



The Synergistic Impact of Atopy and Reduced Upper Airway Microbiome Biodiversity on Asthma Persistence in Early Childhood

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Introduction

Recent studies increasingly suggest that the airway microbiome plays a critical role in respiratory health and disease, including its potential influence on the development and persistence of asthma in children.

Aim

This study aimed to evaluate the clinical, immunological, and microbiological factors associated with asthma persistence from preschool to school age.

Material and methods

We enrolled 82 children aged 4-8 years with asthma, collecting nasopharyngeal swabs for microbiome analysis via next-generation sequencing (NGS) and nasal mucosa samples to measure mRNA expressions of predefined cytokines and innate lymphoid cells (ILCs). Of these, 74 children were observed over five years to assess asthma persistence.

Results

After five years, 23% (17 of 74) of the children continued to have asthma, while 77% (57 of 74) experienced remission. A multivariate logistic regression analysis revealed that asthma persistence was independently associated with atopy (OR=10.3, 95% CI: 2.1 to 51.1) and reduced biodiversity of the upper airway microbiome (OR=3.8, 95% CI: 1.1 to 13.3). Notably,





children with both atopy and reduced microbiome biodiversity showed higher nasal expression of IL-5.

Conclusions

Our findings indicate that reduced microbiome biodiversity, combined with atopy, increases the risk of asthma persistence and is associated with higher nasal IL-5 expression. This study highlights new potential targets for preventing persistent asthma in children.