Methods. Twenty-two veterans with a clinical *E. coli* isolate (11 FQ-resistant [FQ-R], 11 FQ-susceptible [FQ-S]) and their HH members underwent serial stool sampling (2–6 occasions each). Stool samples were cultured selectively for FQ-S and FQ-R *E. coli*. Per sample, 10 *E. coli* colonies underwent PCR-based profiling; one colony per profile underwent pulsotyping and PCR-based ST131 detection, as did all clinical isolates. Each strain's extent of within-HH sharing and colonization were calculated.

Results. Of the 11 FQ-R clinical isolates, seven were ST131 and four non-ST131; all FQ-S clinical isolates were non-ST131. The 22 HHs included 68 total subjects (49 humans, 19 pets), with a per-HH mean of three subjects, 9.5 total fecal samples, and 6.7 unique strains. The index patient's stool yielded the corresponding clinical strain in 91% of FQ-R HHs, but only 45% of FQ-S HHs. Sharing of the clinical strain occurred in 45% of FQ-R HHs (43% if ST131, 50% if non-ST131), vs. 27% of FQ-S HHs. For the 22 clinical strains, the extent of within-HH sharing and colonization was greater for FQ-R than FQ-S strains (sharing index, 0.45 vs. 0.15; colonization index, 0.47 vs. 0.14). The FQ-R HHs also yielded 12 additional (non-clinical) FQ-R strains, the FQ-S HHs only 1. Non-clinical FQ-R strains colonized much less extensively than FQ-R clinical strains and were not shared between HH members.

Conclusion. Compared with FQ-S clinical *E. coli*, FQ-R clinical *E. coli* more frequently colonize the index patient, are shared among HH members, and co-occur with other HH FQ-R strains, all of which may drive population-level resistance. Given the potentially important clinical implications of within-HH strain sharing and colonization, better understandings are needed of its mechanisms, including characteristics of the strain, host, and gut microbiota.

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657. Epstein–Barr Virus Genetic Diversity in Blood vs. Saliva Samples From Patients with Infectious Mononucleosis

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Background. The Epstein–Barr virus (EBV) is associated with several diseases, including infectious mononucleosis as well as malignant disorders. The relationship between strains of the virus and disease manifestation or illness severity is of interest. Such strains have been defined by genetic variations in the major viral genes. As a first step toward a better understanding of the relationship between strains and clinical outcomes, data are required on the patterns of genetic diversity of the virus in different populations. In this study, we examined the genetic diversity of the BZLF-1 gene, which is a major lytic gene of the virus.

Methods. We sequenced the BZLF-1 gene of EBV following amplification from DNA that was extracted from blood and saliva from previously healthy Canadian children and young adults with infectious mononucleosis. Sequencing was done by Sanger methodology (dideoxy DNA sequencing) and the sequences were aligned with a reference strain of EBV using Geneious software. The variant burden and types of single nucleotide variants were compared in blood and saliva samples.

Results. Twenty-six samples were obtained from 24 patients less than 24 years of age (16 saliva and 10 blood samples). Two subjects provided paired blood and saliva samples at the same visit. Among 36 single nucleotide variations (SNVs), 22% were common to both blood and saliva samples. There was a nonstatistically significant trend for more SNVs among blood compared with saliva samples (median 6 and 1, ranges 0–8 and 0–9, respectively). Of the 3 exons of BZLF-1, exon 1 had the greatest frequency of SNVs compared with exons 2 and 3. Among the paired samples of blood and saliva, there were different genetic variants of the BZLF-1 gene in the blood compared with the saliva samples obtained from patients with infectious mononucleosis.

Conclusion. Among patients with infectious mononucleosis, different genetic variants of EBV may be present in blood compared with saliva. Blood samples revealed viral strains with a tendency for more genetic diversity compared with saliva. The potential compartmentalization of strains is of relevance in sample selection for the evaluation of the potential clinical impact of the genetic diversity of EBV. In addition, the potential impact on disease pathogenesis is of interest.

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658. Trends in Mumps Cases and Incidence, United States, January 2016–April 2018

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Background. Since 2012, there has been a steady increase in the number of reported mumps cases and outbreaks in the United States, primarily affecting young, two-dose vaccinated adults. We analyzed epidemiologic characteristics of mumps cases reported nationally from 2016 to 2018.

Methods. We included confirmed and probable mumps cases transmitted from January 2016 to April 2018 by 52 health department jurisdictions (50 states, DC and NYC) that report cases to the National Notifiable Diseases Surveillance System (NNDSS). We calculated overall and age-specific incidence rates (IR) by dividing the annual number of mumps cases by the corresponding US Census Bureau's Bridged Race population estimates. Cases were reported as outbreak-related or non-related in NNDSS by the submitting jurisdiction.

Results. Between January 1, 2016–April 21, 2018, 13,348 mumps cases (n = 6,369 in 2016, n = 6,056 in 2017 and n = 923 in 2018) were reported to NNDSS. IRs were 20, 19, and 2.9/million population in 2016, 2017, and January–April 2018, respectively. Young adults (18–22 years) had the highest IR: 88, 76, and 7.3/million population in 2016, 2017, and 2018, respectively. During January–April timeframe, 348 more cases were reported in 2016 (IR = 3.8/million) and almost four times as many cases were reported in 2017 (n = 3,376, IR = 10.5/million) compared with 2018 ($P < 0.0001$). The number of jurisdictions that reported cases in the first 4 months of each year was 39, 44, and 47 in 2016, 2017, and 2018, respectively. During the same timeframe, the number of outbreak-related cases reported was lower in 2018 (n = 523) vs. 2017 (n = 2,350) and 2016 (n = 1,271) ($P < 0.0001$), and the number of jurisdictions reporting outbreak-related cases was lower in 2018 (n = 16) vs. 2017 (n = 32, $P = 0.002$) and 2016 (n = 22, $P = 0.23$).

Conclusion. Preliminary data suggest that the overall and outbreak-related mumps cases may be decreasing in 2018 after 2 years of increased reports. However, the number of jurisdictions reporting mumps cases has not decreased. Thorough investigations of sporadic cases may lead to improved identification of epidemiologic linkages and earlier identification of outbreaks.

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659. Mumps Outbreak in a High School: Uptake and Parental Perceptions of Third Dose MMR Recommendations, Dallas County, Texas, 2017

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Background. In February 2017, a mumps outbreak was identified in a large Dallas high school among students who had previously completed the two-dose MMR vaccination series. Early notification of recommendations for third dose MMR and free vaccination clinics provided an opportunity to assess vaccine uptake, efficacy, and parental perceptions of third dose MMR recommendations.

Methods. Mumps illnesses were classified as probable or confirmed cases using 2012 CSTE case definitions. Information about vaccination status, exposure history, and illness characteristics was collected from case interviews and medical records. A third MMR vaccine was recommended to all noncase students and offered without charge at school-based vaccination clinics. Supplemental questionnaires assessing parental knowledge and attitudes regarding this third MMR recommendation were administered to guardians of a randomly selected sample of 20 students who received third dose MMR and 50 students who did not receive the vaccine. Fishers exact tests and chi-square were used to compare responses. Data analysis was performed using SAS 9.4.

Results. From February to May 2017, 28 PCR-confirmed and 12 probable mumps cases were identified in students attending one high school campus (24.3 cases per 1,000 students). Of the 1,646 enrolled students, 99.8% had documentation of at least two doses of MMR prior to the outbreak, including all mumps cases. Three undervaccinated students who declined to receive one dose of MMR were excluded from school during the outbreak. Following public health recommendations for a voluntary third MMR dose, 291 students (17.6%) elected to receive a third MMR. No mumps cases occurred in students who received a third vaccine dose. Parental perception of protective benefit of an additional third dose of MMR was significantly associated with decisions to receive third dose MMR (OR: 4.9; 95% CI = 1.6–15.3).

Conclusion. Responsiveness to health department recommendations for third MMR vaccination in this outbreak setting was limited, even with broad educational communications and free school-based vaccine clinics. The challenges in achieving robust voluntary uptake of a third MMR dose may not improve substantially despite recent ACIP recommendations, in the absence of school mandates requiring third dose of MMR during outbreaks.

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660. Are US Clinicians Thinking Measles in the Post-elimination Era? Surveillance for Measles-Like Illness in a Commercially Insured US Population

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Background. In September 2016, the Americas was the first region to eliminate measles, a highly contagious, vaccine-preventable disease that can lead to complications and death. To maintain elimination, the Pan American Health Organization (PAHO) suggested a minimum rate of suspected measles investigations (≥2 per 100,000 population) be conducted annually. However, measles-like illness (MLI) investigations conducted by US clinicians are not tracked by the measles surveillance program in the