Down syndrome in patients with otitis media is associated with changes in the nasopharyngeal microbiome

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Introduction
Otitis media (OM) is inflammation of the middle ear (ME) that is usually due to infection. Globally, OM is a leading cause of hearing loss. OM is the most frequently diagnosed disease in young children and infants, and children with Down syndrome (DS) demonstrate even higher OM incidence rates. Furthermore, children with DS experience more severe OM with worse outcomes, often requiring multiple surgeries. Individuals with DS have increased susceptibility to infections, though no studies to date have investigated the bacterial profiles of DS children with OM. Greater knowledge of microbiota changes associated with DS will aid in pinpointing which mucosal and epithelial processes that regulate the microbiota are disrupted in DS.

Objectives
• Determine differences in nasopharyngeal (NP) microbiota (i.e., alpha- & beta-diversity) between OM patients with and without Down syndrome.
• Identify individual taxa differing in relative abundance between OM patients with and without Down syndrome in NP microbiota samples

Methods
Here, we examined the microbiotas of the NP of 11 children with DS using 16S rRNA gene sequencing data and analyzing diversity indices and relative abundance of individual taxa compared to 84 non-DS children with OM.

The NPs of OM patients with DS demonstrate increased alpha-diversity in microbiota richness and diversity when compared to non-DS OM patients (Figure 1). Beta-diversity was not significant after adjusting for age and batch (Figure 2; PERMANOVA p = 0.08). Upon examination of individual taxa, DS was associated with nominally significant increases in relative abundances of Atopobium, Abiotrophia, Anaerococcus, Enterobacteriaceae, Neisseriaceae, and Halomonas. In contrast, Nocardioides, Erysipelotrichiaceae, Peptostreptococcaceae, and Leptotrichiaceae were nominally significantly enriched in abundance in non-DS OM patients compared to those with DS (Figure 3). After FDR adjustment, Halomonas remains significantly associated with DS (FDR-adjusted p=3.30 × 10^-4).

Conclusions
• DS is associated with increased biodiversity in the NP of pediatric OM patients.
• DS is associated with significant increases in relative abundance of several taxa, particularly Halomonas.

These findings on the NP microbiota in children with DS might be related to increased predisposition to chronicity of OM, which in turn may be due to differences in immune regulation in the mucosa of patients with DS.

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