2634. Human Metapneumovirus in a Children's Hospital: It Should Get More Attention

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Session: 271. Pediatric Respiratory Viral Infections

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Background: Viral respiratory infections are a major cause of hospitalization and intensive care unit (ICU) admission to children's hospitals. Rates of respiratory syncytial virus (RSV) and influenza are closely tracked due to their known morbidity. We had previously observed over one season that human metapneumovirus (hMPV)-infected children have high rates of hospitalizations and ICU admissions, particularly those with chronic lung disease (CLD). We expanded our data to include an additional 5 seasons to compare rates of hospitalizations and hospital-acquired infections (HAIs) due to hMPV, RSV and influenza.

Methods: During the 2014–2019 winter viral seasons, hMPV, RSV and influenza infections were tracked through both PCR testing (Biofire Respiratory Panel) and DFA testing (D3 Ultra DFA Respiratory Virus Screening & ID Kit; Diagnostic Hybrids). For hMPV admissions, rates of hospitalizations, ICU admissions, HAIs and mortalities were assessed and compared with RSV and influenza admissions. Retrospective data were used to study patients infected with hMPV.

Results: During the winter seasons of 2014–2019, the rates of hospitalization due to hMPV were significantly higher than both RSV and influenza (Figure 1). ICU admissions and HAIs for hMPV were similar to RSV and influenza (Figures 2 and 3). There were 9 deaths over this time period; 5 due to RSV, 3 due to influenza and 1 due to hMPV. The proportion of deaths due to hMPV compared with RSV and influenza was similar (P = 0.54, 0.89, respectively). Of the 315 total admissions with hMPV, 43 (13.7%) had CLD and 13 (4.1%) were tracheostomy dependent. Among 67 hMPV ICU admissions from 2014–2019, 56 (84%) had an underlying medical diagnosis, 25 (37%) had CLD, 13 (19%) had tracheostomies, and 17 (25%) required mechanical ventilation. The average age of hMPV infected children in our ICU is 4 years 1 month.

Conclusion: Our large descriptive study of hMPV-infected children over 6 seasons showed higher rates of hospitalization compared with RSV and influenza, similar ICU and HAI rates, and similar rates of mortality. ICU admitted children often had associated co-morbidities, including CLD. Further studies for focused disease surveillance and potential vaccine development for high-risk children are needed.

Figure 1. Winter Viral Patients Requiring Admission

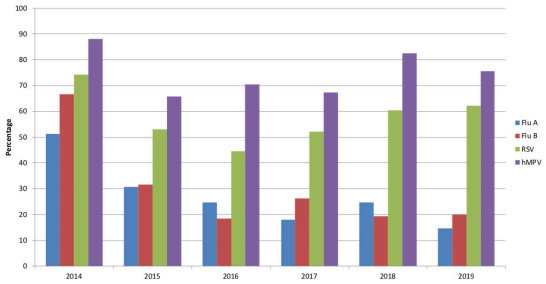


Figure 2. Winter Viral Patients Admitted to PICU/CVICU/NICU

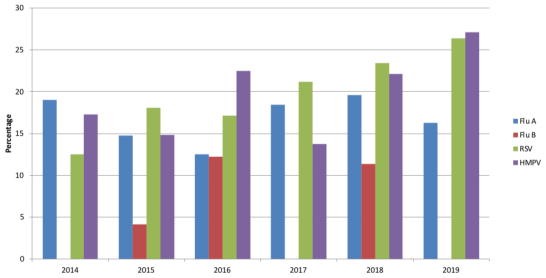
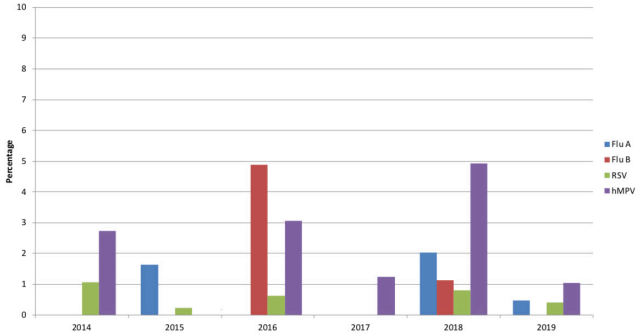


Figure 3. Winter Viral Patients with a Healthcare Associated Infection



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

2635. Outbreak of Enterovirus D68 Among Children in Japan and Simultaneous Circulation of Clade B3 in Europe

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Background: Enterovirus D68 (EV-D68) is a re-emerging, high-morbidity pathogen that causes severe respiratory infection and acute flaccid myelitis in children. EV-D68 is phylogenetically divided into 4 major groups—clade A through D—and each clade has subclades defined by genetic variant. Outbreaks of all strains have been reported in more than 10 countries. However, no study has compared the viral genomic characteristics of EV-D68 in contemporaneous outbreaks in different countries.

Methods: An outbreak of EV-D68 in children younger than 15 years occurred in Niigata, Japan, from October through November 2018. The patients were admitted to hospital with respiratory distress and wheezing episodes. RNA extracted from nasopharyngeal samples was tested by EV-D68-specific PCR. Clade was determined by semi-nested PCR analysis of the VP1 region, and the phylogenetic tree of the VP1 sequence was constructed. To clarify viral genomic characteristics, we compared the clade to those of outbreaks occurring during 2014–2018 in other countries.

Results: EV-D68 testing of 47 patients yielded positive results for 22 (47%) (median age 4.6 years; IQR, 2.9–6.7), and 15 (69%) had a past medical history of allergic disease. No patient developed acute flaccid myelitis. The VP1 sequences from all isolates belonged to clade B3, the same clade detected during the 2015 outbreak in Japan (figure). Interestingly, EV-D68 outbreaks were reported in France and Italy (clades D1/B3 and D1, respectively) during this period. Although the EV-D68 clades responsible for outbreaks in 2014 differed by region, clade B3 is now the dominant clade and has caused concurrent EV-D68 outbreaks in children since 2015 (table).

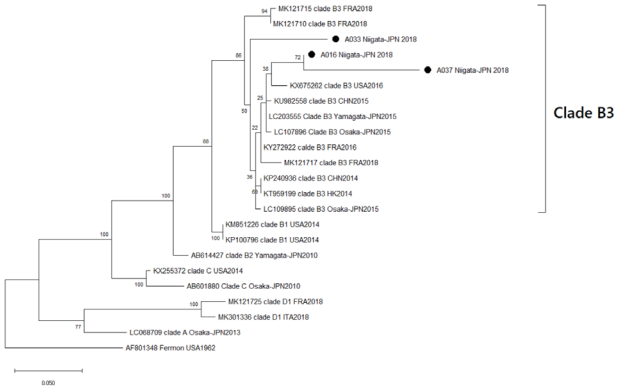
Conclusion: In 2018, an EV-D68 clade B3 outbreak occurred among children in Niigata, Japan. This clade is now dominant and periodically circulates around the world. Because EV-D68 can cause simultaneous outbreaks worldwide and is associated with high morbidity, detailed real-time epidemiological surveillance of EV-D68 is warranted.

Country/Region	2014	2015	2016	2017	2018
United States	A, B1, B2		B3		
Canada	B2				
France	B1, B2		B3		D1, B3
Italy			B3		D1
Sweden			B3		
United Kingdom			B3		
Netherlands			B3		
Hong Kong	B3				
Taiwan	B3				
Japan		B3			B3

Table: Reported Enterovirus D68 clades in outbreaks during 2014-2018, by country/region

Figure. Phylogenetic tree of enterovirus D68 clades, including the current clade B3 outbreaks in Niigata, Japan, in 2018.

●: strains of current outbreak



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