



Non-Differential Microbial Community Composition in Nasal Polyps from Asosmic vs. Normosmic CRSwNP Patients

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Abstract

Nasal polyposis is one of the most globally distributed life-disturbing disease. In patients of Chronic Rhinosinusitis with Nasal Polyposis (CRSwNP) presenting for surgical treatment, 90% suffered from anosmia/hyposmia. Wondering whether the microbiome in nasal polyps of CRSwNP patients related, we studied the microbial community composition in nasal polyps of dysosmic vs. normosmic CRSwNP patients by bacterial 16S rRNA gene sequencing. Results showed no strong separation of grouped samples, which suggested that microbial community composition in nasal polyps might not be an active direction for future study.

Keywords: Nasal polyps; Chronic Rhinosinusitis with Nasal Polyposis (CRSwNP); Microbial community composition; Anosmia; Hyposmia

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Short Communication

Nasal polyposis, characterized as noncancerous excrescence generated from hyperplasia of regional sinonasal mucosa, is one of the most globally distributed life-disturbing disease, even though undeadly. In patients of Chronic Rhinosinusitis with Nasal Polyposis (CRSwNP) presenting for surgical treatment, 90% suffered from anosmia/hyposmia, which substantially decreased their quality of life [1].

The pathogenesis of nasal polyps and underlying mechanisms of dysosmia in CRSwNP are still being investigated to date. Current researches on this issue are mainly focused on dysregulated inflammatory response, with several leading theories pointed out, including immunocyte/IgE/cytokine-driven inflammation, fungus mediated inflammatory process, and Staphylococcus aureus triggered massive inflammatory response [2]. However, a refined convincing explanation on why olfactory dysfunction frequently occurs in CRSwNP patients is highly required.

Considering that the sinonasal microbial community composition is critically involved in normal development of olfactory epithelia and olfactory function, we wondered whether the microbiome in nasal polyps of CRSwNP patients is related to the dysosmia onset [3]. As such, we studied the microbial community composition in nasal polyps of dysosmic vs. normosmic CRSwNP patients by bacterial 16S rRNA gene sequencing.

Six asosmic CRSwNP patients and 6 age-sex-balanced normosmic CRSwNP patients aged 20 to 50 years were selected with exclusion of recent antibiotics consumption, common cold or neurologic/psychiatric/systemic diseases with nasal symptoms. Written informed consent for all participants was obtained. The samples of nasal polyps were collected from subjects to extract DNA, followed by amplification of V1-V3 region of bacterial 16S rRNA gene for subsequent sequencing with Illumina MiSeq/Hiseq platform.

Normalized reads were evaluated for diversity and richness of microbial community composition with alpha diversity index using Shannon diversity (Figure 1A), Chao richness (Figure 1B) and Good's coverage analysis (Figure 1C). No difference was detected in these tests between asosmic and normosmic groups. Then beta diversity was determined through Principal Coordinates Analysis (PCoA) based on Bray-Curtis's dissimilarity (Figure 1D), showing no strong separation of grouped samples, which indicated no differential microbial community composition between two groups.

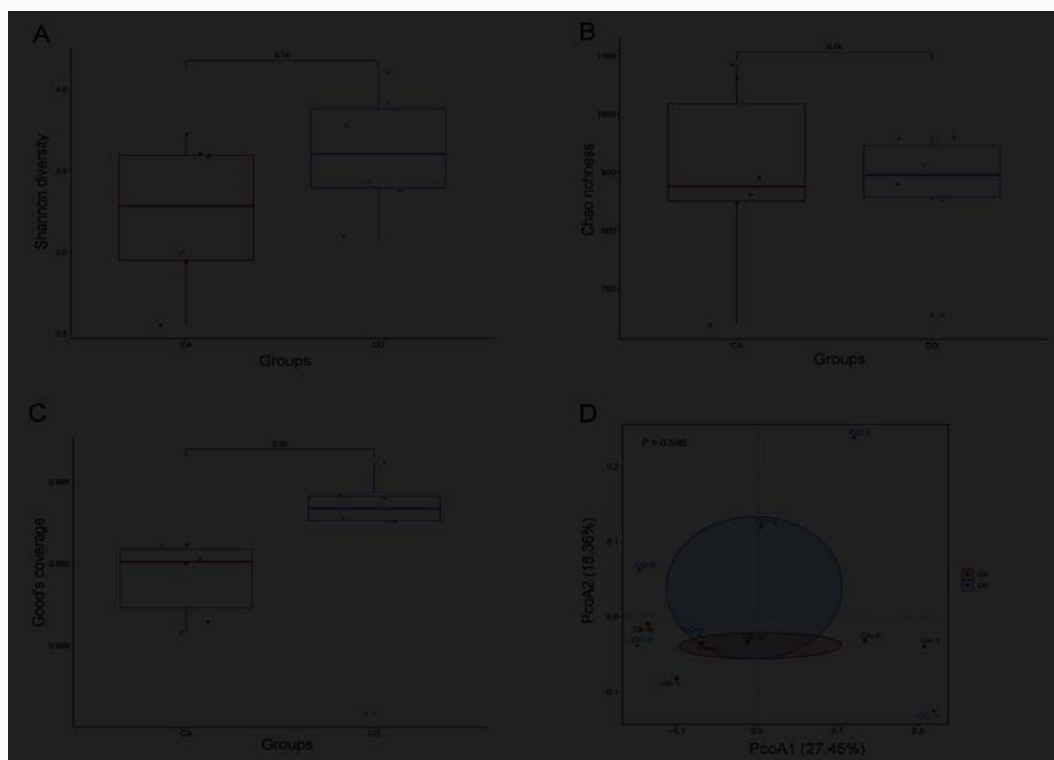


Figure 1: The alpha diversity and beta diversity analysis based on Operational Taxonomic Units (OTUs) level. A: Shannon diversity. B: Chao richness. C: Good's coverage analysis. D: PCoA analysis. The P value was shown on the top for A, B and C, and P value in D was calculated by ANOSIM analysis. CA: Anosmic group; CO: Normosmic group.

Though emerging biologic agents against CRSwNP might help in developing promising therapeutic strategies, the under-expected efficacy of medical therapy and nonnegligible recurrence even after surgical intervention on refractory CRSwNP patients remains a frustrating clinical topic for otolaryngologists [4,5]. Thus, we expected to find out the mechanisms of CRSwNP related dysosmia, and set practical therapy targets to alleviate the suffering of patients. However, our results suggested that microbial community composition in nasal polyps might not be an active direction for future study.

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