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 pediatrics (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, Clostridium 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 sanitisers 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 diagnosis 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 (GA-SA) infection, group B Streptococcus (GB-SA) 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 Anchorage 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 GB-SA 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 33% of invasive GB-SA 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. Naegleri fowleri is a thermophilic ameba 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 ameba typically occurs in warm freshwater lakes and ponds, as well as in hot springs and 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 source and treatment practices for 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 in Waco, Texas. We called off the surf park 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 a 1 bacteriologic sample collected at the cable park venue, and viable thermophilic amebae were detected in all samples collected from the 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 amebic 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 facilities. 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 R-Finder 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 GATKUnifiedGenotyper, and removed the recombined 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 diverse with encoded blaCTX-M-15, which confers extended-spectrum β-lactamase (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 blaCTX-M-15 and 30, 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 clades and may circulate regionally. Multifected 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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Central, Bogotá, Distrito Capital de Bogota, Colombia; 5Universidad Nacional de Colombia, Asociación Colombiana de Infectología – Capítulo Central, Fundación HOMI Hospital de la Misericordia, Fundación Hospital Infantil Universitario de San José, Bogotá, Distrito Capital de Bogota, Colombia; 6Universidad Nacional de Colombia, Bogotá, Colombia; Asociación Colombiana de Infectología – Capítulo Central, Bogotá, Distrito Capital de Bogota, Colombia; 7Universidad Nacional de Colombia, Bogotá, Colombia; 8Hospital Universitario Clínica San Rafael, Universidad Nacional de Colombia, Bogotá, Distrito Capital de Bogota, Colombia; 9Hospital Universitario San Ignacio, Pontificia Universidad Javeriana, Bogota, Distrito Capital de Bogota, Colombia; 10Hospital Universitario San Ignacio, Bogotá, Distrito Capital de Bogota, Colombia; 11Unidad de Servicios de Salud Santa Clara, Subred Centro Oriente, Bogotá, Distrito Capital de Bogota, Colombia; 12Fundación Hospital Infantil Universitario de San José, Bogotá, Distrito Capital de Bogota, Colombia; 13A descriptive, observational, retrospective study was conducted in 5 tertiary care hospitals in Colombia from 2011 to 2017. Methods. A descriptive, observational, retrospective study was conducted in 5 tertiary care hospitals during a 7-year period. Demographic, clinical data and in-hospital outcomes were collected through chart review from all culture-confirmed invasive S. pneumoniae cases in each hospital. The National Health Institute laboratory database was assessed to obtain information about ST (Quellung) and antimicrobial susceptibility (Broth microdilution).

Results. 128 cases of IPD were included in this interim analysis, 70 (54.7%) were males. The median age was 58 ± 16.7 years. Main underlying conditions were cardiovascular disease (32%), smoking (27.9%), diabetes (20.3%), autoimmune diseases (18.4%), and cancer (18%). The main clinical presentation was bacteremic pneumonia (66.4%), followed by meningitis (14.8%), bacteraemia (14.1%) and other (3.1%). Critical care management was required in more than half of the patients: ICU (60.2%), mechanical ventilation (53%) and isotropic support (51.6%). The overall in-hospital mortality rate was 43% and was 39%, 52.6% and 61% for pneumonia, meningitis and bacteremia, respectively. ST was known for 82 (64%) cases, most frequent ST were: 3 (10.9%), 14 (7.3%), 19A (6.1%), 1 (4.8%), 4/8/11A/22F (3.65% for each one). ST contained in 13-valent conjugate vaccine (PCV13), 23-valent pneumococcal vaccine (PPVS23) and non-vaccine serotypes accounted for 43.9%, 54.9%, and 40.2% of IPD cases, respectively (Figure 1). 83% and 80.7% strains were susceptible to penicillin andceftriaxone, respectively.

Conclusion. The two known primary risk factors for herpes zoster (HZ) are age and immunodeficiency yet estimates of HZ risk by immunocompromising medical condition have not been well characterized. We undertook a systematic review of the literature to estimate HZ risk in six categories of immunocompromised patients.

Methods. We conducted a systematic review of evidence for HZ in patients with hematopoietic cell transplants (HCT), cancer (blood and solid tumor), HIV, and solid-organ transplant (SOT; kidney and other). We identified studies in PubMed, Embase, Cochrane, Scopus and clinicaltrial.gov using the following outcome search terms: Herpes Zoster, Shingles, VZV, chickenpox, Varicella-zoster virus, or opportunistic infection. We included articles that presented original data from studies in the United States on risk of HZ in adults and were published after 1992 (1996 for HIV). Case reports and conference abstracts were excluded. We assessed risk of bias with Cochrane (clinical trials) or GRADE (observational) methods and categorized studies as high, medium, or low risk.

Results. We identified and screened 3,765 records; 57 articles were abstracted and 34 deemed low or moderate risk of bias (Figure 1). All articles reported at least one estimate of HZ cumulative incidence, which ranged from 0% to 41%. Thirteen studies estimated HZ incidence, which varied widely within and between immunocompromised populations (Figure 2). The highest estimates were seen in HCT (median = 52 HZ cases/1,000 patient-years), followed by blood cancers and SOT, and then solid tumor cancers and HIV (median = 13 HZ cases/1,000 patient-years). Among 17 studies of HCT patients, longer follow-up time and absent or <1 year of post-transplant antiviral prophylaxis were associated with higher HZ cumulative incidence (Figure 3).

Conclusion. HZ is common among all immunocompromised populations studied—exceeding expected HZ incidence in immunocompetent middle-age adults. Antiviral prophylaxis among HCT patients has an ameliorating effect but long-term HZ risk following discontinuation is unclear. Better evidence for incidence and severity of HZ in immunocompromised populations is needed to inform economic and HZ vaccine policy analyses.