Chronic rhinosinusitis

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Chronic rhinosinusitis (CRS) is the chronic inflammation of the sinus cavities of the upper respiratory tract, which can be caused by a disrupted microbiome. However, the role of the oral microbiome in CRS is not well understood. Polymicrobial and anaerobic infections of CRS frequently increased the difficulty of cultured and antibiotic therapy. This study aimed to elucidate the patterns and clinical feasibility of the oral microbiome in CRS diagnosis. Matched saliva and nasal swabs were collected from 18 CRS patients and 37 saliva specimens from normal volunteers were collected for 16S rRNA sequencing. The α-diversity of the saliva displayed no significant difference between control and CRS patients, whereas the β-diversity was significantly different ($p = 0.004$). Taxonomic indices demonstrated that Veillonella dispar, Rothia mucilaginosa, and Porphyromonas endodontalis were enriched, while Campylobacter and Cardiobacterium were reduced in the saliva of CRS patients. These microbial markers could significantly distinguish CRS patients from control (AUC = 0.939). It is noted that the 16S rRNA results of the nasal swab were consistent with the nasopharynx aerobic culture, and additionally detected multiple pathogens in CRS patients. In summary, these results indicated these oral microbiomes may provide a novel signal for CRS detection and that NGS may be an alternative approach for CRS diagnosis.

chronic rhinosinusitis (CRS) nasal microbiome oral microbiome saliva next-generation sequencing (NGS)

1. Introduction

Chronic rhinosinusitis (CRS) is a common upper respiratory tract disease, defined as a persistent inflammation of the nasal cavity and sinus mucosa for more than 12 weeks. CRS is frequently caused by viral and bacterial infection, resulting in symptoms of nasal congestion/discharge, facial pain/pressure, and loss of smell. These symptoms not only severely impact the patient's quality of life and work ability but also cause an enormous economic burden [1,2]. According to whether nasal polyps are present, CRS is further divided into chronic rhinosinusitis with nasal polyposis (CRSwNP) and chronic rhinosinusitis without nasal polyposis (CRSsNP). When the number of polyps is too many or they become too large, they will further block the nasal cavity, preventing normal mucus discharge and worsening the infection. Until now, the therapeutic approach for CRS has been treatment with antibiotics, corticosteroids, saline lavage, and surgery [3].

2. Specifics

CRS pathogenesis is a complex process of microbial infection and inflammation. Numerous studies have investigated the microbiome in the sinuses of normal subjects and CRS patients [4,5]. However, few studies have reported the patterns and clinical relevance of oral microbiomes in CRS patients. The oral cavity and neighboring nasal cavity are ideal habitats for microbiomes due to the stable oral temperature, pH, and nutrient transportation from saliva [6,7]. It is noted that the oral microbiome is the second most complex microbial system behind the gut microbiota. Approximately 700 species have been reported in the oral cavity; half of them are cultivated and named [8]. The oral cavity is also an important entrance for both the upper and lower respiratory tracts. Oral pathogens have been reported to impact systemic health through the bloodstream, swallowing, or other avenues and are involved in systemic diseases, especially for periodontal disease in cardiovascular disease, diabetes, and Alzheimer's disease [9,10,11].

The clinical characteristics of CRS are a polymicrobial infection and an increased proportion of anaerobes. The polymicrobial infection increases the difficulty of antibiotic therapy, and most of the anaerobic species are uncultivated [4]. Therefore, use of the culture-independent molecular approach has been growing in the past few years with pyrosequencing, quantitative polymerase chain reaction (qPCR), and next-generation sequencing (NGS). However, few studies have assessed different sites of the microbiome in the same CRS patients, especially within the oral microbiome in CRS. Furthermore, conflicting results exist between culture-dependent and culture-independent approaches.

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