Nasal microbiota differences in young infants are associated with early childhood irritability
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Background. The etiology and pathophysiology of childhood mental health are poorly understood. Early childhood irritability is a transdiagnostic marker that portends significant risk for subsequent mental health problems. Robust evidence demonstrates irritability can be quantified early in infancy. The early life microbiome is implicated in defining trajectories of intraspecies and interspecies development. In contrast to the gut microbiome, however, a relationship between the infant nasal microbiome and early childhood irritability remains undefined. We sought to investigate associations between the nasal microbiota of infants <60 days of age and early childhood irritability.

Methods. This control study included infants with archived respiratory nasal samples collected for routine clinical care at ≤60 days of age from an emergency department visit (1/2016-5/2019). Parents completed an online survey when children were 14-42 months of age that included questions about medical history, development, and irritability (Multidimensional Assessment of Preschool Disturbive Behavior, MAP-DB). The upper quartile of the MAP-DB Temper Loss Score was classified as high dysregulation. Additional clinical data were collected from the electronic health record. DNA extracted from archived nasal swabs were sequenced to 150 bp using the Illumina MiSeq for 25 samples. Fifty-two taxa that were abundant (>0.01) in ≥50% of the samples were included for analysis.

Results. Seventy-two children were initially included, with 16 categorized as high dysregulation. The median age at nasal sample collection was 30 days (IQR 14-44), and age at parent survey was 28 months (IQR 19-31). Fifty-weight percent of the cohort was white, 6% Black, 6% Asian, 20% other, and 25% identified as Lantine ethnicity. The infants were 49% female sex, 77% were born by vaginal delivery, and 43% had a virus identified at time of nasal sample. After removal of extraction/PCR contaminants, taxa present only at higher levels in media, and samples with <80 sequences, the final microbiota comparison dataset was n=33 children, 7 with high dysregulation. Alpha-diversity (Shannon index) was lower in the high dysregulation group (p=0.0031) pre-background taxa removal, p=0.1288 post-correction, Figure 1A-B). Of the 18 taxa that were compared, Haemophilus, Streptococcus, Staphylococcus, and Gardnerella were highly abundant in children in the high dysregulation group in false discovery rate corrected significance q<0.005, Figure 1C). Parasutterella was more abundant in a subset of infants that were classed as high dysregulation (p=0.025).

Conclusion. Differences in the nasal microbiota of infants, decreased diversity and abundance of certain respiratory bacteria, are associated with early childhood irritability, a marker of mental health risk. Further study may provide mechanistic insights and potentially guide new risk assessment or treatment options.

Resolution of thrombocytopenia during treatment for symptomatic congenital cytomegalovirus disease
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Background. Congenital cytomegalovirus (cCMV) is the most common congenital viral infection in the United States (4.5 per 1000 live births) and is the leading non-genetic cause of sensorineural hearing loss and developmental disabilities in children worldwide. However, reliable estimates of time to resolution for manifestations of cCMV disease have not been fully elucidated. A better understanding of the resolution of laboratory abnormalities for cCMV is needed to guide decisions about frequency of placental antibody testing and potential benefits of prophylactic antiviral therapy.

Methods. Data from 243 infants with symptomatic cCMV were retrospectively analyzed from four studies conducted by the NIH-funded Collaborative Antiviral Study Group over the years 1989-2011. Individuals were compared based on baseline titers of CMV antibody in the maternal serum following birth. The primary end points of interest. It then can be transfected into other cells in the body. Blood

Results. Predicted curves showed that the interaction between antiviral therapy and platelet value over time was found to be significant (p=0.0106) for individuals with normal baseline platelet counts (Grade 0, defined as ≥ 125,000). For individuals with Grades 1-4 thrombocytopenia at baseline, probability curves showed that both baseline platelet value, utilizing Division of AIDS Toxicity Scale categorization, and treatment received. Kinetics of the trend in platelets over time were compared between groups with Kaplan-Meier plots and binomial analyses of abnormal vs. normal. All analyses were conducted over the 6-week (45 day) time period.

Conclusion. Significant thrombocytopenia during treatment for symptomatic congenital cytomegalovirus disease
Shelby Walcott, University of Alabama, Birmingham

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