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Nasopharyngeal Microbiota and Bronchial Asthma in Children (A Literature Review)

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Abstract: Asthma remains the most prevalent chronic condition in childhood. In recent years, substantial progress has been made in characterizing the microbial communities of the upper and lower airways, clarifying their relevance to pediatric asthma. Early investigations confirmed that both upper and lower airways harbor complex microbiomes and that disturbances in these communities are associated with pediatric asthma. Evidence suggests that the airway microbiome in infancy may predict subsequent asthma development and is modifiable by environmental exposures, including respiratory viral infections. Moreover, airway microbial composition has been linked to asthma severity, disease control, and frequency of exacerbations. Advances in multi-omics technologies have enabled deeper exploration of interactions between airway microbes and host immune responses in children with asthma. Current research increasingly focuses on translating these findings into preventive and therapeutic strategies. The airway microbiome represents a promising avenue for improving understanding of pediatric asthma, with implications for diagnosis, prognosis, and potential treatment approaches. Further studies are required to confirm these associations and integrate microbiome-based insights into clinical practice.

Keywords: airway microbiome; pediatric asthma; upper airway; lower airway; respiratory disease.

Asthma is the most common chronic disease in children, affecting millions worldwide and posing significant burdens on physical health, development, and quality of life. Growing evidence indicates that the airway microbiome plays a meaningful role in asthma pathogenesis. Studies increasingly suggest that airway microbial profiles may contribute to asthma diagnosis, help identify children at risk, and potentially inform therapeutic decisions.

This review summarizes current knowledge regarding the airway microbiome in pediatric asthma, emphasizing key discoveries related to upper and lower airway microbial communities and highlighting recent advances that have shaped the field.

The microbiome encompasses the collective microorganisms inhabiting a specific ecological niche, along with their genetic material and functional interactions. Disruption of this ecosystem, known as dysbiosis, is characterized by altered microbial diversity and imbalance between beneficial and potentially pathogenic organisms.

Historically, the lungs were believed to be sterile and were therefore excluded from early microbiome initiatives. However, modern sequencing technologies have demonstrated that the airways host diverse microbial populations. Techniques such as 16S rRNA sequencing and shotgun metagenomics have enabled detailed taxonomic and functional profiling beyond what was previously achievable through culture-based methods. Integration of omics-based approaches now allows investigation of microbial structure, metabolic activity, and host–microbe interactions.

Although much of the initial research focused on adults, studies examining airway microbiomes in children with asthma have expanded rapidly. Both upper and lower airways are involved in asthma pathophysiology, yet sampling of the lower airway is invasive and technically challenging in pediatric populations. Consequently, upper airway sampling has been more common, though increasing attention is being paid to understanding relationships between microbial communities across airway compartments.

Research in adults has demonstrated that the lower airway microbiome differs between individuals with asthma and healthy controls, as well as across varying levels of disease severity. Similar patterns have been observed in pediatric asthma. Early comparative studies revealed enrichment of Proteobacteria in the lower airways of children with asthma, while healthy controls exhibited higher proportions of Bacteroidetes. These findings provided early evidence of airway dysbiosis in pediatric asthma.

Subsequent investigations have confirmed that children with asthma possess distinct lower airway microbial profiles, though reported dominant taxa have varied across studies. Such variability likely reflects differences in study populations, disease severity, and sampling methodologies. Beyond bacterial communities, fungal components of the airway microbiome have also been implicated, with certain fungi observed more frequently in children with severe asthma.

Compared with the lower airway, the upper airway is more readily accessible, facilitating longitudinal and population-based studies. Research has shown that microbial communities of the upper and lower airways are related but not identical. Differences in nasal microbiota have been documented between children with asthma, those experiencing asthma exacerbations, and healthy peers.

Importantly, the upper airway microbiome appears to influence asthma risk from early life. Studies in asymptomatic infants have demonstrated that early colonization with specific bacterial taxa is associated with increased likelihood of recurrent wheeze and asthma later in childhood. These findings suggest that microbial patterns established during infancy may have long-term consequences for respiratory health.

Respiratory viral infections further modify these relationships. Interactions between viruses and specific bacterial communities in early life have been associated with increased asthma risk, highlighting the dynamic nature of the airway microbiome and its responsiveness to environmental exposures.

The relevance of the airway microbiome extends beyond asthma onset. In children with established asthma, microbial composition has been linked to disease control and exacerbation risk. Certain nasal microbiome profiles have been associated with increased susceptibility to respiratory illnesses and asthma exacerbations, while others appear to confer relative protection.

Experimental studies suggest that some airway bacteria may directly influence epithelial integrity and inflammatory signaling, providing potential mechanistic explanations for observed clinical associations. Together, these findings support an ongoing role for airway microbiota throughout the course of pediatric asthma.

Only a limited number of studies have examined upper and lower airway microbiomes simultaneously in children with asthma. Available data indicate notable differences in microbial

diversity and composition between these compartments. Upper airways often contain dominant "hub" genera that may contribute to microbial stability, whereas lower airway communities appear more heterogeneous.

These compartment-specific differences underscore the importance of studying the airway as an integrated system while recognizing that upper and lower regions may contribute distinctively to asthma pathophysiology.

Asthma is a multifactorial disease with complex underlying mechanisms. Omics-based technologies—including metagenomics, transcriptomics, and metabolomics—have enhanced understanding of how airway microbes interact with host immune and metabolic pathways.

Emerging studies integrating microbial data with host gene expression and metabolite profiles have revealed associations between specific bacterial taxa, immune mediators, and metabolic markers. These insights suggest that airway microbes may influence immune regulation and inflammatory responses relevant to asthma development and severity.

An important clinical question is how airway microbiome research can inform asthma management. Antibiotics are known to alter microbial communities, but recent evidence indicates that pre-existing airway microbiota may also shape treatment responses. Clinical trials have demonstrated that microbial richness and specific taxa can modify the effectiveness of antibiotic therapy in young children with asthma-like symptoms.

These findings highlight a bidirectional relationship between airway microbiota and treatment, suggesting that microbiome-informed approaches could help optimize therapeutic strategies in the future.

Research on the airway microbiome in pediatric asthma has advanced considerably, revealing important associations with disease development, severity, and treatment response. The airway microbiome is influenced by both environmental exposures and host factors, contributing to the heterogeneity observed across studies.

Continued application of advanced omics methodologies will enable more comprehensive investigation of microbiome-related mechanisms in pediatric asthma. Ultimately, translating these insights into clinical practice may improve risk stratification, guide therapy, and reduce the overall burden of asthma in children.

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