1473. Enterovirus (EV)-D68 in Pediatric Patients with Respiratory Tract Infection: the Circulation of new B3 Clade in Italy
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Background. EV-D68 is an emerging infectious agent that has been found associated with both mild and severe respiratory diseases and neurological clinical manifestations. Four clades with a number of subclades that can circulate or co-circulate during different periods have been identified. However, molecular evolution of EV-D68 is not known as it is the possible association between specific genetic variants and the development of severe cases. To solve these problems, genetics of strains identified during an outbreak of EV-D68 infection that occurred in Italy during the period March–October 2016 were studied.
Methods. Nasopharyngeal samples obtained from children admitted to the Emergency Room for respiratory infection were tested with a previously validated specific real-time PCR for detection and quantification of EV-D68. Phylogenetic analysis (PhA) of the virus performed sequencing the major capsid protein (VP1). Moreover, tests for detection of selective pressure were carried out.
Results. Respiratory samples of 390 children were tested. Twenty-two patients (5.6%; median age, 47 months) were infected by EV-D68. All but three had a lower respiratory tract infection and not none of these hospitalized. A consistent reduction of SaO2 level was evidenced at admission. All the strains belonged to the EV-D68 subclade B3. No evidence of increased clinical severity associated with specific molecular signatures of VP1 sequence or viral load was shown. B3 strains had 92.3% and 94.7% nucleotide identity with B3 clades identified in other countries where a number of very severe cases was diagnosed. No sign of selective pressure was found.
Conclusion. EV-D68 subclade B3 was the only cause of the EV-D68 diseases diagnosed in Italy during 2016. The same subclade was found in Northern Europe, China, and USA in the same period. This suggests that the outbreaks had a common origin and EV-D68 B3 has become the preeminent EV-D68 strain causing disease worldwide. No specific characteristic of EV-D68 VP1 has been found associated with disease characteristics, in contrast with what has been evidenced by other studies. Further studies on full-genome sequencing in larger cohorts of patients are needed.
Disclosures. All authors: No reported disclosures.

1474. Asymptomatic Adults and Children Can Transmit Human Parechoviruses and Enteroviruses to Neonates and Young Infants
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Background. Human parechovirus (HPeV) type 3 and enteroviruses (EVs) are the common viruses causing severe diseases in neonates and young infants. Given no specific therapy is currently available and the morbidity and mortality of the diseases are high, understanding the detailed transmission routes is critical for the prevention.
Methods. This prospective study evaluated viral etiologies of neonates and young infants < 4 months suspecting sepsis and/or meningococcpelulitis in 2016 in Niigata, Japan. DNA and RNA from serum/cerebrospinal fluid (CSF) were analyzed for HPeVs, EVs, and/or herpes simplex virus using real-time PCR. Bacterial infection was excluded based on blood/CSF culture results and their clinical course of the patients. To investigate the source of infection, we collected stool samples from available family members of the patients regardless of their symptoms. The stool samples were checked for each virus and if they were positive, the VP1 region for HPeVs and VP1/VP4-2 region for EVs, were determined and typed. Furthermore, clinical information on symptoms of family members of HPeVs- and EVs-infected neonates and young infants. Careful hand hygiene and other standard precaution may contribute to decrease the risk of the transmission during the outbreak of HPeV3 and EVs.
Disclosures. All authors: No reported disclosures.

1475. Characterization of Circulating RSV Strains Among Patients In The Outsmart RSV Program During the 2015–16 Winter Viral Season in the United States
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Background. Respiratory syncytial virus (RSV) is an established cause of serious lower respiratory tract disease in infants and young children. To better describe currently circulating strains, monitor their evolution and characterize the patient populations, genotyping of RSV has been performed since 2010.
Methods. OUTSMART included 14 labs in 4 US regions and Puerto Rico that provided RSV-positive samples and matching demographic data during Dec 2015 to Mar 2016 for subtyping and descriptive analyses. To gauge the representativeness of the OUTSMART patient sample, results were compared with the Nationwide Emergency Department Sample (NEDS) and the National Inpatient Sample (NIS).
Results. Participating labs reported 10,304 RSV-positive samples (10.9%) out of 94,710 tested, of which 525 samples were submitted for further analyses. The majority of samples came from children ≤ 2 years: 1–3 months (17.4%), 4–6 months (13.7%), 7–12 months (21.9%), and 1–2 years (17.5%). The distribution of samples from males (53.0%) and females (47.0%) were similar. Of those with determined RSV subtype (n = 392; 74.7%), 62.8% were subtype A and 38.3% were subtype B. Of the two co-circulating subtypes, A was more prevalent through age 5 while B was more common in those ages 6+.
Hospitalizations were much more common among younger age groups from 0–4 months (25.6%) compared to 5–11 months (11.9%) and 12–17 months (9.2%). The majority of RSV-positive samples were collected February–March. For all databases, the largest disease burden was among those < 1 year old (OUTSMART: 45.1%, NEDS 62.3%, NIS 62.7%), followed by the 1–2 year age group (OUTSMART: 27.6%, NEDS 26.9%, NIS 21.8%). The databases were also similar by gender (% male–OUTSMART: 53.0%, NEDS 53.9%, NIS 53.9%).
Conclusion. The OUTSMART program characterizes circulating RSV strains and monitors their temporal and geographic evolution in the US to inform the development of anti-RSV monoclonal antibodies and vaccines.
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1476. Respiratory Syncytial Virus-Associated Hospitalizations in Young Children in the United States, 2015–2016
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Background. Respiratory syncytial virus (RSV) is a major cause of severe acute respiratory illness (ARI) among young children. With several vaccines and immunoprophylaxis agents for RSV currently in development, updated estimates of severe RSV disease in young children in the United States (US) are needed.

Methods. Prospective active surveillance for hospitalized ARI was conducted from 11/3/2015 to 6/30/2016 among <5 years of age at seven pediatric health sites participating in the New Vaccine Surveillance Network. Demographic and clinical information for enrolled subjects were gathered through parent interviews and medical chart reviews. Mid-turbinate nasal and throat flocked swabs (combined for testing when available) were handled and tested for RSV as per site’s protocol (when pertinent) were collected for respiratory pathogen testing. Specimens were tested for RSV using molecular diagnostic assays at each site.

Results. In preliminary data analyses, 2,948 hospitalized children with a median age of 11 months were enrolled during the study period, of whom 1,030 (35%) tested positive for RSV. Most RSV-positive infections occurred in children <2 years of age (87%; n = 893) with 340 (33%) RSV-positive children aged 0–2 months, 148 (18%) aged 3–5 months, 174 (17%) aged 6–11 months, and 195 (19%) aged 12–23 months. The majority of RSV-positive children (75%; n = 776) had no chart-documented comorbid conditions. Among 893 RSV-positive children <2 years of age, 161 (18%) reported a history of preterm birth, with 99 (11%) reporting birth at 34–36 weeks gestational age (WGA), 33 (4%) at 30–33 WGA, 20 (2%) at <30 WGA, and 9 (1%) with no further gestational age information available. Among all RSV-positive subjects, the median length of stay was 2 days; 708 (69%) received supplemental oxygen during hospitalization, 222 (22%) were admitted to an intensive care unit, and 28 (3%) required mechanical ventilation.

Conclusion. During the 2015–16 season, RSV was associated with one-third of ARI hospitalizations in young children, the majority of which occurred in children aged <24 months. Most RSV-positive children were otherwise healthy, and nearly one-fifth of those <2 years of age reported a history of preterm birth. RSV continues to be a major cause of morbidity among young children in the US.

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1477. Molecular Epidemiology of Respiratory Syncytial Virus A G-Protein for 9 Years and Emergence of ON1 Genotype Having 72 Nucleotide Duplication in Korea

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Background. Respiratory syncytial virus (RSV) is a major pathogen causing seasonal epidemics of lower respiratory tract infection in young children. The attachment (G) glycoprotein is a major virulence factor and a target of human neutralizing antibodies. The G protein shows the evidence of changes in its amino acid over time, making its study important in vaccine development strategies. We aimed to explore the molecular epidemiology of G protein of RSV in Korea.

Methods. One hundred and thirty-six RSV strains were obtained from children who were hospitalized at Seoul National University Children’s Hospital, from October 2005 to September 2014. The frozen stock viruses were propagated in HEP-2 cells and the infected cell lysates were collected when cytopathic effects were apparent. The attachment (G) protein was then purified, and further analysis was performed using cDNA constructed from viral RNA and primers from previous studies. Phylogenetic and putative antigenicity patterns were performed using CLC Main Workbench ver. 6.6.5 software (CLC bio, Aarhus, Denmark).

Results. The entire G genes were sequenced from all 136 RSV A strains: most (n = 99, 72.8%) strains had 895 nucleotide-span, but the others (n = 45, 37.2%) had 72 nucleotide (nt) duplication, which are well-known ON1 genotype. On phylogenetic grouping, three different genotypes 1–3 except ON1 were additionally defined. During the 2005–2006 season, the prevalence of genotypes 1, 2, and 3 were comparable (36.4%, 27.3%, and 36.4%, respectively), but genotype 1 became predominant (69.2%) in the 2006–2007 season. The genotype 3 increased since 2007–2008 (80.8%) and was identified exclusively during three consecutive seasons thereafter (2009–2011). In the 2011–2012 season, the first ON1 strain was identified in Korea, and the prevalence increased to 91.7% in the 2012–2013 season, then to 100% thereafter (2013–2015). In spite of 72-nt duplication, the putative antigenicity patterns of G protein were comparable between ON1 genotype and the others.

Conclusion. Our findings highlight the genotype change of circulating RSV A in 3–4 years interval, which might explain the reason for annual local epidemics of RSV A. Also in Korea, RSV A ON1 genotype increased since 2011 and was circulating exclusively since 2013.

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1478. Hospitalizations in the First Year of Life for Infants with Respiratory Syncytial Virus and Unspecified Bronchiolitis in a Population-Based Cohort

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Background. Respiratory syncytial virus (RSV) can cause serious disease in infants, particularly those with high-risk (HR) conditions or born preterm. In the past 2 decades, interventions to prevent serious RSV disease have been implemented for these infants. This study assessed infant hospitalization trends for RSV and unspecified bronchiolitis (UB) by HR status and gestational age (GA) during the first year of life in a population-based cohort.

Methods. California hospital discharge data from the Office of Statewide Hospital Planning and Development linked to vital statistics for 1997–2011 was used to identify infants 17–47 weeks GA. Trends of RSV- and UB-coded hospital admissions during the first year of life were compared by GA category and by HR status (ICD-9 codes for chronic lung disease, congenital heart disease, and other conditions increasing risk of respiratory infection).

Results. Of 7,406,370 infants discharged after birth, 161,094 (2.2%) had HR status. In the HR cohort, 82,540 non-birth hospitalizations occurred, with 5,765 (7.0%) for RSV and 5,166 (6.3%) for UB. In non-HR infants, 737,326 non-birth hospitalizations occurred, with 99,378 (13.5%) for RSV and 72,442 (9.8%) for UB. For HR infants, RSV hospitalizations decreased from 1997 to 2010 (Figure 1); the highest admission rates occurred in infants <3 mos. For non-HR infants overall, RSV hospitalization rates remained similar throughout the study period. UB hospitalization rates for HR infants were stable and decreased for non-HR infants. For non-HR preterm infants, RSV hospitalizations for all GA categories decreased, with greater decreases in those with earlier GA (Figure 2), whereas UB hospitalization rates were relatively stable (Figure 3).

Conclusion. RSV and UB hospitalizations are common in the first year of life. During the study period, admissions for RSV in non-HR infants and for UB in HR and non-HR infants remained stable from 1997 to 2010; however, admissions for RSV in HR and preterm infants decreased significantly, possibly due to prevention efforts targeting this population.

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S460 • OFID 2017:4 (Suppl 1) • Poster Abstracts