

Correspondence

Potential roles of disordered airway microbiota in patients with severe asthma

To the Editor:

We read with great interest the recent work of Huang et al¹ who investigated the relationships between airway microbiota and severe asthma in adult patients. Using 16S rRNA-based PhyloChip platform, the authors found that specific bronchial microbiota were associated with and might modulate inflammatory processes in patients with severe asthma and related phenotypes. Airway dysbiosis in patients with severe asthma appeared to differ from that observed in those with milder asthma in the setting of inhaled corticosteroid use.

As the gateway of the airway, the healthy nasopharynx harbors diverse microbes on balance that play a fundamental role in the well-being of their host, which is an accessible source of airway microbial communities.^{2,3} The perturbation of the nasopharyngeal microbiota may be a significant determinant of risk for bacterial invasion into the lower airway and may contribute directly and indirectly to the ensuing risk for the development of allergic diseases such as asthma.⁴ To evaluate the specific roles of airway microbiota, a harmonization and accuracy of methodologies for lower airway sample collection is required. However, the specific region sampled in the lower airway cannot avoid nasopharyngeal contamination even with protected bronchial brushings. The microbes in the airway microbiota may not represent the true colonizer of the lower airways. Nasopharyngeal sampling for microbiomic analysis may offer an additional insight into airway microbiota. In addition, the nasopharyngeal microbiota in patients with severe asthma taking regular inhaled corticosteroids might also be distinct from that found in healthy nasopharynx. The altered airway microbiota might be consistent with changes of nasopharyngeal microbiota. Therefore, it remains to be proven definitively whether the true colonizer of airway microbiota without any nasopharyngeal contamination is linked with severe asthma significantly.

It is noteworthy that the diversity and abundance of each habitat's signature microbes vary widely even among healthy subjects, with strong niche specialization both within and among individuals.⁵ For airway microbiomic analysis, alpha diversity (within subjects), beta diversity (among subjects), richness indices, and Good's coverage would provide meaningful information for changes in the overall structure and composition of airway microbiota. However, the diversity analysis seemed to be ignored in Huang et al's study.¹ Biodiversity of microbial communities within hosts may have a protective effect.⁶ Abrahamsson et al⁷ also demonstrated that low diversity of the gut microbiota in early infancy has been shown to be an important

risk factor for the development of allergy. In addition, phylogenetic beta diversity metrics such as unweighted UniFrac distance metrics analysis and principal coordinate analysis are useful for documenting shifts in the membership and/or structure of communities that may occur between sample categories or across environmental gradients. Good's coverage estimator can represent the depth of the sequencing analysis. Without detailed diversity analysis, it is not enough to evaluate the alterations in airway microbiota correctly and deeply.

This study provides new insight, but sample collection and microbiota evaluation were limited, and there was no assessment of nasopharyngeal microbiota in company with airway microbiota. Without understanding the true colonizer of the airway microbiota at a deeper level, it is not possible to decipher the roles of airway microbiota in the development of severe asthma.

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