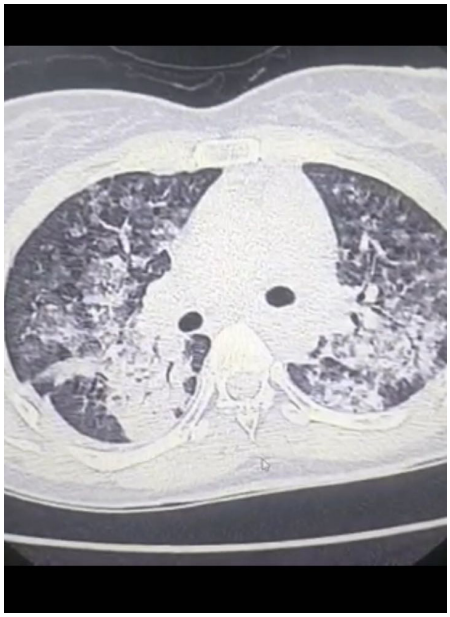

Disclosures. **All authors:** No reported disclosures.

1791. Novel Metabolomics Approach for the Diagnosis of Respiratory Viruses Directly from Nasopharyngeal Specimens

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Background. Respiratory virus infections are important causes of morbidity and mortality among pediatric and adult patients. These viruses infect respiratory epithelial cells, where they may induce specific metabolite alterations. As a proof-of-concept, we investigate the novel use of liquid chromatography (LC) combined with quadrupole time-of-flight mass spectrometry (Q-TOF) for the study of host cell metabolite alterations to diagnose and differentiate respiratory viruses.

Methods. We studied nasopharyngeal swab samples positive for respiratory viruses by the eSensor Respiratory Viral Panel (GenMark Diagnostics, Carlsbad, CA). Banked, frozen samples (−80°C) stored in viral transport media were retrieved and thawed. Aliquots of 100 µL were centrifuged at 13.3 × *g* for 15 minutes, and the filtrate was analyzed by Agilent 6545 Quadrupole LC/Q-TOF (Agilent Technologies, Santa Clara, CA). Compounds were separated using a novel column arrangement based on hydrophobicity and charge using a quaternary solvent manager, followed by accurate mass analysis by LC/Q-TOF. Agilent Mass Profiler 3D principal component analysis was performed, and compound identification was completed using the METLIN metabolite database.

Results. A total of 235 specimens were tested by LC/Q-TOF, including 195 positive specimens [including adenovirus, coronavirus, influenza A H1N1 and H3N2, influenza B, human metapneumovirus, parainfluenza viruses 1, 2, 3, and 4, respiratory syncytial virus (RSV), and rhinovirus] as well as 40 negative clinical specimens. LC/Q-TOF primary component analysis (PCA) allowed preliminary identification of key metabolites that distinguished all virus-positive specimens compared with the negative group, and differentiated respiratory viruses from one another including between influenza A 2009 H1N1 and H3N2 subtypes (Figure 1).

Conclusion. Preliminary data from our LC/Q-TOF analysis show that respiratory viruses exhibit different host cell metabolomic profiles that allow viral differentiation to the species level, and for influenza A virus, the subtype level. This metabolomic approach has substantial potential for diagnostic applications in infectious diseases directly from patient samples, and may be eventually adapted for point-of-care testing.

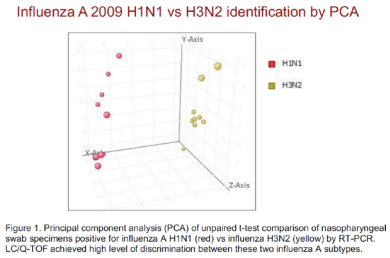

Figure 1. Principal component analysis (PCA) of unpaired t-test comparison of nasopharyngeal swab specimens positive for influenza A H1N1 (red) vs influenza H3N2 (yellow) by RT-PCR. LC/Q-TOF achieved high level of discrimination between these two influenza A subtypes.

Disclosures. **All authors:** No reported disclosures.

1792. Viral DNA Loads in Various Blood Components of Patients with EBV-Positive T/NK Cell Lymphoproliferative Diseases

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Background. Epstein–Barr virus (EBV) is associated with T- and NK-cell lymphoproliferative disorders (EBV T/NK-LPD). For diagnosis of EBV T/NK-LPD, quantification of EBV DNA loads in peripheral blood by real-time PCR has been widely used. However, optimal blood components and cut-off values for diagnosis were not fully evaluated.

Methods. Fifty-nine patients with EBV T/NK-LPD including chronic active EBV infection (CAEBV), severe mosquito bite allergy, hydroa vacciniforme-like lymphoproliferative disorder (HV), and EBV- hemophagocytic lymphohistiocytosis (EBV-HLH) were enrolled. EBV DNA loads were compared among disease categories in each blood component from the same whole blood sample. The association between EBV DNA loads and disease activity were evaluated in CAEBV patients. Furthermore, the diagnostic cut-off value for EBV DNA loads in whole blood from CAEBV patients as compared with infectious mononucleosis patients was determined.

Results. EBV DNA loads in whole blood and peripheral blood mononuclear cells (PBMCs) were not significantly different among disease categories, whereas EBV DNA loads in plasma were significantly higher in EBV- HLH patients than in HV patients. EBV DNA loads in whole blood and PBMCs showed strong correlation (Figure 1). EBV DNA loads in plasma were significantly higher in CAEBV patients with active disease than in those with inactive disease (median: $10^{4.5}$ IU/mL vs. $10^{0.8}$ IU/mL, $P < 0.001$) (Figure 2). Diagnostic cut-off values for whole blood EBV DNA loads of CAEBV patients as compared with those of infectious mononucleosis was $10^{4.2}$ (= 15,800) IU/mL (Figure 3).

Conclusion. Measuring EBV DNA loads in whole blood can be considered as initial evaluation for diagnosis of EBV T/NK-LPD. EBV DNA loads in plasma are more closely related to disease activity of CAEBV than EBV DNA loads in whole blood and PBMCs.

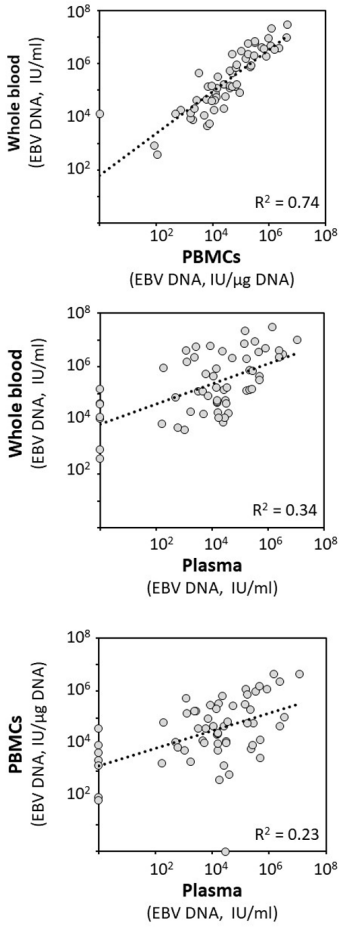

Fig. 1