburi, Thailand, [3]Maesot Hospital, Tak, Thailand, [4]Tak Provincial Health Office, Tak, Thailand, [5]UNICEF, Programme Division, New York, USA
**Background:** Chikungunya virus (CHIKV), the mosquito-borne virus causing chikungunya disease, last caused an outbreak in Southern Thailand in 2008. We describe the epidemiological and clinical characteristics of patients with CHIKV infection in Tak, Northwest Province as part of surveillance for acute febrile illness (AFI) along the Thai-Myanmar border. **Methods:** Patients aged 2-80 years hospitalized with AFI, defined as a temperature ≥38 ºC or history of fever ≤7 days were enrolled. We defined AFI patients with no evidence of respiratory symptoms or diarrheal disease as patients with undifferentiated fever (UF). Demographic and laboratory results were abstracted from medical records. Patients were interviewed for clinical symptoms and risk factors. Blood samples were collected from all UF patients and a randomly selected 20% of AFI patients for CHIKV PCR testing. **Results:** During June 2017 - May 2020, 4,041 febrile patients were included. Samples were collected from 1,734 patients; CHIKV was detected in 137 (7.9%) patients [106/1,100 (9.6%) of UF and 31/634 (4.9%) of AFI]. All cases were detected during May 2019 – January 2020; monthly positive rates ranged from 9-45%, peaking in July 2019. Among 137 PCR positive cases, median age was 36 (range 17-51) years, 49% were male, 87% were Thais, 97% reported mosquito bites and 69% were missed (not clinically diagnosed as CHIKV) on admission. In multivariate analysis, compared to AFI patients that tested negative for CHIKV (N=1,597), CHIKV cases were more likely to have muscle pain [85% vs. 58%, p<0.01], joint/bone pain [84% vs. 33%, p<0.01], back pain [61% vs. 38%, p<0.01], or rash [32% vs. 11%, p<0.01]; they were less likely to have thrombocytopenia [platelet ≤100,000/µl (2.7% vs. 18%, p=0.03)], or leukocytosis [WBC ≥10,000/µl (22% vs. 46%, p=0.02)]. CHIKV patients were more likely to report prior contact with other febrile household members (aOR 2.4; 95%CI=1.7-3.5), coworkers (aOR 3.0; 95%CI=1.9-4.8) or neighbors (aOR 2.4; 95%CI=1.6-3.7). **Conclusions:** A lab-based surveillance system detected a chikungunya outbreak in Tak Province; CHIKV cases were detected by PCR that otherwise would have been missed. Eliminating transmission from mosquitoes and limiting mosquito exposure to febrile persons should be considered if CHIKV is detected by AFI surveillance in the future.

### Poster 376. Strategic and Operational Limitations Likely to Explain the Persistence of the Tenth Ebola Virus Disease Epidemic in Eastern Democratic Republic of the Congo

**N. Taty**[1,2,3], D. Bompangue[1,3], S. Misambu[1], J.J. Muyembe[4], N. Meschnet de Richmond[2]
[1]Research and Training Unit on Ecology and Control of Infectious Diseases, University of Kinshasa, Kinshasa, Democratic Republic of the Congo, [2]Montpellier Geography and Planning Laboratory, University of Paul Valéry, Montpellier, France, [3]National Program for the Elimination of Cholera and the Control of Other Disrheic Diseases,

Ministry of Health, Kinshasa, Democratic Republic of the Congo, [4]National Institute for Biomedical Research, Kinshasa, Democratic Republic of the Congo

**Background:** Ebola Virus Disease (EVD) first revealed in 1976 in the Democratic Republic of Congo (DRC) and southern Sudan. As of June 2020, 30 epidemics have already been reported in Africa, including 11 epidemics in the DRC. The 10th EVD epidemic in the DRC in three provinces in the east of the country is the longest and the most geographically widespread. **Methods:** An analysis of the strategic and operational limits during the management of this epidemic was carried out by a qualitative approach using the documentary review and semi-structured interviews. The critical analysis of the content of five Strategic Response Plans developed during the management of the 10th EVD epidemic in the DRC and of 65 daily situation reports completed by the analysis of the content of the speeches of 26 actors interviewed to respond to the original question. **Results:** It emerges from this investigation that the complexity of the field (insecurity, movement of the population, community resistance) does not fully explain the extent and duration of the 10th epidemic of EVD in the DRC. Intrinsic errors made by the teams in the planning of the management of operations added to the complexity of the field, amplifying resistance, accelerating the spatial spread of the epidemic and sometimes artificially prolonging the duration of the epidemic in the sites. affected. The contextualization of planning and modus operandi on epidemics are just as important as the large financial volumes and human resources often deployed in large numbers in the field. **Conclusion:** Subsequent studies on the governance of epidemics of infectious diseases in the DRC, particularly that of EVD, are necessary to better understand the errors repeated since several epidemics reported not only in the DRC but also in other African countries.

### Poster 377. Emergency Department Visits for Tick Bites Consistently Predict Peak Visits for Lyme Disease in Areas of High and Medium Lyme Disease Incidence

**C.C. Nawrocki**[1], L. Radhakrishnan[2], A.F. Hinckley[1], G.E. Marx[1]

[1]Division of Vector-Borne Diseases, Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Division of Health Informatics and Surveillance, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background**: Syndromic surveillance can be a timely and complementary approach to traditional surveillance of reportable infectious diseases and is currently the only national surveillance system for tick bites. Peak emergency department (ED) visits for tick bites might predict peak ED visits for Lyme disease and could inform timely public health prevention messaging to reduce risk of Lyme disease and other tickborne diseases. **Methods**: Using the Electronic Surveillance System for the Early Notification of Community-Based Epidemics, we applied algorithms identifying ED visits for tick exposure and for suspected Lyme disease across three Health and Human Services (HHS) regions with known high (Region 1), medium (Region 5), and low (Region 8) Lyme disease incidence during 2017 – 2019. We then determined average number and incidence of ED visits for both tick bite and Lyme disease, and average time between peak annual ED visits for tick bite and Lyme disease. **Results**: In Region 1, the average annual number and incidence of ED visits for tick bites was 8,067 (235/100,000 ED visits) and 3,210 (93/100,000 ED visits) for Lyme disease; in Region 5, it was 2,222 (28/100,000 ED visits) for tick bites and 965 (12/100,000 ED visits) for Lyme disease; and in Region 8, it was 181 (11/100,000 ED visits) for tick bites and 77 (4/100,000 ED visits) for Lyme disease. The average peak MMWR week for tick bite was 22 in Regions 1 and 5 and MMWR week 23 in Region 8. Peak ED visits for tick bite preceded peak ED visits for Lyme disease each year in Regions 1 and 5 (on average, by 6 weeks in Region 1 and by 5 weeks in Region 5); no clear peak in ED visits occurred for Lyme disease in Region 8. **Conclusion**: During this 3-year period, syndromic surveillance provided consistent temporospatial trends and was a reliable indicator of healthcare burden of patients presenting to the ED for tick bites and suspected Lyme disease. Peak ED visits for tick bites can be used as an early indicator of Lyme disease risk in regions with high or medium incidence of Lyme disease and might inform public health messaging and clinician awareness.

### Poster 378. *Brucella melitensis* Outbreak in Minnesota Associated with Unpasteurized Soft Cheese Brought Back by a Traveler Returning from Mexico

**M. Bye**[1], K. Smith[1], J. Scheftel[1], M. Sullivan[2], L. Magnuson[1], S. Wang[2], M. Ireland[1], C. Medus[1]

[1]Infectious Disease Epidemiology, Prevention, and Control Division, Minnesota Department of Health, St. Paul, MN, USA, [2]Minnesota Department of Health Public Health Laboratory, St. Paul, MN, USA

**Background:** Brucellosis is caused by direct contact with or consumption of products from infected animals. Each year, 0 – 5 Minnesotans acquire brucellosis, most often during foreign travel. In June 2021, three brucellosis cases who reported eating unpasteurized cheese from Mexico were reported to the Minnesota Department of Health (MDH). **Methods:** MDH conducts passive surveillance for brucellosis, including medical chart abstraction and patient interview. Suspect clinical isolates must be sent to MDH for confirmation and identification to species. A

case was defined as a Minnesota resident with a lab-confirmed *B. melitensis* infection who reported eating locally acquired cheese from Mexico. Cases were interviewed using a structured questionnaire. A sample of the cheese was obtained from a case for testing. **Results:** Eleven outbreak cases were identified. The median age of cases was 44 years (range, 16-52 years), 7 (64%) were male, and all were Hispanic. Nine cases were interviewed by a native Spanish-speaking MDH staff member. Cases reported purchasing or being gifted an unpasteurized homemade queso fresco, likely made with goat milk, from an individual who brought it from Guanajuato, Mexico. Cheese was purchased and consumed from May through July 2021. Cases reported illness onsets from late May through September 11, 2021. All cases reported fever, 7(70%) headache, 7(70%) lack of appetite, and 6(60%) muscle aches. Ten (91%) cases were hospitalized, for a median of 7 days (range, 1-13 days). Cases experienced severe complications including endocarditis (n=3), sepsis (n=3), splenomegaly (n=1), and hepatitis (n=1). Post-exposure prophylaxis and 6 months of symptom and serologic monitoring was recommended for asymptomatic cheese consumers. Cases were given letters to distribute to acquaintances who may have eaten the cheese, encouraging them to seek care. On July 1, a health alert was issued to notify local healthcare providers of the outbreak. The cheese sample was PCR-positive at the Minnesota Department of Agriculture lab; *B. melitensis* was culture-confirmed from the cheese at MDH. **Conclusions:** Unpasteurized cheese brought from other countries can cause locally acquired brucellosis. Clinicians should consider brucellosis in patients with compatible symptoms even without a relevant travel history.

### Poster 379. Canine Dirofilariasis in the Republic of Armenia

**V. Hakobyan**, T. Markosyan, K. Sargsyan, S. Kharatyan, H. Elbakyan
Scientific Centre for Risk Assessment and Analysis in Food Safety Area, CJCS, Yerevan, Republic of Armenia
**Background:** Dirofilariasis is an anthropozoonotic disease caused by the nematode of the genus *Dirofilaria*, in animals and humans. While dogs and wild canids are the natural reservoirs, humans can become incidental hosts. Adult helminths *D. repens*, parasitize under the skin and *D. immitis* are localized in the heart. Infection with dirofilariasis occurs when animals are bitten by mosquitoes infected with microfilariae. The problem of dirofilariasis in Armenia has not been sufficiently studied. We proposed to study the epizootic situation of canine dirofilariasis in two regions of the Republic of Armenia (RA) and to clarify the causes of infection to prevent dirofilariasis. **Methods**. The blood and serum of dogs from Armavir and Shirak regions were studied in 2018-2020. The survey of dogs was carried out twice a year during the period of active flight of mosquitoes. A total of 155 dogs of different breeds, both sexes, and aged from 1 to 10 years were examined. For laboratory diagnostics of dirofilariasis, methods of a thick crushed drop of blood and enrichment according to Knott were used, as well as immunodiagnostic tests for rapid diagnostics. **Results.** We determined that 5.8% (9) of the examined dogs from Armavir and Shirak region were infected by dirofilariasis, and disease was most often recorded in dogs aged 5 to 8 years. The highest infection rate of 4.52% (7) was recorded among the dogs of Armavir region, which can be explained by the presence of mosquitoes of the genus *Aedes, Culex, Anopheles*, which infect dogs during bites. The infection rate of dogs in Shirak marz was 1.29% (2 dogs). **Conclusions.** Thus, local invasion of dirofilariasis has been registered in the territory of the RA. In this regard, it is necessary to prevent the emergence of new foci of the disease. For this purpose, timely registration, analysis of each case of canine disease, promotion of preventative treatment, and the identification of areas with the greatest risk of infection due to the presence of relevant mosquito vectors are needed. As a preventive measure, it is necessary to prevent dogs from contact with blood-sucking insects, using various insecticides and repellents to destroy and deter disease vectors. This will also reduce the dirofilariasis incidence in dogs, which will minimize the risk to humans.

### Poster 380. Histopathology and Immunohistochemistry Methods To Diagnose Fatal Malaria Infection in Minimally Invasive Tissue Sampling (MITS) Samples

**M.R. Bias**[1,2], T.M. Wilson[1,2], J.M. Ritter[2], J.N. Seixas[2], B.E. Ndibile[3], S. Sava[3], D. Adera[3], T. Massawa[3], I.A. Bassey[4], C. Carrilho[5], M.R. Ismail[5], D. Jordao[5], F.C. Fernandes[5], C.B. Traore[6], D.M. Blau[2], S.R. Zaki[2], R.B. Martines[2]
[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3] Kisii Teaching and Referral Hospital, Kisii, Kenya, [4] ICAP-Columbia University, Makeni, Sierra Leone, [5]Department of Pathology, Faculty of Medicine, Eduardo Mondlane University and Maputo Central Hospital, Maputo, Mozambique, [6]Department of Pathological Anatomy and Cytology, University Hospital of Point G, Bamako, Mali
**Background:** Malaria infection is a leading cause of mortality in low-income countries, including in children aged <5. There is a limited data about the use of specialized tissue-based diagnostic methods on minimally invasive tissue sampling (MITS) samples to investigate malaria as cause of death. **Methods:** The CDC's Infectious Diseases

Pathology Branch (IDPB) receives post-mortem formalin-fixed MITS samples from children <5 years in 7 countries in sub-Saharan Africa and South Asia as part of Child Health and Mortality Prevention Surveillance (CHAMPS). Specialized diagnostics at IDPB, including routine histopathological (HP) evaluation and immunohistochemical testing (IHC) for Plasmodium falciparum were performed on brain and liver tissues to identify malaria infection in MITS samples received between January 2017 to July 2021 from 4 countries where malaria is endemic. Pathologists from IDPB and CHAMPS sites performed collaborative pathology review using telepathology, and findings were discussed in online meetings to reach consensus diagnoses and to increase pathology capacity at sites through quality assessment and training for identification of HP patterns and interpretation of IHC. **Results:** We identified 169 (12%) deaths among 1412 evaluated as having suspected malaria based on histomorphological features of malaria infection, including presence of hemozoin pigment and/or intraerythrocytic protozoan. Among these, 423 *P. falciparum* IHC tests were performed on liver and brain MITS samples from 169 cases deaths. Of these, malaria was detected in 113 (67%) cases in one or both tissues. IDPB demonstrated features of malaria and of IHC staining during virtual meetings with the CHAMPS sites to increase diagnostic capacity for malaria at the sites. **Conclusions:** Malaria is an important cause of child mortality in low-income countries. HP evaluation in combination with specialized IHC testing in MITS samples is useful for the diagnosis of malaria infection. The sequestration of parasitized erythrocytes in the microvasculature of vital organs is central to the pathogenesis of severe malaria, and recognition of HP and IHC features of malaria infection is crucial for the diagnosis.

### Poster 381. *Francisella tularensis* Bone and Joint Infections – United States, 2004-2020

**A. Beeson**[1], M. Baker[2], B. Dell[3], H. Schnitzler[4], T. Woodall[5], A. Schwartz[1], J. Petersen[1], A. Hinckley[1], G. Marx[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Missouri Department of Health and Senior Services, Jefferson City, MO, USA, [3]Public Health – Seattle and King County, Seattle, WA, USA, [4]Washington State Department of Health, Seattle, WA, USA, [5]Colorado Department of Public Health and Environment, Denver, CO, USA

**Background:** Tularemia is caused by the highly infectious bacterium *Francisella tularensis* which is recognized as a Tier 1 bioterrorism agent. Tularemia has a range of recognized clinical manifestations, but only 6 bone or joint infections have been reported in the worldwide literature. We sought to identify cases of *F. tularensis* septic arthritis or osteomyelitis in the United States and describe risk factors, diagnosis, treatment, and outcomes for this rare but severe form of tularemia. **Methods:** A case was defined as a patient in the US with a positive *F. tularensis* culture from a bone or joint. Cases were identified from reports made to CDC from 2004 – 2021 as well as from a comprehensive literature search. Supplemental clinical and laboratory data were obtained from medical records. Variables were systematically abstracted and summarized. **Results:** Eleven cases were identified, 8 from CDC reports and 3 from the literature. Most were male (n=9); median age was 61 years (range 10 – 81). Six states were represented. Exposures included lawnmowing (n=7), animal handling (n=4), and insect bites (n=1). Infected sites included 1 finger, 2 elbows, 1 ankle, 1 prosthetic shoulder, 2 prosthetic hips, and 4 prosthetic knees. Five individuals were immunocompromised due to medication (n=3) and/or underlying comorbidities (n=3). All presented with localized symptoms including pain, effusion, warmth, and/or erythema at the site of infection; 5 (45%) also had systemic symptoms including fever, headache, altered mental status, and/or night sweats. Median approximate time from onset of localized symptoms to diagnosis was 3 months (range 0.5-36). Bacteria were visible on gram stain of joint fluid in 2 cases. None had positive blood cultures. Antibiotic choice and duration varied widely. Six case patients underwent surgery, including 2 joint explantations; 5 were hospitalized and no deaths were reported. **Conclusions:** Clinicians should be alert to the possibility of bone or joint infection with *F. tularensis* in those with compatible exposures and history of joint replacement or immunosuppression. Such infections may present as localized pain with or without systemic illness. Blood cultures are not a sensitive diagnostic tool for this form of tularemia. Information on long-term outcomes is needed to guide treatment recommendations.

### Poster 382. Interpolation of Data of Field Researches as a Method of Modeling the Number of Common Voles and Their Fleas and Ticks

**R. Danielyan**, L. Paronyan
National Center for Disease Control and Prevention, Yerevan, Armenia

**Background:** The common vole is a host of infectious diseases like plague, tularemia, leptospirosis, yersiniosis, and erysipeloid in Armenia. The source of the spatial information regarding the ecology of the host and vectors are based on the numbers of rodents and ectoparasites within an area. To improve the quality and effectiveness of surveillance, we need to convert geographic data collected during field research into a digital format. The proposed method is based on the use of global positioning systems (GPS) in field studies to obtain accurate data. **Methods:** To evaluate this method, we utilized field research data collected in the northwestern part of Armenia during the summer of

2021. During this period, 234 survey points were analyzed and samples collected in the field were delivered to the laboratory: 1,874 common voles, 7,780 fleas, and 3,711 ticks. To interpolate the data, we used the *Spatial Analyst Tools* and the *Inverse Distance Weighted* method in *ArcGIS* program. **Results:** After the computer processing of point data, we produced an interpolated raster format of the model with the values of the number of collected common voles, fleas, and ticks in the studied territory. The minimum and maximum abundance of 234 surveyed points were from 0 to 65 individuals of common voles, from 0 to 203 fleas, and from 0 to 37 ticks. Next, we create a simulated surface in the form of maps, where the number of the hosts and vectors by gradations is visualized. Interpolation of data also made it possible to obtain predicted geographic data that can be used to plan autumn field studies. **Conclusions:** This technique can be used as a means of fast and high-quality processing of large arrays of geographical point data. The proposed method can be considered as a broader technology that can be adapted and used in various field studies, for reporting results of large datasets, and improved infectious disease surveillance.

### Poster 383. Understanding Parent and Pediatrician Perceptions of Anthrax Vaccination Use in Children During a Bioterror Emergency

**V.M. Carter**[1], E.M. Allen[1], R. Devchand[2], L. Koehler[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Hager Sharp, Washington, DC, USA
**Background:** During an anthrax emergency, public health officials will recommend a post-exposure prophylaxis (PEP) regimen of antibiotics and multidose anthrax vaccine, adsorbed (AVA). Currently there are no data on AVA use in children, making it available to children <18 years old only under an Investigational New Drug (IND) protocol. Parents will have to make decisions quickly, weighing the benefits of unlicensed AVA use in their children against the high risk for illness and death from anthrax. **Methods:** The Centers for Disease Control and Prevention conducted 12 in-person focus groups with parents and 25 telephone in-depth interviews (IDIs) with pediatricians to understand attitudes and knowledge gaps related to pediatric AVA use. Parent focus groups took place in Washington, DC and Dallas, TX and followed a human-centered design approach to immerse parents in a scenario that detailed a hypothetical anthrax bioterror attack. Focus group findings informed IDIs with pediatricians to understand their knowledge about anthrax PEP in children and barriers to discussing AVA use with parents. Pediatricians represented a range of U.S. regions and a mix of practice settings. Findings supported material development and testing with parents. **Results:** 91 parents and 25 pediatricians participated. Parents had questions about the vaccine's safety and efficacy, its use as PEP, and the antibiotic regimen. Pediatricians anticipated challenges related to AVA use in children, including limited parental understanding of how PEP works, adherence challenges—especially for the vaccine/antibiotic combination—and hesitancies about the IND protocol. Both groups indicated that they would seek guidance from trusted, evidence-based sources. **Conclusions:** Both parents and pediatricians will need information about AVA use in children following an anthrax bioterror attack. This project underscores that (1) effective communication from trusted experts during a public health emergency is essential for disease prevention and anthrax vaccine uptake, and (2) pediatricians are well-positioned to address knowledge barriers and improve PEP uptake in a bioterror emergency but need resources to support their efforts. Lessons learned could inform actions to improve uptake of other investigational vaccines among children.

### Poster 384. Brucellosis in Cattle, a One Health Perspective: Assessing the Associated Risk Factors in District Kasur, Pakistan, 2021

**T. Munir**[1,2], M.U.Z. Khan[3], S. Khalid[2], A. Chaudhry
[1]Field Epidemiology & Laboratory Training Program Pakistan, Islamabad, Pakistan, [2]Livestock & Dairy Development Department, Punjab, Pakistan, [3]Faculty of Veterinary Sciences, Superior University, Lahore, Punjab, Pakistan
**Background**: Brucellosis is the most important zoonotic disease spread via aerosol or pathogen infection, or direct contacts of skin abrasions. Brucellosis has been reported in 86 countries comprising of developing countries in majority. In Pakistan, prevalence of bovine brucellosis is around 8.7%. This study was designed to assess the risk factors associated with brucellosis in cattle and to assess the level of engagement of farmers with these risk factors. **Methods**: A case-control study was conducted in District Kasur from March 2021 to May 2021 to determine the risk factors and knowledge, attitude, practices of cattle handlers associated with the development of bovine brucellosis. Seropositive samples were considered as cases while negative were controls. A sample of 56 with a case-control ratio of 1:3 was calculated using EpiInfo7™. A pre-tested semi-structured questionnaire was used for face-to-face interviews. **Results**: The mean age of the cattle and livestock handlers was 4.73 years (SD ± 1.35) and 32 years (SD ± 8.4) respectively. Around 71% (n=40) of the respondents lived in farm premises, 46% (n=26) reported handling abortions themselves. Around 68% (n=38) knew about brucellosis but only 27% (n=15) knew its zoonotic potential. Multivariate analysis of risk factors indicated that handling of abortion at the farm (OR=10.36, CI=1.5-68.6, *P*-

value=0.015), breeding practices (OR=27.7, CI=1.3 – 596.2, *P*=0.03) and history of abortion in the farm (OR=6.3, CI=1.2 – 32.5, *P*=0.02) were mainly associated with brucellosis. Multivariate analysis of knowledge of farmers specified that only mode of transmission of brucellosis from animals to humans (OR=2.89, CI=1.05-7.9, *P*-value=0.04) was statistically significant. **Conclusion**: This study helped to understand the potential risk factors associated with brucellosis in cattle and knowledge of farmers towards brucellosis and mal-practices in management of dairy farming, which will lead to improved herd management practices resulting in the reduction of brucellosis infection. It also revealed that farmers have limited knowledge and awareness about brucellosis.

### Poster 385. Identification of Risk Zones for Leptospirosis in Lviv Oblast

**O.O. Zubach**[1], I.I. Ben[1], O.B. Semenyshyn[2]
[1]Danylo Halytsky Lviv National Medical University, Lviv, Ukraine, [2]State Institution Lviv Oblast Center for Disease Control and Prevention of the Ministry of Health of Ukraine, Lviv, Ukraine
**Background**: In Ukraine, the incidence rate of leptospirosis varies between 0.64 – 2.03 per 100,000 population. In some areas of Lviv Oblast, the incidence exceeds 10 per 100,000 population. Therefore, the determination of risk zones for leptospirosis in Lviv Oblast is relevant due to the need for disease prevention. **Methods**: A retrospective analysis of medical records of patients hospitalized with leptospirosis at the Lviv Oblast Clinical Hospital of Infectious Diseases in 2008-2019 was conducted. At the same time, reports on Leptospira infection in rodents (rats, mice) of the Laboratory of Especially Dangerous Infections of the Lviv Oblast Center for Disease Control and Prevention were analyzed. Leptospirosis detection in humans and in rodents was carried out using microagglutination test with 13 Serovars of Leptospira. An electronic database of leptospirosis cases in humans and infected mouse-like rodents was created using Microsoft Excel. The QGIS 2.0.1 was used to analyze the obtained data, the map of the 259 human and 3524 rodent cases of Leptospirosis in Lviv Oblast was created. Data processing was performed using Statistica software. **Results**: Layered plotting of the data on Lviv Oblast map demonstrated the diversity and distribution of leptospirosis cases in humans and rodents. Further comparisons took into account the geographical landscape of the Lviv Oblast (Ukrainian Carpathians, Forest-steppe and Forest zones). The greatest number rodents that tested positive was observed in the forest-steppe zone (13.16%), 10.66% of all positive animals came from the forest zone, and 10.26% of test-positive animals came from the zone of the Ukrainian Carpathians ($p < 0.05$). A similar pattern was found in humans: significantly more cases of the disease were recorded in forest-steppe zone - 62.94%, compared with the forest zone (24.32%) and the zone of the Ukrainian Carpathians (12.74%), $p < 0.001$. **Conclusions**: The GIS technologies allowed to obtain a spatial understanding of the Leptospira geographical distribution in Lviv Oblast. These differences may allow us to identify specific risk factors associated with these differences. More detailed studies on the epidemiology of Leptospirosis in the Lviv Oblast are needed.

### Poster 386. Formative Evaluation of Two Ebola Survey Instruments in Three African Languages: A Cognitive Interview Study in the Democratic Republic of Congo

**H. Bulambo**[1], G. Earle-Richardson[1], J. Hemingway-Foday[2], V. Anne-Lyne[2], A. Leumbou[3], P. Kimpanga[3], J. Kahehero[3], G. Kasereka[3], D.B. Misati[4], R.K. Mangamfu[5], C.E. Prue[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Research Triangle Institute International (RTI), Durham, NC, USA, [3]Research Triangle Institute International (RTI), Goma, Democratic Republic of Congo, [4]Division Provincial de la Santé (DPS), Goma, Democratic Republic of Congo, [5]Ministère de la Santé Publique, Kinshasa, Democratic Republic of Congo
**Background**: Ebola outbreaks in Sub-Saharan Africa are becoming more frequent. Despite advances in prevention and treatment, affected communities' support for epidemic control measures is still challenging. Knowledge, Attitude and Practice (KAP) surveys are frequently used during outbreaks to understand community perceptions and concerns. However, a scan of published Ebola KAP surveys did not reveal any that reported performing cognitive testing in local languages. The objective of this assessment was to conduct cognitive interviews with two Ebola KAP surveys in French and three African languages with volunteers from a variety of backgrounds to ensure consistent, accurate interpretation of the questions and to identify areas of potential linguistic and cultural misunderstanding. **Methods:** Interviews were conducted in respondents' native language. Participants included males and females of varying social classes, educational levels, and ages from the cities of Goma and Kinshasa. The interviewers explored participants' understanding of survey questions and responses. Noted areas of confusion were shared among interviewers, and revisions tested until questions were understood. **Results:** Sixty-five interviews were conducted, 17 in French, 15 in Kiswahili, 17 in Kinande, and 16 in Lingala. For the African languages, there were three main findings: 1) languages did not have widely understood words for Ebola-specific terms (e.g., "contact tracing"), or for some diseases (e.g., typhoid). Preferred terms were in French or a blend of languages; 2) some terms related to daily life were unclear (e.g., "community") and were revised to follow the original intent of

the question; 3) there were instances in which participants did not understand words in their own language, indicating that comprehension varied within languages. **Conclusions:** Cognitive interviewing revealed ways to improve the clarity of survey questions and response options, but also underscored the need for survey pre-testing in a specific language with a diverse sample of the intended respondent population before use.

### Poster 387. Knowledge and Practices by Community Members in Human African Trypanosomiasis Endemic Areas - Nyimba and Mambwe Districts of the Luangwa Valley, Zambia, 2020

**J.E. Zulu**[1,2], J. Banda[2], S. Ngalande[3], C. Simukoko[4], M. Mbewe[4], L. Soko[4], E. Bulaya[4], J. Mulambya[2], G. Zulu[2], N. Sinyange[5]
[1]Zambia Field Epidemiology Training Program, Lusaka, Zambia, [2]Eastern Provincial Health Office, Chipata, Eastern Province, Zambia, [3]Eastern Provincial Livestock and Fisheries Office, Chipata, Zambia, [4]Nyimba District Health Office, Nyimba, Eastern Province, Zambia, [5]Zambia National Public Health Institute, Lusaka, Zambia
**Background:** Human African Trypanosomiasis (HAT) caused by *Trypanosoma brucei Rhodesiense* is a neglected tropical disease (NTD) transmitted by the bite of an infected tsetse fly. This disease is still endemic at very low scale in North-Eastern and Southern Zambia. In 2019 seven cases of HAT were reported in the valley areas of Mambwe and Nyimba Districts, and four (57%) of them died. Early identification of this disease in the community improves patient outcomes. We sought to describe the knowledge and practices of the community members in the affected areas in order to institute control measures. **Methods:** We conducted a cross sectional survey of community members from the 13th to the 22nd of March 2020. Catchment populations for health facilities (HFs) which reported cases of HAT and those in the tsetse fly-infested belt in Nyimba and Mambwe districts, were purposively selected. We assessed knowledge and practices of community members in these health centre catchment areas on HAT symptoms, health seeking behaviour as well as control of the disease. **Results:** We interviewed 228 respondents with a median age of 32 years (range= 17-95 years), 55.3% were males. Of the 180 that knew about HAT, 55.0% mentioned being sleepy/drowsy as one symptom while 27.8% mentioned malaise as one of the symptoms. On traditional beliefs, 21.6% said they knew of some traditional beliefs surrounding HAT. Of these, 70.7% talked about its linkage to witchcraft, while 7.3% said you get the disease when you either have sexual relations with a woman who is older than you, or while the woman is having her menses. Asked if HAT is preventable, 75.5% said it was preventable. **Conclusions:** There is a knowledge gap among populations in the tsetse fly-infested areas on the identification, prevention and control of HAT. The known symptoms are those of late-stage disease, leading to delayed presentation at HFs. Health education on identification and prevention of HAT should be conducted, and these should cover all communities in the tsetse fly-infested belt in Zambia.

### Poster 388. Estimating Dengue, Chikungunya, and Zika Transmission Intensity over a Decade in Ponce, Puerto Rico

**S. Kada**, L.A. Adams, M.A. Johansson
Centers for Disease Control and Prevention, Dengue Branch, San Juan, PR, USA
**Background:** Arboviruses are a significant health burden in the Americas. Puerto Rico has experienced decades of dengue epidemics with all four dengue viruses (DENV 1-4). In the last decade, the emergence of chikungunya virus (CHIKV) and Zika virus (ZIKV) in 2014 and 2016, respectively, led us to investigate how incidence of these successive arboviral outbreaks impacted population immunity and how that might impact dengue transmission in coming years. **Methods**: We used the age distribution of reported symptomatic cases between 2010 and 2019 and a catalytic model to estimate the annual force of infection of DENV, CHIKV and ZIKV in Ponce, Puerto Rico. We compared various hypotheses of immune interaction between the three arboviruses. **Results**. We found that CHIKV incidence in 2014–2015 followed a pattern of primary infection, confirming that the population was completely naïve to CHIKV. ZIKV incidence followed a pattern of secondary infection, which confirms the immune-mediated interaction of successive DENV and ZIKV infections, and the potential consequences for future DENV outbreaks. **Conclusions.** This study provides insights into epidemiologic trends observed during the spread of multiple arboviruses in Puerto Rico.

### Poster 389. Combating Concurrent Outbreaks of Hemorrhagic Fever with Renal Syndrome and Tularemia in a Wake of COVID-19 Pandemics

**M. Korva**, N. Knap, K. R. Rus, M. Sagadin, M. Jelovšek, T. Avšič-Županc
Institute of Microbiology and Immunology, Faculty of Medicine, University of Ljubljana, Slovenia
**Background**: Hemorrhagic fever with renal syndrome (HFRS) is endemic in Slovenia with annual sporadic cases and seasonal epidemic outbreaks. The overall incidence of HFRS in Slovenia is modest, but in epidemic years 2012 and 2019, 188 and 246 case were diagnosed respectively. Also, the complex ecology of the Balkan Peninsula supports the existence of diverse rodent species, which harbor not only several genetic lineages orthohantaviruses,

but also other zoonotic pathogens like bacterium *Francisella tularensis*. Tularemia has a broad geographical distribution with sporadic cases occurring in many European countries. In last 20 years 35 patients with a clinical diagnosis of tularemia were treated in Slovenia. Most of the patients have ulceroglandular form of tularemia, which correlates with epidemiological data indicating transmission by a tick bite in 50% of patients. In March 2020, shortly after the WHO declared COVID-19 pandemic, the first case of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection was confirmed in Slovenia too. COVID-19 pandemic has dominated the attention of healthcare professionals. The screening for COVID-19 was the first step in all healthcare encounters, when symptoms such as fever, myalgia, gastrointestinal signs and fatigue were present. However, this unspecific signs and symptoms are very common also for other zoonotic diseases that are endemic in Slovenia. **Methods**: The Laboratory for zoonoses at the Institute of Microbiology and Immunology, Faculty of Medicine, University of Ljubljana is the central laboratory for the diagnostics of zoonoses in the country. The laboratory has a knowledge, infrastructure (BSL3+ laboratory) and materials for classical, direct and indirect microbiological methods. **Results**: Due to the COVID-19 pandemic the laboratory's furthermost effort were focused in ensuring quick and reliable molecular diagnosis of SARS-CoV-2. Since the beginning of the pandemic, we have tested more than 730.000 samples identifying 113.340 SARS-CoV-2 positive cases. In spite the heavy COVID-19 diagnostic burden, our longstanding experience in HFRS led us to recognize, already in February 2021 the early cases of HFRS, which usually predict a seasonal outbreak. Using ELISA and multiplex RT-PCR we tested 1591 samples and 565 patients were HFRS positive. In June, at the peak of HFRS epidemics and slight decrease of COVID-19, an increased number of cases with unknown diagnosis appeared in the same geographical region. Due to the overlapping symptoms and increased zoonotic activity, a suspicion of tularemia was raised by the laboratory. In retrospective and prospective analysis of samples, the biggest outbreak of tularemia in Slovenia was discovered, with more than 55 infected patients with various clinical picture. **Conclusions**: The unforeseen upsurge of COVID-19 cases globally caused the disruption of health services due to the overwhelming burden and lead to a prioritized COVID-19 testing. In our case, although HFRS is endemic in Slovenia, more than 30% of HFRS patients were first tested with PCR for SARS-CoV-2 and in case of tularemia patients prior to the recognition of the outbreak, the diagnosis was delayed for a few weeks.

### Poster 390. Knowledge, Attitudes, and Practices of Livestock Raisers Regarding Anthrax Vaccination of Livestock in Bangladesh

**I.S. Shanta**[1], M. Kadzik[2], A. Vieira[2], K. Hossain[1], T. Rahman[3], M.S. Islam[1], F. Haque[1,4], M.B. Hossain[1], S.S.U. Ahmed[5], S.S. Islam[6], E.D. Kennedy[2], M.S. Friedman[2], J.S. Salzer[2]
[1]International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, [2]Centers for Disease Control and Prevention (CDC), Atlanta, GA, USA,[3] Bangladesh Livestock Research Institute, Savar, Dhaka, Bangladesh, [4]University College London, London, UK, [5]Department of Epidemiology and Public Health, Sylhet Agricultural University, Sylhet, Bangladesh, [6]Department of Livestock Services, Dhaka, Bangladesh
**Background:** Anthrax is an endemic disease in Bangladesh and zoonotic outbreaks are reported annually. Between 2009 and 2015, 1,857 suspected human cases of cutaneous anthrax were reported. Annual livestock vaccination against anthrax is one of the primary prevention and control methods; however, livestock vaccination practices are largely unknown. We aimed to determine the knowledge, attitude and practices of livestock raisers regarding the use of anthrax livestock vaccination in Bangladesh. **Methods:** From October 2017 to March 2018, we conducted a cross-sectional survey in four districts with the highest number of suspected human cases and four districts having no reported cases in Bangladesh. We randomly selected 10-11 villages per district; 81 villages in total. From each village, we randomly enrolled 20 households with at least one domestic animal (cattle/buffalo/goat/sheep). We interviewed the primary livestock raiser from each household. **Results:** Among the 1,620 livestock raisers interviewed, 82% raised cattle, 57% raised goats, 4% raised sheep and 1% raised buffalo. Approximately 36% of respondents had heard of the livestock disease "anthrax" or "Torka" (the local name); 48% in outbreak districts and 24% in non-outbreak districts ($p<0.001$). Only 11% of respondents were aware anthrax caused human disease; 19% in outbreak districts and 3% in non-outbreak districts ($p<0.001$). Overall, 25% of respondents reported that they vaccinated their livestock for any diseases. Among those that vaccinate, only 18% of respondents reported vaccinating their livestock against anthrax; 23% in outbreak districts and 12% in non-outbreak districts ($p<0.05$). The majority (73%) of the livestock raisers who did not vaccinate their animals reported they were unaware of the vaccine; 44% reported vaccinators did not come to their village. Livestock raisers reported being willing to pay an average of 0.12 USD per vaccine for cattle or buffalo and 0.06 USD per vaccine for goats or sheep. **Conclusion**: Although respondents in outbreak districts were more likley to have heard about anthrax and aware of its zoonotic potential, the reported use of livestock vaccination is low. There is a need for community engagement with targetted education, and risk communication to livestock raisers regarding knowledge of the disease, the importance of vaccination, and to minimize the gap in the accessibility of the vaccine in endemic villages.

### Poster 391. Unique Case of Tenosynovitis Caused by Dog Heartworm

**A. Amjad**, G. Decker, V. Raheja, B. Sharma
The Wright Center for GME, Scranton, PA, USA

A 24-year-old Caucasian male with a past history significant for mild remote COVID 19 pneumonia initially presented to his company doctor with complaints of a swollen left hand and pain in his second through fourth digits. He denied any insect bites. Review of systems was negative. His occupational history was significant for lifting and carrying hides at a meat packing plant. His exam was unremarkable except a small wound on his left mid palm which had a small eschar which was healing. There was mild pain elicited on both flexion and extension of his left third and fourth digits with minimal fusiform swelling of his third digit. No unusual rashes were noted. The patient was initially prescribed Naprosyn with minimal relief. He subsequently underwent an MRI, which revealed fourth finger tenosynovitis. He was next prescribed a Medrol dose pack for persistent pain with little relief. Due to unrelieved symptoms by medical management, he was referred to an orthopedic hand surgeon. He subsequently underwent surgery for tenosynovitis and pathology of his synovium and flexor tendon of the long finger revealed chronic inflammation and granulomas with the parasite Dirofilaria seen in the biopsy specimen. He was prescribed a single dose of Ivermectin with a month of meloxicam with resolution of his symptoms. Dirofilaria are a group of parasitic roundworms that usually infect animals. Infections in humans are extremely rare. The most common species seen in humans are D. immitis, D. repens and D. tenuis. D immitis is usually seen in dogs in the form of larvae. These parasites are transmitted to humans through mosquito bites. Most infections are seen in the lungs as the larvae accumulate in the pulmonary arteries, which trigger an immune response to form granulomas. These appear as coin-like lesions on chest x rays. Very few cases of extra pulmonary dirofilaria infections have been reported, when the larvae were found in the eyes, brain and testes. We report one of the first cases of Dirofilaria infections seen in the hand of a young male, leading to tenosynovitis. Definitive treatment includes surgical removal of the granulomas and inflammatory nodules. Antimicrobials such as ivermectin and doxycycline in conjunction with anti-inflammatories have been tried but further research regarding the effectiveness of these medications is required.

### Poster 392. Association between Tick Bites and Positive Alpha-gal Specific IgE Testing among People with and without Alpha-gal Syndrome

**K. Nichols Heitman**[1], E.S. Jones[2], A.M. Binder[1], B.J. Biggerstaff[2], P.A. Armstrong[1], S.K. Choudhary,[3], C.B. Beard[2], L.R. Petersen[2], S.P. Commins[3], G.J. Kersh[1], J.S. Salzer[1]
[1]Rickettsial Zoonoses Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Office of the Director, Division of Vector-Borne Diseases, Centers for Disease Control and Prevention, Fort Collins, CO, USA, [3]University of North Carolina, Chapel Hill, NC, USA

**Background**: Alpha-gal syndrome (AGS) is an allergy to mammalian meat products due to an immunoglobulin-E (IgE)-mediated reaction to galactose-alpha-1,3-galactose (alpha-gal). Evidence in the United States suggests recent bite from a lone star tick (*Amblyomma americanum*) predisposes people to AGS. Nearly all patients are diagnosed based on clinical history and a positive blood test (≥0.1 IU/mL) for alpha-gal specific IgE (sIgE). **Methods**: We performed a case-control (1:2 ratio) study with cases aged ≥18 years presenting with AGS at an allergy clinic in North Carolina during 2018–2020 and compared them to controls, who reported tolerating mammalian meat products, from a nearby internal medicine clinic. An interviewer-administered questionnaire gathered epidemiologic and tick exposure data in the year before AGS onset (cases) or time of enrollment (controls), and blood was obtained for sIgE and other testing. **Results**: Eighty-two cases (98% positive for alpha-gal sIgE at ≥ 0.1 IU/mL and 191 controls (33% positive for alpha-gal sIgE) were enrolled; they did not differ by age or sex, but cases were less likely to report Black race (2% vs. 14%; OR [95% CI]: 0.2 [0.04–0.6]). Nearly all cases (n=75; 94%) reported tick bite compared to 54% (n=99) of controls (OR [95% CI]: 12.7 [5.0–32.0]). Case-patients reported more encounters with ticks compared to controls (median 5 vs. 3 encounters) and spent more time in outdoor wooded areas (median 10 vs. 4 hours per week). Cases were also more likely to report bites that took a long time to heal or were unusually large (OR [95%CI] = 24.9 [5.9, 103.4]). Controls who were positive for alpha-gal sIgE were 3.8 times more likely to report tick bites compared to controls who tested negative (OR [95% CI]: 3.8 [2.0-7.4]). **Conclusions**: We found a strong association between self-reported tick bite and both elevated alpha-gal sIgE antibodies and clinical AGS. One-third of controls also tested positive for alpha-gal sIgE, suggesting further investigation is needed to understand the mechanisms governing IgE response and cut-off values used for diagnosing AGS. These findings also highlight the importance of both an appropriate clinical history and supporting blood test to establish an accurate AGS diagnosis.

### Poster 393. Recent Trends of Viral Hemorrhagic Fever Suspect Cases in Uganda

**A.N. Whitesell**[1], L. Nyakarahuka[2], J. Baluku[2], S. Balinandi[2], J. Klena[1], T.R. Shoemaker[1], J. Montgomery[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Uganda Virus Research Institute, Entebbe, Uganda

**Background:** Since its formal establishment in 2011, the Uganda Viral hemorrhagic fever (VHF) surveillance program has successfully detected more VHF outbreaks between 2011-2020 than in all the years prior. However, the coronavirus disease 2019 (COVID-19) pandemic has impacted healthcare and public health systems worldwide. To determine how the recent COVID-19 pandemic affected this program, VHF surveillance data was used to compare the recent trend in VHF suspect cases with previous trends. **Methods:** VHF surveillance data from August 2010-June 2021 was used to calculate the average number of suspect cases per month for various time periods. Data were compared across three defined timepoints: before the declaration of the 2018 Ebola Virus Disease (EVD) outbreak in bordering DRC provinces, during EVD outbreaks in bordering DRC provinces, and during peaks of COVID-19 infections in Uganda. Data were also compared across 12-month time periods from June-July. **Results:** While no significant difference was detected between the average number of suspects per month during the COVID-19 peaks and before the 2018 EVD outbreak, the average was significantly higher during the EVD outbreaks in bordering DRC provinces (p=0.00). Additionally, the average number of suspects per month during July 2020-June 2021 was lower than the three previous 12-month periods, decreasing to 8.3 from 31.4 during the previous 12-month period. While differences were detected across all 12-month timepoints, the average number of suspects from July 2020-June 2021 only significantly differed from July 2018-June 2019 during which an average of 57.3 suspects per month was reported (p=0.02). **Conclusions:** The recent trend of average number of VHF suspects per month was lower than the three previous 12-month periods; however, when comparing across all 12-month periods, the average number of suspects per month during July 2020-June 2021 did not significantly differ from any other period besides July 2018-June 2019. And while the average number of suspects per month was lower during peaks of COVID-19 cases compared to during the EVD outbreaks, it did not significantly differ from the average prior to 2018. Additional analyses will be performed to determine if this recent trend of VHF suspects represents a decline due to the COVID-19 pandemic or a return to the previous trends after the 2018 DRC EVD outbreak.

### Poster 394. Cardiovascular Manifestations of Leptospirosis: A Retrospective Study of Patients Admitted at a Tertiary Care Hospital in Coastal Karnataka Region

**M.S. Rao**[1], J. Samanth[2],K. Nayak[2]
[1]Department of Cardiology, Kasturba Medical College, MAHE, Manipal, Karnataka, India,[2] Department of CVT, MCHP, MAHE, Manipal, Karnataka, India

**Background:** Leptospirosis is an emerging global zoonosis and there is limited clinical data on the cardiac manifestations of leptospirosis including myocarditis. **Methods:** This was a retrospective study conducted at a tertiary care hospital in South India and patients admitted between January 2016 to September 2020 who met the clinical criteria for leptospirosis; ELISA IgM positive and age>18 years were included. Patients with known cardiac disease and mixed infection (Scrub typhus, Dengue, blood culture septicaemia, Enteric fever and covid+) were excluded. A comprehensive assessment comprising of clinical presentation, electrocardiography (ECG), 2D echocardiography and outcomes including all-cause mortality and myocarditis were studied and binomial logistic regression was performed to identify independent predictors of all-cause mortality and myocarditis. **Results:** Out of 510 patients, 339 (66.5%) were males and 171 (33.5%) were females. The mean age was 48.4±13.73 years. The mean hospital stay days was 10.11±6.133 days in which 204 (40%) patients had longer hospital stay days (>10 days). 85(16.7%) patients were diabetic and 86 (16.9%) were hypertensive. 54 (10.6%) patients were diagnosed with acute respiratory distress syndrome (ARDS). 143 (28.0%) patients developed Multi Organ Dysfunction Syndrome (MODS) during their hospitalization. 91 (17.8%) patients underwent hemodialysis. Most common ECG findings were prolonged corrected QT interval (21.0%) and Sinus Tachycardia (20.8%). Echocardiographic evidence of myocarditis was seen in 53 (10.4%) patients. 21 (4.1%) had Isolated LV dysfunction, 20 (3.9%) patients had Isolated RV dysfunction and 12 (2.4%) had bi-ventricular dysfunction. All-cause mortality was seen in 41(8%) patients. Multivariable binary logistic regression analysis showed age, sinus tachycardia, Prolonged QTc interval, hypertension, need for hemodialysis and presence of myocarditis were the independent predictors of mortality among patients with leptospirosis. **Conclusions:** In the largest retrospective cohort of leptospirosis patients, cardiac sequelae in form of myocarditis occurred frequently. Therefore, clinical vigilance pertaining to cardiac status is paramount in these patients.

### Poster 395. A Quartan Malaria Local Case in Armenia, 2021

**K. Gevorgyan**[1], L. Paronyan[1], G. Sargsyan[1], A. Gevorgyan[2], A. Keshishyan[1], L. Avetisyan[1], A.Vanyan[1]

[1]**National Center of Disease Control and Prevention,** Infectious Diseases Clinical Hospital Nork, Yerevan, Armenia, [2]Ministry of Health of the Republic of Armenia, Yerevan, Armenia
**Background:** Historically, in Armenia, local transmission of quartan malaria was interrupted in 1949; the country eliminated all forms of malaria in 2005 and is in the malaria re-introduction prevention stage. In 2021, *Plasmodium malariae* was found in a resident of Ejmiadzin town. This form of malaria is characterized by low and long-term parasitemia (up to 40-50 years) due to prolonged erythrocytic schizogony, a self-developing nephrotic syndrome with edema, proteinuria, and hypertension, which is often found in children. In children, gastrointestinal disorders are the most often malaria symptom manifested. The main goal of the study was to determine the status of the Ejmiadzin case and the place/time of infection. **Methods:** Historical, clinical, epidemiological, and laboratory data were analyzed. Three options were considered: departure to a malaria-endemic country, infection at the hospital in May 2021, and infection in childhood. **Results:** The 60-year-old patient, who has never left Armenia, was admitted to the hospital «Best life» due to heart attack, leg swelling, and history of chronic arterial hypertension, diabetes, and COVID-19. Revascularization of coronary vessels was performed, and blood-thinning medicines were prescribed. Forty-two days after treatment, the patient had an attack of malaria which was diagnosed at Erebuni and Nork Hospitals. It was determined that she could not have been infected in the hospital, during April-May, as there were no patients with confirmed malaria or from malaria-endemic countries. The patient has also never received a blood transfusion. Ultimately, it is most likely that the patient could have contracted quartan malaria in childhood, and this infection was benign. This hypothesis is supported by the fact that in childhood, the patient had repeated bouts of nausea, vomiting, and abdominal pain (symptoms associated with malaria in children), due to which appendectomy was performed about 52 years ago. **Conclusions**: Considering the non-specificity of signs of quartan malaria in children, and low long-term parasitemia, it is important to organize an awareness campaign among clinicians and laboratory workers to raise the sensitivity of the malaria surveillance system.

## Foodborne and Enteric Diseases

### Poster 396. Single and Multiple Enteric Infections in a Longitudinal Study in British Columbia, Canada, 2005-2014

**M. Taylor**[1], M.R. Gohari[2], M.C. MacKinnon[2], D. Panagiotoglou[3], E. Galanis[1,4], S.E. Majowicz[2]
[1]British Columbia Centre for Disease Control, Vancouver, BC, Canada, [2]University of Waterloo, Waterloo, ON, Canada, [3]McGill University, Montreal, QC, Canada, [4]Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada
**Background**: Enteric infections can cause long-term sequelae, but assessing such associations is challenging as individuals can experience >1 infection concurrently or over time. Our aims were to describe the occurrence of new infections within individuals, and to determine appropriate time periods to define incident infections, for the population of British Columbia (BC), Canada. **Methods**: We analysed laboratory-confirmed infections (*Campylobacter*, *Cryptosporidium*, *Cyclospora*, *Giardia*, hepatitis A, *Listeria*, *Salmonella* spp., STEC, *Shigella*, *Yersinia*, and *Vibrio*) reported from 2005 to 2014. Time at-risk for infection was the number of days individuals were enrolled in BC's mandatory health insurance plan. We reviewed time between onset dates for people with >1 infection. **Results:** There were 42,309 incident infections (96.4/100,000 person-years). Subsequent incident infection of the same pathogen had an onset date >2 years for *Giardia*, and >90 days for all other infections, with no recurrence for hepatitis A. 276 non-incident infections in the 5.8 million people under study. Multiple incident infections occurred in 1,641 individuals (range: 2-5 infections); 1,227 had two incident infections from different pathogens, of whom 919 (75%) had the two at different times and 308 (25%) had them concurrently. The most frequent concurrent pathogen were *Campylobacter* and non-typhoidal *Salmonella* (n=118) and the most frequent pair at different times were *Campylobacter* and *Yersinia* (n=142). Those with >1 incident infection were more often male (59%) compared to those with 1 incident infection (52%) and were slightly younger (median ages: 37.8 vs. 36.1 years). A small number (n=303; 19%) of individuals had three to five incident infections over the 10 years, all from the same pathogen; nearly all were *Campylobacter* (n=122), *Yersinia* (n=58), or Giardia (n=58). **Conclusions:** Multiple infections were rare, and most were with the pathogens with the highest incidence in BC. Those with >1 incident infection were different demographically than those with 1 infection, which may reflect different risk factors. Identifying pathogen-specific time periods to define incident infections allowed us to differentiate repeat testing of the same infection from re-infection, which is needed to assess post-infection sequelae risk.

### Poster 397. Enteric Infections Lead to Infrequent but Severe Renal Outcomes, British Columbia (BC), Canada

**E. Galanis**[1,2], M. Gohari[3], D. Matsell[2], P. Yenson[2], M. Taylor[1], D. Panagiotoglou[4], S. Majowicz[3]

[1]British Columbia Centre for Disease Control, Vancouver, BC, Canada, [2]Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada, [3]University of Waterloo, Waterloo, ON, Canada, [4]McGill University, Montreal, QC, Canada
**Background:** Enteric infections can lead to acute kidney injury (AKI) through Shiga toxin-mediated effects (hemolytic uremic syndrome-HUS), sepsis or dehydration. HUS and AKI can lead to chronic kidney injury, renal transplant and death. We measured the risk of renal conditions subsequent to enteric infections within a retrospective, population-based, longitudinal cohort study. **Methods:** We linked province-wide reportable disease data to physician claims, hospitalization, and vital statistic data in BC in 2005-14. Infections leading to AKI included *Campylobacter*, hepatitis A, *Salmonella* spp, Shiga toxin-producing *E. coli* (STEC), *Shigella* and *Yersinia*; AKI was defined as ≥1 hospitalization with ICD10 codes N17.0, N17.8 or N17.9 within 90 days of infection. Infections leading to HUS included STEC and *Shigella;* HUS was defined as >2 physician claims occurring within 2 years with ICD9 codes 283.11 or ≥1 hospitalizations with ICD10 code D59.3, within 45 days of infection. Chronic kidney disease (CKD) was defined as ≥1 hospitalization with ICD code N18.9, renal transplant was defined as ≥1 hospitalization with ICD code Z94.0, death from AKI/HUS was defined as N17.0, N17.8, N17.9 or 283.11 in any of the 10 death codes. We estimated odds ratios (OR) adjusted for age and sex using logistic regression. **Results:** 83,777 AKI episodes and 168 HUS episodes occurred in the 10 years. The AKI hospitalization rate increased from 122 to 307/100K person-years; the HUS rate remained stable (avg incidence=0.4/100K person-years). 827 (3%) AKI episodes occurred in 33,477 infected individuals: 620 (75%) occurred after *Salmonella* spp or *Campylobacter* infections, 261 (32%) occurred within 14 days of infection and 762 (92%) occurred in ≥40-year-olds. 49 (2%) HUS episodes occurred in 3,174 infected individuals: 48 (98%) had STEC infection, 42 (86%) occurred within 14 days of infection and 24 (49%) occurred in 1–9-year-olds. The odds of AKI were higher among those with prior infection (OR=2.0, 95% CI: 1.9-2.2). Among infected individuals with AKI or HUS, 308 (35%) developed CKD, 39 (4%) had a renal transplant and 23 (3%) died. **Conclusions:** Enteric infections are associated with rare but severe renal outcomes in children and adults. Measuring the chronic sequelae of infections provides a more accurate reflection of their burden of illness.

### Poster 398. Use of Genomic Data to Identify Animal Feed as a Possible Source of *Salmonella* Serotype Infantis Infections, United States, 2020–2021

**B.E. Karp**[1], Z. Ellison[2], B. Tolar[1], B. Ge[3], M.C. Nichols[1], L. Gieraltowski[1], G.Z. Fortenberry[4], K.B. Hise[1], G.E. Langley[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [3]Food and Drug Administration Center for Veterinary Medicine, Laurel, MD, USA, [4]US Department of Agriculture Food Safety and Inspection Service, Washington, DC, USA
**Background:** Nontyphoidal *Salmonella* cause ~1.35 million U.S. infections each year. The relative importance of animal feed as a source of *Salmonella* strains that enter the food supply is not known. Protein-rich oilseed feed ingredients, like soybean and canola meal, are often contaminated with *Salmonella*. *Salmonella* strains sometimes persist in feed processing plants for months or years. **Methods:** Using NCBI's Pathogen Detection Isolates Browser, we identified a subcluster of closely related *Salmonella* Infantis isolates from humans, cattle, pork, chicken, and canola meal within a single-nucleotide polymorphism cluster of ~300 isolates. We obtained isolate and patient demographic data from PulseNet and assessed strain relatedness using core genome multilocus sequence typing. We collected patient exposure and illness information from interviews conducted by health departments, and information on food, feed, and animals from routine screening programs conducted by FDA and USDA. **Results:** We found 33 highly related (0–11 alleles) *Salmonella* Infantis isolates; all were from samples collected in the United States March 2020–July 2021 from humans (15), bob veal calves (7), dairy cattle (3), ground pork (3), and imported canola meal (3) and chicken (2) from Canada. The canola meal was produced by 1 processing plant in Canada and collected over 6 months. Patient isolates aligned geographically with those from food animals, food, and canola meal—most were from the Northeast or from the East North Central census division. Patients were <1–60 (median 18) years old; 6 were children and 8 were female. Live poultry (5) or livestock (1) exposure was reported for 6 of 12 patients with available information. Two patients had exposure to chickens fed the same brand of layer feed. **Conclusions:** Genetic and epidemiologic data suggest that *Salmonella* Infantis-contaminated canola meal was incorporated into animal feed and that people became infected through contact with infected animals or their environment, consumption of contaminated food animal products, or contact with contaminated food or feed. A more comprehensive surveillance system for *Salmonella* in feed and feed ingredients with timely data reporting and submission of feed isolate data to PulseNet would help identify microbial threats to the food supply and prevent illnesses.

### Poster 399. Identification and Monitoring of a Persisting Multidrug Resistant *Salmonella* enterica Serotype Infantis Strain Using Whole Genome Sequencing

**M. Leeper**[1], B. Tolar[1], K. Hise[1], Z. Ellison[2], J. Chen[1], J. Folster[1], L. Francois Watkins[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA

**Background:** Whole genome sequencing (WGS) is facilitating identification of reoccurring, emerging, and persisting (REP) strains of enteric bacteria. Illnesses caused by REP strains may be linked to a common source but may not present as acute outbreaks. PulseNet, the national laboratory network for foodborne disease surveillance, and CDC's National Antimicrobial Resistance Monitoring System (NARMS), review WGS data to identify REP strains based on core genome multi-locus sequence typing (cgMLST) and additional genomic markers. PulseNet and NARMS monitor selected REP strains to investigate sources of illness and inform prevention efforts. **Methods:** *Salmonella* Infantis sequences generated by WGS were uploaded to the PulseNet national *Salmonella* database by certified PulseNet laboratorians and resistance profiles were characterized by NARMS using BioNumerics genotyper. Isolates were further evaluated using cgMLST and allele code (a population-based form of nomenclature) designation to identify genetic relatedness. **Results:** To date, 5853 *Salmonella* Infantis isolates from human and non-human sources, with collection years as early as 2012, have been designated REP strain REPJFX01 based on allele code and cgMLST analysis. 93.9% of 3753 REPJFX01 isolates from food sources are from chicken. 416 isolates have been associated with 7 temporally-related clusters of illness, in which epidemiologic investigations revealed chicken as the source. Antibiotic resistance and plasmid analysis shows that >99% of isolates have a *gyrA*(D87Y) mutation, which reduces susceptibility to ciproflaxacin, and an IncFIB(pN55391) replicon associated with a resistance plasmid reported in *S.* Infantis. Additionally, 52% harbor $bla_{\text{CTX-M-65}}$, a gene conferring resistance to ampicillin and ceftriaxone. cgMLST analysis shows that all isolates differ within 0-70 alleles. **Conclusions:** Our results highlight the utility of WGS and allele code nomenclature in identifying and monitoring strains of public health concern that may not present as acute outbreaks. Continuing to assess the prevalence and genetic characteristics of such strains may help identify common sources and create opportunities for new prevention approaches.

### Poster 400. Microbiological and Molecular Characterization of *Salmonella* species in Frozen Meat and Organs Imported into Egypt: A Public Health Importance

**A. Abdelaziz**[1], M. Ghafar[2]
[1]Food Microbiology Department, Central Public Health Laboratories, Abdien, Egypt, [2]Department of Zoonoses, Faculty of Veterinary Medicine, Cairo University, Giza, Egypt

**Background:** Non-typhoidal *Salmonella* (NTS) constitutes one of the major worldwide zoonotic food-borne pathogens. The disease caused by NTS is mainly manifested by gastroenteritis; however, bacteraemia and localization in different organs with chronic sequelae may also occurs. Many pathogenic mechanisms are involved in NTS-induced diarrhea including production of enterotoxin which is encoded by *stn* gene. The most encountered serotypes in majority of food-borne human salmonellosis are *S.* Typhimurium, *S.* Enteritidis, *S.* Heidelberg, and *S.* Newport .Egypt, like most of developing countries, depends mainly on importation of frozen meat and organs to face the continuous increase of human population and shortage of local animal protein. The aims of this study are to isolate and microbiologically characterize *Salmonella* spp. in frozen meat and organs imported into Egypt and to evaluate the potential virulence of the isolates by detecting the presence of the *stn* enterotoxin gene using PCR. **Method:** A total of 1363 imported frozen meat and organ samples (962 meat, 281 liver, 69 heart, 51 kidney) were collected from original packets while lots are in their primary destination (Cairo Airport, Port Said Port, Alexandria Port) before market distribution. All samples were transferred refrigerated under aseptic conditions to Food Microbiology Laboratory at Central Public Health Laboratories (CPHL) for further processing and testing. Isolation and identification of *Salmonella* spp.: Isolation and identification of *Salmonella* spp. were executed according to ISO 6579/2002. Briefly, the pre-enrichment step in non-selective medium was executed by inoculation of homogenized 25g of each sample in 225 ml buffered peptone water and incubation at 37 °C for 24 h. Enrichment was carried out by inoculation of 0.1 ml aliquots of pre-enrichment broth in the selective Rappaport-Vassiliadis with soya (RVS broth) medium and incubation at 42 °C for 24 h. A loopful from RVS broth was streaked on Xylose lysine deoxycholate agar (XLD agar) then the plates were incubated at 37°C for 24 h. Suspected colonies were biochemically confirmed by triple sugar iron (TSI), lysine decarboxylation iron agar (LIA), urea, indole, and citrate utilization tests. Pure cultures were also serologically tested using slide agglutination test according to White Kauffman scheme. Molecular identification of enterotoxin (*stn*) gene: DNA extraction: *Salmonella* pure colonies on XLD agar were grown overnight in 5 ml buffer peptone water at 37°C. One ml of culture medium was centrifuged and the pellet was washed twice and then resuspended in 200 µl TE buffer. For cell lysis, the suspension was boiled

at 100°C for 10 minutes and then placed in refrigerator for 5 minutes. Finally, the mixture was centrifuged at 13,000 xg for 5 minutes and 5 µl of supernatant was used as DNA template in PCR reaction. PCR and agarose gel electrophoresis*:* All PCR amplifications were performed in 25-µl reaction mixtures containing 5 µl of each DNA template, 5 µl of 5X PCR Master Mix and 10 pmoles of each *Stn* P1-Forward (5- TTG TGT CGC TAT CAC TGG CAA CC -3) and *Stn* M13-Reverse (5- ATT CGT AAC CCG CTC TCG TCC -3) primer supplied by Metabion, Germany. Statistical analysis: The analysis of the results was conducted using the computer software SPSS (SPSS Inc., Chicago, IL, USA; version 16.0). The significance difference of *Salmonella* prevalence among potential countries, from which meat and organs were imported, was evaluated by chi-square test. Post hoc test for determination of source of difference was performed. The *p*-value < 0.05 was considered statistically significant. **Results:** The general chi-square test showed a significant difference between the prevalence of isolated *Salmonella* species among the potential meat and organ exporters to Egypt (Brazil, India, Australia and USA). The post hoc test with the adjusted *p*-value of 0.00625 (level of significance), due to multiple testing, showed that India had the highest significant prevalence of *salmonella* (3.39%) followed by Brazil (1.20%), USA (0.83%) and Australia (0%). **Conclusion:** This study revealed that imported frozen meat and organs might constitute a foodborne illness hazard due to contamination with enterotoxin producing *Salmonella* spp. In addition, our results demonstrated that India has the highest significant prevalence of *Salmonella* followed by Brazil, USA and Australia. This is a flashing warning signal for the concerned authorities on the hygienic measures employed in slaughterhouses in countries from which frozen meat and organs are imported.

### Poster 401. Foodborne Gastro-Intestinal Illness Outbreak amongst People Who Ate from a Restaurant in Chingola, Kitwe and Ndola Districts, Zambia 2021

**T. Emmanuel**[1], A. Hamukale[1], H. Moonga[1], J. Simwanza[1], C. Musenge[3], C. Sakulanda[3], R. Zulu[3], E. Kateule[1,2], D. Banda[1,2], N. Sinyange[1,2]
[1]Zambia Field Epidemiology Training Program, Lusaka, Zambia, [2]Zambia National Public Health Institute, Lusaka, Zambia, [3]Copperbelt Provincial Health Office, Ndola, Zambia
**Introduction:** On 30th August 2021, 4 hospitals in the Copperbelt province recorded mass admissions of patients complaining of diarrhea, vomiting, and abdominal pain of acute onset. All the patients had history of eating from a common food outlet from three different cities (Kitwe, Ndola, and Chingola) within 24hrs of onset of symptoms. From 30th August to 3rd September 2021, 372 patients were line listed. We investigated the suspected foodborne outbreak in the Copperbelt province to establish the cause of the outbreak. **Methods:** We conducted a case control study among people who presented with diarrhoea, vomiting and abdominal pain at the 4 Hospitals between 25th August and 3rd September 2021. We administered a questionnaire to patients and non-patient household contacts which included questions about food exposures and clinical details. Multivariable logistic regression was used to calculate odds ratios (OR) for factors associated with the acute gastrointestinal illness. Analysis conducted in R version 4.0.5. **Results**: We interviewed 183 cases and 133 controls. The median age was 24 years (IQR:14, 35) and 52.2% were females. Those who ate from After 10 restaurant outlets [OR==35.49; (95% CI :14.83,84.88) p=0.001] were associated with the foodborne illness. *Salmonella* was detected in 50% (19/38) of patients with laboratory results. *Staphylococcus aureus,* total coliforms 93*, Escherichia coli,* faecal coliforms, and *Klebsiella* species were detected in food and food preparation/storage surfaces. The outbreak was not associated with drinking water from any source, contact with pets and attending any event where food was served. **Conclusion:** The outbreak was associated with eating from after 10 food outlets. *Salmonella* was found to be the most probable cause of the outbreak. Contamination of food and working surfaces with pathogens indicates poor food safety practices. The Ministry of Health and the Local Authorities should strengthen food safety and hygiene practices in food premises.

### Poster 402. PulseNet International (PNI): Understanding Challenges towards Implementing WGS for Foodborne Surveillance: PulseNet International Experience

**K. Kubota**[1], C. Nadon[2], T. Davedow[2], M.M. Freeman[3], H. Carleton[3]
[1]Association of Public Health Laboratories, Silver Spring, MD, USA, [2]Public Health Agency of Canada, Winnipeg, Manitoba, Canada, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** PulseNet international is a network of networks encompassing 7 regions on 5 continents dedicated to the surveillance and detection of outbreaks caused by enteric bacterial pathogens. Established in the 2000s, the network has since expanded to more than 80 countries worldwide. Using standardized methods and utilizing a common platform for data sharing, PulseNet International has demonstrated regional and international success in identifying foodborne outbreaks at the regional and international levels. The aim of this study was to identify barriers and challenges at the local level for implementing WGS within PulseNet international laboratories. **Methods:** A 25 question survey was developed using Google forms and sent to PulseNet regional coordinators for

further distribution to network laboratories. The survey was distributed to collect qualitative data assessing the status and challenges of implementing WGS within the laboratories during the 2019 calendar year. **Results:** A total of 41 laboratories responded, representing 34 of 54 countries surveyed. Our study found that barriers for implementing WGS for foodborne surveillance include lack of analysis capacity, insufficiently skilled workforce, and lack of knowledge using WGS data for cluster detection. Sharing sequence data within and across countries for real-time surveillance is uncommon. Some of the challenges include limited experience generating high quality sequence data, limited bioinformatics capacity and skills, and lack of platforms for exchanging data and communicating. **Conclusions:** This survey was a key systematic study to better understand barriers and challenges for implementing WGS among low-to-middle-income countries within the PulseNet International network. Developing implementation plans at regional levels, training laboratory personnel, and establishing a common platform for data sharing and information exchange are the highest needs to fully implement WGS technology for foodborne surveillance. The use of genomic epidemiology worldwide during the COVID-19 pandemic for tracking the spread of variants has accelerated WGS implementation and changed the landscape for utilization for foodborne surveillance activities at the local and regional levels.

### Poster 403. Trends in *Salmonella* Serotypes Causing Outbreaks Associated with Four Meat Categories, 1998-2019

**B.L. Gleason**, Z. Cui, P.M. Griffin
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** *Salmonella* is the leading bacterial cause of foodborne illness in the United States. In 2018, ~40% of foodborne *Salmonella* illnesses were attributed to chicken, pork, turkey, and beef. Determining major and emerging serotypes in outbreaks associated with specific meats can guide prevention measures. **Methods:** We examined *Salmonella* serotypes that caused outbreaks from specific meats during 1998–2019 using data from the Foodborne Disease Outbreak Surveillance System. We ranked serotypes in each meat category based on numbers of outbreaks and illnesses. **Results:** During 1998–2019, 394 *Salmonella* outbreaks associated with meat consumption were reported, resulting in 12,738 illnesses. Chicken-associated outbreaks caused 1.7 times more illnesses than pork, 1.8 times more than turkey, and 1.9 times more than beef outbreaks. During 2010–2019, 1) chicken-associated outbreaks increased compared with 1998–2009; 2) Enteritidis was among the top three serotypes that caused outbreaks in all meat categories; 3) Enteritidis caused 2.3 times more chicken-associated outbreaks than during 1998–2009; 4) Typhimurium was the top serotype for pork but declined for chicken and turkey compared with 1998–2009; 5) I 4,[5],12:i:- appeared as a cause of outbreaks associated with pork (in 2011), turkey (2015), and chicken (2016); and 6) Newport was the top serotype causing beef outbreaks. Trends for outbreak-associated illnesses were similar to those for outbreaks. **Conclusions:** Chicken was responsible for more *Salmonella* outbreaks than other meat categories. The increase in *Salmonella* outbreaks from chicken, the prominence of Enteritidis in outbreaks associated with all meat categories, the emergence of I 4,[5],12:i:- in three meat categories, and the persistence of Newport as a major cause of beef-associated outbreaks indicate that prevention measures on farms and in slaughter plants are inadequate. The decline in Typhimurium outbreaks associated with poultry may be due to industry-initiated poultry vaccination. Serotype trends can inform on-farm control methods and improvements in meat inspection.

### Poster 404. Foodborne Botulism Cases in Armenia, 2016-2020

**A. Papoyan**[1,2], A.P. Jimenez[2], L. Avetisyan[1], G. Melik-Andreasyan[1], N. Bakunts[1], A. Vanyan[1]
[1]National Center of Disease Control and Prevention, Ministry of Health of the Republic of Armenia, Yereven, Armenia, [2]Mediterranean and Black Sea Programme for Intervention Epidemiology Training (MediPIET), Instituto de Salud Carlos III, Madrid, Spain
**Background**: Foodborne botulism is a life-threatening intoxication caused by ingestion of food containing botulinum neurotoxin. In Armenia, the National Botulism Surveillance System collects reports of all suspected botulism cases for early detection of outbreaks. Food canning at home is very common in Armenia. A potential increase in botulism cases due to the 2020 lockdown prompted this study. **Methods**: Available information on all suspected botulism cases during 2016-2020 was extracted from the National Center of Disease Control and Prevention database and all paper notification cards were reviewed to verify. We estimated the annual botulism incidence and characterized all probable and laboratory confirmed cases by demographic factors and risk exposures using STATA 16. **Results**: During 2016-2020, a total of 160 suspected cases of foodborne botulism were reported. Among them, 112 were either probable (patients with compatible clinical presentation and an epidemiological risk factor) or laboratory confirmed with an annual incidence that ranged 0.7-0.9/100,000 population. Most cases were notified in winter. Median age was 37 years (IQR=24yrs) and 55% (61) were females. There were 5 deaths. While

54% (60) were part of outbreaks, sporadic cases (52) occurred in every Armenian region, except for Syunik. A significantly higher proportion of outbreak cases were from rural areas (p=0.01). All 112 cases were attributed to home canned vegetables, with an alarming proportion of outbreak cases due to canned chervil (p<0.001). **Conclusion**: No increase in foodborne botulism was observed during the 2020 lockdown in Armenia. Over the last five years, foodborne botulism incidence was stable at a worldwide record level with large outbreaks, nationwide sporadic cases and fatal outcomes. Because all cases were attributable to home-canned vegetables, educational campaigns on appropriate washing, preservation and canning should be implemented.

### Poster 405. *Listeria monocytogenes* in Enoki Mushrooms: A Recurring Concern?

**A. Palacios**[1], A. Conrad[1], E. Pereira[2], A. Tesfai[2], M. Bazaco[2], J. Huffman[1], L. Gieraltowski[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Food and Drug Administration, College Park, MD, USA

**Background:** Outbreaks of listeriosis have been linked to fresh produce. In 2020, investigators linked a multi-year outbreak to enoki mushrooms, popular in Asian cuisine. After this outbreak, state partners and FDA increased testing of imported enoki mushrooms. We describe clusters of genetically related clinical and enoki mushroom isolates and the challenges identifying enoki mushrooms as a vehicle. **Methods:** All *Listeria monocytogenes* isolates from enoki mushrooms were whole genome sequenced (WGS). Sequences were uploaded to the National Center for Biotechnology Information (NCBI) and PulseNet. PulseNet identified clusters of clinical and enoki mushroom isolates related within 25 allele differences by whole genome multi locus sequence typing (wgMLST) for all years available in NCBI. We reviewed demographic and mushroom consumption data for ill people. **Results:** We identified eight strains of *L. monocytogenes* from enoki mushrooms resulting in six product recalls. Four strains were related to 25 clinical isolates across four clusters. The clusters had illnesses occur in multiple years (2-12 years). Cluster 1, investigated in 2015, included 13 patients; 6 of 10 (60%) reported Asian race (indicating a possible preference for Asian cuisine). Two patients reported fresh mushroom exposure; mushroom consumption was unknown for eight patients. Cluster 2, investigated in 2021, included five patients; one patient of Asian race and reported eating unknown types of mushrooms. For the two remaining clusters (3 and 4 patients, respectively) limited epidemiologic information was available. **Conclusions:** Our analysis identified four genetically related clusters of clinical and enoki mushroom isolates. Two clusters had some epidemiologic data consistent with enoki mushrooms as a plausible vehicle. Enoki mushrooms are not included on the standard *Listeria* case report form, complicating assessment of mushroom exposure. Enoki mushrooms are often consumed raw in the United States. People who are at higher risk for listeriosis should consider cooking enoki mushrooms to prevent illness.

### Poster 406. Estimating the Burden of Foodborne Illness for *Campylobacter*, *Salmonella*, and *Vibrio parahaemolyticus* in Japan, 2006-2019

**K. Kubota**[1], H. Amanuma[1], M. Tamura[1], Y. Kumagai[2], H. Asakura[1], F. Kasuga[3]
[1]National Institute of Health Sciences, Kawasaki, Kanagawa, Japan, [2]Wayo Women's University, Ichikawa, Chiba, Japan, [3]National Institute for Environmental Studies, Tsukuba, Ibaraki, Japan

**Background:** In Japan, the numbers of food poisoning incidence and cases are reported mandatory; however, these do not exactly reflect the real burden of foodborne illnesses due to the passive surveillance nature. We estimated the burden of foodborne illnesses associated with three pathogens in Japan from laboratory confirmed numbers of infections for *Campylobacter*, *Salmonella* and *Vibrio parahaemolyticus* in Japan for 2006-2019. **Methods:** Data on laboratory-confirmed infections of three pathogens were collected from clinical laboratories that test stool samples submitted from all over Japan or from Miyagi Prefecture, from January 2006 to December 2019. The physician consultation rate and the stool submission rate were estimated from telephone population surveys conducted for whole of Japan and for Miyagi prefecture. Each estimate was introduced into the Monte-Carlo simulation model as a probability distribution, which was run for 10,000 iterations. **Results:** The estimated mean numbers per year of foodborne illnesses for *Campylobacter*, *Salmonella* and *V. parahaemolyticus* in whole of Japan were 5.5 -13.6 million, 1.2 -2.8 million, and 44-438 thousand during 2006-2019, respectively. Those estimated for whole of Japan from data on Miyagi prefecture were 0.64 -1.6 million, 78-220 thousand, and 2-63 thousand during 2006-2019, respectively. The numbers of reported foodborne illnesses per year in Japan during 2006-2019, for *Campylobacter*, *Salmonella* and *V. parahaemolyticus*, were 1,600-3,300, 440-3,600 and 50-1,300, respectively. **Conclusions:** These data reveal a significant difference in numbers and trends between our estimates of burden of foodborne illnesses and the reported foodborne disease cases associated with three pathogens. Need for continuing active surveillance system to complement the present passive surveillance is strongly suggested, in order to identify and prioritize food safety measures more precisely and to monitor the effectiveness of risk management options.

## Fungal Diseases

### Poster 407. Fungal Necrotizing Exernal Otitis: Place of Antifungal Treatment

**R. Lahiani**, I. Riahi, M. Ghabi, O. Gabsi, O. Kharrat, H. Jaafoura, S. Manoubi, M. Tbini, M. Ben Salah
ENT Department - EPS Charles Nicolle, Tunis, Tunisia

**Introduction:** Necrotizing extrernal otitis (NEO) is a serious condition. We are increasingly seeing the emergence of fungal agents that cause this condition. **Methods:** A retrospective study carried out over a period of 10 years, from 2010 to 2020, including 21 patients with fungal NEO treated in our department. The fungal origin was retained in front of an ear sample isolating a fungal agent. **Results:** The mean age was 65.76 ± 7.3 years. The sex ratio M / F was 1.6. All our patients were diabetic and 13 patients had hypertension.The main complaint was otalgia followed by otorea in 16 cases and hearing loss in 4 cases .The median time between symptom onset and hospitalization was 30 days [14-120].Oral antibiotic therapy before admission was prescribed in 20 patients, 8 of whom also received topical antibiotic treatment. Otoscopy showed that external auditory canal(EAC) was stenotic in all cases with an average degree of stenosis of 49.7%.Three patients had clinical involvement of the temporomandibular joint (TMJ) (14.3%). Six patients had peripheral facial palsy. Biological examination, the mean sedimentation rate was 74, the median CRP level was 16.6, the median fasting blood sugar level was 2.3. Bacteriological and mycological samples were taken in all cases and redone in 6 cases. The fungal agents isolated were Candida Albicans in 7 cases, Candida Parapsilosis in 5 cases, Aspergillus Niger in 4 cases, Aspergillus Flavus in 3 cases, Candida Tropicalis in 1 cases, Candida Famata in 1 case. Nine bacterial cultures were positive. Aspergillus serology was carried out in 11 cases and were positive in only 2 cases. computed tomography was performed in all patients within a median of 2 days of admission, revealed EAC filling and lysis of the tympanic bone in all cases, extension to TMJ in 11 cases ,an extension to the deep spaces of the face in 8 cases (38.1%),an involvement of the soft parts in 5 cases, an extension to the deep spaces of the face in 8 cases, osteitis of the base of the skull in 2 cases and lysis of the facial nerve canal in one case. A probabilistic double antibiotic therapy targeting Pseudomonas was started after taking samples from all patients. Eleven patients received antifungal treatment (8 received voriconazole and 3 received fluconazole). The median length of hospital stay was 29 days [14-117]. Six patients retained PFP after a 3-month follow-up. Four of the 11 patients treated with an antifungal were readmitted (19%). **Conclusion:** The isolation of fungal agents during NEO is probably a result of infection secondary to local and oral antibiotic therapy initially initiated. The initiation of antifungal therapy during an OEN should be carefully considered given its many side effects. Confirmation of the diagnosis must be based on biopsies rather than a superficial sample to be able to incriminate the fungal agent in the genesis of this pathology.

## Waterborne Diseases and Hand Hygiene

### Poster 408. Outbreaks associated with Drinking Untreated or Improperly Treated Water During Outdoor Activities—United States, 1971–2019

**A.D. Miller,** M.E. Gleason, K.M. Benedict, S.A. Collier, J.S. Yoder, J.R. Cope, V.A. Roberts
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Outdoor freshwater sources (e.g., rivers, streams, or springs) can be contaminated by microbial pathogens. People who spend time outdoors (e.g., campers, backpackers, and hikers) and consume water from these sources without treating it properly can become ill. To better understand illnesses associated with consuming water from outdoor freshwater sources, we summarized outbreaks reported to CDC's Waterborne Disease and Outbreak Surveillance System (WBDOSS). **Methods:** Waterborne disease outbreaks are voluntarily reported by public health officials in U.S. states, the District of Columbia, territories, and freely associated states through WBDOSS. We summarized outbreaks that included drinking water directly from outdoor freshwater sources during 1971 through 2019 (the latest year of available data). We examined seasonality and common etiologies, as well as water settings, sources, and treatment. **Results:** In total, 48 outbreaks occurred in 22 states during 1971 through 2019, resulting in 678 illnesses (range 2–102 cases per outbreak), four hospitalizations, and no known deaths. Most outbreaks began during May–September (n=36; 75%); among the 36 outbreaks with a suspected or confirmed etiology, most were caused by with *Giardia* (n=25; 69%) or *Campylobacter* (n=5; 14%). Rivers and streams were the most common water source (n=34; 71%); common settings included national and state parks (n=11; 23%), public outdoor areas (n=11; 23%), and wilderness and forest settings (n=10; 21%). In 33 outbreaks (69%), no water treatment was attempted; in seven outbreaks (15%), only disinfection was used; in three outbreaks, filtration and disinfection (the recommended treatment strategy) were used. **Conclusions:** These findings emphasize the importance of water treatment when consuming fresh water from rivers, streams, or springs. Educational materials should include

detailed information on potential pathogens found in freshwater sources and how to treat water to remove these pathogens. Promotion of health messages should occur around times of peak outdoor recreational activity.

### Poster 409. Epidemiology and Evolving Prevention of Treated Recreational Water–associated Outbreaks — United States, 2015–2019

**S.K. Aluko**[1,2], S. Lee[1], J.P. Laco[1], E.J. Hannapel[1], V.R. Hill[1], M.C. Hlavsa[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA

**Background:** The number of annually reported US outbreaks associated with treated recreational water (e.g., in pools, hot tubs, or water playgrounds) has increased substantially since the late 1990s. This increase is driven by Cryptosporidium and Legionella. Chlorine is effective in reducing transmission of most pathogens in treated recreational water. However, the outer oocyst wall and biofilm protect Cryptosporidium and Legionella, respectively, against chlorine inactivation. The latest outbreak data new prevention tools are highlighted. **Methods:** U.S. public health officials voluntarily reported waterborne disease outbreaks to CDC. We defined an outbreak as similar illness in ≥2 persons, epidemiologically linked by location and time of exposure to treated recreational water—or aerosols or volatiles from such water. We examined data on treated recreational water– associated outbreaks, which started during 2015–2019 and had a report finalized in the National Outbreak Reporting System by February 4, 2021. Outbreak data include earliest illness onset date, case count, hospitalization and death counts, etiology, and outbreak exposure setting and venue. **Results:** For 2015–2019, 36 states and D.C. voluntarily reported 208 outbreaks. These outbreaks resulted in 3,646 cases, 286 hospitalizations, and 13 deaths. Cryptosporidium caused 76 (37%) outbreaks, resulting in nearly 70% of all cases (n=2,492 [68%]). Legionella caused 65 (31%) outbreaks, which resulted in all 13 deaths. More than one-third (n=71 [34%]) of the 208 outbreaks were associated with a hotel or resort; half of all outbreaks (n=107 [51%]) started during June–August. **Conclusions:** Prevention measures beyond chlorination are needed to prevent treated recreational water– associated outbreaks. CDC's Model Aquatic Health Code incorporates the latest science into guidelines that protect public health (e.g., calling for ultraviolet light disinfection to prevent Cryptosporidium transmission, daily inspection for and removal of biofilm) and address emerging public health threats (e.g., pathogen occurrence in novel aquatic venues). Additionally, CDC's new Legionella Control and Water Management Program Toolkits aim to prevent outbreaks caused by Legionella, including specific considerations for hotels and resorts.

### Poster 410. Withdrawn

### Poster 411. Implementation of a National-Level Baseline Capacity Review for Water, Sanitation, and Hygiene Related Enteric Diseases — Kenya, 2021

**M. Daud**[1], N. Mwanyalu[1], E. Langat[1], B. Bodha[1], A.M. Medley[2], R. Williams[2], C. Adibe[2,3], V. Petrenko[2,3], C. Ashton[4], A. Abade[5], P. Amoth[6], F.N. Kuria[6], J. Githaiga[1], F. Odhiambo[1], M. Nunga[1], M.O. Owiny[1]
[1]Kenya Field Epidemiology and Laboratory Training Program, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]RWD Consulting LLC, [4]Washington State Department of Health, USA, [5]African Field Epidemiology Network, [6]Kenya Ministry of Health, Nairobi, Kenya

**Background**: Enteric diseases caused an estimated 2,701,449 diarrheal illnesses in Kenya in 2020. To promote the continuous improvement, prevention and control of water, sanitation, and hygiene (WASH) related enteric diseases at the national level, Kenya partnered with the U.S. Centers for Disease Control and Prevention (CDC) to implement the WASH Baseline Capacity Review (WASH BCR). **Methods**: During 2020-2021 the Kenya Field Epidemiology and Laboratory Training Program (FELTP) partnered with CDC to prepare for and implement the WASH BCR at the national level. During July-August 2021, 24 expert respondents from the Ministry of Health, Ministry of Water, and non-governmental stakeholders were interviewed on various WASH competencies, including WASH preparedness and outbreak response, workforce capacity, surveillance of waterborne diseases, sampling and microbiology, and quality management systems. Interview responses were electronically recorded, and a Microsoft Excel tool instantly scored the quantitative responses. CDC subject matter experts (SME) will review the qualitative questions, determine an overall national capacity level, and generate a final report to provide actionable public health recommendations. **Results**: Approximately two-thirds of the questions were quantitative and could be instantly scored on a 10-point scale. Preliminary quantitative findings show competency scores ranging from 8-10, with Clinical Sampling and Microbiology scoring the highest. Qualitative responses are currently being analyzed. **Conclusions:** The WASH BCR engaged Kenyan stakeholders in a robust assessment of WASH and enteric disease surveillance national capacity. Preliminary quantitative findings indicate a range of capacity levels for the competencies assessed. Evaluation of the qualitative data is ongoing and will enhance the interpretation of the quantitative findings. A final report with national capacity determination is anticipated in January 2022 and will be

the subject of our presentation. The WASH BCR can be used to inform tailored action plans to enhance Kenya's enteric disease prevention and control programs.

### Poster 412. Qualitative Evaluation of Hand Hygiene Perception and Practices among Healthcare Workers in Guatemala in the Context of COVID-19

**P. Garzaro**[1], C. Craig[2], C.Q. Pratt[2], C. Cordon-Rosales[1,3], M.J. Lozier[2], D. Call[3], B. M. Ramay[1,3]
[1]Universidad del Valle de Guatemala, Guatemala City, Guatemala, [2] Centers for Disease Control and Prevention,[3] Paul G. Allen School for Global Health, Washington State University, Pullman, WA, USA
**Background:** Healthcare workers (HCWs) are at increased risk of SARS-CoV-2 infection due to regular patient contact. Proper hand hygiene (HH), which includes handwashing (HW) with soap and water or sanitizing with alcohol-based hand rub (ABHR), remains an effective strategy for preventing transmission of SARS-CoV-2. Implementing HH strategies that are both contextually relevant and effective is imperative for both HCWs and their patients to protect against transmission of infectious diseases like COVID-19. **Methods:** To better understand HH practices and preferences among HCWs and to make appropriate recommendations for improving adherence, we conducted a qualitative assessment with 10 HCWs from healthcare facilities (HCFs) in Quetzaltenango, Guatemala in July 2021. In-depth interviews were conducted with clinical staff, and collected information was translated and transcribed verbatim, coded using MaxQDA, and analyzed using a thematic analysis approach. **Results:** ABHR and HW with soap and water were common HH practices, although there was greater confidence and affinity for HW. ABHR was described as an alternative form of HH, used when there was limited access to water or time. Some HCWs described using the same HH methods regardless of type of procedure carried out during patient interaction, while others emphasized the need for HW with soap and water for invasive procedures. All participants demonstrated a high level of knowledge about proper HH in a HCF setting, yet lack of resources (water, sinks, soap, or ABHR) and time were barriers to regular HH practice. Participants expressed that proper HH was motivated by the desire to protect self, family, and patients; belief in benefits of HH; concerns about COVID-19; and visual cues. Interviewees suggested that increasing access to resources, periodic training on HH, and improvements in internal supply management processes could enhance practices among HCWs. **Conclusions:** This study has identified appropriate intervention strategies, including designing messages to promote HH and increasing access to ABHR in HCFs as potential methods to improve HH practices among HCWs. These strategies will be shared with the Ministry of Health for development of interventions for improving HH practices in HCFs.

### Poster 413. Norovirus-associated Acute Gastroenteritis (AGE) in a Peruvian Andean Community: Population Epidemiology and Incidence in a Multi-Year Community Cohort

**W.R. Campbell**[1], J. Neyra[2], L.E. Calderwood[3,4], C. Romero[2], G. Soto[2], A.K. Kambhampati[3], A.J. Hall[3], Y. Tinoc[2], J. Vinjé[3], S.A. Mirza[3]
[1]Division of Infectious Diseases, Department of Internal Medicine, Walter Reed National Military Medical Center, Bethesda, MD, USA, [2]US Naval Medical Research Unit No. 6, Lima, Peru, [3]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Cherokee Nation Assurance, Arlington, VA, USA
**Background:** Norovirus is the leading contributor to the burden of acute gastroenteritis (AGE) globally; however, estimates vary widely by socioeconomic setting and study design, with few estimates obtained via active community surveillance. **Methods:** Active surveillance for AGE was conducted in an annual median of 256 households during April 2015–April 2019 in a peri-urban suburb of Cusco, Peru. The cohort consisted of 1,645 participants, who contributed a total of 4,176 person-years (PY) of observation. Study staff conducted 2–3 visits per week to identify AGE cases of all ages, based on reported vomiting and/or diarrhea. Clinical data were collected 15 days following symptom onset, and stool specimens were collected within 10 days. Asymptomatic control households were matched to every 5$^{th}$ index case of AGE and a stool specimen was collected. Norovirus identification was made using real time reverse transcriptase polymerase chain reaction (qRT-PCR). Incidence was determined as a function of PY contributed by the annual at-risk study population. **Results:** A total of 1,099 AGE episodes were reported, for an incidence of 26.3 AGE episodes per 100 PY (95% Confidence Interval [CI]: 24.8 – 72.9). Testing of stool samples from 1,014 AGE episodes identified 186 (18.3%) norovirus episodes in 149 individuals, corresponding to a norovirus AGE incidence of 4.5 episodes per 100 PY (95% CI: 3.9 - 5.1). Norovirus incidence was highest in those aged <2 years with 200.5 episodes per 100 PY (95% CI: 173.4 – 232.0). Women aged 18 to <65 years accounted for 303 (27.6%) episodes of AGE and 44 (23.7%) of norovirus AGE reported in the cohort. Among 678 asymptomatic controls, 58 (8.2%) were positive for norovirus. The odds of norovirus detection were significantly higher among AGE cases compared to controls (OR = 2.4 [95%CI: 1.8 – 3.3]). **Conclusions:** The incidence of norovirus AGE was highest among infants, and the greatest number of norovirus episodes occurred among adult women. The data presented will help shape public health interventions in specific at-risk sub-populations.

### Poster 414. Strengthening National Water Sanitation and Hygiene Surveillance by Implementing a Baseline Capacity Review Assessment Tool

**A.M. Medley**[1], H.J. Mikoleit[2], M.M. Freeman[1], D. Berendes[1], M. Turnsek[1], J. Murphy[1], C. Adibe[1,3], V. Petrenko[1,3], C. Ashton[4], K. Carr[1], G.G. Rao[5], V. Bampoe[2], V. Hill[1], J. Concepción-Acevedo[6], R.Y. Williams[1]
[1]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Division of Bacterial Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]RWD Consulting, LLC, [4]Washington State Department of Health, [5]University of North Carolina, Chapel Hill, NC, USA, [6]Center for State, Tribal, Local and Territorial Support, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background**: Enteric diseases caused an estimated 1.4 million deaths worldwide in 2015. The U.S. Centers for Disease Control and Prevention (CDC) developed the water, sanitation and hygiene (WASH) Baseline Capacity Review (BCR) assessment tool to identify national capacity to prevent, detect, and respond to enteric disease outbreaks and advance global health security. **Methods**: Twelve BCR sections assess WASH preparedness and outbreak response, workforce development, waterborne disease surveillance, and laboratory capacity. Early versions of the BCR were piloted in Sierra Leone, seven Central American countries and the Dominican Republic between 2016-2019. Based on user and subject matter expert (SME) feedback, CDC developed the current version (version 3), which was piloted in Kenya in 2021. Version 3 is comprised of an Excel-based data collection and analysis tool, virtual training materials, and an implementation guide. Version 3 can instantly score 352 of the 538 (65%) questions to determine a capacity level ranging from low to high. Additional CDC SME input determines an overall national capacity level and generates a final report to provide actionable public health recommendations. **Results**: Ten countries completed the BCR as a tabletop exercise or through key informant interviews. In 2020, the 8 Central American and Caribbean countries used their findings to inform capacity building for national-level laboratories and enteric disease surveillance training opportunities. Based on facilitator feedback, versions 1 and 2 of the BCR were too long and the lack of a standardized data entry process made the assessment challenging to complete. Therefore, reports for the 8 Central American and Caribbean countries were not finalized until 2020. A preliminary capacity level from version 3 was available within one month of completing the assessment in Kenya. **Conclusion**: The WASH BCR engages national stakeholders in a robust assessment of WASH and enteric disease surveillance national capacity. Version 3 provides rapid feedback to stakeholders for prompt action and findings can drive the implementation of tailored activities to improve enteric disease prevention and control programs. A final report with recommendations for system strengthening is expected in early 2022.

### Poster 415. Strategic Sampling Design and Adaptive Sampling for COVID-19 Wastewater Surveillance: Case Studies in South Atlanta and Emory University Campuses

**Y. Wang**[1], P. Liu[1], M. Wolfe[1], J. VanTassell[1], P.F.M. Teunis[1], C.L. Moe[1]; L. Freeman[2], W. Rose[2], C. Holt[2], M. Browning[2]
[1]Center for Global Safe Water, Sanitation, and Hygiene, Rollins School of Public Health at Emory University, Atlanta, GA, USA, [2]City of Atlanta Department of Watershed Management, Atlanta, GA, USA

**Background:** Wastewater surveillance has been utilized to supplement information from clinical diagnostic testing to monitor COVID-19 in communities. COVID-19 Wastewater surveillance is complicated by many factors, including the geographic distribution of infections, fecal shedding, dilution and possible degradation of virus in the wastewater, wastewater characteristics, sample collection methods, and lab assays. Strategic sampling design can mitigate many of these complications, reduce uncertainty, and provide actionable information to control the spread of COVID-19. **Method:** We conducted network analyses of the Atlanta sewer network and developed a method to identify the catchment area of each manhole. COVID-19 Wastewater surveillance can provide information on temporal trends in infection at a city level, identify spatial hotspots at a community level, and flag surges in cases at an institutional level. We examined several sampling strategies based on target population, target catchment size, and nested catchment for different goals and illustrate these strategies with two case studies in South Atlanta and Emory University campuses. An adaptive sampling process was developed to transform the wastewater surveillance into a dynamic system that relocates sampling sites based on the most recent results. **Results:** The Atlanta sewer network is a tree network with some net topology structures within the center of the city. Detection rates for SARS-CoV-2 varied even between manholes in close proximity. With the strategic sampling design, the wastewater surveillance can provide actionable results to meet the goal of wastewater surveillance. The adaptive sampling approach improved the performance of nested sampling by continuously relocating sites to identify and monitor areas with high SARS-CoV-2 infection. **Conclusions:** Understanding the sewer network topology and catchment area of sampling sites are critical for designing sensitive and actionable COVID-19 wastewater surveillance.

Strategic sampling design should be based on the goal of wastewater surveillance, infection prevalence, and public health evidence needed for action.

### Poster 416. Spatial and Temporal Dynamics of Cholera Epidemics in Lake Tanganyika Areas from 2008 to 2021

**S. Mako**[1,2], N. Taty[2,3], Doudou Batumbo[4], P. Welo[2], T. Vita[4], N. Meschnet de Richmond[3], D.Bompangue[4]
[1]Master 1 in Ecology of Infectious Diseases, University of Kinshasa, Democratic Republic of Congo, [2]National Program for the Elimination of Cholera and the Fight against Other Diarheic Diseases, Ministry of Health, Democratic Republic of Congo, [3]Montpellier Geography and Planning Laboratory, University of Paul Valéry, Montpellier, France, [4]Research and Training Unit on Ecology and Control of Infectious Diseases, University of Kinshasa, Democratic Republic of the Congo

**Background**: Lake areas in Tanganyika province are reporting cholera cases continuously. Three of these Zones out of the total of 11 zones in this province (Kalemie, Moba and Nyemba) constitute the Kalemie sanctuary site. Despite the implementation of numerous response activities, the epidemiological profile does not appear to be improving. The present study aims to identify the micro-hotspots in these sanctuary areas as well as the factors of persistence of cholera epidemics. **Methods**: A descriptive cross-sectional study was conducted in Tanganyika. Epidemiological, environmental and biological data were collected. The field investigation was carried out from July 29 to September 4, 2021. **Results**: The lake areas of Tanganyika recorded 80% of cases and 50.5% of deaths from 2008-week 30.2021. In these areas, during periods of lull, cases retract in 14 micro-hotspots (6 in Kalemie, 5 in Nyemba and 3 in Moba) out of the 94 health areas in this region. The persistence of cholera epidemics in these micro-hotspots suggests the existence of potential environmental and human reservoirs. Five strains of *Vibrio cholerae* were found in samples taken from Lake Tanganyika and 2 stool samples taken from asymptomatic fishermen came back positive out of 44 samples taken during the lull. The health areas adjacent to the lake are the most affected at the level of sanctuary areas. The presence of a train station and a large market with significant activity make these areas particularly vulnerable to cholera epidemics. **Conclusion:** The association of "water-hygiene and sanitation" type actions with community sensitization primarily targeting micro-hotspots of persistent epidemics could avoid the seasonal trend of cholera epidemics highlighted by this study. The continued epidemiological and environmental monitoring of parameters of the yaw and the genetic characterization of strains of *Vibrio cholerae* in the environment should contribute to the early.

### Poster 417. Moving Cholera Rapid Diagnostic Tests Beyond Role as Simple Screening Tool

**A.K. Debes**[1*], D.M. Olson[2*], D.G. Nichols[3], S. Xiao[1], M. Turnsek[4], P. Barboza[1,5]
[1]Department of International Health, Johns Hopkins Bloomberg School of Public Health, Baltimore MD, USA, [2]World Health Organization, Geneva Switzerland, [3]Chenega Professional & Technical Services, LLC, [4]Centers for Disease Control and Prevention, Atlanta, GA, USA, [5] Secretariat, Global Task Force on Cholera Control
*Authors contributed equally

**Background:** Cholera causes an estimated 2.86 million cases and 95,000 deaths annually. Timely diagnosis by classic microbiology methods, the mainstay for confirming outbreaks, is constrained by lack of local culture capacity and delayed transport to reference centers. Cholera rapid diagnostic tests (RDT) are a crucial tool for early detection of cholera cases but are deemed to lack adequate specificity and sensitivity for widescale use. Given constraints on the use of culture methods, adapted use of RDTs offers an alternative for early outbreak monitoring and improved cholera burden estimates. **Methods:** A literature review identified RDT performance evaluations conducted between 1990 – 2020. A meta-analysis focused on Crystal VC, SD Bioline anwzzd Cholkit compared to culture or PCR as gold standard. Model estimated means were calculated for direct specimen performance evaluations (sensitivity and specificity) and used with estimated situation-specific prevalence to calculate positive and negative predictive values (PPV and NPV) for RDT performance. We then estimated needed testing outcomes at differing levels of cholera prevalence to have confidence that, among those testing RDT positive, at least one is a true cholera case. **Results:** Of 100 abstracts reviewed, 20 articles were included in the final analysis. The median number of samples evaluated by RDT was 170. The model estimated mean for RDT Sensitivity on direct specimens, 93% surpassed WHO acceptable limit of 90%. The model estimated mean for Specificity on direct specimens, 79%, did not meet WHO lower limit (85%). Using the described methodology, our calculations show that there is >90% probability (PPV) that at least 1 RDT positive case is a true cholera case when cholera prevalence (based on context-typical proportion of clinic care seekers that are culture positive for cholera) is 20% and 3 of 6 patients tested are RDT positive. **Conclusions:** Based on model estimated means for performance and probabilities derived from this analysis, grouped positive RDT results (with the required number of positive tests adapted to context-typical cholera prevalence) can indicate the true presence of *V. cholerae* O1 with high confidence, to monitor cholera

epidemiological situations and to better inform response measures and control programs using microbiologically derived data.

## Health Communications

### Poster 418. Health Communications for Migrant Produce Workers in the United States

**C.K. Rodriguez Morales**
Rollins School of Public Health, Emory University, Atlanta, GA, USA
**Background:** In 2020, produce workers were declared "essential workers" to protect America's food supply chain. Produce workers had to work during stay-at-home orders enacted nationwide. Workers were disproportionally impacted by COVID-19 outbreaks creating the need to inform this community on COVID-19 preventive measures. High prevalence of limited literacy, a monolingual Spanish population, and complex guidance produced gaps in information among workers. The goal of this project was to protect produce workers and their community by informing them on COVID-19 protective measures through the development of a series of infographics with COVID-19 information using visuals and plain language. **Methods:** Twenty messages were developed based on information obtained from federal and non-federal resources. The messages covered topics on direct and indirect transmission of COVID-19, masks, and symptoms. These messages were transformed into infographics with concise messaging and visuals that could deliver the message to workers with limited literacy. The English versions of these infographics were analyzed to determine the readability level and were later translated into Spanish. To ensure that the content and visuals were meeting the project's goal, partners from Oregon State University and Mexico provided important feedback during the development of the infographics. After feedback, several changes were made to improve the messages and general aesthetics of the infographics. **Results:** Forty-two infographics were developed with the English versions ranging from 3rd to 8th grade level of readability. A guiding document on how to use these infographics was created describing original source content, usage, placement, grade level of the infographics, and descriptions of the images included in each infographic. **Conclusion:** This project produced new communications materials available to workers and growers to download for free, helping close some gaps in access to information. Lastly, it has provided one more tool to the food and agriculture industry to help keep produce workers informed on COVID-19.

### Poster 419. Examining Reach and Impact of *Emerging Infectious Diseases*® during the COVID-19 Pandemic

**B. Breedlove**, R. Tucker, B. Segal, S. Richardson, S.L. Gregory, S. O'Connor, W. Hale, M. Boggess, M. Kuehnert, P. Drotman
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** *Emerging Infectious Diseases (EID)*, an externally peer-reviewed, open-access journal published monthly by the Centers for Disease Control and Prevention, was launched in 1995 and transitioned to an online-only journal starting in 2020. Approximately half the members of *EID*'s Editorial Board do not work for CDC. Starting the journal was a key part of CDC's response to a 1992 Institute of Medicine report, *Emerging Infections: Microbial Threats to Health in the United States*, that warned of the increasing threat to American and global public health from new, previously unknown, or reemerging diseases. During its first 27 years, *EID* has published more than 11,750 peer-reviewed articles, providing a link between the scientists uncovering potential health threats and the professionals who respond to those threats. *EID* provides readers with an array of search tools and spotlight collections to help them explore its ever-increasing content. Each issue of the journal features a theme, and recurrent themes include antimicrobial resistance, food safety, fungal infections, mycobacterial infections, respiratory diseases, vectorborne infections, and zoonotic infections. *EID* does not record or track any personal information for visitors to its website. The journal uses aggregated metrics to evaluate its reach and influence and to understand how well *EID* brings attention to, and improves the understanding of, disease emergence and reemergence, prevention, and elimination. **Methods:** To better understand *EID*'s reach and influence, we monitor these metrics: *EID's Journal Impact Factor;* Scopus CiteScore Metrics; and Google Scholar h-Index rankings; usage of *EID* content accessed through PubMed Central; attention in lay media, as measured by Altmetric Attention Scores; most frequently cited articles, as tracked by Scopus; website page views, as tracked by Adobe Analytics; number of subscribers to *EID*'s online email notifications; number of articles submitted to *EID*. **Results:** Journal Citation Impact Factor, CiteScore Metrics, and Google Scholar h-index scores measure the number of citations of *EID* articles within other scientific journals and rank compare *EID*'s influence with that of similar journals. *EID*'s 2020 Journal Citation Impact Factor is 6.883—2nd among open-access infectious disease journals and 7th among tracked infectious disease journals. In 2020, *EID*'s content available from PubMed Central, the U.S. National Library of

Medicine's digital repository, was accessed 8,858,952 times—up 4,862,751 from 2019 and to date has been accessed more than 4,000,000 times in 2021. Altmetric scores for *EID*'s articles show that among the journal's most popular articles are those about COVID-19, and 13 of those articles are ranked among the 1,000 most popular of more than 19,300,000 tracked articles. *EID*'s most highly cited articles include those on foodborne infections, antimicrobial resistance, influenza, vectorborne diseases, and zoonotic diseases. **Conclusion:** Multiple journal metrics indicate that EID's exposure and influence have increased over time, and many of those metrics, including website page views, PubMed usage, and Altmetric rankings, have reached all-time highs since the start of the COVID-19 pandemic.

### Poster 420. Operationalizing Risk Communication and Community Engagement (RCCE): An Assessment of 2020 Capacity in 26 Countries

**L. Dick**, J. Moodie, A. Greiner
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Public health emergencies have revealed the critical need for immediate and effective risk communication and community engagement (RCCE). Even with Global Health Security Agenda Joint External Evaluation (JEE) RCCE indicators helping guide countries to meet International Health Regulations, RCCE is often under-resourced, unprepared, and overlooked in response operations. As countries responded to COVID-19, we examined critical gaps in RCCE capacity to strengthen this integral component of global health security. **Methods:** From August to November 2020, we assessed COVID-19 RCCE response capacity in 26 countries. Through structured interviews of CDC Country Office staff, we assessed the existence of 1) a dedicated and trained RCCE team and 2) a RCCE strategic plan. We also abstracted JEE Version 1.0 data (indicator R.5.1 [Risk Communication Systems]) from February 2017 to November 2019 for reference. RCCE capacity was scored on 3-point scale for ease of reporting but ensured congruency to the JEE 5-point scale. **Results:** The 26 countries represented five World Health Organization (WHO) regions: African (76.9%), South-East Asian (11.5%), Western Pacific (3.8%), Eastern Mediterranean (3.8%), and European (3.8%), with a median 2020 GDP per capita of $1,346 (range: $448-7,189). RCCE team capacity varied widely, with six (23.1%) countries at full capacity, 15 (57.7%) at partial capacity, and five (19.2%) at no capacity. For RCCE strategic plan, 16 (61.5%) had partial capacity and seven (26.9%) had no capacity. Only three (11.5%) countries had both a dedicated RCCE team and strategy during COVID-19. For JEE indicator R.5.1, 13 (50.0%) of the countries scored a one, eight (30.8%) scored a two, four (15.4%) scored a three, and only one (3.8%) scored a four. Aligning the different JEE scores from 2017-2019, 42.3% performed better and 38.5% performed consistently. **Conclusions:** Despite some improvement since JEE scoring, countries demonstrated an overall low RCCE operational capacity during COVID-19. The findings in this assessment highlight the need to focus on essential operational resources for a sustainable and ready RCCE program, including resources, staffing and strategic planning. As a critical component of International Health Regulations, global health security initiatives should prioritize sustainable RCCE program implementation.

### Poster 421. WHO Competence Framework to Build a Response Workforce to Manage Infodemics

**T.D. Purnat**[1], S. Rubinelli[2], J. Lamichhane[3], S. Briand[3], T. Nguyen[3]
[1]Digital Transformation Unit, European Centre for Disease Prevention and Control, Stockholm, Sweden, [2]University of Lucerne and Swiss Paraplegic Research, Luzerne, Switzerland, [3]World Health Organization, Geneva, Switzerland

**Background:** An infodemic is an overflow of information of varying quality that surges across digital and physical environments during an acute public health event. It leads to confusion, risk-taking and behaviors that can harm health and lead to erosion of trust in health authorities and public health responses. Infodemic management can support the management of epidemics and of epidemic risk. The practice requires health workforce to have multidisciplinary and cross-functional skillsets. **Methods:** The framework was developed in stages. First, lessons about infodemic management were synthesised from the three WHO infodemic management conferences and other events during 2020. This was followed by a qualitative interview study, and then by two facilitated expert panels to validate the results and reach consensus. This resulted in a competence framework to build a response workforce for managing infodemics. **Results:** The competence framework comprises four domains: (i) infodemic management - competencies in infodemiology; (ii) prepare and monitor - competencies in the use of effective tools to listen to communities and in design and sharing of high quality health information; (iii*)* detect and intervene- competencies to design, implement and evaluate interventions to promote resilience to the infodemic and health misinformation and to empower individuals and communities to exercise their right to access quality health information; (iv) strengthen - competencies to strengthen health systems to promote healthier populations through better management of infodemics in health emergencies and preparedness. **Conclusions:** Infodemic management requires enhancement of skills and is innovating the next generation of public health system capacities and tools for more effective

management of epidemics and of epidemic risk. The competence framework can guide and support the design, development, and evaluation of the needs of health workforce. Because the infodemic management practice and the science of infodemiology are quickly developing, the competence framework will be regularly reviewed and updated.

### Poster 422. Evaluation of a Geographic, Community-focused Infodemiology Intervention Addressing COVID-19 Vaccine Misinformation on Social Media Using an Implementation Science Framework

**D.A. Scales**[1,2], J.M. Gorman[2], L.J. Leninger[3]
[1]Division of General Internal Medicine, Weill Cornell Medicine, New York, NY, USA, [2]Critica, The Bronx, NY, USA, [3]Tuck School of Business at Dartmouth, Hanover, NH, USA
**Background:** Misinformation surrounding Covid-19 vaccines has affected vulnerable communities in different ways. We describe an online effort to address Covid-19-vaccine related misinformation on social media (Facebook) according to a flexible, multi-dimensional protocol derived from evidence on effective persuasion and debunking methods online. Intervening on news media posts based in Newark, Central Texas and Chicago media markets, infodemiologists employed multiple engagement techniques including empathy in accordance with motivational interviewing, reflective practice, appeals to scientific consensus, reframing, personal anecdotes, in-group linguistic and cultural frames to demonstrate in-group identity and trustworthiness, and referencing sources likely to be trusted by commenters. **Methods:** 146 pilot interventions collected December 2020 – April, 2021 were qualitatively and quantitatively evaluated by adapting categories of the RE-AIM implementation science framework: reach, effectiveness, adoption, implementation and maintenance. Two coders engaged in qualitative examination of infodemiologists' fealty to the protocol, commenter engagement, behavior of other commenters, other commenters relative engagement with infodemiologists, and focusing on "bystanders" versus active commenters. Coding discrepancies were resolved through deliberation. Social media platform user agreements prohibiting data scraping as well as IRB restrictions limited data collection. **Results:** 64% (93/146) of interventions demonstrated engagement (comments and/or likes) and 55% (80/146) resulted in direct text responses from other users. Protocol fealty was high according to qualitative metrics though there was significant variation in empathic opening statements, commenter responses and engagement by bystanders. In only 1% of interventions (2/146) was evidence of a backfire effect found and these corresponded with deviations from the recommended protocol. **Conclusions:** Infodemiologists can be effective within public, community-specific parameters on social media, providing counterweight to misinformed comments without precipitating significant psychological reactance. Facebook platform and IRB limitations inhibited full-scale evaluation of the impact of the intervention on bystanders, leading to heavy emphasis on process-oriented metrics. Subsequent infodemiologist work has expanded to other social media platforms. Mixed-methods evaluations leveraging implementation science frameworks are an effective approach to evaluating both fealty to protocol and, to the degree made feasible by native platform metrics, an intervention's relative impact.

## Special Populations

### Poster 423. Infectious Agents Associated with Stillbirths and Early Neonatal (0-2 days) Deaths in Sub-Saharan Africa and South Asia: Findings from Child Health and Mortality Prevention Surveillance, 2016-2019

**A. Rahman**[1], M. Alam[1], K.H. Lee[2], M.I. Jahan[1], M.Z. Hossain[1], M. Rahman[1], S. El Arifeen[1], I.U. Ogbuanu[3], S. Samura[4], E. Kaluma[3], S.O. Sow[5], A.M. Keita[5], M.D. Tapia[6], A. Mehta[6], K.L. Kotloff[6], S.A. Madhi[7], S. Mahtab[7], P. Mutevedzi[7], B.N. Thwala[7], C. Mugah[8], S. Sava[9], E. Oele[9], R. Omore[8], A.K. Igunza[8], I. Mandomando[10,11], Q. Bassat[10,12-15], S. Ajanovic[12], R. Varo[10,12], A. Sitoe[10], N. Assefa[16], J.A.G. Scott[17], L. Madrid[16,17], M. Mulatu[18], F. Temesgen[19], B. Dewey[20], L. Liu[21], C.G. Whitney[20], D.M. Blau[22], R.F. Breiman[23], E.S. Gurley[1,2]
[1]International Center for Diarrhoeal Diseases Research (icddr,b), Dhaka, Bangladesh, [2]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [3]Crown Agents, Freetown, Sierra Leone, [4]World Hope International, Makeni, Sierra Leone, [5]Centre pour le Développement des Vaccins (CVD-Mali), Ministère de la Santé, Bamako, Mali, [6]Center for Vaccine Development and Global Health, University of Maryland School of Medicine, Baltimore, MD, USA, [7]South African Medical Research Council Vaccines and Infectious Diseases Analytics (VIDA) Research Unit, Johannesburg, South Africa, [8]Kenya Medical Research Institute, Center for Global Health Research (KEMRI-CGHR), Kisumu, Kenya, [9]Kisumu County of Department of Health, Kisumu, Kenya, [10]Centro de InvestigaçãoemSaúde de Manhiça [CISM], Maputo, Mozambique, [11]Instituto Nacional de Saúde [INS], Maputo, Mozambique, [12]ISGlobal - Hospital Clínic, Unversitat de Barcelona, Barcelona, Spain,

[13]InstitutóCatalana de Recerca I EstudisAvançats [ICREA], Barcelona, Spain, [14]Pediatrics Department, Hospital Sant Joan de Déu, Universitat de Barcelona, Esplugues, Barcelona, Spain, [15]Consorcio de Investigación Biomédica en Red de Epidemiología y SaludPública [CIBERESP], Madrid, Spain, [16]College of Health and Medical Sciences, Haramaya University, Harar, Ethiopia, [17]Department of Infectious Disease Epidemiology, London School of Hygiene & Tropical Medicine, United Kingdom, [18]Ayder Specialized Comprehensive Hospital, Mekelle University, Mekele, Ethiopia, [19]Addis Ababa University, Addis Ababa, Ethiopia, [20]Emory Global Health Institute, Emory University, Atlanta, GA, USA, [21]Public Health Informatics Institute, Task Force for Global Health, Atlanta, GA, USA, [22]Center for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, USA, [23]Department of Global Health, Rollins School of Public Health, Emory University, Atlanta, GA, USA
**Background**: Infection causes more than 50% of stillbirths and about 25% of newborn deaths in low-and middle-income countries. The causative pathogens have changed significantly over time but epidemiologic evidence is scanty. We aimed to characterize the pathogens contributing to stillbirths and neonatal deaths occurring within the first two days of life in sub–Saharan Africa and South Asia. **Methods**: CHAMPS is a multi-country project designed to investigate the causes of stillbirths and children under-5 years old deaths using multiple diagnostic platforms, including postmortem minimally invasive tissue sampling. Expert panels review the data and assign underlying, immediate, and morbid causes of death ("causal chain"). **Results**: We examined 440 stillbirths and 433 neonatal deaths occurring in the first two days of life between December 2016 and December 2019. Among stillbirths, 12% (53/440) had a congenital infection in the causal chain, with 64 infectious pathogens being identified. Half were gram-positive bacteria (50%, 32/64), 36% (23/64) were gram-negative, and 14% (9/64) were viruses. The most common pathogens were *Streptococcus species* including group B streptococci (36%, 23/64), followed by *E. coli/Shigella species* (14%, 9/64) and Cytomegalovirus (13%, 8/64). Among 124 neonatal cases with infection in the causal chain, congenital infection caused 54% (67/124) of early neonatal deaths. We identified 140 pathogens in the causal chain for neonates; 60% (84/140) were gram-negative bacteria, 34% (47/140) gram-positive, and 4% (6/140) viruses. Among them *Acinetobacter baumannii* (12%, 17/140), *E. coli* (16%, 23/140) and *Klebsiella pneumoniae* (22%, 31/140) followed by *Streptococcus agalactiae* (16%, 22/140) were the most common bacteria. High rates of multidrug resistant gram-negative bacteria associated with post-mortem specimens were reported from Mozambique and Bangladesh. **Conclusion**: The frequency of Gram-positive vs Gram-negative bacteria was dissimilar when comparing stillbirths and neonatal deaths. The differences highlight the need for better characterization of cascades contributing to utero-fetal infection scenarios. A better understanding of the source of infection by effective screening during pregnancy is crucial to prevent their associated morbidity and mortality.

### Poster 424. Characterization of *Ureaplasma* isolates from neonatal deaths in the global multi-center Child Health and Mortality Prevention Surveillance Network

**J.L, Waller**[1], E. Yang[1,2], M.H. Diaz[1], J.M. Winchell[1] Child Health and Mortality Prevention Surveillance Consortium[3]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]IHRC, Inc., Atlanta, GA, USA, [3]Emory Global Health Institute, Atlanta, GA, USA
**Background**: *Ureaplasma* species, including *U. urealyticum* and *U. parvum*, commonly colonize the female urogenital tract and are transmissible to neonates during birth. Recent studies in South Asia and South Africa revealed *Ureaplasma* species as a leading cause of severe neonatal infections. However, diagnostic testing of clinical specimens and comprehensive genomic studies of *Ureaplasma* are limited. **Methods:** Whole blood, cerebrospinal fluid (CSF), and tissue specimens were collected from neonates post-mortem via a minimally invasive tissue sampling (MITS) procedure at seven Child Health and Mortality Prevention Surveillance (CHAMPS) sites in sub-Saharan Africa and South Asia from May 2017 to October 2021. *Ureaplasma* species were detected by real-time reverse transcription polymerase chain reaction (RT-PCR) using custom TaqMan Array Cards for multipathogen detection. Cause of death was determined by a committee of experts upon review of multiple data sources according to diagnostic standards. Specimens were transferred to CDC for additional testing and culture. Whole genome sequencing was performed on all isolates using Illumina MiSeq benchtop sequencr. **Results:** Isolates were recovered from 8 of 22 primary specimens, including lung tissue (n=4), blood (n=2), and CSF (n=2), from 5 CHAMPS cases enrolled in South Africa from May 2017 to January 2018. *U. parvum* and *U. urealyticum* isolates were recovered from two cases each. In one case *U. parvum* was recovered from both blood and CSF while *U. urealyticum* was recovered from tissue; both species were identified in primary blood and CSF specimens from this case. Three (60%) of 5 cases were early neonates (1-6 days), one (20%) was a late neonate (7-27 days), and one (20%) death occurred in the first 24 hours of life. *Ureaplasma* was not attributed in the causal chain in any case. RT-PCR performed on 22 primary specimens revealed *U. urealyticum* in 9 (41%), *U. parvum* in 6 (27%), and both species in 2 (9%); neither species was determined in 5 (23%) specimens. **Conclusions:** Analysis of additional

specimens from cases enrolled at other CHAMPS sites is ongoing to further investigate the factors underlying development of severe *Ureaplasma* infections in neonates. Comprehensive genomic analysis will allow for identification of bacterial features related to severe disease and death.

### Poster 425. Congenital Cytomegalovirus Infections Mother-Newborn Pair Study in Southern Ethiopia

**M. Hailemariam**[1,2,3], Z. Mekonnen[2], E. Loha[4], E. Padalko[3,5]
[1]School of Medical Laboratory Sciences, Hawassa University College of Medicine and Health Sciences, Hawassa, Ethiopia, [2]School of Medical Laboratory Sciences, Jimma University Institute of Health Jimma University, Jimma, Ethiopia, [3]Department of Diagnostic Sciences, Ghent University, Ghent, Belgium,[4]Centre for International Health, University of Bergen, Bergen, Norway,[5] Laboratory of Medical Microbiology, Ghent University Hospital, Ghent, Belgium

**Background**: Congenital cytomegalovirus is a common cause of neurodevelopmental delays and sensorineural hearing loss of infants yet remain unnoticed in the entire world. So far, the prevalence of congenital cytomegalovirus (cCMV) and associated factors in Ethiopia are not studied. Hence this study was the first to assess the prevalence and associated factors of cCMV in Ethiopia. **Methods**: A mother-newborn pair cross-sectional study was conducted at Hawassa University comprehensive and specialized hospital, Ethiopia. Newborn's saliva sample was collected after one hour of the breastfeed and tested for cCMV using Alethia CMV molecular assay. Mothers' sera were tested serologically for anti-CMV IgM and IgG by EUROIMMUN ELISA. Pregnant women responded to a questionnaire about their previous and current obstetric history and socio-demographic characteristics. Possible associated factors for cCMV were assessed by bivariable and multivariable logistic regression. **Results**: A total of 593 mother-newborn pair was assessed. CMV was detected in 14 of 593 newborn saliva swabs (2.4%; 95% CI 1.2–3.7). As assessed by CMV IgM positive results, maternal CMV seropositivity was 8.3% thus; the rate of congenital transmission was 28% (14/49). Congenital CMV infection was significantly associated with maternal exposure through nursery school children in the household, women sharing a feeding cup with children, and any of the detected curable STIs during pregnancy. Birth weight was negatively associated with CMV infection. Maternal age, gravidity, level of education, and sharing of children feeding utensils were not associated with cCMV infection. **Conclusion**: A high rate of cCMV infection in the absence of a maternal diagnostic facility and lack of awareness is a serious challenge for Ethiopia. Thus, policymakers must take appropriate action through the antenatal care system for prevention strategies and put in place a constant health education and awareness creation of pregnant women about the causes of infection and hygienic measures.

### Poster 426. Impact of Cirrhosis on Outcomes of Patients Hospitalized with Pneumonia: Analysis of the National Inpatient Sample

**H. Laswi**[1], A. Abusalim[1], R. Musa[2], M.S. Warraich[1]
[1]John H. Stroger Hospital of Cook County, Chicago, IL, USA, [2]East Tennessee State University, Johnson City, TN, USA

**Background:** Liver cirrhosis imposes a substantial health burden and is a major cause of morbidity and mortality. It leads to dysfunction of both the innate and acquired immunity resulting in an increased risk of infections. Pneumonia is one of the most common infections in cirrhotic patients and one of the most frequent primary diagnoses for inpatient stays in the US. The goal of this study is to compare clinical outcomes of cirrhotic patients admitted with a primary diagnosis of pneumonia to those without cirrhosis. **Method:** Using the 2016 to 2018 nationwide inpatient sample databases, we included all patients admitted with a primary diagnosis of pneumonia, with and without cirrhosis, as a secondary diagnosis. International Classification of Diseases-tenth revision codes were used. The primary outcome was in-hospital mortality. Secondary outcomes included length of stay and total hospital charges. Results: Out of 2101783 pneumonia hospitalizations, 33394 (1.58%) had cirrhosis. Compared to patients without cirrhosis, cirrhotic patients had a lower mean age (63.3 years vs. 68.6, P=0), were mostly males (56.9% vs. 46.8%, P=0), and had higher mean Charlson comorbidity index (4.1 vs 2.4, P=0). Hospitalizations for pneumonia with cirrhosis had 1.1 day increase in mean LOS (P=0), higher total hospital charges (56103 USD vs 41115 USD, P=0), and inpatient mortality (4.6% vs 2.5%, P=0) compared to those without cirrhosis. **Conclusion:** Compared to patients without cirrhosis, cirrhotic patients admitted with a primary diagnosis of pneumonia were younger and had higher Charlson comorbidity index. Moreover, patients with cirrhosis had worse outcomes in terms of inpatient mortality, length of stay, and total hospital charge.

### Poster 427. Care for Latent Tuberculosis Infection at Kaiser Permanente Southern California: 2009 – 2018

Moved to Poster Session 5, Wednesday, August 10, 12:30 PM – 1:30 PM (at end of Respiratory Diseases and Influenza section, after Poster 372**)**

## Late-breakers

### Poster LB-86. A Systematic Review of Zoonotic Enteric Parasites Carried by Flies, Cockroaches, and Dung Beetles

**A.N. Barnes**[1], A. Patel[1], M. Jenkins[1], K. Rhoden[1]
[1]Department of Public Health, Brooks College of Health, University of North Florida, Jacksonville, FL, USA, [2]Stanton College Preparatory School, Jacksonville, FL, USA
**Background:** Insect vectors such as filth flies, cockroaches, and dung beetles have the ability to transmit a variety of zoonotic enteric parasites (ZEPs) of public health importance. Recognizing which pathogens each vector has been shown to carry can assist in our understanding of parasite exposure risks for households and communities. The purpose of this systematic review was to outline the parasites which have been documented in each vector, risk factors for human and animal exposure, and potential One Health interventions for their prevention and control. **Methods:** A systematic review was conducted across 15 databases using PRISMA guidelines for the screening process. Peer-reviewed journal articles with English abstracts or full-text that comprised primary research showing natural or experimental vector infection with one or more ZEP were included. **Results:** A total of 85 articles published between 1926-2021 were included in the final qualitative analysis. The most common parasites associated with these insect vectors included, but were not limited to: *Ascaris* spp., *Trichuris* spp., *Entamoeba* spp., and *Cryptosporidium* spp. Risk factors for potential exposure for humans and animals included inadequate or unsafe water, sanitation, and hygiene practices or services, unsafe food handling, human-animal contact, favorable environmental conditions for vector habitats, insect behaviors and preferences, and ingestion of contaminated vectors. **Conclusions:** Many of the pathogens are related to inadequate water, sanitation, and hygiene within household practices, community services, or animal husbandry operations. These unsafe environments serve as feeding and breeding sites for filth flies, cockroaches, and dung beetles. Addressing these risk factors using a One Health framework would be helpful in the prevention of global ZEP exposure for humans and animals.

### Poster LB-87. Antimicrobial Action of Oxytetracycline in the Composition of Polyphosphate Ester Type Transporter

**M. Kozak**[1], A. Stasiuk[2], V. Vlizlo[3], D. Ostapiv[1], Y. Bodnar[1], N. Kuzmina[1], N. Figurka[2], N. Nosova[2], R. Ostapiv[4], I. Kotsumbas[4], S. Varvarenko[2], V. Samaryk[2]
[1]Institute of Animal Biology of the NAAS of Ukraine, Lviv, Ukraine, [2]Lviv Polytechnic National University, Lviv, Ukraine, [3]S. Gzhytskyi National University of Veterinary Medicine and Biotechnologies, Lviv, Ukraine, [4]State Research Control Institute of Veterinary Medicinal Products and Feed Additives, Lviv, Ukraine
**Background:** Long-term use of tetracyclines for the treatment of infectious diseases formed resistance to antibiotics. Therefore, given the emergence of antibiotic-resistant microorganisms and the reduced effectiveness of antibiotics, it is advisable to develop and implement polymeric transport systems to increase the therapeutic effect and decrease the toxic effects of antibiotics. The aim of this study was to evaluate the effect of new polyphosphate ester type transporters in complexes with oxytetracycline on microorganisms' growth. **Methods:** Polyphosphate esters (phosphorus-containing pseudopolyamino acids) were obtained by activated polycondensation according to the Steglich reaction of N-derivatives of dicarboxylic α-amino acids and di-polyethylene glycol (ethyl) phosphates. Oxytetracycline by phosphorus group was attached to the synthesized polyphosphates. Quantitative content of oxytetracycline in the samples was measured by high performance liquid chromatography. Disks diffusion tests were used to determine the effectiveness of the antibiotic action on the growth of microorganisms. Microorganisms were also cultured in liquid medium. Culture growth in the presence of oxytetracycline and its complexes was compared to control. **Results:** Two complexes of oxytetracycline with polyphosphateester type transporters (P4 and P6) were synthesized. Oxytetracycline contents in these complexes were 11.9 mg/ml (P4) and -12.2 mg/ml (P6). P4 strongly inhibits *S. aureus* growth at 2.3 μg/disk concentration. The growth inhibition area is 37.5% ($p < 0.01$) higher compared to the action of the traditional form of antibiotic and P6 complex. P6 is more effective in inhibiting the growth of *S. aureus* at the concentration 3.8 μg/disk compared to control. A similar result was found during the cultivation of *S. aureus* in the liquid medium. Both P4 and P6 caused growth inhibition of *E. coli* in solid medium at 8 μg/disk. **Conclusions**: Oxytetracycline in the complex with polyphosphate ester type transporters has a higher antimicrobial effect compared to the traditional form of antibiotic. The effectiveness of the complexes depends on the composition of the transporters and the microorganism sensitivity to the antibiotic.

### Poster LB-88. Assessment of Risk Factors for Coronavirus Disease 2019 in Healthcare Workers: A Nested Case-control Study, Bishkek, Kyrgyzstan, June 2020-May 2021

**V. Alymkulova**[1], D. Nabirova[2], N. Kemelbek kyzy[1], S. Alaverdyan[3], N. Abamuslimova[4], C. Zhumalieva[5], D. Otorbaeva[4]
[1]Central Asia Field Epidemiology Training Program, Bishkek, Kyrgyzstan, [2]US Centers for Disease Control and Prevention, Regional Office of Central Asia, Almaty, Kazakhstan, [3]American University of Armenia, Yerevan, Armenia, [4]Department of Disease Prevention and State Sanitary and Epidemiological Supervision, Bishkek, Kyrgyzstan, [5]Republican Scientific and Practical Center for Infectious Control of Scientific and Production Association "Preventive Medicine", Bishkek, Kyrgyzstan
**Background:** Despite mitigation measures against coronavirus disease (COVID-19) implemented in Kyrgyzstan hospitals, 3173 healthcare workers (HCW) had been diagnosed with COVID-19 by September 13, 2020, amounting to 22 COVID-19 cases/100 HCW. We aimed to identify risks for COVID-19 among HCW exposed to COVID-19 patients in Bishkek. **Methods:** We conducted a case-control study of HCW in six hospitals with high COVID-19 incidence among HCW using incidence-density sampling. HCW in the national COVID-19 registry with SARS-CoV-2 PCR-positive and SARS-CoV-2 IgG-negative results June 2020-May 2021 were recruited as cases if exposed to COVID-19 patients <14 days. Controls were randomly selected among HCW working concurrently at the same hospitals with SARS-CoV-2 PCR- and IgG-negative results. We collected sociodemographic, work, clinical, and laboratory information, and used logistic regression to identify factors significantly ($p<0.05$) associated with COVID-19. **Results:** We included 132 cases and 406 controls; 479 (89%) were women, and 256 (48%) were ages <40 years. Medical respirators (FFP3) were used by 49% of cases vs 28% of controls; 90% of cases vs 91% of controls stayed in shift-dormitories. Comorbidities were reported in 34% of cases vs 14% of controls. Odds of COVID-19 was greater for HCW who used FFP3 vs not (adjusted odds ratio=2.9, 95% confidence interval [CI]: 1.1–3.9), shared a shiftwork dormitory with another HCW diagnosed with COVID-19 vs not (2.9, CI: 1.5–5.5), and had a comorbidity vs not (2.3, CI:1.4–5.0). **Conclusions:** Results suggest need for increased quality assurance of and training in the correct fitting and donning of personal protective equipment, especially respirators, and improved communication for HCW promoting personal responsibility in protecting staff, patients, and themselves. HCW at higher risk for severe COVID-19 with comorbidities could be assigned to lower risk areas of the hospital, and improved mitigation measures could be adopted for shared at-work housing and communal spaces.

### Poster LB-89. Comparing the Impact of Two Different COVID-19 Vaccination Strategies in the United States and Italy in the Elderly Population

**P.K. Mathur**[1], L. Gallon[1], M. Cartabia[2], R. Campi[2], A. Clavenna[2]
[1]Northwestern University Feinberg School of Medicine, Chicago, IL, USA, [2]Istituto di Ricerche Farmacologiche Mario Negri IRCCS, Milan, Italy
**Background:** This study aimed to compare vaccine distribution and impact in Italy and the US. The study focused on the elderly as this population was prioritized for vaccination in both countries and hypothesized that the first impact of vaccination could be evident in this age group. Comparing COVID-19 vaccine distribution strategies and impact will serve to inform future public health initiatives. **Methods:** Data analyzed includes (1) vaccine coverage in the elderly (2) percent reduction in the number of COVID-19 cases (3) cumulative number of COVID-19 deaths in the elderly in the first 5 months after the starting of rollout. The difference in the number of cumulative deaths in Italy vs US from January 14th (4 weeks after vaccine rollout in the US) to May 31$^{st}$, 2021 was estimated as an indicator of potentially avoidable deaths. Data sources on COVID-19 vaccinations, cases and deaths include the CDC and Italian Ministry of Health. The temporal trend of the indicators reported above was described by plotting the estimates on a graph and interpolated using GraphPad Prism. **Results:** The vaccine rollout started on December 14$^{th}$, 2020 in the US and on December 27th 2020 in Italy. Until May 2021, Italy had less relative available doses than the US. *Vaccine Distribution:* On December 31st, 2021, vaccine coverage of the elderly was 95% in the US (84.6% with two doses) and 94.6% in Italy (91.4% with two doses). In Italy, at the end of February 2021 less than 10% of the elderly were vaccinated versus 59.8% with the first dose and 32.4% with two doses in the US. 90% coverage was reached on June 17$^{th}$, 2021 in Italy and September 22nd 2021 in the US. *Vaccine Impact :* From the peak seen on January 12$^{th}$, 2021 the US saw a 100% reduction in cases in the 75+ population ~50 days later while the same reduction in Italy was not seen until ~100 days later. A possible 10,170 preventable deaths of those 80+ in Italy since January 14$^{th}$, 2021 were estimated. **Conclusions:** The US vaccination strategy resulted in early but slow uptake of vaccines reaching 90% coverage 3 months later than Italy but did find a faster percent case reduction within the elderly population. The major limitation of Italy's strategy was the number of vaccine doses available. If Italy could have started vaccination when the US did with the same number of doses, there would have been a possible 10,170 avoidable deaths of those 80+.

### Poster LB-90. COVID-19 Vaccine Acceptability among Health Workers in the Democratic Republic of Congo

**M. Nzaji**[1], A. Manyong[1], C. Standley[1], K. Stolka[1], S.F. Meyou[1], C.K. Kasendue[2]
[1]RTI International, Research Triangle Park, NC, USA, [2]The Bizzell Group, Kinshasa, Democratic Republic of the Congo

**Background:** COVID-19 vaccine coverage in countries in sub-Saharan Africa has lagged behind the rest of the world, with the Democratic Republic of Congo (DRC) among those with the lowest rates. While supply was initially a major barrier, there have been concerns over low levels of uptake, especially among high-risk groups such as health workers. There is limited evidence concerning COVID-19 vaccine acceptability among health workers in DRC. The objective of this study was to conduct a knowledge, attitudes, and practices survey among health workers in the DRC, and determine factors associated with acceptance and non-acceptance of COVID-19 vaccination. **Methods:** From January – April 2022, a questionnaire was distributed electronically among health workers in North Kivu, Haut Katanga, and Kinshasa provinces. Health facilities were selected through simple random sampling, and snowball sampling was utilized for widespread dissemination of the questionnaire. Questionnaires were completed online and submitted anonymously. **Results:** The survey received 422 responses in North Kivu, 832 in Haut Katanga, and 900 in Kinshasa. In North Kivu, 33% of health workers reported at least one dose of the COVID-19 vaccine received versus 43% in Haut Katanga and 43% in Kinshasa. Overall, 83% perceived a moderate or elevated risk of contracting COVID-19. Among health workers who had not received the vaccine, 34% reported other adult vaccinations, including for yellow fever, cholera, and Ebola. The most commonly cited reasons for non-acceptance of the COVID-19 vaccine included insufficient safety data (22%), side effects (28%), and perceived inefficacy of the vaccine (22%). **Conclusions:** Results of this study confirmed low COVID-19 vaccination acceptance among health workers in three provinces of the DRC with the highest COVID-19 incidence rates in the country. While health workers perceive a high-risk of transmission of COVID-19, concerns around safety, side effects, and efficacy may drive vaccine reticence. Relatively high reported rates of vaccine uptake for other epidemic-prone diseases indicate that outbreaks perceived as more severe may motivate health workers to receive vaccines. Risk communication and engagement efforts should emphasize COVID-19 vaccine safety and efficacy as potential opportunities for improving uptake.

### Poster LB-91. Donor-derived *Strongyloides stercoralis* Infection in Two of Three Organ Transplant Recipients — California, Michigan, Ohio, 2022

**A.O. Adeyemo**[1,2], S. Montgomery[1], R. Chancey[1], P. Annambhotla[1], J. Coyle[3]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Michigan Department of Health and Human Services, Lansing, MI, USA

**Background:** Infection with the soil-transmitted parasite *Strongyloides stercoralis* can cause life-threatening complications among organ transplant recipients. Not all organ procurement organizations (OPOs) test solid organ donors for strongyloidiasis. In December 2021, an OPO was notified of *Strongyloides* infection confirmed 102 days posttransplant in a right kidney recipient. The Organ Procurement and Transplantation Network Ad Hoc Disease Transmission Advisory Committee (DTAC) was notified of the possible donor-derived event. CDC was asked to investigate. **Methods:** On January 5, 2022, CDC initiated the investigation by contacting the OPO to obtain information about donor history, testing, and the three organs transplanted. To determine donor infection status, the OPO submitted a specimen for antibody testing. Transplant coordinators in California, Michigan, and Ohio were interviewed about recipient *Strongyloides* testing, treatment, and risks factors. The DTAC case classification was used to determine case status. The investigation concluded January 31, 2022. **Results:** The organ donor emigrated from an area endemic for strongyloidiasis and was employed in landscaping; his banked specimen was antibody positive for *Strongyloides*. The right kidney recipient was serologically negative pretransplant. Gastrointestinal symptoms were present 98 days posttransplant; small bowel and stomach biopsies revealed *Strongyloides* infection. The left kidney and heart recipients were not screened pretransplant. The left kidney recipient was born in an endemic area, lives in a rural area, and had no clinical illness compatible with strongyloidiasis; two posttransplant *Strongyloides* antibody tests were negative. The heart recipient had no known risks. Bronchoalveolar lavage showed *Strongyloides* infection; she developed disseminated strongyloidiasis and hyperinfection syndrome 131 days posttransplant. Based on the investigation, donor-derived strongyloidiasis was proven in two of three recipients. **Conclusions:** Testing donors whose histories suggest strongyloidiasis risk can help avert donor-derived infections. Although testing donors for strongyloidiasis is not standard for all OPOs, increased testing can improve patient outcomes through preemptive treatment of transplant recipients.

### Poster LB-92. Early Changes in Ferritin among COVID-19 Inpatients and Risk for Invasive Mechanical Ventilation and Mortality

**D. Ramonfaur**[1], G.M. Aguirre-García[2], C.A. Diaz-Garza[2], G. Torre-Amione[2], V.M. Sanchez-Nava[2], R. Lara-Medrano[2], M.T. Ramírez-Elizondo[2], A.C. Esparza-Sandoval[2], F.J. Ortega-Hernández[2], M.F. Martínez-Reséndez[2,3]
[1]Harvard Medical School, Division of Postgraduate Medical Education, Boston, MA, USA, [2]Instituto Tecnológico y de Estudios Superiores de Monterrey, School of Medicine and Health Sciences, Monterrey, Nuevo Leon, Mexico, [3]Hospital San Jose-Tec Salud, Epidemiological Surveillance Unit, Monterrey, Nuevo Leon, Mexico
**Background:** Ferritin is an acute phase reactant that has been described as a marker of severity in COIVD-19 inpatients. Results in different studies evaluating admission levels of ferritin and risk for adverse in-hospital outcomes have been conflicting. The relationship between 48-hour changes (delta) in ferritin and the risk for invasive mechanical ventilation (IMV) and in-hospital death is unclear. We evaluate the relationship between 48-hour delta in ferritin upon admission and the risk for in-hospital death and IMV in COVID-19 inpatients. **Methods:** A retrospective cohort among 2,523 adult patients hospitalized with COVID-19 was conducted. Ferritin was assessed upon admission and 48 hours post-admission. Winsorization was applied to both the admission and 48-hour value to account for outliers. Delta in ferritin was derived from the difference in ferritin in micrograms/liter (48-hour ferritin – admission ferritin). Delta in ferritin and the risk for IMV and in-hospital death was assessed using multivariable logistic regression models adjusting for demographics and comorbidities. **Results:** A total of 1,044 patients had complete data for both admission and 48-hour ferritin. Winzorization further excluded 22 patients with extreme values. Ultimately, 1,022 patients were included in the analysis. Mean age was 52 ± 14, 73% were male, 207 (20%) had the IMV outcome and 124 (12%) had the in-hospital death outcome. Mean ferritin at admission was 1,525 ± 1,278, and mean delta in ferritin was -0.71 ± 931. Delta in ferritin was associated with a higher likelihood of IMV (OR 1.00035; 95%CI 1.00014- 1.00055; p= 0.001) and in-hospital death (OR 1.00032; 95%CI 1.00007-1.00056; p< 0.001) in a near-linear relationship. For every 100 units increase of delta in ferritin, the risk for IMV and in-hospital death increases by 3.5% and 3.2%, respectively. **Conclusions:** Delta in ferritin is independently associated with IMV and in-hospital death. These findings suggest delta in ferritin may be a powerful predictor of in-hospital outcomes among COVID-19 inpatients.

### Poster LB-93. EARS - A WHO AI-Supported Platform for Real-Time Online Social Listening of COVID-19 and COVID-19 Vaccine Conversations

**C. Czerniak**[1], I. Cesar[2], C. Pi[1], T. Purnat[1], S. Briand[1], T. Nguyen[1]
[1]World Health Organization, Geneva, Switzerland, [2]Media Measurement Ltd, London, UK
**Background:** Listening to people's questions and concerns is an important way for health authorities to learn about what matters to communities in response to COVID-19. WHO infodemic management framework emphasizes the need for faster insights into concerns of citizens. The WHO EARS online social listening platform summarizes real-time information about how people are talking about COVID-19 in public spaces online, so risk communication and infodemic response interventions can be better designed and more effectively implemented. **Methods:** The platform allows for exploration of the online public conversations at global and country level, a private country-specific dashboard for in-depth analysis, and an open API with the aggregated and anonymized data. The platform covers 30 pilot countries from all WHO regions globally, 9 languages, and tracking 41 COVID-19 conversation categories. It is being expanded with an additional set of categories related to conversations about COVId-19 vaccines. **Results:** Analysis results are presented normalized by the relative proportion of the conversation per country to ensure comparability across countries. The dashboards show how the topics of conversation change and evolve country by country over time, such as: what are the most popular categories and those gaining traction, and their patterns; what are the top and rising terms and hashtags within each category; what are the differences in conversations by; the composition of the conversation by intention: questions (confusion), complaints (frustration) or praise. The platform is used for training and empowering health information professionals to respond earlier to the infodemic, with daily analysis of changing COVID-19 conversations shared publicly online. **Conclusions:** The EARS platform provides a public social listening tool and an integrative analytical service bringing together disparate data sources to help countries detect changing attitudes and critical information gaps. Big data and AI analytics complements surveys and epidemiological data for near-real-time infodemic insights helping decision-makers adapt public health programmes to best serve their communities.

### Poster LB-94. Evaluation of the National Immunization Program by Estimating Immunoglobulin G Antibody Prevalence of Measles and Rubella in Lao People's Democratic Republic

**C. Pattamavone**[1], S. Miyano[5], P. Nouanthong[2], K. Phounphenghack[1], C. Tengbriacheu[1], B. Khamphaphongphane[3], L.Y. Ichimura[5], K. Komada[4], M. Hachiya[4]

[1]National Immunization Programme, Vientiane, Lao, PDR, [2]Institute Pasteur du Laos, Vientiane, Lao PDR, [3]National Center Laboratory Epidemiology, Ministry of Laos, Vientiane, Lao PDR, [4]Bureau of International Health Cooperation, National Center for Global Health and Medicine, Tokyo, Japan
**Background:** To eliminate measles and rubella, it is critical to develop strategic and efficient immunization programs. This study aimed to evaluate the population immunity and the measles-rubella program's effectiveness by estimating anti-measles and anti-rubella IgG prevalence in the general population of the Lao People's Democratic Republic (PDR). **Methods:** A nationwide seroprevalence survey was conducted in Lao PDR between May and June 2019, using the multi-stage cluster sampling method. In the first and second stages, 26 districts and two villages each from participated provinces were selected using probability proportional to size sampling. In the third stage, 42 people were randomly selected from the residents' list in each village. Dried blood spot samples were collected onto Whatman™ 903 filter paper by finger prick. IgG titers were measured by Enzygnost® enzyme-linked immunosorbent assay, and the results were considered positive at ≥120 mIU/ml for measles and ≥ 10 IU/ml for rubella. **Results:** We approached two thousand forty-three people and enrolled one thousand nine hundred ninety-three people (females: 53.0%, mean age: 23.1 years (1-89 years)), excluding 50 inappropriate specimens. IgG prevalence was estimated to be 98.3% [95% CI: 97.7-98.8] for measles and 87.8% [86.4-89.2] for rubella. Measles IgG prevalence was estimated to be greater than 95% except for those aged 1-2 years, and rubella was estimated to be greater than 80% except for those aged 1-2 years and 25-34 years. **Conclusions:** Overall, IgG prevalence of measles and rubella was higher than those herd immunity thresholds required to eliminate both viruses. However, the prevalence of both antibodies in people aged 1-2 years was lower than herd immunity, indicating a need for a more robust immunization program. Special attention should be paid to the rubella vaccinations in 25-34-year-old to minimize the potential risk of creating congenital rubella syndrome.

### Poster LB-95. Experiments To Evaluate Respirable Aerosols Produced during Different Poultry Slaughtering Methods

**N.A. Rimi**[1], M.H. Fahad[1], A. Clark[2], J.A. Mott[3], R. Sultana[1], D.E. Swayne[4], K. Hossain[1], S.M.G. Mortaza[1], M.K. Saifullah[1], I.S. Shanta[1], M. Giasuddin[5], M.Z. Hassan[5], J.C. Kile[3], W.G. Lindsley[6]
[1]icddr,b, Dhaka, Bangladesh, [2]Private Veterinary Consultant, [3]Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]U.S. Department of Agriculture, Athens, GA, USA, [5]Bangladesh Livestock Research Institute, Savar, Dhaka, Bangladesh, [6]National Institute for Occupational Safety and Health, Centers for Disease Control and Prevention, Morgantown, WV, USA
**Background:** Influenza viruses can be aerosolized during slaughter of infected chickens, increasing the risk of zoonotic transmission. We evaluated aerosol generation during different poultry slaughtering methods used in Bangladeshi live bird markets. **Methods:** Chickens were slaughtered by severing the cervical blood vessels and placing them in different containers to exsanguinate inside an air movement control booth within a temperature-controlled room. A total of 675 chickens were divided into two groups: 135 for single slaughter (i.e., 1 chicken/experiment) and 540 for multiple slaughter (i.e., 4 chickens in a group/experiment) using a barrel without a lid (method-1), a barrel with a solid lid (method-2), a barrel with a star-cut lid (method-3), a small cone (method-4) and a large cone (method-5). Three PATS+ aerosol monitors were placed 148 cm above the floor during slaughtering, corresponding to a worker’s breathing level to measure concentrations of airborne particles <2.5 µm at baseline and during slaughtering. We also conducted in-depth interviews with the slaughterers to collect feedback on different methods used. **Results:** The average particle concentrations were 38.4 µg/m$^3$ (SD 25) during single slaughter and 120.1 µg/m$^3$ (SD 27.5) during multiple slaughter for method-1; 4 µg/m$^3$ (SD 5.3) during single slaughter and 36 µg/m$^3$ (SD 13.6) during multiple slaughter for method-2; 3.3 µg/m$^3$ (SD 5.2) during single slaughter and 34.3 µg/m$^3$ (SD 21.2) during multiple slaughter for method-3; 47.1 µg/m$^3$ (SD 47.1) during single slaughter and 112 µg/m$^3$ (SD 52.3) during multiple slaughter for method-4; and 32.9 µg/m$^3$ (SD 30.9) during single slaughter and 131 µg/m$^3$ (SD 60.1) for method-5. Method-2 or method-3 reduced particle concentrations significantly (P< 0.001) compared to method-1, the most widespread method. The slaughterers preferred method-2, followed by method-1 and method-3. They did not like the cones, as those were not suitable for rapidly slaughtering poultry and were costlier. **Conclusions:** Closing barrels with a solid lid or star-cut lid reduced particle concentrations during poultry slaughtering and were preferred by the slaughterers. The findings can be used to promote methods that can minimize human exposure to potentially hazardous aerosol particles during poultry slaughtering.

### Poster LB-96. Galago: An Exploration and Reporting Tool Making Pathogen Genomic Data More Actionable during Outbreak Investigations

**S.M. Bell**, C. Megill

CZ Science Initiative Foundation, Redwood City, CA, USA
**Background:** Pathogen whole-genome sequencing (WGS) provides high-resolution data about how cases are connected to one another during an infectious disease outbreak. While recent funding has increased the availability of WGS data, especially for SARS-CoV-2, this data is often presented in the form of phylogenetic trees which can be difficult for public health officials to interpret or take action on. Here, we present Galago, a web-based tool that helps epidemiologists and other public health officials interpret phylogenetic trees to make pathogen genomic data more interpretable and actionable during outbreak investigations. **Methods and results:** Foundational user research was conducted via an extended field study during the first 18 months of the SARS-CoV-2 pandemic, wherein we tightly collaborated with local departments of public health across California to provide genomic epidemiological data and interpretation. Through this work, we identified a set of epidemiological questions that are critical to public health response and can be answered reliably based on basic observations of a phylogenetic tree topology (without requiring custom inferential models). These include “How closely related are my samples of interest?”; “How distinct is this putative outbreak from background circulation?”; “When did this putative outbreak start?”; and “How much downstream transmission has there been?”, among others. To answer these questions, we then built an open-source tool called Galago which takes a phylogenetic tree and optional epidemiological metadata (e.g., a line list) as input. Galago first helps users identify subtrees of interest based on epidemiological case definitions; a list of samples defined a priori; or clustering methods from Matutils and Treetime. Once a subtree/cluster of interest is identified, Galago then traverses and makes observations about the tree. These observations are then automatically translated into reports with narrative text and visualizations, using terminology and plots that are familiar to public health users. **Conclusions:** Galago is freely available at https://chanzuckerberg.github.io/galago/. We warmly welcome feedback and contributions from the public health community.

### Poster LB-97. Hand Hygiene Infrastructure in Schools in Belize during the COVID-19 Pandemic: A National Survey and Assessment

**A. Ly**[1], R.I .Manzanero[2], K. McDavid[3], C. Craig[3], Y. Gongora[4], G. Morazan[1], D. Maheia[4], M.J. Lozier[3], K.O. Murray[1]
[1]Baylor College of Medicine and Texas Children’s Hospital, Houston, TX, USA, [2]Belize Ministry of Health and Wellness, Belmopan, Belize, [3]Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Belize Ministry of Education, Culture, Science and Technology, Belize City, Belize
**Background:** COVID-19 pandemic has brought to the forefront the importance of a well-collaborative network of clinical data sharing between healthcare providers and public health agencies. Despite, the numerous challenges that the providers face such as data security, privacy, confidentiality, disparate vocabulary and lack of technological infrastructures, most are still able to establish a shared digital platform. This study aimed to describe the experiences and lessons learned from using providers shared electronic databases and traditional reporting systems and the implications to case investigations, contract tracing and interventions during COVID-19 pandemic. **Methods:** Data used for this assessment was based on Covid-19 cases reported to Houston Health Department (HHD) between March 2020 to March 2022. A total of 33,150,000 cases was reported to HHD by approximately 279 medical providers and laboratories through electronic feeds (Electronic lab report (ELR)), roster imports, and facsimile/secured emails/Courier services during the period. **Results:** Of the total number of cases reported during the study period, 92.73% (n=30,740,000) was received through electronic feeds, 7.03% (n=2,330,528) through roster imports, and 0.24% (n=79,717) through facsimile/secured emails/courier services. The turnaround time during the period under review varied significantly from 1.46 to 5.74 days with an average of 2.29 days (95%CI:2.07-3.25) due mainly to increased electronic reporting. We noted a significant difference ($p<0.001$) in the turnaround time during the COVID-19 onset year (2020) and 2021, being 4.17 days (95%CI: 3.41-4.92) and 1.95 days (95%CI: 1.42-2.48), respectively. **Conclusion:** This study highlights the importance of collaborative data exchange between providers and public health agencies. Electronic data sharing conserved providers time and efforts, allowed them to fulfill the reporting mandates and enhanced HHD COVID-19 response through timely investigations, contact tracing and interventions. This partnership led to a more coordinated and effective risk management and informed local decision making to keep Houstonians safe as the COVID-19 outbreaks unfold.

### Poster LB-98. Healthcare Providers Secured Data Sharing for Public Health Surveillance: Houston Health Department’s Perspective During COVID-19 Pandemic

**M.K. Ahmed**, S. Khuwaja, O. Mgbere, L. Carrillo, J. Lin, K. Sapkota
Disease Prevention and Control Division, Houston Health Department, Houston, TX, USA

**Background:** COVID-19 pandemic has brought to the forefront the importance of a well-collaborative network of clinical data sharing between healthcare providers and public health agencies. Despite, the numerous challenges that the providers face such as data security, privacy, confidentiality, disparate vocabulary and lack of technological infrastructures, most are still able to establish a shared digital platform. This study aimed to describe the experiences and lessons learned from using providers shared electronic databases and traditional reporting systems and the implications to case investigations, contract tracing and interventions during COVID-19 pandemic. **Methods:** Data used for this assessment was based on Covid-19 cases reported to Houston Health Department (HHD) between March 2020 to March 2022. A total of 33,150,000 cases was reported to HHD by approximately 279 medical providers and laboratories through electronic feeds (Electronic lab report (ELR)), roster imports, and facsimile/secured emails/Courier services during the period. **Results:** Of the total number of cases reported during the study period, 92.73% (n=30,740,000) was received through electronic feeds, 7.03% (n=2,330,528) through roster imports, and 0.24% (n=79,717) through facsimile/secured emails/courier services. The turnaround time during the period under review varied significantly from 1.46 to 5.74 days with an average of 2.29 days (95%CI:2.07-3.25) due mainly to increased electronic reporting. We noted a significant difference ($p<0.001$) in the turnaround time during the COVID-19 onset year (2020) and 2021, being 4.17 days (95%CI: 3.41-4.92) and 1.95 days (95%CI: 1.42-2.48), respectively. **Conclusion:** This study highlights the importance of collaborative data exchange between providers and public health agencies. Electronic data sharing conserved providers time and efforts, allowed them to fulfill the reporting mandates and enhanced HHD COVID-19 response through timely investigations, contact tracing and interventions. This partnership led to a more coordinated and effective risk management and informed local decision making to keep Houstonians safe as the COVID-19 outbreaks unfold.

### Poster LB-99. Incidence of COVID-19 Vaccines Related Adverse Events Following Immunization in Qatar: A Descriptive Study

**S. Albayat**
Ministry of Public Health, Doha, Qatar

**Introduction:** The emergence and availability of the Novel Coronavirus 2019 (COVID-19) vaccines was a major scientific success in the fight against the COVID-19 pandemic. However, the safety of vaccines is of utmost importance as its efficacy. With the deployment of the COVID-19 vaccines, Qatar activated its adverse events following immunization (AEFI) surveillance system to monitor the safety of COVID-19 vaccines. This study aimed to identify and classify the COVID-19 vaccines' related AEFI. **Methods:** AstraZeneca, Moderna and Pfizer were the COVID-19 vaccines used in Qatar. All population were targeted by the COVID-19 vaccines according to the vaccine specific age eligibility. Passive AEFI surveillance system was implemented where reports were sent from health care facilities to ministry of public health. Assessment and classification of AEFI were done according to the updated World Health Organization manual. **Findings:** Among a total of 6742968 COVID-19 vaccine doses administered in Qatar since the start of the vaccination in December 2020 and up to 26 April 2022, a total of 115 AEFI were reported through surveillance system that gives an overall incidence of 0.02 AEFI per 1000 doses. Of reported AEFI, 90 (78%) were classified as vaccine related of which 38 (34%) were serious events. The most common reported AEFI were urticaria (42 events) followed by anaphylactic reaction (17 events). There were 17 events of carditis reported. **Conclusion:** The incidence of the reported COVID-19 vaccines AEFI was very low with the majority classified as minor events. Despite its few numbers, anaphylaxis and carditis events are of concern.

### Poster LB-100. Introducing Patient COVID-19 Screening as Part of Infection Prevention and Control (IPC) at Antiretroviral Therapy (ART) Clinics in Nigeria: Lessons Learned

**R. Okonkwo**[1], T. Sorungbe[1], C. Ibe[1], L. Tompkins[2], P. Malpiedi[2], A. Enoma[1], C. Igbokwe[1], K. Ayodeji[1], E. Edemeka[1], E. Kombu[1], D.F. Rodriguez[3], B. Gleason[3], M. Peterson[3], C. Onyenuobi[4], T. Okwor[5], A. Abimiku[1,6]
[1]International Research Centre of Excellence-Institute of Human Virology Nigeria (IRCE-IHVN), Abuja, Nigeria, [2]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Division of Global HIV & TB, Centers for Disease Control and Prevention, Atlanta, GA, USA, [4]Division of Global HIV & TB, U.S. Centers for Disease Control and Prevention, Abuja, Nigeria, [5]Antimicrobial Resistance and Infection Prevention and Control Programme, Nigeria Centre for Disease Control, Abuja, Nigeria, [6]University of Maryland School of Medicine Institute of Human Virology, Baltimore, MD, USA

**Background:** The rapid identification and separation of suspected COVID-19 cases is essential to prevent transmission in health facilities (HFs), particularly in clinics treating patients with compromised immunity, such as people living with HIV. This project implemented infection prevention and control (IPC) interventions that included establishing patient screening for COVID-19 and triage using multimodal approaches at 29 antiretroviral therapy (ART) clinics in North Central Nigeria (convenience sample). We present data and lessons learned from

implementation. **Methods:** Prior to initiating screening, IPC and quality improvement (QI) trainings were provided to HF and state IPC teams. Screening stations were established at clinic entry points using QI tests of change. All patients were screened upon entry, and symptomatic patients were sent for evaluation that may result in referral for testing. Patients referred for testing were isolated, and services were fast tracked. Onsite supportive supervision, HF and state IPC team meetings, and peer learning meetings between HFs provided opportunities to share successes and address gaps. **Results:** From November 2021 to April 2022, we screened 51,972 patients; 1699 (3.2%) screened positive for COVID-19 symptoms. After evaluation, 56.2% (955/1699) were sent for testing and 3.5% (33/955) tested positive. Results of incremental tests of change guided scaling of each HF's screening program. Peer learning meetings facilitated sharing of best practices that included establishing a single point of entry, using tags to identify patients screened, and educating patients on the screening process. Following supportive supervision, screening registers were improved to monitor linkage to testing after screening. **Conclusions:** Screening yield of 3.5% for COVID-19 highlights the importance of IPC practices for early disease detection, timely preventive measures, and risk mitigation, particularly as new SARS-CoV-2 variants emerge. Successful implementation and continued improvement of patient screening programs relied on multiple approaches, including trainings, QI methods, HF supervision, and peer meetings. Key next steps are for HFs to expand screening programs to include staff and for states to adopt IPC policies to guide screening program implementation at HFs.

### Poster LB-101. Measuring the Burden of Infodemics on Health Behaviors and Outcomes through Harmonized Global Metrics and Collaboration

**A. Ishizumi**[1], A.G. Dunn[2], T.D. Purnat[1], B. Yau[1], C. Bertrand-Ferrandis[1], B. White[1], S. Briand[1], T. Nguyen[1]
[1]Department for Epidemic and Pandemic Preparedness and Prevention, Emergency Preparedness Division, World Health Organization, Geneva, Switzerland, [2]Biomedical Informatics and Digital Health, School of Medical Sciences, Faculty of Medicine and Health, The University of Sydney, Sydney, NSW, Australia
Background**:** Infodemics happen when an excess of information makes it difficult for people to discern what they see and hear to make good health decisions. Several challenges limit the usefulness of applying infodemiology research to the practice of managing infodemics including inconsistency in how information exposure is measured and a lack of focus on assessing associations with health behaviors. Methods: In 2021, WHO partnered with the University of Sydney to develop a study toolkit. We sought to create novel tools for measuring information exposure that can be easily deployed, linked to surveys measuring health behaviors, and implement a standardized study protocol so that data can be directly synthesized into a global analysis of information risk factors associated with health behaviors. Results: A web-based study platform was developed, comprising tools for capturing information exposures within studies that link to health behavior surveys. The first tool is a smartphone application that asks users to actively record relevant information they see or hear in diary. The second application is a web browser plugin that passively tracks webpages with relevant keywords. Because localized studies follow a standardized protocol and de-identified participant data are recorded in a common format, local study investigators can opt-in to contributing study data to support global surveillance efforts. Conclusions: Through standardization of measurement tools and relevant study protocols, the toolkit can be used to quickly collect and synthesize data for global or regional analysis of infodemic burden of disease. Validation of the toolkit in the field is needed to inform its open-source release.

### Poster LB-102. Metagenomics for Pathogen Detection and Characterization: Saponin-based Eukaryotic DNA Depletion Improves Detection of *Listeria spp*.

**J. Rumore**[1,2], M. Walker[2], C. Nadon[1,2], A. Reimer[2], N. Knox[1,2]
[1]Department of Medical Microbiology & Infectious Diseases, University of Manitoba, Winnipeg, Manitoba, Canada, [2]National Microbiology Laboratory, Canadian Science Centre for Human and Animal Health, Public Health Agency of Canada, Winnipeg, Manitoba, Canada
**Introduction:** Metagenomic sequencing of primary selective enrichment cultures from food samples may expedite pathogen detection and improve public health response. However, high eukaryotic:prokaryotic ratios can impede detection. A saponin-based eukaryotic DNA depletion method has proven effective for removing up to 99.9% host DNA in clinical specimens for metagenomic diagnostics, but this has not been evaluated in foods. This pilot study aimed to assess the impact of a saponin-based eukaryotic DNA depletion method on pathogen detection in foods. **Methods:** Pathogen-food combinations common in outbreaks, *Shigella sonnei* (carrots), *Escherichia coli* O157:H7 (lettuce, ground beef), and *Listeria monocytogenes* (ready-to-eat; RTE ham, and turkey deli meat), were artificially created with outbreak and non-outbreak strains (*S. flexneri*, *E. coli* O26:H11, *E. coli* O103:H25, *L. innocua, and L.*

*welshmeri*). Isolates were included at three levels of contamination: high ($10^3$ CFU $ml^{-1}$), medium ($10^2$ CFU $ml^{-1}$) and low ($10^1$ CFU $ml^{-1}$). Genomic DNA was extracted from overnight-enriched cultures (22 ±2H) with and without a saponin-based eukaryotic DNA-depletion step. Metagenomic sequencing was performed on the Illumina NextSeq. Low-quality reads were filtered using fastp, followed by *in silico* removal of eukaryotic reads with bowtie2. Taxonomic classification was performed using Kraken 2 and a custom-built reference database. **Results:** Compared to unprocessed samples, eukaryotic DNA depletion increased the average genome coverage depth of the spike-in *Listeria* spp. strains by a minimum 80-fold and increased reads classified to the genus and species level by more than 20-fold across all spike-in levels in RTE ham and turkey deli meat. Eukaryotic DNA depletion did not improve the detection of *S. sonnei*, *E. coli* O157:H7, and corresponding non-outbreak strains, and in some cases, it led to pathogen DNA loss. **Conclusions:** Saponin-based eukaryotic DNA depletion improved detection of *Listeria spp*. in RTE meats but may not be appropriate for all pathogen-food combinations and must be assessed according to the pathogen and sample type.

### Poster LB-103. Real-time Pandemic Surveillance Using Hospital Admissions and Mobility Data

**S.J. Fox[1]***, M. Lachmann[2]*, M. Tec[1], R. Pasco[1], S. Woody[1], Z. Du[3], X. Wang[1], T.A. Ingle[1], E. Javan[1], M. Dahan[4], K. Gaither[4,5], M.E. Escott[6], S.I. Adler[6], S.C. Johnston[5], J.G. Scott[1], L.A. Meyers[1,2,5]
[1]The University of Texas at Austin, Austin, TX, USA, [2]Santa Fe Institute, Santa Fe, NM, USA, [3]School of Public Health, The University of Hong Kong, Hong Kong, [4]Texas Advanced Computing Center, Austin, TX, USA, [5]Dell Medical School, Austin, TX, USA, [6]City of Austin, Austin, TX, USA
*Authors contributed equally.
**Background**: Forecasting the burden of COVID-19 has been impeded by limitations in data, with case reporting biased by testing practices, death counts lagging far behind infections, and hospital census reflecting time-varying patient access, admission criteria, and demographics. **Methods:** Here, we show that hospital admissions coupled with mobility data can reliably predict severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission rates and healthcare demand. **Results**: Using a forecasting model that has guided mitigation policies in Austin, TX, we estimate that the local reproduction number had an initial 7-d average of 5.8 (95% credible interval [CrI]: 3.6 to 7.9) and reached a low of 0.65 (95% CrI: 0.52 to 0.77) after the summer 2020 surge. As precautionary behaviors increased safety in public spaces, the relationship between mobility and transmission weakened. We estimate that mobility-associated transmission was 62% (95% CrI: 52 to 68%) lower in February 2021 compared to March 2020. In a retrospective comparison, the 95% CrIs of our 1, 2, and 3 wk ahead forecasts contained 93.6%, 89.9%, and 87.7% of reported data, respectively. **Conclusions**: We find that our mechanistic model is better able to forecast critical time periods (e.g., rapid surges and declines) compared with baseline phenomenological models. Developed by a task force including scientists, public health officials, policy makers, and hospital executives, this model can reliably project COVID-19 healthcare needs in US cities.

### Poster LB-104. Resolving Discrepancies in the Identification of *Vibrio* Species: Biochemical, Proteomic, and Genomic Methods to Identify *V. cholerae*

**T. Davedow[1,2]**, S. Banerjee[3], R. Boone[3], B. Shutinoski[3], S. Christianson[2], C. Nadon[1,2]
[1]Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, MB, Canada, [2]Public Health Agency of Canada, National Microbiology Laboratory, Winnipeg, MB, Canada, [3]Bureau of Microbial Hazards, Food Directorate, Health Canada, Ottawa, ON, Canada
**Background**: *Vibrio* species are abundant in marine environments worldwide. Some *Vibrio* species are pathogenic to humans and have been implicated in foodborne diseases. The main sources of *Vibrio* infection in Canada are shellfish. Non-epidemic *V. cholera*e causes human disease in Canada and targeted surveillance systems are lacking. Whole genome sequencing (WGS) combined with powerful bioinformatics tools already provides basis for other enteric disease surveillance in Canada. Developing its use for *Vibrio* species is a crucial next step to better understand and protect the public from this emerging pathogen and the pandemic threat of *V. cholerae* O1/O139 and its variants. This research aims to utilize proteomic, genomic and bioinformatics tools to uncover the identity of isolates that were previously characterized as presumptive *V. cholerae* via biochemical tests. The hypothesis is that the previous gold standard phenotypic methods are insufficient for distinguishing *V. cholerae* from other *Vibrio* species in shellfish. **Methods:** A population of *Vibrio* species that were previously isolated from Canadian retail and harvested shellfish and characterized as presumptive *V. cholerae* were utilized. Isolates were analyzed in depth using matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry, WGS and bioinformatics tools to compare methods and determine an accurate species-level classification. A maximum likelihood tree was built using IQ-tree and results were analyzed and visualized in RStudio using the ggtree package. **Results:** Out of 55 isolates, only 20% were identified as *V. cholerae* by proteomic, genomic and bioinformatics

tools. WGS and bioinformatics analysis illustrated a comprehensive view of *Vibrio* species diversity in shellfish samples. Taxonomic classification revealed the presence of known pathogenic species to humans (*V. algninolyticus, V. cholerae, V. parahaemolyticus, V. vulnificus*), coral (*V. mediterranei*), shellfish (*V. aestuarianus*), and a potentially novel *Vibrio* species. **Conclusions:** WGS provided accurate identification of *Vibrio* bacteria that were previously masked by other species. Without accurate identification tools we do not have a complete picture of the risks posed by this organism and its potential threat to Canadians in the future.

### Poster LB-105. SARS-CoV-2 AY.25 (Delta) Variant Infections Among Staff and Afghan Evacuees at an Operation Allies Welcome Safe Haven Site — November – December 2021

**L. Gosdin**[1], A. Siu[1], J. Meeker[1], L. Turner[2], E. Mosites[1], L. Talley[1], A. Boyd[1]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]Division of Consolidated Laboratory Services, Virginia Department of General Services, Richmond, VA, USA
**Background:** In August 2021, the US government began evacuating eligible people from Afghanistan for relocation in the US. Afghan evacuees were temporarily housed at US congregate living facilities, called Safe Havens. A SARS-CoV-2 outbreak response was initiated at one facility with 600 staff and 2,062 evacuees. **Methods:** Data on testing, vaccination, symptoms, treatment, and close contacts were collected for evacuees and staff with confirmed SARS-CoV-2 infections. Symptomatic individuals and close contacts were tested per CDC guidelines via antigen and/or reverse transcription–polymerase chain reaction tests. Four SARS-CoV-2-positive samples underwent genomic sequencing. Attack rates were calculated using facility census data. **Results:** During November 24 – December 18, 2021, 27 SARS-CoV-2 infections occurred among staff (attack rate: 45.0 per 1,000) and five among evacuees (attack rate: 2.4 per 1,000). Among 27 infected staff, 26 were fully vaccinated (22 received a two-dose mRNA series [one boosted], and four a single-dose vaccine); one was vaccination status unknown. Twenty-one were booster-eligible. Among five infected evacuees, two were unvaccinated (ages three and eleven), and three had received a single-dose vaccine and were booster-eligible. Thirty had symptomatic illness; two were hospitalized. Genomic sequencing indicated SARS-CoV-2 AY.25 infections, the Delta variant. Contact tracing suggested staff as sources of the outbreak. Implementation of CDC-recommended mitigation measures included: 10-day isolation of infected people, 14-day quarantine of unvaccinated close contacts, vaccine boosting, pediatric vaccination, enforced mask mandates, staff serial testing, symptoms screening, improved ventilation, and physical distancing. **Conclusions:** Vaccination, boosting, and other mitigation measures are critical to slowing SARS-CoV-2 transmission in congregate settings. Higher attack rates among staff who commuted daily, compared to evacuees who remained on site, highlight staff as key to preventing outbreaks linked to community transmission. These findings have applications to similar settings, e.g., emergency intake shelters for unaccompanied children crossing the southern border, homeless shelters, and correctional facilities.

### Poster LB-106. What You Need to Know to Prevent Zoonoses Associated with Fancy Rats, Bearded Dragons, Baby Chicks, and Other Non-Traditional Pets!

**D. Stanek**1,2, J.A. Brown1,3, B. Lipton1,4, J. Dunn1,5, K. Varela6
1National Association of State Public Health Veterinarians, Baltimore, MD, USA, [2]Florida Department of Health, Tallahassee, FL, USA, [3]Indiana Department of Health, Indianapolis, IN, USA, [4]Seattle & King County Public Health, Seattle, WA, USA, [5]Tennessee Department of Health, Nashville, TN, USA, [6]One Health Office, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Non-traditional pet (NTP) ownership in the U.S. is increasing by 4% annually, with approximately 13% of households owning an NTP in 2016. Three groups of NTPs are consistently associated with outbreaks of zoonotic diseases in people: rodents, reptiles, and backyard poultry. In response to a need for zoonotic disease prevention guidance for NTPs, the National Association of State Public Health Veterinarians developed a new NTP Compendium for human, veterinary and public health practitioners, pet owners, people at occupational risk and other partners. **Methods:** A literature review was conducted to characterize documented U.S. outbreaks and cases associated with NTPs during 1996–2017. Reported NTP-associated outbreaks during 2009–2017 were also retrieved from the Centers for Disease Control and Prevention Animal Contact Outbreak Surveillance System (ACOSS). A committee of subject matter experts convened and used a One Health approach to summarize these data and reach a consensus on preventive recommendations. **Results:** A total of 223 outbreaks and 20 case reports linked to NTP species were identified. These were largely attributable to *Salmonella* and associated with backyard poultry (105 outbreaks), reptiles (62 outbreaks, 6 case reports), rodents and other small mammals (17 outbreaks), along with fish and amphibians (8 outbreaks). Outbreaks and case reports attributed to lymphocytic choriomeningitis virus, *Streptobacillus moniliformis*, and Seoul hantavirus were also identified. The literature review and ACOSS reports described 8,028 human illnesses attributable to these pathogens, with 1,245 (16%) occurring in children younger

than 5 years old. A total of 1,444 (18%) hospitalizations and 26 (0.3%) deaths were associated with these illnesses. Common NTP zoonotic pathogens and activities that increase or decrease the risk for zoonotic diseases are summarized by animal type. Antimicrobial stewardship, wildlife-NTP interface risks; responsible pet ownership, zoonotic disease risk for NTPs aquatic environments, special exposure settings and NTP source and supply chains are also considered. **Conclusions:** The new NTP Compendium provides data-driven recommendations to inform prevention messaging and guide investigations of NTP-associated zoonotic disease cases and outbreaks.

## Oral Presentation Abstracts

## O1. Healthcare and Healthcare-associated Infections

**3:15 PM – 4:45 PM**

**Centennial Ballroom I**

### Risks Associated with Reusable Bronchoscopes and Urologic Endoscopes

**C.L. Ofstead**, K.M. Hopkins, A.G. Smart
Ofstead & Associates, Inc., Saint Paul, MN, USA
**Background:** In 2021, the United States Food and Drug Administration released two safety communications regarding inadequately reprocessed and maintained bronchoscopes and urological endoscopes based on more than 1,300 adverse event reports filed in the past six years. These warnings follow similar communications regarding duodenoscopes in the wake of widely publicized reprocessing failures and outbreaks. Following growing international awareness of duodenoscope reprocessing challenges, we sought to determine whether similar risks existed with other types of endoscopes. **Methods:** During the past six years, our team has evaluated real-world reprocessing effectiveness for bronchoscopes and ureteroscopes during three studies conducted in seven hospitals in the United States. Assessments included tests for organic soil, microbial cultures, visual inspection with magnification and borescopes, and audits of reprocessing practices. **Results:** Of 35 bronchoscopes that were high-level disinfected in five hospitals, 71.4% (16.7% - 100%) tested positive for organic soil; 65.7% (58.3% - 83.3%) harbored viable, culturable microbes; and 100% had visible residue or damage. High-concern organisms or actionable levels of microbial growth (>100 CFU) were present in 28.6% (16.7% - 29.2%) of patient-ready bronchoscopes. Potential pathogens included *Stenotrophomonas maltophilia*, *Escherichia coli/Shigella*, and mold. For 16 ureteroscopes that had been sterilized with hydrogen peroxide gas in two hospitals; 100% tested positive for organic soil, including protein (100%) and hemoglobin (63%); 13% harbored viable, culturable microbes; and 100% had visible irregularities (debris, fluid, or damage). Substandard reprocessing was observed at all seven hospitals. **Conclusions:** The current pandemic has strained infection control efforts internationally, and surges of healthcare-associated infections associated with medical devices and instruments have been documented. Bronchoscopes and ureteroscopes are exposed to extensive contamination during procedures, and these data show that current reprocessing practices are insufficient to ensure patient safety. Additional research is needed to drive evidence-based interventions

### Prevalence of Colonization with Antimicrobial-resistant Bacteria in a Guatemalan Community: An Antibiotic Resistance in Communities and Hospitals (ARCH) Study

**B.M. Ramay**[1,2], L. Grajeda[1], M.R. Lopez[1], C. Castillo[1], M. Freitas Ning[3], G.H. Palmer[2,4], C. Cordón[1], C. Herzig[5], R.M. Smith[5], D.R. Call[2]
[1]Universidad del Valle de Guatemala, Guatemala City, Guatemala. [2]Paul G. Allen School for Global Health, Washington State University, Pullman, USA. [3] CDC Central American Regional Office, Guatemala City, Guatemala, [4]Washington State University Global Health-Kenya, Nairobi, Kenya. [5]Centers for Disease Control and Prevention, Atlanta, USA
**Background:** Antimicrobial resistance (AMR) is driven, in part, by transmission of microorganisms within and among communities and healthcare systems. This study aimed to determine the prevalence of these organisms in human residents in a community located in western Guatemala. **Methods:** Household residents in the Department of Quetzaltenango, Guatemala were selected using a three-stage (randomly selected geographic cluster, household, and participant) cross-sectional study design. We collected socio-demographic information and a stool sample from one participant per household. Samples were plated onto CHROMagar™ to select for presumptive extended-spectrum cephalosporin-resistant Enterobacteriaceae (ESCrE) and carbapenem-resistant Enterobacteriaceae (CRE). Up to three distinct colonies were selected from each plate for species identification and antibiotic susceptibly testing

using a VITEK 2®. Pearson chi squared test was used to detect differences in ESCrE prevalence by sex, age, or urban/rural locations. **Results:** From November 2019 to March 2020, 381 participants were enrolled of whom 343 (90%) were adults ≥18 y, 289 (76%) were female and 258 (67%) lived in rural areas. Stool samples from 49% (186/381) of participants were positive for presumptive ESCrE using CHROMagar™, of which 93% (173/186) were confirmed by VITEK 2. Few participants (2%, 7/381) had stool samples that were positive for presumptive CRE, of which 29% (2/7) were confirmed by VITEK 2. Among the 193 participants with colony growth on ESCrE or CRE CHROMagar™ plates, 449 bacterial isolates were recovered. The most commonly identified organisms were *Escherichia coli* (n=406, 90%), followed by *Enterobacter cloacae* (n=12, 3%), and *Klebsiella pneumoniae* (n=9, 2%). Of all organisms with identifiable Minimum Inhibitory Concentration MIC data (n=444), 32% (142/444) were resistant to three antibiotic classes, followed by 20% (88/444) and 15% (65/444) being resistant to four and five antibiotic classes, respectively. Confirmed colonization with ESCrE was not associated with sex, age, or urban/rural locations (P>0.05). **Conclusion:** A high proportion of participants were colonized with ESCrE, which is consistent with transmission occurring in the sampled community. Resistance to carbapenems was largely absent from this population.

### Development of a Database System to Support the Rapid Detection and Containment of Emerging Antimicrobial Resistance Threats by the CDC's Global Action in Healthcare Network Antimicrobial Resistance Module (GAIHN-AR)

**A. Espinosa-Bode**, O. McGovern, N.E. Brown, J. Safstrom, K. Wilson, J.Y. Huang, A.C. Brown, F.C. Lessa
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Antimicrobial resistance (AR) is a growing global threat, however, integrated health information systems that capture actionable data for rapid implementation of infection prevention and control (IPC) measures to stop AR spread are not readily available**.** The CDC's Global Action in Healthcare Network Antimicrobial Resistance Module (GAIHN-AR) is a new global initiative to rapidly detect and contain emerging AR threats in healthcare settings. Based on U.S. lessons learned for containment of multi-drug resistant organisms, rapid communication and integration of laboratory and IPC data are essential for GAIHN-AR partners to contain emerging AR threats effectively. **Methods:** We developed a database model and a prototype to facilitate integrating and communicating laboratory testing results and IPC containment response data. The process encompassed an informatics approach with three phases. First**,** we assessed if similar functional systems existed in the pilot countries. Second, we developed the GAIHN-AR's database model and prototype using a multi-step strategy. Lastly, we tested the prototype to assess content and functionality. **Results:** A gap analysis at the pilot countries indicated that the needed database model did not exist. Then, we built the model with two key components: 1) Alerts, for rapidly notifying IPC teams when laboratories detect targeted AR pathogens and adapted from the U.S. Antibiotic Resistance Laboratory Network Alerts system, and 2) IPC response for management of the containment response. Using REDCap®, we built a proof-of-concept database prototype. The prototype involved data collection from laboratory and IPC teams at hospital and national levels. CDC used specific, simulated resistance threat test cases for initial prototype testing before sharing with partners for broader testing to support upcoming in-country system adoption under their existing AR information environments. **Conclusions:** Emerging AR threats emphasize the need for rapid data sharing and collaboration between laboratories and IPC teams for action from local to global levels. The early planning, development, and adoption of information-based resources can be a strategic approach to support more efficient AR containment responses.

### *Klebsiella Pneumoniae* Associated Child Mortality in the Child Health and Mortality Prevention Surveillance (CHAMPS) Network

**A. Wadhwa**[1], D.M. Blau[1], S.A. Madhi[2], D. Onyango[3], I. Mandomando[4,5], S.O. Sow[6], S. El Arifeen[7], E.S. Gurley[7,8], M. Alam[7], A. Rahman[7], K.M. Islam[7], B.A. Tippett-Barr[1], V. Akelo[1], J.R. Verani[1], K.L. Kotloff[9], Q. Bassat[5,10,12-14], I.U. Ogbuanu[15], J.A.G. Scott[11], N. Assefa[16], L. Madrid [11,16], J.O. Oundo[11,16], M. Brhane[16], O. Ita[17], J. Ojulong[18], S. Lako[19], J. Bunn[20], R. Omore[21], K. Otieno[21], S. Mahtab[2], V. Baillie[2], B.N. Thwala[2], S. Velaphi[22], M.D. Tapia[9], S.M. Tennant[9], H. Badji[6], A. Massinga[5], E. Dora[5], J. Miguel[5], R.F. Breiman[23], C.G. Whitney[23]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]South African Medical Research Council Vaccines and Infectious Diseases Analytics Research Unit, University of Witwatersrand, Johannesburg, South Africa, [3]Kisumu County Department of Health and Sanitation, Kisumu, Kenya, [4]Manhiça Health Center, Maputo, Mozambique, [5]Centro de Investigacao en Saude de Manhica (CISM), Maputo, Mozambique, [6]Center for Vaccine Development-Mali, Bamako, Mali, [7]International Centre for Diarrhoeal Disease Research, Bangladesh, Dhaka, Bangladesh, [8]Department of Epidemiology, Johns Hopkins University, Baltimore, MD, USA, [9]Department of Pediatrics, Center for Vaccine Development and Global Health, University of Maryland School of Medicine,

Baltimore, MD, USA, [10]ISGlobal - Hospital Clínic, Unversitat de Barcelona, Barcelona, Spain, [11]London School of Hygiene & Tropical Medicine, London, UK, [12]Institució Catalana de Recerca I Estudis Avançats (ICREA), Barcelona, Spain, [13]Hospital Sant Joan de Déu, Barcelona, Spain, [14]Consorcio de Investigación Biomédica en Red de Epidemiología y Salud Pública [CIBERESP], Madrid, Spain, [15]Crown Agents, Freetown, Sierra Leone, [16]College of Health and Medical Sciences, Haramaya University, Harar, Ethiopia, [17]University of Calabar Teaching Hospital, Calabar, Nigeria, [18]ICAP –Columbia University, Freetown, Sierra Leone, [19]Aberdeen Women's Centre, Freetown, Sierra Leone, [20]World Health Organization – Sierra Leone, Freetown, Sierra Leone, [21]Kenya Medical Research Institute – Center for Global Health Research (KEMRI-CGHR), Kisumu, Kenya, [22]Department of Pediatrics, Chris Hani Baragwanath Academic Hospital, School of Clinical Medicine, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa, [23]Emory Global Health Institute, Atlanta, GA, USA
**Background**: *Klebsiella pneumoniae* (Kp) is an important cause of nosocomial infections, characterized by antimicrobial resistance and high case fatality. Limited data are available on illness and death due to nosocomial or community-acquired Kp in resource-poor settings. The Child Health and Mortality Prevention Surveillance (CHAMPS) network aims to generate accurate data on deaths in children under-5 to inform prevention strategies. **Methods**: CHAMPS surveillance occurs in defined catchment sites in seven countries (Bangladesh, Ethiopia, Kenya, Mali, Mozambique, Sierra Leone and South Africa). Under-5 child deaths reported within 24 hours, with obtained consent, undergo minimally invasive tissue sampling (MITS) and comprehensive diagnostic testing in addition to collection of clinical data and verbal autopsy. Kp was detected by culture and/or PCR in blood, CSF, or lung tissue. The complete data on each death was reviewed by local experts using a standardized process (Determination of Cause of Death) to identify all relevant conditions leading to death (causal chain). **Results**: Of 1644 deaths in children under-5 years enrolled from 2016-2020 that had causes of death assigned, Kp-associated conditions were listed in the causal chain leading to death in 348 (21%), ranging from 8% (49/640) of neonates aged 0 -<3days, 40% (133/331) of neonates 3-28 days and 25% (166/673) of children 29 days to 5 years. Of these 348 Kp associated deaths, 44% (154) were deaths that occurred in the community or within 72 hours of hospitalization. The most common clinical syndrome among deaths with Kp in causal chain was sepsis (73%), followed by pneumonia (52%); only 2% had meningitis without pneumonia or sepsis. **Conclusions**: Preliminary findings support increasing the focus on preventing invasive disease caused by Kp and its associated child mortality, and further work to understand burden of illness caused by Kp outside of health facilities.

### Impact of Biosafety and Infection Control and Prevention Training Program on Sudanese Health Workers Practices During Covid-19 First Wave in Sudan, March-August 2020

**M.M. Elkarsany**[1], M.E. Hamad[1], R.E. Mohamed[2]
[1]Kararay University, Khartoum, Sudan, [2]Ministry of Health, Khartoum- Sudan
**Background:** The aim of this study is to high light the importance of health staff training during health emergencies involving highly pathogenic agents. **Methods:** A cohort group of 47 health workers including ER staff, laboratory personnel, and intensive care unit nurses were selected from 8 tertiary hospitals, in 4 states of Sudan, as a core group for a Training of Trainers (TOT) on basic biosafety, infection prevention and control training with special emphasis on respiratory pathogens using WHO guidelines. A pre-test questionnaire to assess their baseline knowledge followed by a series of lectures and small group discussion involving problem solving methods were performed during a 5-day workshop**.** The group was followed over 5-month period at their respective hospital using a structured questionnaire and direct observation methods plus the relevant hospital data with regard to health staff hospital acquired Covid-19 infection rates .4 other tertiary hospitals were selected as control group. **Results:** Following the TOT a statistically significant increase (9% to 67%) in knowledge, attitude and skills was observed among the trainees, with a p-value of < 0.002.The cascade training done by the core group reached 250 secondary trainees in 5 months period .In all the 8 hospitals involved the staff infection rate was less than 1.2% compared with a rate of 8% in control group hospitals .The above training also reflected on favourable patient outcome relative to control group hospitals. **Conclusion:** The training above highlighted the significance of involving health workers and improving their knowledge and awareness of biosafety and infection prevention and control during Covid-19 ongoing pandemic.

### Strengthening Infection Prevention and Control for COVID-19 in Primary Health Facilities in Sub-Saharan Africa Using a Performance Management Approach

**L.N. Patel**[1], A.E. Barrera[1], K. Brudney[1], A. Haile[1], S. Kozikott[1], O. Manzi[1], M. Thomas[1], C.T. Lee[1]
[1]Resolve to Save Lives, an Initiative of Vital Strategies, New York, NY, USA
**Background:** SARS-CoV-2 has taken a disproportionate toll on health care workers (HCWs), with substantial costs to health systems. In collaboration with Ministries of Health and partners, we implemented an initiative to improve

infection prevention and control (IPC) to protect HCWs and patients. During April 2020—January 2021, the collaborative trained 42,058 HCWs from 8,444 facilities, including 7,574 primary health care facilities in 22 African countries. Monitoring visits using a standardized tool were conducted and resources including personal protective equipment (PPE) were provided. Findings from this first phase were used to design a second phase of the initiative beginning in January 2021, with a stronger focus on behavior change, mentorship and strengthening of national IPC programs. **Methods:** The second phase was designed to provide longitudinal supportive supervision to and mentorship of HCWs at primary health care facilities and use data to inform performance improvement and development of national policies. Mentors conducted monthly visits to assess IPC performance using a tool developed in collaboration with Africa Centres for Disease Control and Prevention. The tool measured performance in areas including availability and appropriate use of PPE and hand hygiene behaviors. Mentors reinforced IPC concepts, implemented behavior change interventions and developed tailored solutions to context-specific challenges. **Results:** Data from eight countries from the first phase showed statistically significant improvement in all IPC measures except availability of PPE and cleaning supplies. Interim data from the second phase, implemented in nine countries, have demonstrated continuous improvement in IPC measures from the first phase, including increasing PPE availability and improvement in hand hygiene behaviors and the appropriate use of PPE. **Conclusions:** We transformed an emergency COVID-19 training program into a multimodal strategy to improve IPC at primary health care facilities in nine countries. Preliminary phase II data show improvement in overall IPC scores. Institutionalization of IPC, including the strengthening of national programs and domestic and global investments, will be needed to sustain these gains and protect HCWs and patients from SARS-CoV-2 and other future pathogens.

## O2. Health Equity and Special Populations: Globally and Locally

**3:15 PM – 4:45 PM**

**Centennial Ballroom II**

## Integrating Health Equity Principles in Public Health Communication and Scientific Products

**R.M. Calanan**, S. Laird, S.R. Bedrosian, N. Patel, Y.P. Springer, H. Talley-McRae, M.E. Bonds
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** Public health communication and education efforts are essential interventions to protect and promote the health of all people in all communities. Public health practitioners must be intentional about content communicated, the language and terminology used, and methods and channels employed for dissemination. **Methods:** In August 2020, the U.S. Centers for Disease Control and Prevention (CDC) developed an internal resource for CDC COVID-19 response staff to apply a health equity lens in developing scientific communication and data products. This resource was expanded to a set of guiding principles and reviewed by a broad and diverse group of internal and external subject matter experts. It was subsequently made publicly available on CDC's website in August 2021. **Results:** CDC's *Health Equity Guiding Principles for Inclusive Communication* is a resource for public health practitioners at all levels, community organizations, and other public health partners. CDC encourages application of these principles through use of a health equity lens when framing information about health disparities. Key principles include using person-first language, avoiding unintentional blaming, and using preferred terms for specific population groups. Meaningful community engagement is foundational to the process of developing non-stigmatizing, unbiased communication for health promotion, research, or policy making. CDC is applying these principles in all types of public health communications during development, review, and dissemination processes, including drafting content, selecting images, and assessing cultural and linguistic responsiveness. The resource is a living document that is not prescriptive, and its implementation is intended to be an iterative process. **Conclusions:** Public health programs and practices must recognize and respect the diversity of the communities they serve. These guiding principles are intended to help public health professionals use inclusive, accurate, and accessible language intended to show respect for all audiences and communities. Achieving health equity requires ongoing efforts to address avoidable inequities so that all people have a fair and just opportunity to achieve optimal health and well-being.

## Causes of Death Identified in Neonates Enrolled Through Child Health and Mortality Prevention Surveillance (CHAMPS), December 2016 – December 2019

**S. Mahtab**[1], S.A. Madhi[1], V.L. Baillie[1], T. Els[1], B.N. Thwala[1], D. Onyango[2], B.A. Tippet-Barr[3], V. Akelo[3], K.A. Igunza[4], R. Omore[4], S. El Arifeen[5], E.S. Gurley[5, 6], M. Alam[5], A.I. Chowdhury[5], A. Rahman[5], Q. Bassat[7-11], I. Mandomando[8, 12], S. Ajanovic[7], A. Sitoe[8], R. Varo[7, 8], S.O. Sow[13], K.L. Kotloff[14], H. Badji[13], M.D. Tapia[14], C.B. Traore[15], I.U. Ogbuanu[16], J. Bunn[17], R. Luke[18], S. Sannoh[19], A. Swarray-Deen[20], N. Assefa[21], J.A.G. Scott[22], L. Madrid[21, 22], D. Marami[21], S. Fentaw[23], M.H. Diaz[24], R.B. Martines[25], R.F. Breiman[26], D.M. Blau[27], C.G. Whitney[26]
[1]South African Medical Research Council Vaccines and Infectious Diseases Analytics Research Unit, University of the Witwatersrand, Johannesburg, South Africa, [2]Kenya County Department of Health, Kisumu, Kenya, [3]Centers for Disease Control and Prevention, Kisumu, Kenya, [4]Kenya Medical Research Institute-Center for Global Health Research (KEMRI-CGHR), Kisumu, Kenya, [5]International Center for Diarrhoeal Diseases Research (icddr,b), Dhaka, Bangladesh, [6]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA, [7]ISGlobal - Hospital Clínic, Unversitat de Barcelona, Barcelona, Spain, [8]Centro de Investigação em Saúde de Manhiça, Maputo, Mozambique [CISM], [9]Institutó Catalana de Recerca I Estudis Avançats [ICREA], Barcelona, Spain, [10]Hospital Sant Joan de Déu, Universitat de Barcelona, Esplugues, Barcelona, Spain, [11]Consorcio de Investigación Biomédica en Red de Epidemiología y Salud Pública [CIBERESP], Madrid, Spain, [12]Instituto Nacional de Saúde [INS], Maputo, Mozambique, [13]Centre pour le Développement des Vaccins (CVD-Mali), Ministère de la Santé, Bamako, Mali, [14]Center for Vaccine Development and Global Health, University of Maryland School of Medicine, Baltimore, MD, USA, [15]University Hospital of Point G, Bamako, Mali, [16]Crown Agents, Freetown, Sierra Leone, [17]World Health Organization – Sierra Leone, Freetown, Sierra Leone, [18]Ola During Children's Hospital, Freetown, Sierra Leone, [19]St. Luke's University Health Network, Easton, PA, USA, [20]University of Ghana Medical School, Accra, Ghana, [21]College of Health and Medical Sciences, Haramaya University, Harar, Ethiopia, [22]Department of Infectious Epidemiology, London School of Hygiene & Tropical Medicine, London, United Kingdom, [23]Bacterial and Mycology Unit, Ethiopian Public Health Institute, Addis Ababa, Ethiopia, [24]Respiratory Diseases Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [25]Infectious Diseases Pathology Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA, [26]Emory Global Health Institute, Emory University, Atlanta, GA, USA, [28]Center for Global Health, Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background**: Each year, 2.4 million children die within their first month of life. Child Health and Mortality Prevention Surveillance (CHAMPS) aims to generate accurate data on why such deaths occur and inform prevention strategies. **Methods**: CHAMPS sites were established in seven countries. After obtaining consent, investigators collected clinical information, verbal autopsy, and minimal invasive tissue sampling (MITS). MITS included needle core biopsies for histopathology, microbiological culture, and molecular tests. The full set of data was reviewed by local experts using a standardized process to identify all relevant conditions leading to death (causal chain). Analysis examined deaths within 24-hours of birth, early (1-<7 days) and late (7- <28 days) neonatal deaths and deaths occurring during first 3 years from December 2016 through December 2019. Deaths were categorized using WHO, International Classification of Diseases. **Results**: We analyzed 675 deaths, 42% occurring within 24-hours, 39% early and 20% late neonatal deaths. Leading underlying causes of death were complications of prematurity (34%), complications of intrapartum events (26%), infections (18%), congenital malformations (10%), and respiratory disorders (6%). In addition to the underlying cause, 67% of deaths had additional conditions and 19% had $\geq$3 other conditions in the causal chain. The most common causes considering the whole causal chain were infection (47%), prematurity (41%) and respiratory distress syndrome (29%). The most common Gram-negative bacterial infections were *Klebsiella pneumoniae* (37%), *Acinetobacter baumannii* (36%), and *Escherichia coli* (12%). *Streptococcus agalactiae* (9%) and *Staphylococcus aureus* (7%) were most common among Gram-positive infections. **Conclusions**: Obstetric care and infection play significant role in neonatal death. Unravelling the source of infection and development of appropriate preventive and therapeutic measures will help to reduce neonatal death in low- and middle-income countries. Showing the full causal chain of events that lead to death highlights the complexities involved in each death along with the multiple opportunities for prevention.

## Nationwide Measles and Rubella Outbreaks in South Sudan, 2019

M. Peck[1], S. Maleghemi[2], **L. Kayembe**[1], M. Hercules[1], A. Anyuon[3], S. Bunga[4], J. McFarland[1], O. Olu[2]
[1]Centers for Disease Control and Prevention, Atlanta, GA, USA, [2]World Health Organization Country Office, Juba, South Sudan, [3]Ministry of Health, Juba, South Sudan, [4]Centers for Disease Control Country Office, Juba, South Sudan

**Background:** South Sudan, a country experiencing a Grade 3 protracted humanitarian emergency with more than six million people affected by civil war (2013-2016) and 1.87 million internally displaced persons, has many

inaccessible areas and hard-to-reach-populations for vaccination. To ensure adequate population immunity against measles, the World Health Organization (WHO) recommends two doses of measles-containing vaccine (MCV); South Sudan currently provides one dose. In December 2018, South Sudan confirmed a measles outbreak. The Ministry of Health, WHO, and the U.S. Centers for Disease Control and Prevention collaborated to investigate the outbreak. **Methods:** Analysis was conducted to characterize measles outbreak, assess potential concurrent outbreaks of other pathogens, assess causes, and evaluate the potential for ongoing outbreaks. Data sources included vaccination coverage derived from WHO and UNICEF estimates, country administrative vaccination coverage estimates, and measles case-based surveillance data. Specimens for suspected measles cases were tested for measles and rubella immunoglobin (IgM) antibody by enzyme-linked immunoassay at the National Measles Laboratory in Juba. **Results:** In 2019, there were 3,727 suspected measles cases reported nationally. Nine hundred and thirteen (913) specimens were tested for measles IgM antibody; among these, 317 (35%) tested measles IgM positive. Among 596 cases that tested measles IgM negative, 149 (25%) were rubella IgM positive. Among suspected measles cases, 2,589 occurred in children under the age of five, with 861 (23%) under 1 year of age. More than a third (1,262) of patients were hospitalized; there were 36 reported measles-related deaths. Twenty-seven (34%) of 80 counties did not report case-based surveillance data. The three counties (Abyei, Wau and Pibor) with the highest number of reported cases have ongoing civil war and a large number of displaced persons. Among all counties that reported cases, administrative coverage for the first dose of MCV ranged from 0%-84%. **Conclusions:** To address measles and rubella immunity gaps, South Sudan needs to achieve >95% coverage with two doses of MCV as recommended by WHO. Populations typically inaccessible due to insecurity and armed conflicts should be targeted in vaccination campaigns.

### "*I have to ask*": A Mixed Methods Study on the Challenges of Collecting Sexual Orientation and Gender Identity Data among San Francisco COVID-19 Case Investigators and Contact Tracers

**L. Gutierrez-Mock**[1], H. Burgess[2], Y.X. Ho[2], J. Gagliano[3], M. Persson[3], N. Lesh[2], M. Reid[1,4,5]
[1]Institute for Global Health Sciences, University of California, San Francisco, CA, USA, [2]Dimagi Inc, Cambridge, MA, USA, [3]San Francisco Department of Public Health, San Francisco, CA, USA, [4]Division of HIV, Infectious Diseases and Global Medicine, University of California, San Francisco, CA, USA, [5]School of Medicine, University of California, San Francisco, CA, USA
**Background:** In September 2020, SB932 was signed into law in California, requiring the collection of sexual orientation and gender identity (SOGI) in the electronic reporting of communicable diseases. However, jurisdictions committed to collecting SOGI data, such as San Francisco, struggled to accurately collect this data within COVID-19 case investigation and contact tracing (CICT) interviews. The CICT workforce consists primarily of redirected state and city employees, most of whom are inexperienced in SOGI data collection. This analysis sought to determine how San Francisco COVID-19 CICTs were documenting SOGI data, and what, if any, obstacles precluded this. **Methods**: We used a mixed-methods study design in which we analyzed data from two sources: (1) survey form data from the San Francisco CalCONNECT CICT COVID database collected between November 15, 2020 and April 15, 2021 to assess SOGI item completeness and (2) qualitative data from 37 in-depth, semi-structured 90-minute virtual interviews with the San Francisco CICT workforce conducted in November 2020. **Results:** Among COVID-19 cases investigated during the study period (N=15,416), sexual orientation data are missing from 20% of records. Furthermore, the prevalence of transgender and non-binary individuals among those reported cases is 0.32%, far below the overall San Francisco transgender population estimate of 0.76%. CICT interview respondents indicated observing or experiencing SOGI questions asked incorrectly, such as including qualifiers or skipping the questions altogether. Many respondents reported not understanding the rationale behind SOGI data fields and feeling uncomfortable asking the questions. **Conclusion**: Qualitative and quantitative data on SOGI parameters in COVID-19 epidemiologic and surveillance records suggest that these data may have been under-reported in San Francisco. To improve our understanding of the true impact of COVID-19 among LGBTQ populations, our results strongly suggest that comprehensive training and quality assurance are crucial in supporting the state mandate of collecting more accurate and reliable SOGI data among COVID-19 cases and their close contacts.

### Severity of COVID-19 Hospitalization Outcomes among US Adults Differ by Disability Status and Disability Type

**K. Clarke**, K. Hong, M. Montgomery, M. Schoonveld, A. Greenspan, J. Thierry
Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** One in four US adults report living with a disability and may be at increased risk for severe COVID-19 outcomes. There is a lack of published analyses on COVID-19 severity in U.S. adults by disability type from

national datasets. This study analyzed electronic health record (EHR) data to explore differences in COVID-19 outcomes between people with and without disability and by disability types. **Methods:** Multivariable regressions of Premier Healthcare data for adults with COVID-19 hospitalized between April 2020 and June 2021 were performed, adjusting for age, sex, race/ethnicity, region, underlying condition, and urbanicity. Disability status and type (mobility, visual, hearing, or intellectual developmental disability [IDD]) was classified by ICD-10-CM code. Outcomes included intensive care admission, mechanical ventilation, in-hospital mortality, and 30-day readmission for COVID-19 among people with a disability compared to those without a disability. Among community-dwelling adults, rate of discharge to long term care (LTCF) or skilled nursing facilities (SNF) was assessed. **Results:** Adults with any disability (n=88,238) had increased risk of mechanical ventilation (aRR: 1.04; 95%CI: 1.02-1.07), in-hospital mortality (1.04; 1.01-1.06), and 30-day readmission (1.24; 1.20-1.28) compared to those with no disability (n=513,448); risk was highest among adults with IDD ([1.35; 1.29-1.42], [1.34; 1.28-1.41], [1.53; 1.42-1.64]), respectively). Risk varied by disability type; risk of readmission was significantly increased among every disability type (aRRs: 1.13-1.53). Among community-dwelling adults, risk of discharge to a LTCF or SNF was increased for every disability type (aRRs: 1.14-2.53) compared to people without a disability. **Conclusions:** Severity of COVID-19 hospitalization outcome in U.S. adults varies by disability status and type; IDD was associated with the highest risk of severe outcomes. Increased risk of readmission across disability types may indicate a need to improve discharge planning and follow up support services for adults with disabilities. Increased risk for adults with disabilities to be discharged to LTCF or SNF may be in part due to COVID-19 severity but may also reflect a need for improved assessments of the ability of people with disabilities to function independently after discharge.

### Emerging Infectious Diseases among People Experiencing Homelessness: A Systematic Review

**C.S. Saldana**[1], A.A. Meehan[2], C.K. Lin[3], E. Mosites[2]
[1]Division of Infectious Disease, Emory University School of Medicine, Atlanta, GA, USA, [2]Centers for Disease Control and Prevention, Atlanta, GA, USA, [3]Department of Medicine, Emory University School of Medicine, Atlanta, GA, USA
**Background:** People experiencing homelessness (PEH) are at an increased risk for infectious diseases. However, the extent of the infectious disease risk associated with homelessness is not clear. We conducted a systematic review of literature to identify emerging infections among PEH and areas where further research is needed. **Methods:** We followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses guidelines. Peer-reviewed literature published in English from the United States and Canada between January 2003 and March 2021 with epidemiologic data on infectious diseases among PEH were included. Vaccine preventable diseases were excluded because they have recently been reviewed. Two reviewers independently searched for articles and extracted data for each article. A third reviewer resolved discrepancies when needed. **Results:** Of 1540 articles were screened, 187 met inclusion criteria with epidemiologic data for 24 infectious diseases. Over half of articles provided data on Hepatitis C virus or *M. tuberculosis* (64 and 53 articles, respectively). Respiratory virus studies included COVID-19 (n=16) and respiratory syncytial virus (n=1). Fifteen articles described prevalence of *S. aureus* colonization and 10 reported Group A Streptococcus colonization or infection. Articles on five sexually transmitted infections, *C. trachomatis* (n=10), *N. gonorrhoeae* (n=8), *T. pallidum* (n=4), *T. vaginalis* (n=3) and Herpes Simplex Virus (n=1) were included. Vector-borne disease reports, including *Rickettsia* spp. (n=1), *Bartonella* spp. (n=6), *Leptospira* spp. (n=2) and West Nile Virus *(n*=2), commonly included seroprevalence estimates. Aside from *Shigella* (n=2), no reports on diarrheal pathogens (*Salmonella* spp. (n=1), Noroviruses (1), *E. coli* (1), and *G. duodenalis* (1)) reported human disease data. Seven articles described exposure to ectoparasites, including head lice, fleas, scabies and Triatominae, the vector for *T. cruzi*. Of 58 articles with comparative epidemiologic data, all demonstrated increased risk for PEH compared to the general population. **Conclusion:** Aside from Hepatitis C, tuberculosis, and COVID-19, published data that quantify the infectious disease risks associated with homelessness were sparse. However, increased risk of disease associated with homelessness was evident.

## O3. Zoonotic Diseases and One Health

**3:15 PM – 4:45 PM**

**Centennial Ballroom III**

### Prioritizing Zoonotic Diseases Using a One Health Approach: Highlights from 30 Subnational, National, and Regional Prioritizations, 2014–2021

**G.W. Goryoka**, N.L. Oussayef, K. Varela, R. Ghai, I. Zecca, H. Belles, C. Basler, C. Barton Behravesh
Centers for Disease Control and Prevention, Atlanta, GA, USA

**Background:** Zoonotic diseases pose a significant threat to human and animal health. Prioritizing zoonotic diseases requires a multisectoral, One Health approach and provides an opportunity to improve coordination, collaboration, and communication among One Health partners. CDC's One Health Zoonotic Disease Prioritization (OHZDP) Process brings together representatives from human, animal, and environmental health and other relevant sectors to prioritize zoonotic diseases of greatest concern for One Health collaboration. **Methods:** Data from OHZDPs conducted from 2014–2021 were analyzed by geographical location, participants, criteria, priority zoonotic diseases, and action items identified during the workshops. Zoonotic diseases, criteria, questions, and action items were standardized, categorized, and aggregated around common themes. **Results:** CDC and partners facilitated 30 OHZDPs in multiple regions globally: Africa (n=20), Asia (n=7), and the Americas (n=3). Voting members from human, animal, and environmental health sectors were represented in 25 (83%) workshops. Common criteria included epidemic/pandemic potential (n=29; 97%), disease severity (n=27; 90%), ability to prevent and/or control (n=29; 97%), social, economic, and/or environmental impacts (n=25; 83%), and bioterrorism potential (n=9; 30%) of the zoonoses. Frequently prioritized zoonotic diseases were rabies (n=29; 97%), zoonotic influenza (n=28; 93%), brucellosis (n=21; 70%), Ebola and other viral hemorrhagic fevers (n=20; 67%), and anthrax (n=19; 63%). Common action items included strengthening One Health coordination (n=27; 90%), data sharing (n=25; 83%), and workforce (n=23; 77%) and improving surveillance (n=27; 90%), outbreak response (n=26; 87%), and laboratory capacity (n=26; 87%) for the priority zoonoses. **Conclusions:** CDC's OHZDP Process utilizes a transparent method for prioritizing zoonoses and eliciting recommendations through a One Health approach. Strengthening One Health coordination and workforce and improving surveillance, response, laboratory capacity, and data sharing for zoonoses were commonly identified as priority follow on actions. These findings highlight the importance of a One Health approach to address endemic and emerging zoonoses at the national and regional levels.

### One Health Approach Increased COVID-19 Diagnoses in Ghana

**B. Nkrumah**[1], W.K. Ampofo[2], G. Boateng[3], F. Aseidu-Bekoe[4], J. A. Frimpong[1], M. Gyansa-Lutterodt[5], D.T. Barradas[1], P. Kuma-Aboagye[6]
[1]Division of Global Health Protection, US Centers for Disease Control and Prevention, Accra, Ghana, [2]National Laboratory Network Coordination Committee for COVID-19, Accra, Ghana, [3]National Public Health and Reference Laboratory, Ghana Health Service, Accra, Ghana, [4]Public Health Division, Ghana Health Service, Accra, Ghana, [5]Technical Coordination Directorate, Ministry of Health, Accra, Ghana, [6]Director General, Ghana Health Service, Accra, Ghana,
**Background:** Ghana reported its first case of COVID-19 in March 2020. At the time, there were only two human research laboratories with SARS-CoV-2 molecular testing capacity of about 2000 samples per day. In April 2020, Ghana adopted an enhanced contact tracing approach during a partial lockdown in the two main cities - Accra and Kumasi -which led to increased daily testing of up to 50,000 samples per day. Here we outline how a One Health approach was used to increase the number of COVID-19 testing laboratories and increase testing capacity in Ghana. **Methods:** The Ministry of Health (MoH) and Ghana Health Service (GHS) formed the National Laboratory Network Governance for COVID-19 Testing. This consisted of laboratory technical expertise mainly from the human and animal health sectors. In addition, to the Noguchi Memorial Institute for Medical Research and Kumasi Center for Collaborative Research, other laboratories (2 human, 3 animal, 1 academic and 1 environmental) were identified. The MoH developed National Guidelines for COVID-19 PCR testing where the national regulatory bodies - Food and Drugs Authority and Health Facilities Regulatory Agency (HeFRA) - accredited laboratories to conduct PCR testing for SARS-COV-2. The MoH and GHS provided reagents, consumables, and staffing. Interlaboratory comparison was used to monitor testing quality and performance. **Results:** Between March and June 2020, testing sites increased from two to nine and these laboratories were all approved for COVID-19 PCR testing. Overall testing capacity increased from 2000 to 8300 tests per day with the animal and environmental laboratories contributing significantly. Turnaround time reduced from over 4 weeks to 48 hours. **Conclusions:** The One Health approach helped Ghana to rapidly scale up SARS-CoV-2 testing capacity resulting in improved turnaround time supporting surveillance and COVID-19 case management. Our findings are applicable to other similar settings when laboratory capacity needs to be expanded rapidly to confront a public health emergency.

### Suspected Anthrax Outbreak Associated with Handling and Consuming Cow Meat in Kapchorwa District, Uganda, April 2021

**J. Morukileng**[1], J. Namayanja[1], F. Monje[1], N. Chelangat[2], J. Buule[3], J. Kayiwa[4], D. Kadobera[1,5], L. Bulage[1,5], A.R. Ario[1,5], J.R. Harris[6]
[1]Uganda Public Health Fellowship Program, Ministry of Health, Kampala, Uganda, [2]Kapchorwa District Local Government, Kampala, Uganda, [3]Uganda Virus Research Institute, Kampala, Uganda, [4]Ministry of Health Public

Health Emergency Operation Center, Kampala, Uganda, [5]Uganda National Institute of Public Health, Ministry of Health, Kampala, Uganda, [6]Division of Global Health Protection, Centers for Disease Control and Prevention, Atlanta, GA, USA
**Background:** During 2018-2020, Kween District in Eastern Uganda faced annual anthrax outbreaks during April-May. On 24 April 2021, the neighbouring district of Kapchorwa reported suspected human anthrax cases following the sudden death of a cow on 14 April from suspected anthrax. We investigated the outbreak to establish scope and exposures and recommend evidenced-based control measures. **Methods:** A suspected cutaneous anthrax case was acute onset of skin vesicles, lesions, or eschars plus ≥2 cutaneous symptoms plus regional lymphadenopathy. Suspected gastrointestinal anthrax was acute onset of ≥2 of abdominal pain, vomiting, diarrhoea, or sore throat; all were in residents of Kapchorwa District during April 2021. We conducted a retrospective cohort study among all residents in households receiving or having contact with the meat of the dead cow. We collected demographic, clinical, and exposure history data and calculated risk ratios (RR) to identify exposure factors**.** We collected skin blister exudates from suspected case-patients for real-time polymerase chain reaction (rtPCR) tests. **Results:** Among 215 cohort members, 24 (12%) were suspected cases, including 5 cutaneous, 19 gastrointestinal, and 1 both. None was laboratory-confirmed due to non-viable samples. Butchering (RR=46, 95%CI 9.3–226), skinning (RR=55, 95%CI 11–262), and removing internal organs from the cow carcass (RR=39, 95%CI 7.7–198) were associated with suspected cutaneous anthrax. Consuming boiled, fried, and/or roasted meat was not associated with gastrointestinal anthrax. **Conclusion:** This was the fourth anthrax outbreak associated with handling and/or eating meat from cattle that died suddenly in eastern Uganda in four years. Health education targeting socio-behavioral factors associated with handling meat from animals that die suddenly needs to be intensified among butchers. Laboratory capacity to collect viable samples needs to be enhanced for prompt diagnosis and action.

### Clinical and Epidemiologic Characteristics of *Borrelia miyamotoi* Disease

**D.W. McCormick**[1], H. Sohail[2,3], C.M. Brown[4], J. Bjork[5], E. Schiffman[5], A.A. Mathewson[6], M. Notarangelo[6], K. Cervantes[7], J. Garrett[8], C. McGinnis[8], N.A. Kwit[9], R. Osborn[10], A.M. Schwartz[1], A.F. Hinckley[1], K.J. Kugeler[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Maine Center for Disease Control and Prevention, Augusta, ME, USA, [3]University of Southern Maine, Portland, ME, USA, [4]Massachussetts Department of Public Health, Boston, MA, USA, [5]Minnesota Department of Health, Saint Paul, MN, USA, [6]New Hampshire Department of Health and Human Services, Concord, NH, USA, [7]New Jersey Department of Health, Trenton, NJ, USA, [8]Rhode Island Department of Health, Providence, RI, USA, [9]Vermont Department of Health, Burlington, VT, USA, [10]Wisconsin Department of Health Services, Madison, WI, USA
**Background:** *Borrelia miyamotoi* is a newly recognized pathogen transmitted to humans by blacklegged ticks. The clinical features and incidence are poorly defined. The U.S. geographic distribution is expected to be similar to that of Lyme disease, occurring primarily in the Northeast and Upper Midwest. Staff from CDC and state health departments developed a draft surveillance case definition in 2016 for jurisdictions initiating surveillance for this emerging disease. We summarize clinical and epidemiologic data for *B. miyamotoi* cases reported during 2013-2019 among states where Lyme disease is common. **Methods:** A confirmed case was defined as illness with fever or chills with ≥1 of many other possible symptoms combined with molecular evidence or evidence of seroconversion against GlpQ protein; a possible case was defined as the same clinical signs or symptoms but with a single positive serology result. **Results:** Eight states reported ≥1 confirmed or possible case of *B. miyamotoi* disease during 2013-2019; two additional states reported no cases. A total of 293 cases were identified; 164 (56%) were classified as confirmed, 151 (52%) occurred among males, and median patient age was 52 years (range 1-86 years). Most cases (70%) occurred during June-September, peaking in August. Common symptoms included fever (93%; 41% had a relapsing fever), fatigue (88%), and headache (82%); 22% reported a rash. Twenty percent (38/190) were hospitalized; there were no reported deaths. **Conclusions:** These initial *B. miyamotoi* disease cases reported through public health surveillance represent the largest sample size of human disease characteristics to date in the U.S. Cases were associated with a more diverse range of symptoms than has been reported in published case series including a higher prevalence of rash and relapsing fever. Persons with *B. miyamotoi* disease became ill most commonly in late summer, timing associated with questing behavior of larval blacklegged ticks, suggesting tick of that lifestage play a role in transmission. Under-ascertainment is likely and case identification may be biased toward more severe cases due to limited clinical awareness and test availability. Ongoing surveillance of *B. miyamotoi* disease will improve detection and better define its incidence, geographic distribution, and severity.

### A Qualitative Study with Parents and Key Informants Assessing Acceptability of the Dengvaxia Vaccine among Puerto Rico Residents

**C. Rosado-Santiago**[1], C. L. Pérez-Guerra[1], C. Colón-Burgos[1], K. M. Marrero-Santos[2], S. H. Waterman, G. Paz-Bailey[1]
[1]Dengue Branch, Division of Vector-Borne Diseases, Centers for Disease Control and Prevention, San Juan, Puerto Rico, USA, [2]Division of Global Migration and Quarantine, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, San Juan, Puerto Rico, USA
**Background:** A new dengue vaccine, Dengvaxia, was approved by the US Food and Drug Administration for children 9-16 years of age with prior laboratory confirmed dengue infection living in areas where dengue is endemic, including the US territory of Puerto Rico[1]. In children who haven't had dengue before, the vaccine could increase the risk of hospitalization or severe dengue if the child is later infected with dengue. To limit this risk, doctors must order a blood test before vaccination. Parents should bring the results back to doctors to evaluate vaccination eligibility. Therefore, assessing perceptions of Puerto Rican parents and key informants about Dengvaxia was imperative. **Objective(s): (1)** Examine acceptability, barriers, and motivators to participate in a Dengvaxia vaccination program. **(2)** Evaluate best dissemination strategies for vaccine education to Puerto Rican parents. **Methods:** We conducted 5 focus groups with parents of children 9-16 years of age (n=38) and 15 in-depth interviews with key informants (pediatricians, physicians from immunization clinics, university researchers, school officials). A snowball sample was used, and a content analysis was carried out. **Results:** Parents agreed to vaccinate their children if they have ample and clear information about Dengvaxia. Barriers to vaccination included lack of information, distrust towards new vaccines, vaccine side effects and risks, and high cost/lack of insurance coverage for laboratory tests and the vaccine. Motivators involved prevention of future dengue infections, having a previous dengue infection or awareness of dengue fatality, vaccine and laboratory test covered by health insurance, availability of rapid test results and vaccine appointments, and support of health institutions in Puerto Rico. Preferred strategy for vaccine information dissemination was orientation from healthcare providers to parents. **Conclusions:** Dengvaxia information should be disseminated before the implementation of an immunization program in Puerto Rico. Dengvaxia education to healthcare professionals will help them answer parents' questions. By addressing motivators and barriers, and disseminating vaccine information in plain language, acceptability of Dengvaxia in Puerto Rico could increase.

### Characterizing Lyme Disease Diagnoses using Electronic Medical Records in a Large Midwestern Healthcare System

**K.J. Kugeler**[1], A.M. Schotthoefer[2], K.M. Cooley[1], E. Scotty[2], J. Mayer[2], A.M. Schwartz[1], J. Meece[2], A.F. Hinckley[1]
[1]Centers for Disease Control and Prevention, Fort Collins, CO, USA, [2]Marshfield Clinic Research Institute, Marshfield, WI, USA
**Background:** Lyme disease (LD) is among the most common of all notifiable diseases in the northeastern, mid-Atlantic, and upper Midwest United States. Alternative data sources are increasingly needed to provide information on the epidemiology of LD and serve as an adjunct to public health surveillance. We explored data from electronic medical records (EMR) at one large healthcare system in an area with high LD incidence to better understand characteristics of possible LD diagnoses and inform development of an algorithm for surveillance and research. **Methods:** We created a retrospective cohort of persons evaluated for LD during 2016–2019. Records were included with at least one of: ICD-10 codes for LD; codes for diagnostic tests performed for LD; and/or prescriptions for an antibiotic used for LD treatment. Records for an individual were grouped into event windows ("events") that incorporated all codes occurring within +/- 30 days of any other associated code. Events were categorized according to presence/absence of: ICD code for LD, tests for LD, and antibiotic prescriptions. **Results:** A total of 62,103 unique patients contributed 76,101 possible LD events during 2016–2019; 58% of possible LD events were associated with LD treatment. Events commonly began in May–July. Patient age distribution was bimodal with peaks among children and older adults. Overall, 52% were female; female predominance occurred among persons aged 15–59 years. Most patients (51,658; 83%) contributed one event, 8,034 (13%) two events, and 2,411 (4%) >2 events. Most events (44,936; 59%) reflected single day encounters. An ICD-10 LD code occurred for 5,249 (7%) events. LD testing occurred for 42,662 (56%) events; 5,496 (13%) were positive. ICD-specific LD codes occurred with LD treatment more often (78%) than codes for testing occurred with LD treatment (27%). **Conclusions:** The age distribution of patients and seasonality of possible LD diagnoses were similar to that of national surveillance. Most patients had one, short duration LD event during 4 years, suggesting most LD diagnoses do not require extended clinical care. Use of LD-specific ICD codes was relatively rare. LD testing was common yet infrequently linked to treatment. Use of specific code combinations will be necessary to maximize predictive value of an EMR-based algorithm for LD diagnoses.

## O4. Late-breakers III: Emergency Preparedness and Response

**3:15 PM – 4:45 PM**

**Centennial Ballroom IV**

### Excess Mortality in Ukraine during the Course of COVID-19 Pandemic in 2020-2022

**A. Shishkin**[1], P. Lhewa[1], C. Yang[2], P. Skums[3], A. Kirpich[1]
[1]Department of Population Health Sciences, School of Public Health, Georgia State University, Atlanta, GA, USA, [2]Department of Biology, College of Arts & Sciences, Georgia State University, Atlanta, GA, USA, [3]Department of Computer Science, College of Arts & Sciences, Georgia State University, Atlanta, GA, USA
**Background:** The ongoing pandemic of COVID-19 caused by SARS-CoV-2 coronavirus was originally detected in Wuhan, China in late 2019. Within just months the virus has rapidly spread around the planet. Now, in the middle of 2022 the devastating effects of the pandemic can be evaluated over time for each specific country. In this work we investigate and compare the excess mortality for Ukraine before and during the last two years of the pandemics. Ukraine is the second largest country in Europe by area where COVID-19 has not always been thoroughly studied. **Methods:** In this work we fill that knowledge by studying the excess mortality in Ukraine during that time. The excess mortality is studied using statistical modeling methods for reported time-series data with subsequent forecasting and comparisons using standardized P-scores. Non-parametric scores as well as parametric scores computed based on the Prophet and ARIMA models forecasts are produced and compared. The excess mortality is compared with COVID-19 reported mortality during the pandemic, demographic changes over time as well as with other potential excess mortality causes. **Results:** There are indications of substantial increase in excess mortality during COVID-19 pandemic. The most deaths were observed in three waves in November-December 2020, March-April 2021 and November-December 2021. The highest excess in mortality was observed During November 2021 in the amount of 80.88% while the lab-confirmed mortality contributed only 21.8% of the overall mortality for the same month. Therefore, the diagnosed COVID-19 mortality represents only the portion in the overall mortality excess. The excess mortality was also compared to the neighboring countries in the region. **Conclusions:** Overall, there are indications of the substantial mortality increase in Ukraine during the two pandemic years.

### Mitigation Matters: SARS-CoV-2 Infection Rates among Two South Dakota School Districts

**H. Parsons**, A. Ortiz, A. Miller, J. Clayton
South Dakota Department of Health, Pierre, SD, USA
**Background:** CDC recommends mitigation strategies for combatting the spread of SARS-CoV-2 in K-12 schools. South Dakota schools had drastically different mitigation approaches during the pandemic. Our objective was to compare SARS-CoV-2 case rates for two school districts with different mitigation strategies. **Methods:** School district A followed CDC guidance consistently by implementing universal indoor masking, close contact tracing, and physical distancing. School district B followed CDC guidance throughout the 2020 timeframe but halted all mitigation efforts in 2021. From August 26 to October 31 in 2020 and 2021, confirmed and probable SARS-CoV-2 cases among students were reported for school districts A and B into the South Dakota Department of Health's (SD-DOH) electronic disease surveillance system. Student enrollment counts were obtained from the South Dakota Department of Education. Along with an analysis of other factors, case rates were calculated by school district and year for comparison. **Results:** In 2020, school district A and B implemented three key mitigation strategies recommended by the CDC. In 2020, 42 SARS-CoV-2 cases (1.5%) were reported from 2,791 students in school district A, and 154 cases (1.2%) were reported from 12,690 students in school district B. There was no statistically significant difference in case rates comparing school district A and B (p-value= 0.22). In 2021, 18 SARS-CoV-2 cases (0.7%) were reported from 2,742 students in school district A, and 381 cases (3.0%) were reported from 12,751 students in school district B. In 2021, students in school district B had a 4.5 times greater likelihood of SARS-CoV-2 infection compared to school district A (p-value= <0.0000001). **Conclusion:** COVID-19 mitigation measures recommended by the CDC can significantly reduce transmission of SARS-CoV-2 in K-12 school settings. School board officials should consider a layered approach of mitigation measures to support in-person learning during times of high community transmission of SARS-CoV-2.

### Community Pharmacists' Perspective as Frontline Vaccinators in the COVID-19 Pandemic in the State of Louisiana: A Qualitative Report

**C. Gillard**, S. Al-Dahir, D. Davis, M. Earls, B. Singleton

Xavier University of Louisiana, New Orleans, LA, USA
**Background:** The state of Louisiana experienced over 17,000 deaths from COVID-19. Over 5 million vaccines were administered in Louisiana, mostly by community pharmacists. Pharmacists have been on the frontlines providing COVID education, vaccination, and testing. The purpose of this project is to describe the perspectives of pharmacists providing vaccination in their communities. **Methods:** Community pharmacies in Louisiana were recruited to participate in a pharmacist led interventional model to increase COVID-19 vaccine uptake. The pharmacists participated in a focus group to understand their experiences providing COVID-19 vaccination. Pharmacists were recruited from areas of the state based on the Louisiana Department of Health designated regions. Focus groups were conducted on a virtual platform and consisted of a combination of poll and open-ended discussion questions related to their experiences providing COVID-19 vaccination such as challenges to vaccination they have encountered, experiences with vaccine hesitancy, and also their opinions on ways to improve vaccine uptake. **Results:** A total of 5 focus groups were conducted with 51 community pharmacists from different Louisiana regions. Most of the pharmacists that participated were from Baton Rouge and the Greater New Orleans area. Pharmacists stated that they have encountered COVID-19 vaccine hesitancy. Over 70% of the pharmacists stated that patients are seeking counseling about the COVID vaccine before making their decision about vaccination. Over 80% of the pharmacists felt the concerns around the COVID-19 vaccine are different from that of other vaccines. The top challenges to vaccination reported by pharmacists included time, staffing, and workload. The pharmacist discussed that vaccine hesitancy in their communities has decreased as more people are becoming vaccinated. They also stressed concerns about vulnerable populations such as the elderly and African Americans. **Conclusion:** Pharmacists expressed challenges they encountered while providing COVID-19 vaccination yet are still motivated to vaccinate and education patients and aid vulnerable populations during the pandemic.

### COVID-19 Community-level Development

**M.J. Panaggio**, P. Graff, E. Peterson
Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA
**Background:** On February 25, 2022, the Centers for Disease Control and Prevention announced the COVID-19 community levels, a county categorization scheme designed to summarize key COVID-19 indicators to help communities make decisions about prevention strategies. These levels are based primarily on COVID-19 hospital admissions and inpatient bed utilization with confirmed cases as a secondary indicator and mark a shift in focus from transmission to healthcare burdens. **Methods:** We will discuss the development of the community levels and highlight the considerations that led to the current level definitions. We will address the quantitative and qualitative criteria used to select the current indicators and thresholds including their capacity to predict severe outcomes three weeks later, as measured by correlation with deaths and ICU utilization, and geospatial analysis. We will also describe the threshold validation process using metrics such as the area under the receiver operating characteristic as well as the resulting implementation of the community levels. **Results:** We will demonstrate that these community level definitions provide significant improvements over the previous community transmission level framework in identifying counties that will experience severe outcomes. We will also show that the spatiotemporal patterns generated by this categorization scheme have historically provided more informative descriptions of the trajectory of the pandemic. **Conclusions:** This work underscores the challenges inherent in public health communication of complex metrics. This work also highlights the need for simple and reliable tools for summarizing this information in a digestible format for decision-makers and the general public. Tools like the COVID-19 community levels can help health officials make more timely and effective decisions about prevention strategies.

### Introducing a Conceptual Framework To Guide Epidemic and Pandemic Preparedness: Epidemic Vulnerability Assessment (EVA) Initiative

**N. Shindo**[1], M.M. Mathis[1], A. Beresniak[2], G. Duru[2], S. Singaravelu[3], S. Burzo[4], S. Garnier[1], V. del Rio Villas[5], S. Briand[1]
[1]World Health Organization, Geneva, GE, Switzerland, [2]Data Mining International, Geneva, GE, Switzerland, [3]Independent scholar, FL, USA, [4]University of British Columbia, Vancouver, British Columbia, Canada, [5]World Health Organization, Southeast Asia Regional Office, New Delhi, India
**Background:** We developed Epidemic Vulnerability Assessment (EVA) framework to evaluate countries' epidemic vulnerability by introducing a novel approach for constructing synthetic indicators. EVA comprises three dimensions: Epidemic Risk (EPR), Health System Resilience (HSR) and Multi-sector Vulnerability (MSV). The ongoing COVID-19 pandemic provides a test case to compare EVA outputs with observed health outcomes. **Methods:** Relevant quantitative and qualitative indicators were selected for each of the three dimensions through an expert-driven consensus process: 15 epidemic risk, 11 health systems and 28 multi-sector vulnerability indicators.

Pre-COVID-19 country-specific data were mainly derived from WHO database, CRED EM-DAT and UN sites. Aggregation to compute a composite indicator (calibrated from 0 and 100) for each of the three dimensions of a country was based on multiple correspondence analyses. Correlations of the outputs with cumulative COVID-19 deaths /100000 population were tested using Spearman rank correlation tests. **Results:** WHO Africa region countries appear to have lower HSR, and higher EPR. WHO America and Europe region countries appear to have higher HSR and lower EPR, while WHO South-East Asia region countries and WHO Western Pacific region countries appear between the Africa and Europe regions. WHO Eastern-Mediterranean region countries appear to have greater MSV compared to AFRO-WHO region, lower EPR and HSR to that of the South-East Asia region countries. Highly significant ($p<0.0001$) moderate positive correlations of EPR, HSR and MSV are established with COVID-19 mortality with Spearman correlation coefficient 0.40, 0.42 and 0.66, respectively. **Conclusions:** EVA can be used to assess, monitor and guide understanding of countries' overall vulnerability against epidemics; dimension-specific scores support more targeted advice. The EVA facilitates identification and prioritization of regions, or countries within a region where more efforts are needed and which dimension(s) to improve epidemic vulnerability thereby to improve epidemic and pandemic preparedness. Statistical correlations of pre-COVID EVA outcomes with COVID-19 mortality confirm the utility of this approach in assessing counties' epidemic vulnerability.

### A New Paradigm for Pandemic Preparedness: Pathogen Wargaming

F. de Rosa[1,2], A. Ballew[1], M. Pieroni[1], P. Siegel[1], M. Polski[3], S. Scarpino[4], **L.A. Meyers**[1,5]
[1]Center for Advanced Pathogen Threat & Response Simulation (CAPTRS), Austin, TX, USA, [2]NATO STO Centre for Maritime Research and Experimentation, La Spezia, Italy, [3]US Naval War College, Newport, RI, USA, [4]Pandemic Prevention Institute, Rockefeller Foundation, New York, NY, USA, [5]University of Texas at Austin, Austin, TX, USA

**Background:** Despite decades of pandemic planning, global health agencies and policy makers struggled to effectively track and mitigate COVID-19. Future preparedness exercises should consider a much wider range of plausible pathogen threats, force the design of innovative countermeasures, and capture cascading social, economic, and political interdependencies that ultimately shape the course of epidemics. **Methods:** Drawing on the Knowledge Acquisition Analytical Game for military wargarming, which makes use of knowledge engineering paradigms for interactive cognitive environments, we developed a formal preparedness game to guide the design and implementation of infection surveillance systems. Designed for individual and small group training, the game forces the players to articulate data collection objectives, assess the timeliness, reliability and trustworthiness of diverse data sources, and identify gaps in data and reasoning. The plug-and-play game structure allows for training across a range of historic and hypothetical pathogen threats, each encoded in a short deck of data snapshot cards. **Results:** The Pathogen Situational Awareness (PSA) game is an evidence-based training tool for improving the collection of surveillance data, analysis, and decision, with respect to current and future pathogen threats. In partnership with the Pathogen Preparedness Institute, we conducted pilot exercises in which players conduct threat assessments for a hypothetical emerging respiratory virus in a temperate region of the globe based on noisy multi-source data. We found that the approach provides actionable insights into both the utility of novel data sources and the cognitive processes that emerge during time-sensitive threat scenarios. Moreover, the game serves as an effective training tool that enables discussion and confrontation among players in a safe-to-fail environment. **Conclusions:** Although research and development of pathogen preparedness games is in its infancy, they provide an effective modality for training decision makers to navigate unexpected and uncertain threats and for developing robust pathogen surveillance systems and response plans.