Results. The metagenomics analysis of viral sequences verified that human adenovirus was the leading cause of gastroenteritis among infants and children in Kuwait, and was detected in 23% of the samples, rotavirus A was detected in 16% of the samples, and the combined infection of human adenovirus and rotavirus was detected in 7% of the samples. Also, newly discovered viruses known to cause gastroenteritis were identified: astrovirus MLBL1 and primate bocaparvovirus-1 were detected in 5% of the samples. Also, each of the following new viruses was detected in 2% of the samples: archivirus A, cardioivirus, parechovirus A, astrovirus V44, cosavirus F, and bufavirus-3. On the other hand, multiplex real-time PCR showed that the combined infection of human adenovirus and rotavirus was the leading cause of gastroenteritis among infants and children in Kuwait, which was detected in 27% of the samples. However, the rotavirus was the second most common cause of diarrhea, which was detected in 20% of the samples. And the human adenovirus alone was detected in 18% of the samples. Our results showed a 69% agreement between both methods. By applying the Cohen’s Kappa statistics for a measure of agreement, the result gave fair agreement between the two methods (k = 0.388, P = 0.0).

Conclusion. Our findings revealed the capability of a metagenomic approach to detect many viruses causing gastroenteritis in stool samples from infants and children in Kuwait.

Disclosures. All authors: No reported disclosures.

1778. Epstein–Barr Virus Genetic Diversity: Evaluation of BZLF1 Variants among Bone Marrow Transplant Patients and Individuals with Infectious Mononucleosis

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Background. Epstein–Barr virus (EBV) is associated with several diseases, including infectious mononucleosis (IM) and malignant disorders, including post-transplant lymphoproliferative disorder (PTLD). The relationship between strains of the virus and disease manifestations or illness severity is of interest. Such strains have been defined by genetic variations in the major viral genes. Data involving the patterns of genetic diversity of the virus in different populations are required. We examined the genetic diversity of the BZLF1 gene, which is a major lytic gene of the virus.

Methods. We sequenced the BZLF1 gene of EBV following amplification from DNA that was extracted from blood obtained from pediatric bone marrow transplant (BMT) patients and children and young adults with IM. 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 (SNV) were compared across the 3 exons of the BZLF1 gene.

Results. We sequenced the BZLF1 gene using 21 patients with IM (median age 14, age range 2-19 years) and 11 who underwent bone marrow transplantation (median age 6, range 3-13 years). Three of 11 BMT patients developed post-transplant lymphoproliferative disorder (PTLD). The relationship between strains of the virus and disease manifestations or illness severity is of interest. Such strains have been defined by genetic variations in the major viral genes. Data involving the patterns of genetic diversity of the virus in different populations are required. We examined the genetic diversity of the BZLF1 gene, which is a major lytic gene of the virus.

Methods. We performed a retrospective analysis of the BZLF1 gene sequences from samples (median 4.5 and 0, respectively; \( P > 0.05 \)). Additionally, 2/11 \( P \) BMT samples contained more than 1 SNV compared with 7/21 (33.3%) IM sequences \( (P > 0.05) \).

Conclusion. There was a tendency for more genetic diversity among samples from patients with IM compared with bone marrow transplant patients, notably those with EBV infection. Further studies will determine if this tendency is due to selective pressures in the transplant setting, including but not limited to the use of antiviral agents directed at the lytic phase of EBV.

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1779. Comparison of Two Zika IgM Antibody Capture Enzyme-linked Immunosorbent Assays (MAC-ELISA) in Symptomatic Patients from Dominican Republic

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Background. Zika virus (ZIKV) is a Flavivirus transmitted to humans by Aedes mosquitoes. To assess the clinical presentation in 434 symptomatic patients (64 men, 370 women [65 pregnant; 305 nonpregnant]) during a ZIKV outbreak in the Dominican Republic (DR) in 2016, we evaluated clinical symptoms, ZIKV by qualitative detection of ZIKV RNA and ZIKV IgM by two MAC-ELISA assays, one from CDC and performed by the Florida Department of Health, Jacksonville, Florida1 and one from InBios International Inc., Seattle, WA (Zika Virus Detect). The results from the two MAC-ELISA assays were evaluated by linear regression analysis. The two MAC-ELISA assays were reported as optical density (OD) ratios from a sample with three different antigens (P/N ratio for CDC Zika MAC-ELISA and Zika Immunostatus Ratio or ISR for InBios Zika Virus Detect MAC-ELISA).

Results. There was a bias in ZIKV detection in April and late May-June 2016 in the 434 symptomatic patients. All 434 had one or more of four symptons including rash, fever, conjunctivitis, and arthralgia. Linear regression analysis (log scale) of results from subject samples tested on the two MAC-ELISAs (282 total) revealed a slope of 1.172, y-intercept of 0.1584 and \( R^2 = 0.587 \). In 88 RT-PCR-negative patients, 48 (54.5%) were positive by both MAC-ELISAs; 27 (30.7%) were negative by both MAC-ELISAS and 13 (14.7%) had discrepant results with a sensitivity of 85% for the InBios MAC-ELISA. The InBios also detected IgM in 54.4% of samples that were positive for ZIKV by RT-PCR attributable to errors in determining the days post symptom onset.

Conclusion. In 2016 there was a biphasic spike of ZIKV-positive infections in 434 symptomatic men and women tested in DR. Both linear regression analysis and our comparative analysis in the ZIKV RT-PCR-positive and negative cohorts demonstrated that the InBios Zika Virus Detect MAC-ELISA provides diagnostic results comparable to the CDC Zika MAC-ELISA.

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1780. Congenital Cytomegalovirus: What Are the Rates of Maternal Screening, Diagnostic Amnioncentesis, and Elective Termination?

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Background. Congenitally transmitted cytomegalovirus (CMV) is the leading infectious cause of deafness and intellectual impairment among infants. Due to lack of effective preventive and curative treatments, routine CMV screening of pregnant women is generally not recommended by clinical guidelines or public health authorities, but is conducted on an opportunistic basis by specific healthcare systems and providers. This targeted review describes the rate of reported maternal screening for CMV infection and subsequent pregnancy outcomes.

Methods. PubMed and Embase were searched to identify English-language articles reporting the rate of screening for CMV maternal infection (Objective 1), the acceptance rate for diagnostic amnioncentesis (Objective 2), and the elective termination rates due to CMV infection (Objective 3) in Europe and Israel. No date limit was applied.

Results. Seventeen articles published between 2000 and 2018 were included. Routine CMV screening of pregnant women in the absence of country-level guidelines appears to be common in France and Israel (table). Conversely, in Portugal, where country-level guidelines exist for preconception screening, a high proportion of women are not screened (table). Acceptance rates of diagnostic amnioncentesis among women with CMV infection vary considerably across countries, with the highest rates reported in Israel (73%) and the lowest in Italy (16%). Elective termination rates were higher among women who underwent amnioncentesis vs. those who did not and those with primary CMV infection vs. those with nonprimary infection. Conversely, one study in Israel showed higher termination rates among patients who did not undergo amnioncentesis vs. those who did (35.5% vs. 7.3%).

Conclusion. The available data indicate that routine screening is carried out in some countries to a variable degree. There is an unmet need for effective prevention and management options to help prevent unnecessary termination of pregnancy.