

# Late-Breaking Reports



## 56<sup>th</sup> Annual Epidemic Intelligence Service Conference April 16–20, 2007



DEPARTMENT OF HEALTH AND HUMAN SERVICES



**Friday, April 20, 2007**

**Late-Breaking Reports**

- 10:30** Late-Breaking Reports. Moderators: Douglas H. Hamilton and Kashef Ijaz
- 10:35** Outbreak of an Unusual Computer Virus — Washington DC, 2007. *Shua Chai*
- 10:45** Malnutrition and Micronutrient Deficiencies in a Long Term Refugee Population—Jhapa and Morang Provinces, Nepal, 2007. *Sapna Bamrah*
- 10:55** Cluster of Severe Methicillin-Resistant *Staphylococcus aureus* Community-Acquired Pneumonia During the Influenza Season — Louisiana, December 2006–January 2007. *Joan Brunkard*
- 11:05** Multistate outbreak of *Salmonella* serotype Tennessee infections associated with consumption of peanut butter – United States, 2006-2007. *Anandi Sheth*
- 11:15** Investigation of *Mycobacterium tuberculosis* Transmission among a Social Network of Family and Friends—Connecticut, 2006. *Ann Buff*
- 11:25** Hepatitis C Virus Infections Among Patients in a Liver Transplant Center, Florida — 2007. *Laurence Cohen*
- 11:35** Social Distancing During a School Closure Because of Communicable Disease — Rhode Island, 2007. *Sara Luckhaupt*
- 11:45** Swine Influenza in a Child with Remote Exposure — Iowa, 2006. *Deborah Dufficy*

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## **Outbreak of an Unusual Computer Virus — Washington DC, 2007**

**Shua J. Chai, R. Diggs, A. Diallo, H. Kan, C. Glymph, B. Furness**

**Background:** Contact with fomites has been implicated in transmission of enteric pathogens. School children are at high risk because of close quarters and less developed hygiene practices. On February 8, 2007, the District of Columbia Department of Health was notified of a gastrointestinal illness outbreak in an elementary school. We investigated to determine etiology and risk factors and to recommend control measures.

**Methods:** We administered a questionnaire to students and staff. Active case-finding was conducted by the school nurse. Ill persons were identified as students or staff with nausea, vomiting, or diarrhea onset during February 2–18. We collected stool samples from two ill persons and 25 environmental samples from shared items throughout the school, including toilets, sinks, doorknobs, computers, and toys for reverse-transcriptase polymerase chain reaction (RT-PCR) analysis and culture.

**Results:** Of 391 students and staff, 100 (26%) were ill, comprising 78/319 (24%) students and 22/72 (31%) staff. Illness onsets occurred during February 4–17; although incidence peaked on February 7, the outbreak persisted. Fifty-two percent (204/391) of students and staff returned questionnaires. Illness was associated with being in first-grade Classroom A (relative risk [RR]=1.8; 95% confidence interval [CI]=1.3–2.7) and contact with an ill person (RR=1.9; 95% CI=1.3–3.0). We identified norovirus strain GII in both stool samples. Staff cleaned shared surfaces before our environmental sampling; a noncleaned computer keyboard and mouse in the implicated first-grade classroom were the only surfaces positive for norovirus.

**Conclusions:** This outbreak likely persisted through person-to-person spread and contact with fomites. Environmental disinfection should be thorough and include atypical fomites that are shared but not commonly cleaned (e.g., computers) to decrease their potential for disease transmission.

**Key words:** norovirus, gastroenteritis, disease outbreaks, fomites

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## **Malnutrition and Micronutrient Deficiencies in a Long Term Refugee Population—Jhapa and Morang Provinces, Nepal, 2007.**

**Sapna Bamrah, O. Bilukha, T. Handzel, L. Talley, B. Tomczyk**

**Background:** Approximately 106,000 Bhutanese refugees have been living in 7 camps in south-eastern Nepal since 1993. Previous surveys have shown micronutrient deficiencies and elevated levels of malnutrition. United Nations High Commissioner for Refugees and the World Food Programme requested that CDC conduct a nutritional survey to evaluate the current levels of malnutrition and provide a baseline for future public health programs.

**Methods:** We completed a cross-sectional survey using systematic random sampling of households to evaluate children aged 6-59 months and their mothers to determine levels of malnutrition, and manifestations of micronutrient deficiencies, in February 2007. The sample consisted of 497 children and 413 mothers throughout the 7 camps. We collected anthropometric measurements on all children, and evaluated both children and mothers for angular stomatitis and hemoglobin (Hb) levels. We also collected information on child morbidity, household food purchases, and infant feeding practices.

**Results:** The prevalence of acute (weight-for-height Z score <-2) and chronic (height-for-age Z score <-2) malnutrition in children aged 6-59 months was 4.2% (95% CI 2.8, 6.4) and 27.0% (CI 23.2, 31.0), respectively. The prevalence of anemia in children (Hb <11 g/dL) was 43% (CI 39.0, 47.7) and in non-pregnant mothers (Hb <12g/dL) was 12.6% (CI 9.7, 16.1). In children, anemia decreased with increasing age from 78.8% (CI 66.0, 87.8) in those aged 6-12 months to 20.0% (CI 13.6, 28.4) in those aged 48-59 months ( Chi-square test for trend: p=0.0001). Active angular stomatitis was present in 1.0 % (CI 0.4, 2.3) of children and 0% of mothers.

**Conclusions:** High prevalence of anemia, especially in youngest children, requires urgent prevention and control measures. These should include improving infant feeding practices, and supplementation or fortification interventions.

**Key words:** refugee health, anemia, micronutrient deficiency, nutrition

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## **Cluster of Severe Methicillin-Resistant *Staphylococcus aureus* Community-Acquired Pneumonia During the Influenza Season — Louisiana, December 2006–January 2007**

**Joan M. Brunkard**, J. Hageman, R. Gorwitz, K. Anderson, G. Fosheim, B. Limbago, M. Pogue, S. Burton, P. Kreyling, J. Guarner, S. Zaki, R. Ratard

**Background:** Methicillin-resistant *Staphylococcus aureus* (MRSA) is an infrequently reported cause of community-acquired pneumonia (CAP), but it can be rapidly fatal, especially among patients coinfecting with influenza. In December 2006, four cases of MRSA pneumonia from one city, including two pediatric deaths, were reported to the Louisiana Office of Public Health. An investigation was initiated to determine if cases were related, identify additional cases, and assess risk factors.

**Methods:** We conducted enhanced surveillance for additional MRSA CAP cases and reviewed patients' medical charts, antibiotic treatment, and risk factors (e.g., history of MRSA skin and soft-tissue infections [SSTI]). MRSA isolates and pathology specimens were collected for characterization at CDC.

**Results:** No epidemiologic links were identified among the original four patients. An additional two cases of MRSA CAP were identified during December 2006–January 2007. Three of the patients had laboratory-confirmed influenza A coinfection, including two children who died within 78 hours of symptom onset. The four surviving patients were hospitalized for a median of 24 days. Five (83%) of the six patients were aged <30 years and three (50%) had recent history of MRSA SSTI. MRSA isolates were available for five patients; all tested positive for the Panton-Valentine leukocidin toxin genes and had an indistinguishable pulsed-field gel electrophoresis pattern USA300-0114.

**Conclusions:** MRSA CAP resulted in severe morbidity and mortality in otherwise healthy persons. A history of MRSA skin infections or coinfection with influenza should lead to a heightened index of suspicion for MRSA CAP when patients present with severe respiratory symptoms. Further research is needed to determine if the rising national prevalence of MRSA SSTIs might lead to an increasing incidence of MRSA CAP.

**Key words:** Methicillin-resistant *Staphylococcus aureus* (MRSA), community-acquired pneumonia, influenza, pediatric mortality

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## **Multistate outbreak of *Salmonella* serotype Tennessee infections associated with consumption of peanut butter – United States, 2006-2007**

**Anandi N. Sheth** for the *Salmonella* Tennessee Outbreak Investigation Team

**Background:** In January 2007, we began investigating a large, multistate outbreak of *Salmonella* Tennessee infections, a rare cause of salmonellosis.

**Methods:** We defined a case as *Salmonella* Tennessee infection in a patient whose isolate demonstrated one of three similar pulsed-field gel electrophoresis patterns and whose illness began after July 31, 2006. We developed hypotheses by comparing patient food histories from an extensive food item questionnaire to U.S. population food consumption survey data. We conducted a case-control study among adult residents of 22 states. State and federal public health laboratories tested implicated product for *Salmonella*.

**Results:** We identified 453 cases in 45 states; 76 (20%) patients were hospitalized and none died. Illness onsets ranged from August 1, 2006 to February 23, 2007; 69% were after November 30. Among 65 cases and 124 controls, illness was associated with consuming peanut butter more than once a week [matched odds ratio (mOR) 3.5, 95% confidence interval (CI) 1.4 – 9.9], consuming Brand X peanut butter (mOR 12.1, CI 3.6 – 66.3), and consuming Brand Y peanut butter (mOR 9.1, CI 1.0 – 433). Brands X and Y were produced in a single plant, which ceased production and recalled all products on February 14, 2007. Laboratories isolated outbreak strains of *Salmonella* Tennessee from 21 jars of Brands X and Y peanut butter produced between July and December 2006 and from two plant environmental samples obtained in February 2007.

**Conclusion:** This is the first foodborne outbreak linked to peanut butter in the United States. Contamination of peanut butter continued for at least several months. Coordinated, multistate epidemiologic and laboratory efforts identified the outbreak vehicle, resulting in a nationwide recall and cessation of the outbreak.

**Key words:** *Salmonella*, outbreak, pulsed-field gel electrophoresis, peanut butter

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## Investigation of *Mycobacterium tuberculosis* Transmission among a Social Network of Family and Friends—Connecticut, 2006

Ann M. Buff, L. Sosa, A. Hoopes, D. Buxton-Morris, T. Condren, M. Lobato, M. Haddad, P. Moonan, J. Hadler

**Background:** Despite the low incidence of tuberculosis (TB) in Connecticut (<3.5 cases per 100,000 persons), high-risk groups (e.g., homeless and incarcerated) continue to challenge TB control efforts. In 2006, eight TB cases in a social network of family and friends and a related ninth TB case were identified. We investigated this outbreak to determine factors associated with *Mycobacterium tuberculosis* transmission.

**Methods:** We reviewed medical records and interviewed adult patients to determine their contacts, activities, and locations frequented while they were contagious. *M. tuberculosis* isolates were genotyped using spacer oligonucleotide typing (spoligotyping) and mycobacterial interspersed repetitive unit (MIRU) methods.

**Results:** All patients were U.S.-born, HIV-negative, and had pulmonary TB. All six adults were female and aged 21–36 years. The three pediatric patients were aged 10–19 months. In 1996, the source patient had smear- and culture-positive TB but completed only 2 weeks of treatment. While contagious for 15 months prior to her TB diagnosis in May 2006, the source patient lived in six locations, including a correctional facility, where she shared sleeping accommodations with each of the secondary patients. Isolates from five secondary patients had the same spoligotyping and MIRU patterns except two isolates that differed by one repeat at a single MIRU locus. Isolates from the source patient showed a mixed population of *M. tuberculosis* with both MIRU patterns.

**Conclusions:** Field and molecular epidemiology confirmed that all secondary patients were linked to the source patient. The source patient's delay in diagnosis, unstable housing situation, and incarceration resulted in eight secondary TB cases. Adequate treatment of her initial TB in 1996 or early diagnosis of her recurrent TB in 2005 could have prevented this outbreak.

**Key words:** pulmonary tuberculosis, *Mycobacterium tuberculosis*, disease transmission, outbreak, molecular epidemiology, genotype

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## **Hepatitis C Virus Infections Among Patients in a Liver Transplant Center, Florida — 2007**

**Laurence P. Cohen**, N. Thompson, R. Kay, P. Ragan, R. Voss, B. Mull, L. Yulin, G. Xia, L. Ganova-Raeva, Y. Khudyakov, J. Perz, I. Williams

**Background:** Hepatitis C virus (HCV) is the nation's leading indication for liver transplantation. HCV transmissions in healthcare settings have been associated with improper handling of parenteral medications, infected donors, or infected healthcare workers (HCWs). During January 2007, two patients who underwent liver transplantation in 2006 at Hospital A were diagnosed with post-transplant incident HCV infection. We investigated to identify additional cases and the sources and modes of transmission.

**Methods:** We reviewed public health surveillance records, hospital A's surgical/procedure logs, and inpatient census and medical records, including those of all patients who underwent liver transplantation during 2006. Blood/organ donors and HCWs were evaluated as sources of HCV infection. Relatedness of isolates from case-patients was examined using the NS5B/HVR1 regions of the HCV genome. Infection control practices were visually observed.

**Results:** Transplant HCWs common to both patients and donors were HCV RNA-negative. Chronic HCV infection was identified among 37% (79/212) of liver transplant patients. No additional incident cases were identified; post-transplant HCV infection status was not obtained for 18% (33/212) of patients. The two case-patients were infected with HCV genotype 1a, but their isolates were unrelated (16% HVR1 minimum distance). Both case-patients had numerous invasive procedures following transplantation, and no additional HCV risk factors were identified. Obvious infection control deficiencies were not identified. Fourteen potential source patients with HCV genotype 1a shared a healthcare worker, procedure area, or in-patient unit with a case-patient.

**Conclusions:** Our findings indicate that transmission of HCV occurred on two occasions but not from a common source. The high prevalence of HCV infection among liver transplant patients highlights the need for strict adherence to aseptic technique and infection control precautions in these settings.

**Key words:** hepatitis C virus, liver disease, transplant, infection control

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## **Social Distancing During a School Closure Because of Communicable Disease — Rhode Island, 2007**

**Sara Luckhaupt, H. Hastings, D. Hunter, A. MacWhorter, K. Kornlyo, P. Edelson**

**Background:** Social distancing through school closure has been recommended to mitigate the spread of pandemic influenza. However, data are limited regarding the effectiveness of school closure in achieving social distancing. In January 2007, schools in three districts (20,000 students) in Rhode Island were closed for 2–4 days because of an outbreak of mycoplasma pneumonia associated with one death. In conjunction with the epidemiologic investigation of illness, we investigated the prevalence and predictors of social distancing.

**Methods:** We administered telephone surveys to a random sample of student households. Parents were asked about children’s activities during school closure and perceptions of children’s risk for illness before and after schools closed and inside and outside of school. Children were classified as practicing social distancing if they did not visit any public places or spend time with more than six persons. We also conducted a self-administered survey of high school students.

**Results:** According to parental report, 187/479 (39%) children practiced social distancing, which was weakly associated with the belief that keeping children away from others would decrease illness risk (odds ratio [OR]=1.09, 95% confidence interval [CI] 0.67–1.77). Fourteen of 101 (14%) high school students practiced social distancing. Among high school students, social distancing was associated with the belief that staying away from others would decrease illness risk (OR=1.99; CI=0.60–6.64) and the perception that illness risk was high outside of school (OR=1.55; CI=0.38–6.33).

**Conclusions:** Closing schools because of communicable illness does not by itself result in social distancing of students. Public health messages advising students and their parents that children should stay away from groups might increase the effectiveness of school closure in achieving social distancing.

**Key words:** pandemic influenza, non-pharmaceutical interventions, schools

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## Swine Influenza in a Child with Remote Exposure — Iowa, 2006

**Deborah L. Dufficy**, M. Harris, V. Shinde, X. Xu, C. Smith, B. Shu, V. Deyde, A. Balish, A. Foust, K. Soyemi, L. Finelli, P. Quinlisk

**Background:** Swine influenza is an uncommonly reported human zoonotic illness usually associated with swine exposure. Person-to-person transmission rarely occurs and was last reported in 1988. In November 2006, a female, aged 4 years, without recent swine exposure, was hospitalized with influenza-like illness (ILI). Routine influenza surveillance detected a nonhuman influenza A virus subtype. Further characterization revealed a triple reassortant A(H1N1) swine influenza virus with human, avian, and classical swine influenza components. We investigated to determine possible sources of transmission to the patient.

**Methods:** We interviewed eight relatives and seven community contacts. We conducted environmental investigations at the patient's home, preschool, child care, grandparents' home, great-grandparents' hog farm, and mother's meat-processing plant workplace. We collected blood samples from eight relatives, and a convenience sample of 10 of 240 of her great-grandparents' unvaccinated hogs.

**Results:** Grandparents had visited the great-grandparents' hog farm twice in September, once with the patient. Influenza-like-illness was present in at least one hog in September. ILI occurred in the grandfather approximately 10 days after the first farm visit and in the grandmother 9 days after the second visit. A cousin experienced ILI 7 days after contact with the ill grandmother. The patient experienced ILI 6 days after contact with the ill cousin. Interviews and environmental investigation determined the patient had had no direct swine exposure. Influenza testing of relatives' and hogs' sera is pending.

**Conclusions:** Routine influenza surveillance was important in identifying this novel human swine-influenza illness. This investigation revealed no recent or direct contact between the patient and swine and, thus, person to person transmission was the most likely source of infection. Ongoing testing might clarify the transmission links among family members.

**Key words:** influenza A virus, H1N1 subtype, reassortant viruses, swine, zoonoses, surveillance