

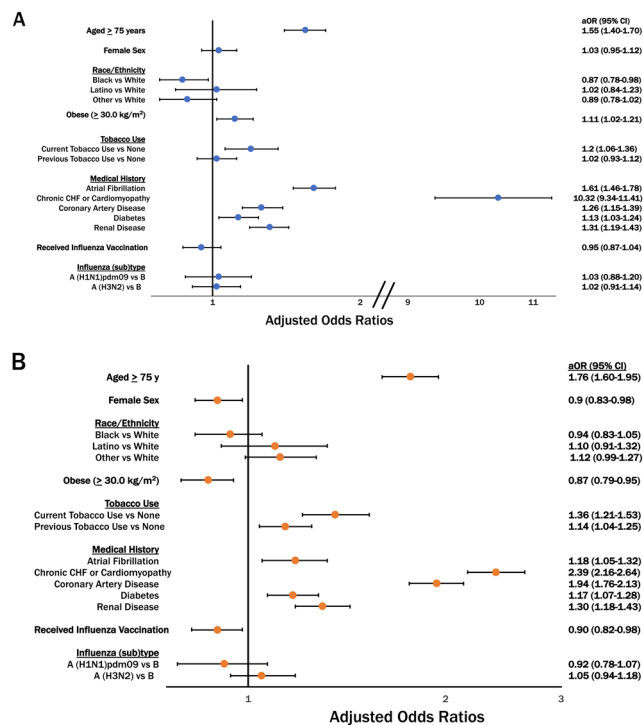
Background. Influenza virus infection most commonly causes acute respiratory tract illness, however may also lead to non-respiratory complications including acute cardiovascular (CV) events. We describe the frequency of and risk factors for acute CV events in adults hospitalized with influenza in the United States.

Methods. We included adults aged > 18 years hospitalized during influenza seasons 2010–2011 through 2017–2018 in FluSurv-NET, a multi-state population-based surveillance system that includes detailed medical chart review of patients hospitalized with laboratory-confirmed influenza. We defined acute CV events by International Classification of Diseases (ICD) primary and secondary discharge diagnosis codes for acute heart failure (aHF), acute ischemic heart disease (aIHD), hypertensive crisis, cardiogenic shock, acute myocarditis, acute pericarditis and cardiac tamponade. We calculated the frequency of acute CV events and used multivariable logistic regression among the 87% treated with influenza antivirals to identify independent factors associated with aHF and aIHD, the two most common diagnoses.

Results. Of 80,374 adults hospitalized with laboratory-confirmed influenza, 12% had > 1 acute CV event. We found that aHF (46%) and aIHD (42%) were the most common, followed by hypertensive crisis (8%), cardiogenic shock (3%), acute myocarditis (0.7%), acute pericarditis (0.4%) and cardiac tamponade (0.2%). Compared with treated patients without an acute cardiovascular event, treated patients with aHF (Figure A) and aIHD (Figure B) were more likely to be older, currently/formerly use tobacco and have underlying conditions including cardiovascular disease, diabetes mellitus, and kidney disease.

Conclusion. Among adults hospitalized with laboratory-confirmed influenza, acute CV events are common, particularly among those with prior cardiovascular disease. During the influenza season, clinicians should consider influenza virus infection in hospitalized adults who present with acute CV events. Non-respiratory complications, specifically aHF and aIHD, may be an under-recognized contributor to the burden of influenza.

Figure: Factors Associated with (A) Acute Heart Failure and (B) Acute Ischemic Heart Disease Among Adults Hospitalized with Influenza, 2010-2018 (N=69,758)



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1622. Clinical and Environmental Surveillance of *Legionella pneumophila* in a Tertiary Healthcare Center in India

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Background. Legionellosis is a form of pneumonia caused by Gram-negative bacilli belonging to the *Legionella* genus. In India, sporadic cases of legionellosis have been reported, but the incidence of this infection is still believed to be underestimated. We conducted a proactive clinical–environmental surveillance in a tertiary healthcare center to determine the frequency of legionellosis, and to identify the pathogen in the hospital water systems.

Methods. During February 2015–February 2019, we enrolled 533 cases (310 males, 223 females) with a diagnosis of pneumonia; a respiratory secretion was collected from each patient and tested for *L.pneumophila* by using a real-time PCR targeting *mip* gene. To identify *Legionella* spp. present in hospital water systems, we collected 201 hospital water samples and were analyzed by cultivation in BCYE agar. Legionella speciation and identification of Lp1 was done by real-time PCR assay.

Results. Among 533 cases, 11(2.1%) [6 male, 5 female] tested positive for *L.pneumophila* by real-time PCR. Of these, all were community-acquired sporadic cases not associated with a cluster or outbreak. Risk factors including smoking, alcohol use, malignancy, underlying respiratory disease, hypertension were identified in 8 (72.7%) cases. The duration of hospitalization for *Legionella* patients was 8–24 days; 5/11 (45.5%) patients were admitted to intensive care units. Of 11 patients 8 (72.7%) survived, and 3(27.3%) died. Among the 201 water samples tested, 38 (18.9%) tested positive for *L.pneumophila* by culture. The presence of Lp1 was detected in 25 (12.4%) water samples. *Legionella* spp. was recurrently isolated from patient areas, cooling towers, residential areas, and other areas inside the hospital campus.

Conclusion. The study indicates a low prevalence of legionellosis in this region. Even though *Legionella* colonization was detected in the hospital water system, no cases of hospital-acquired legionellosis were discovered during the study period. However, considering the risk of nosocomial legionellosis to patients we formulated *Legionella* control strategies in this hospital. Point-of-use filters were installed to the potable water units from where *Legionella* was isolated and repeat sampling from these sites were found to be negative for the contagion.

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1623. Implementation of Electronic Readmission Alert for Discharged Patients Reduces Risk of Secondary Measles Exposure Events

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Background. Measles is a highly infectious illness that is causing increased numbers of outbreaks in the United States. Patients involved in a healthcare measles exposure and who have been discharged before identification of exposure are at risk of becoming infectious in the community, and may seek healthcare within their infectious window, creating a secondary exposure risk for healthcare systems. A measles exposure in an integrated healthcare system occurred, resulting in patient exposures in multiple locations at three campuses, including two community-based emergency departments and three inpatient units. There were 159 patients who were included in the exposure group; 123 were exposed in an ED, and 36 were exposed in an inpatient setting. Ninety-four percent (149/159) of the patients had been discharged at the time of measles case identification and were in the pre-infectious phase of illness. Of those, 36 percent (54/149) presented back to the healthcare system within the potentially infectious window; these 54 patients had 97 individual healthcare contacts in the potentially infectious period following the exposure event. Sixty-one of the 97 return visits (63%) were within the window in which the exposed patients were potentially infectious. Return locations included the three exposure facilities and inpatient and outpatient locations at 10 other system campuses.

Methods. An alert system was developed within the electronic medical record that identified patients that were involved in the exposure, and guided clinicians to mask and place in airborne isolation until measles immunity was verified.

Results. The alert activated 13 days after the exposure was identified, and identified 100% of returns to healthcare at all sites within the system, representing 48% of all potential secondary exposure events (29 /61). No secondary exposures or transmission occurred.

Conclusion. Measles exposures are an enormous burden on healthcare organizations and public health systems. When exposures occur, healthcare organizations need systems to rapidly identify discharged patients who may return within the potentially infectious window. Rapid development of electronic readmission alerts can help standardize identification and reduce the risk of subsequent exposure.

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1624. Primary Care Physician Knowledge, Attitudes, and Diagnostic Testing Practices for Norovirus and Acute Gastroenteritis

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Background. Norovirus is a leading cause of acute gastroenteritis (AGE) across the age spectrum; candidate vaccines are in clinical trials. While norovirus diagnostic testing is increasingly available, stool testing may not be performed routinely, which can hamper surveillance and burden of disease estimates. Our objectives were to understand physicians' stool testing practices in outpatients with AGE, and physician knowledge of norovirus, in order to improve surveillance and prepare for vaccine introduction.

Methods. Internet and mail survey on AGE and norovirus conducted January to March 2018 among national networks of primary care pediatricians (Peds), family practice (FP) and general internal medicine (GIM) physicians.

Results. The response rate was 59% (820/1,383). During peak AGE season, physicians estimated they ordered stool tests for a median of 15% (interquartile range: 5–33%) of their outpatients with AGE. Stool tests were more often available for ova and parasites, *Clostridioides difficile*, and bacterial culture (>95% for all specialties) than for norovirus (6–33% across specialties); even when available, norovirus-specific tests were infrequently ordered. Most providers were unaware that norovirus is a leading cause of AGE across all age groups (Peds 80%, FP 86%, GIM 89%) or that alcohol-based hand sanitizers are ineffective against norovirus (Peds 51%, FP 66%, GIM 62%).

Conclusion. Physicians infrequently order stool tests for outpatients with AGE, and have knowledge gaps on norovirus prevalence and hand hygiene for prevention. Understanding the limitations of surveillance that relies on physician-ordered stool diagnostics, and closing physician knowledge gaps, can help support norovirus vaccine introduction.

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1625. Risk of Invasive Group A *Streptococcus*, Group B *Streptococcus*, and *Streptococcus pneumoniae* Infection Among Adults Experiencing Homelessness—Anchorage, Alaska, 2002–2015

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Background. People experiencing homelessness (PEH) have an increased risk of infectious disease. However, for many infections, this increased risk has not been clearly quantified. For example, the risk of invasive streptococcal infection has not been established among PEH in the United States.

Methods. We compared the incidence of detected cases of invasive group A *Streptococcus* (GAS) infection, group B *Streptococcus* (GBS) infection, and *Streptococcus pneumoniae* (pneumococcal) infection among adult PEH to that in the general adult population in Anchorage, Alaska from 2005 through 2015 using data from the CDC Arctic Investigations Program surveillance system, the US census, and the Anchorage Point in Time count (PIT [a yearly census of PEH]).

Results. During 2005–2015, the PIT counted a mean number of 970 adults (minimum 795, maximum 1486) in Anchorage who were homeless, which accounted for 0.4% of the total population. Compared with the general population, PEH were 53 times as likely to have invasive GAS infection (95% CI 47–61), 7 times as likely to have invasive GBS infection (95% CI 6, 8), and 36 times as likely to have invasive pneumococcal infection (95% CI 33, 40). Of all invasive GAS cases in Anchorage over the time period, 19% occurred within the homeless population, while 3% of invasive GBS cases and 14% of invasive pneumococcal cases were within the homeless population. Additionally, the predominant subtypes of GAS and pneumococcus differed among PEH compared with the general population.

Conclusion. A disproportionate burden of invasive streptococcal disease in Anchorage was detected among PEH, indicating a need for further focus on this high-risk group.

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1626. A Primary Amebic Meningoencephalitis Case Associated with Surfing in an Inland Surf Park

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Background. *Naegleria fowleri* is a thermophilic amoeba that is found in freshwater and causes primary amebic meningoencephalitis (PAM; 0–8 infections per year in the United States) when it enters the nose and migrates to the brain. Patient exposure to water containing the amoeba typically occurs in warm freshwater lakes and ponds during recreational water activities. In September 2018, a 29-year-old man died of PAM after visiting a Texas inland surf park.

Methods. To determine water exposures, we reviewed medical records and conducted interviews with family and individuals who had traveled with the patient. To further investigate the inland surf park as a possible exposure source, we visited the facility and collected water, biofilm, and sediment samples from the surf park and other venues (water slides, lazy river, and cable park) within the facility. We assessed water sources and treatment practices, performed water quality tests, and tested for the presence of *N. fowleri* by culture and real-time PCR.

Results. Interviews revealed that the case-patient's most probable water exposure in the 10 days before becoming ill occurred while surfing in an inland freshwater surf park where he fell off the surfboard into the water multiple times. The on-site investigation of the facility revealed a practice of manual chlorine treatment with monitoring, but no water filtering or record keeping to document water quality. Surf park water temperature was warm (25°C) and chlorine residual was negligible. *N. fowleri* was detected in 1 water and 1 sediment sample collected at the cable park venue, and viable thermophilic amoebae were detected in all samples collected from the surf park, water slide, and cable park venues, as well from the sediment in the open-air groundwater reservoir feeding the venues.

Conclusion. This investigation documents a novel exposure in an inland surf park as the likely exposure causing PAM. Conditions in the surf park were conducive to amoebic growth. Novel types of recreational water venues that do not meet traditional definitions of swimming pools, such as this surf park, might not meet the water quality standards for pools or similar treated venues. Clinicians and public health officials should remain vigilant for nontraditional exposures to water.

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1627. Outbreaks of *Klebsiella pneumoniae* in Special Care Nurseries (SCN) in Jamaica: Role of Whole-Genome Sequencing

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Background. *Klebsiella pneumoniae* is a frequent cause of neonatal sepsis and carries a high mortality rate in lower and middle-income countries (LMICs). From March–November 2015, two Jamaican hospitals experienced *K. pneumoniae* outbreaks in their Special Care Nurseries (SCNs). New admissions to both SCNs were temporarily halted while additional infection control strategies were implemented. 31 babies were infected, of which 15 died. International collaboration was requested to help investigate if the sepsis cases were nosocomial transmission, repeated introductions from the community, or both using whole-genome sequencing

Methods. We sequenced DNA from 19 outbreak isolates ($n = 13$ from Hospital A, $n = 6$ from Hospital B) on an Illumina HiSeq2500 instrument and assembled short-reads using SPAdes. We used ResFinder v3.1.0 to screen resistance genes and assigned MLSTs using in-house scripts. To compare the outbreak isolates, we selected a reference genome from among the assembled isolates, aligned raw reads using the Burrows–Wheeler Aligner (BWA), identified SNPs using GATK UnifiedGenotyper, and removed the recombinant regions using Gubbins v2.3.4. We further contextualized the 19 outbreak isolates against a global collection of more than 300 *K. pneumoniae* genomes.

Results. All 13 isolates from Hospital A appeared to be from a single source. All were ST45 and encoded *bla*_{CTX-M-15}, which confers extended-spectrum β-lactam (ESBL) resistance. Five of 6 isolates from Hospital B appeared to be from a separate, single source. These 5 isolates were ST268 and susceptible to most antibiotics. 1 isolate from Hospital B was ST628, encoded *bla*_{CTX-M-15}, and grouped separately from other Hospital B outbreak isolates. Hospital A and B outbreak isolates formed independent, unique clades within a global *K. pneumoniae* collection.

Conclusion. Our findings indicate nosocomial transmission was responsible for both neonatal *K. pneumoniae* outbreaks, rather than repeat introductions from the community. The main sequence types we detected (ST45 and ST268) are not known pandemic clones and may circulate regionally. Multifaceted infection control measures were implemented for effectively halting outbreaks.

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1628. Clinical, Epidemiological and Microbiological Characterization of Invasive *Streptococcus pneumoniae* Disease in Hospitalized Adults from 5 Tertiary Hospitals in Bogotá, Colombia: A Descriptive Study

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