

The Comparison Study of Human Microbiome in Chronic Rhinosinusitis between Adults and Children

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Abstract : Introduction: The human microbiota is the aggregate of microorganisms, and the bacterial microbiome of the human digestive tract contributes to both health and disease. In health, bacteria are key components in the development of mucosal barrier function and in innate and adaptive immune responses, and they also work to suppress the establishment of pathogens. In human upper airway, the sinonasal microbiota might play an important role in chronic rhinosinusitis (CRS). The purpose of this study is to investigate the human upper airway microbiome in CRS patients and to compare the sinonasal microbiome of adults with children. Materials and methods: A total of 19 samples from 19 patients (Group1; 9 CRS in children, aged 5 to 14 years versus Group 2; 10 CRS in adults aged 21 to 59 years) were examined. Swabs were collected from the middle meatus and/or anterior ethmoid region under general anesthesia during endoscopic sinus surgery or tonsillectomy. After DNA extraction from swab samples, we analysed bacterial microbiome consortia using 16s rRNA gene sequencing approach (the Illumina MiSeq platform). Results: In this study, relatively abundance of the six bacterial phyla and tremendous genus and species found in substantial amounts in the individual sinus swab samples, include *Corynebacterium*, *Hemophilus*, *Moraxella*, and *Streptococcus* species. Anaerobes like *Fusobacterium* and *Bacteroides* were abundantly present in the children group, *Bacteroides* and *Propionibacterium* were present in adults group. In genus, *Haemophilus* was the most common CRS microbiome in children and *Corynebacterium* was the most common CRS microbiome in adults. Conclusions: Our results show the diversity of human upper airway microbiome, and the findings will suggest that CRS is a polymicrobial infection. The *Corynebacterium* and *Hemophilus* may live as commensals on mucosal surfaces of sinus in the upper respiratory tract. The further study will be needed for analysis of microbiome-human interactions in upper airway and CRS.

Keywords : microbiome, upper airway, chronic rhinosinusitis, adult and children

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