Results: Of 192 patients, 39 were Native American and 153 were non-native American. We found no differences in gestational age, gender or age (median age was 5 and 7 months, respectively) between groups. We found no difference in rates of vaccination, upper respiratory symptoms, cough, wheezing, crackles, increased work of breathing or peripheral white blood cell count at presentation. In addition, we found no differences in antibacterial use or length of antimicrobial therapy during hospitalization. Native American children had a statistically significant higher length of hospitalization ($P = 0.01$) as well as days of oxygen supplementation (mean 4.9 vs. 3 days; $P = 0.006$) compared with non-native Americans. Furthermore, Native American children had a significantly higher percentage of PICU admissions (28% vs. 10.4%; $P = 0.008$) as well as intubation rate (26% vs. 8%; $P = 0.04$) compared with non-native Americans.

Conclusion: Native American children had increased length of hospitalization associated with severe illness including longer oxygen supplementation, higher PICU admission rate and need for mechanical ventilatory support.

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

2616. Genetic Susceptibility to Life-Threatening Respiratory Syncytial Virus Infection in Previously Healthy Infants

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Session: 270. Pediatric Respiratory Infections

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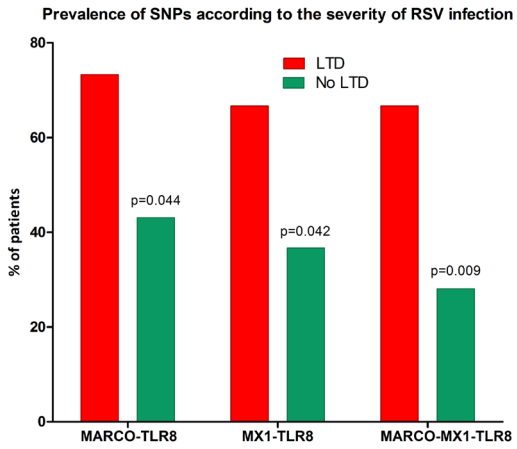
Background: Differential expression of selected immunity genes may have a role in susceptibility to Respiratory Syncytial Virus (RSV). There are few data about some candidate gene single nucleotide polymorphisms (SNPs) associated with the severity of respiratory infections (e.g., Toll-like receptor 4 [TLR4], Toll-like receptor 8 [TLR8], macrophage receptor with colagenous structure [MARCO], myxovirus resistance 1 [MX1]). The aims of this study were to detect the presence of SNPs in selected genes of previously healthy infants infected with RSV, to assess viral load (VL) and to analyze their relationship with life-threatening disease (LTD)

Methods: Prospective cohort study including previously healthy full-term infants < 12 months, hospitalized with a first RSV infection during 2017–2018. RSV diagnosis, virus quantification and genotyping for SNPs (TLR4 rs4986790, TLR4 rs4986791, MARCO rs1318645, MX1 rs469390, TLR8 rs3761624) were performed by qRT–PCR in nasopharyngeal aspirates obtained on admission. Patients with LTD were those admitted to the intensive care unit needing mechanical or non invasive ventilation

Results: 75 patients, mean age 3.9 months (±2.8), 41 (54.7%) male. Fifteen developed LTD. Infants who were homozygous (−/−) or heterozygous (+/−) for MX1rs469390 and TLR8rs3761624 or MARCOrs1318645 and TLR8rs3761624 had significantly more risk of developing LTD (OR 3.45, $P = 0.042$; OR 3.63, $P = 0.048$, respectively). Multivariable logistic regression analysis showed that concurrent MARCOrs1318645, MX1rs469390 and TLR8rs3761624 SNPs increased the risk of LTD (aOR 4.7, $P = 0.018$), fig 1. These SNPs also associated with prolonged length of stay (LOS) ($P = 0.026$) and > 7 days of hypoxemia ($P = 0.031$). No differences were seen in VL of patients with LTD compared with those with better outcome ($P = 0.737$). No differences in VL were seen in patients with SNPs. VL did not correlate with LOS or days of hypoxemia. No other socioeconomic, pregnancy or infant variables associated with LTD

Conclusion: To the best of our knowledge, this is the first study assessing the presence of concurrent SNPs and their association with life-threatening disease in previously healthy infants with RSV infection. These findings provide evidence on the importance of the host and its immune response for the severity of RSV infection.



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

2617. Increased Nasopharyngeal Pneumococcal Density During Asymptomatic Respiratory Virus Infection Is Associated with Subsequent Development of Acute Respiratory Illness

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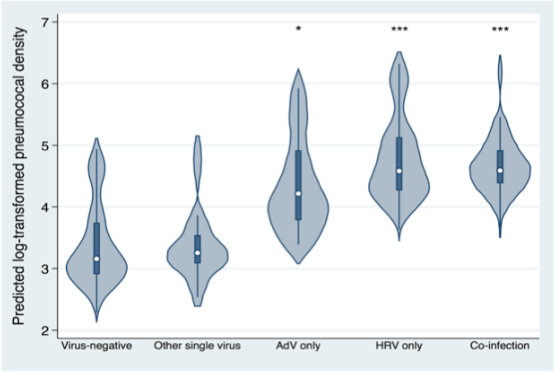
Background: Increased density of nasopharyngeal (NP) pneumococcal colonization has been associated with invasive pneumococcal disease in children. However, factors that lead to increased pneumococcal density are poorly understood. We sought to determine whether viral detection during asymptomatic periods in young children was associated with increased NP pneumococcal density and the subsequent development of acute respiratory illness (ARI).

Methods: Using NP samples obtained during asymptomatic periods from children less than 3 years of age in the rural Peruvian Andes, we determined NP pneumococcal colonization density by quantitative polymerase chain reaction (qPCR) and identified respiratory viruses by RT–PCR. We examined the association between viral detection and pneumococcal density adjusting for relevant covariates using a multivariable quantile mixed effects regression model. We also assessed the association of pneumococcal density during asymptomatic periods in these children on the time to the next ARI using survival analysis.

Results: During asymptomatic periods, the presence of NP pneumococcal colonization was more common when respiratory viruses were detected. In addition, in the multivariable model, $\log_{10}$-transformed pneumococcal densities were significantly higher during asymptomatic periods when viruses were detected [median 4.52 (4.14, 5.01) $P < 0.001$], specifically human rhinovirus (HRV) [median 4.58 (4.27, 5.12), $P < 0.001$] and adenovirus (AdV) [median 4.21 (3.79, 4.91), $P = 0.014$], compared with when no virus was detected [median 3.16 (2.92, 3.73), Figure 1]. Increased pneumococcal density was also significantly associated with a higher rate of subsequent ARI (p = 0.008, Figure 2).

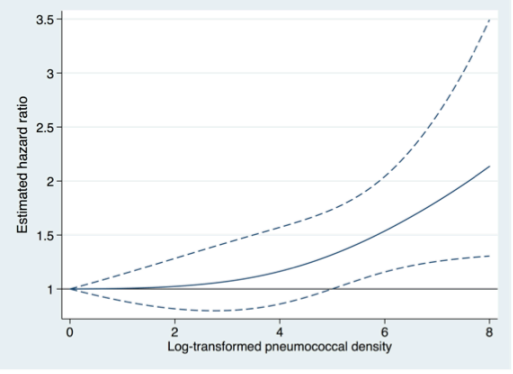
Conclusion: Among young children, detection of respiratory viruses during asymptomatic periods was associated with increased pneumococcal colonization density, which, in turn, was associated with higher rate of subsequent ARI.

Figure 1. Predicted $\log_{10}$-transformed colonization densities by detection of specific viruses among children <3 years



*Predicted densities were estimated from the final multivariable linear quantile mixed effects model. Circles indicate median densities, bars represent interquartile range (IQR), lines extend through the upper and lower adjacent values, and the density plot width indicates the predicted frequency of observations. Asterisks (*) indicate significantly increased predicted densities relative to the reference group (virus-negative), with p<0.05 considered statistically significant (***: p<0.001, *: p<0.05).*

Figure 2. Association between asymptomatic pneumococcal densities and risk of subsequent ARI



Estimated hazard ratios correspond to comparisons of increasing log-transformed pneumococcal density relative to the lowest detectable densities (p=0.013). Estimates were obtained from a frailty model that adjusted for age, sex, month, prior antibiotic exposure, viral detection, and PCV vaccination status. Pneumococcal densities were modeled using restricted cubic splines to allow examination of non-linear associations.

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