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MEETING ABSTRACT Open Access

The early life gut microbiota and atopic disease

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Background

Asthma is the most prevalent of all childhood diseases and accounts for the majority of hospitalizations and school absences in children [1]. Current mouse model research has identified the early life gut microbiota as a potential therapeutic target for the prevention of asthma and atopic diseases [2-4]. We hypothesize that the early life gut microbiota could play a similar preventative role against atopic disease development in humans.

Methods

1262 children enrolled in the Canadian Healthy Infant Longitudinal Development (CHILD) Study with complete skin prick test and wheeze data at one year were grouped into four clinically relevant phenotypes: atopy + wheeze, atopy only, wheeze only, and control. Bacterial 16S rDNA from 3-month and 1-year stool samples of 319 children in these four phenotypes was extracted, amplified, and subjected to high throughput Illumina sequencing. Quantitative polymerase chain reaction (qPCR) and short chain fatty acid (SCFA) analysis were also conducted on 44 children in the two extreme phenotypes (atopy + wheeze vs. control).

Results

16S sequence analysis of our sample cohort (319 subjects) identified bacterial populations that differed in abundance in the atopy + wheeze group at 3-months of age but not at 1-year of age. Additionally, significant changes in the abundance of certain bacterial genera were found in the atopy + wheeze group when compared to controls by qPCR at 3-months of age only. Changes in stool short chain fatty acid production between the atopy + wheeze group and the control group were also observed at 3-months of age only.

Conclusions

Shifts in the relative abundance of certain gut bacterial populations and differences in the levels of stool SCFAs before 3-months of age are associated with atopy and wheeze at one year of age.

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