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 MBL3 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, cardiovirus, parechovirus A, astrovirus VA4, 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 the 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, 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 the 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.

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