

Correspondence

Compositional similarity between indoor and human sputum microbiome

To the Editor:

We read with great interest the article “Type 2-high asthma is associated with a specific indoor mycobiome and microbiome” by Vandenberg et al published online on September 12, 2020, by the *Journal of Allergy and Clinical Immunology*.¹ This is the first study to report the associations between the indoor microbiome exposure, human sputum microbiota, and the occurrence of severe asthma among patients, revealing many novel results. The study showed that patients with type 2-high severe asthma were exposed to increased bacterial and decreased fungal diversity in the indoor environment compared with patients with type 2-low severe asthma. Also, the indoor microbiome composition clustered according to the endotypes of patients with asthma, which suggests that environmental microbiome is associated or even potentially affect the endotypes of asthma. However, there is still an issue in the study that needs to be addressed.

One of the major findings in this study was that a high amount of fungal taxa was shared between the indoor environment and the sputa of patients with asthma during the exacerbation periods. The authors showed that more than 80% proportion of OTUs (operational taxonomic units) was commonly shared between the indoor and sputum microbiome (stable and exacerbation state in Fig 3, *E*, and exacerbation state in Fig 3, *F*). For each OTU, the proportion was counted as a percentage of the number of reads (relative abundance) in samples. It is unclear whether the authors set any cutoff or threshold in the analysis, but the proportion of common OTUs was too high, which contradicted the expectation and their own results in Fig 3, *C* and *D*. In the PCoA (principal coordinates analysis) analysis, the overall taxonomic composition of the indoor and respiratory microbiome was significantly different (Fig 3, *C* and *D*; Bray-Curtis distance > 0.5 between the 2 sample types), indicating high microbial compositional variation between indoor and respiratory microbiomes. The

discrepancy between Fig 3, *C/D*, and Fig 3, *E/F*, could confuse the readers and lead to the misinterpretation of the results. This is an important issue because a high similarity between indoor and respiratory microbiome may imply that environmental microorganisms can be transferred and colonized into the human respiratory tract, posing potential health effects to the occupants. A recent study by Gupta et al² reported a minor correlation between bed dust and airway microbiota compositions among infants, indicating limited microbial transfer and colonization between the 2 ecological niches.² In the study by Gupta et al, a co-occurrence network analysis was applied with false-discovery rate adjustment to assess the shared taxa, and we suggest the authors could also try this approach to identify potential microbial transfer between the indoor environment and human respiratory tract. The new evidence can facilitate a reliable inference of the potential health effects of the indoor microbiome for the occupants.

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