

Association Between Neonatal Gut Microbiome and Infant Wheeze

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Background: Asthma is a chronic respiratory disease that affects 10% of children. Infant wheeze at 1 year and the subsequent development of asthma in early childhood has been associated with infant gut dysbiosis. However, little is known about the relationship between neonatal gut microbiome and the development of wheeze during the first 18 months of life. We hypothesize that the gut microbiome at birth and throughout the first 18 months of life is associated with infant wheeze.

Project Methods: Stool samples were collected from infants at birth, 1, 3, and 12 months of age. The Illumina Miseq system was used to sequence the bacterial V4 region of 16S-rRNA gene. Mothur software was used for analysis. Statistical analysis was used to measure stool shannon diversity and evenness as they relate to timepoint and wheeze vs no wheeze groups.

Results: The study population consisted of 28 infants (18 males and 10 females). 11% of participants reported they had been diagnosed with wheeze by a physician (n=3). Statistical analysis of shannon diversity showed no differences in the stool between participants who wheeze vs those who do not wheeze (p=0.78). No difference in stool evenness was detected between participants who reported wheeze vs no wheeze (p=0.71). However, this analysis includes multiple timepoints. Analysis of stool shannon diversity across timepoints did show a significant difference in stool microbiome (p=0.01).

Conclusion: No differences in stool microbiome were found between infants who do not wheeze and those who do. Further studies can investigate a greater number of samples at each timepoint and relate these to objective measures such as pulmonary function tests. Understanding the association between infant gut dysbiosis and wheeze could have implications for predicting development of asthma in early childhood and potentially lead to targeted interventions.