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 MLB2 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

Carmen de la Plaza de la Salud, Santo Domingo, Distrito Nacional, Dominican Republic, 2016

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.

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Conclusion. The ideal cut-off for “high” serum ferritin was determined to be 876 ng/mL, with levels above that predicting severe thrombocytopenia with a sensitivity of 90% and specificity of 91%. The ROC curve had an area-under-curve (AUC) of 0.846, implying a good test accuracy.

Methods. We included 64 patients in the study. The receiver-operating characteristics (ROC) curve was used to determine the cut-off level for serum ferritin that could discriminate between patients at high risk and those at lower risk for severe thrombocytopenia. The area under the ROC curve (AUC) was used to assess the test's accuracy.

Results. The cut-off value of serum ferritin was 876 ng/mL. Patients with serum ferritin levels above this threshold had a significantly higher risk of severe thrombocytopenia compared to those with levels below this threshold. The AUC of the ROC curve was 0.846, indicating a good test accuracy.

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1782. Real-World HIV Diagnostic Testing Patterns in the United States

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Background. Current HIV diagnostic laboratory testing guidelines from the US Centers for Disease Control and Prevention (CDC) recommend a sequence of tests for detection, differentiation, and confirmation of HIV-1 and HIV-2 diagnosis. There is a gap in knowledge about real-world implementation of the testing algorithm. The aim of this study was to characterize the population that underwent HIV antibody differentiation and confirmatory testing and to describe subsequent testing patterns from a large US clinical laboratory database.

Methods. Patients who received one or more HIV-1/2 antibody differentiation test (BioRad Genius® HIV 1/2 Supplemental Assay [Genius]) in the Quest Diagnostics laboratory database between January 1, 2017 and December 31, 2017 were identified from the study; earliest test date was index date. Genius tests, HIV-1 qualitative RNA (Aptima HIV-1 RNA Qualitative Assay [Aptima]), and HIV-2 DNA/RNA confirmatory tests subsequent to index date were captured. Study measures included point demographic characteristics, testing frequency and sequencing, and test results. For patients with >1 Genius test in 2017, concordance between index and subsequent test results was assessed.

Results. There were 26,319 unique patients identified who received >1 HIV antibody differentiation test result from the Genius assay. Mean age was 40.7 ± 14.3 years, 66.4% were male, and 42.5% were from southern states. Among the study population, there were 28,954 Genius, 7,234 Aptima, and 298 HIV-2 DNA/RNA confirmatory tests. 26.4% of Genius test results were discordant with the initial positive fourth-generation HIV screening results and required subsequent confirmatory testing. In terms of sequencing, the CDC-recommended HIV diagnostic algorithm was followed 74% of the time after screening. 8.5% of patients had >1 Genius test in 2017, concordance between index and subsequent test results was assessed.

Conclusion. The CDC-recommended algorithm for HIV diagnosis is complex for laboratories to implement and currently available assays do not support testing efficiency. To mitigate observed inefficiencies and reduce the laboratory burden of HIV testing, a more accurate and reliable approach for HIV differentiation and confirmatory testing is needed.

Disclosures. All authors: No reported disclosures.

1783. More than Which Molecular Test: Following the Directions in How and Who to Test in the Diagnosis of Influenza

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Background. Centers for Disease Control and Prevention (CDC) recommend a sequence of tests for detection, differentiation, and confirmation of influenza in the United States. Both PCR and a rapid isothermal nucleic acid amplification test (NAAT) for influenza detection are available at the University of Utah Health (UU). The UU has required the more-sensitive PCR to discontinue isolation for suspect-influenza patients, but we hypothesized the NAAT could be sufficient in most patients.

Methods. We included patients with suspected influenza using molecular assays, in part to implement precautions to prevent transmission. Both PCR and a rapid isothermal nucleic acid amplification test (NAAT) for influenza detection are available at the University of Utah Health (UU). The UU has required the more-sensitive PCR to discontinue isolation for suspect-influenza patients, but we hypothesized the NAAT could be sufficient in most patients.

Results. There were 26,319 unique patients identified who received >1 HIV antibody differentiation test result from the Genius assay. Mean age was 40.7 ± 14.3 years, 66.4% were male, and 42.5% were from southern states. Among the study population, there were 28,954 Genius, 7,234 Aptima, and 298 HIV-2 DNA/RNA confirmatory tests. 26.4% of Genius test results were discordant with the initial positive fourth-generation HIV screening results and required subsequent confirmatory testing. In terms of sequencing, the CDC-recommended HIV diagnostic algorithm was followed 74% of the time after screening. 8.5% of patients had >1 Genius test in 2017, concordance between index and subsequent test results was assessed.

Conclusion. The CDC-recommended algorithm for HIV diagnosis is complex for laboratories to implement and currently available assays do not support testing efficiency. To mitigate observed inefficiencies and reduce the laboratory burden of HIV testing, a more accurate and reliable approach for HIV differentiation and confirmatory testing is needed.

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