The association between faecal microbiota and asthma or wheezing: A systematic review and meta-analysis

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Background: Studies have shown inconsistent associations between the composition of early life gut microbiota and allergies. The primary objective of this systematic review and meta-analysis was to investigate associations of components of the faecal microbiota with any individuals experiencing asthma or wheezing. Secondary objectives were to summarise factors associated with asthma or wheezing which may also influence faecal microbiota composition.

Methods & Materials: A literature search for published articles in peer-reviewed journals was performed up to 7 August 2013 in Medline, Scopus, Academic Search Premier, Africa-Wide Information, CINAHL, and Web of Science, using applicable and controlled vocabulary. Eligible studies—those reporting association between faecal microbiota and asthma or wheezing—were selected for inclusion by two independent reviewers after which a random-effects meta-analysis was conducted separately for asthma and wheezing outcomes using qualitative data only.

Results: Fourteen eligible studies were identified, of which seven met the inclusion criteria for the meta-analysis. There were no eligible adult studies. The meta-analysis results showed that Clostridium difficile was significantly associated with increased odds of wheezing (Odds Ratio (OR) = 1.50; 95% confidence interval (CI) = 1.19, 1.89). In addition, C. difficile was associated with increased odds of asthma (OR = 2.06; 95% CI = 1.16, 3.64), although a meta-analysis was not performed. Eligible studies reported that vaginal delivery and breastfeeding was significantly associated with changes in Clostridia and Bifidobacteria, respectively. A single study reported that factors significantly influencing both asthma and the composition of gut microbiota were mode and place of delivery.

Conclusion: These results confirm the likely role of C. difficile with childhood wheezing illness. Large-scale longitudinal birth cohort studies, implementing massively parallel sequencing of the 16S rRNA gene of faecal bacteria or culturomics, are needed to better determine the role of faecal microbial profiles in the development of asthma or wheezing illness. Quantitative analysis is essential in association studies seeing that the relative species abundance contributes to the overall composition of the gut microbiota and eventually to disease states.

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