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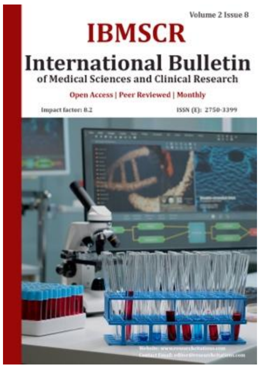

«THE ROLE OF THE NASOPHARYNGEAL MICROBIOTA IN THE PREDISPOSITION TO CHRONIC SINUSITIS»

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Abstract

The nasopharyngeal microbiota plays a critical role in maintaining upper respiratory tract health by protecting the mucosa from pathogenic microorganisms and regulating local immune responses. Dysbiosis, characterized by an imbalance between beneficial and pathogenic microorganisms, increases susceptibility to chronic sinusitis by promoting inflammation and recurrent disease. Modern molecular techniques, including 16S rRNA sequencing, metagenomic, metatranscriptomic, and metabolomic analyses, enable comprehensive characterization of microbial communities, identification of dysbiosis, and prediction of disease risk. Understanding the composition and function of the nasopharyngeal microbiota offers opportunities for early diagnosis, personalized preventive strategies, and potential prognostic markers in chronic sinusitis. Systematic investigation of these microbial communities represents a promising direction for improving the prevention and management of chronic ENT disorders.

Keywords:*Nasopharyngeal microbiota; Dysbiosis; Chronic sinusitis; 16S rRNA sequencing; Metagenomics; Immune regulation; Probiotics; ENT disorders.*

Introduction

The nasopharyngeal microbiota plays a key role in maintaining the health of ENT organs by participating in the protection of the mucosal surface against pathogenic microorganisms and supporting immune homeostasis (Man W.H. et al., 2017; De Boeck I. et al., 2020). An imbalance of the microbial ecosystem, or dysbiosis, may lead to the development of chronic inflammatory processes, including chronic sinusitis, which is one of the most common ENT pathologies in both children and adults (Abreu N.A. et al., 2012; Ramakrishnan V.R. et al., 2019).

According to global epidemiological studies, chronic sinusitis affects approximately 10–15% of the population in different countries, and a significant proportion of patients experience recurrent disease and a reduced quality of life (Fokkens W.J. et al., 2020; Orlandi R.R. et al., 2016). Recent studies indicate that the composition of the nasopharyngeal microbiota directly influences susceptibility to chronic inflammation, while disruption of the balance between “beneficial” and “pathogenic” microorganisms is associated with an increased frequency of disease exacerbations.

In Uzbekistan, precise data on the prevalence of chronic sinusitis remain limited; however, clinical observations indicate a high frequency of recurrent forms of the disease among both children and adults, particularly in urban areas with increased air pollution and frequent respiratory infections (Safina L.A., 2021). Considering the growing interest in the microbiota as a factor influencing the health of ENT organs, the study of its role in susceptibility to chronic sinusitis has become an important task in modern clinical practice.

Objective

The objective of this review article is to analyze the role of the nasopharyngeal microbiota in the development and predisposition to chronic sinusitis.

Normal Nasopharyngeal Microbiota

The nasopharyngeal microbiota comprises bacteria, fungi, and viruses inhabiting the nasal and pharyngeal mucosa, playing a crucial role in maintaining immune homeostasis and protecting against pathogens (Man W.H. et al., 2017). Key bacterial genera include Streptococcus, Corynebacterium, Staphylococcus epidermidis, and Moraxella, which compete with pathogenic microorganisms.

Microbiota composition is established early in life and influenced by environmental exposures, diet, prior infections, and antibiotic use (De Boeck I. et al., 2020). In healthy individuals, microbial communities remain relatively stable, supporting mucosal defense and preventing inflammation.

The microbiota also modulates local immune responses by promoting immunoglobulin, interferon, and antimicrobial peptide production, thereby reducing pathogen colonization and maintaining the balance between immune activation and protection (Abreu N.A. et al., 2012).

Advances in 16S rRNA sequencing and metagenomic analyses have enabled precise characterization of nasopharyngeal microbial communities, identifying key species relevant to health. These insights offer potential for early detection of microbial dysbiosis and risk stratification for chronic ENT disorders (Ramakrishnan V.R. et al., 2019).

Dysbiosis and Its Causes

Nasopharyngeal dysbiosis is a disruption of the normal microbiota balance, characterized by an increase in pathogenic microorganisms and a decrease in beneficial bacteria. This imbalance contributes to heightened susceptibility to chronic inflammatory processes, including chronic sinusitis (Abreu N.A. et al., 2012; Ramakrishnan V.R. et al., 2019).

The primary causes of dysbiosis include frequent upper respiratory tract infections, inappropriate or excessive use of antibiotics, and viral illnesses that alter microbiota composition (Man W.H. et al., 2017). Additional contributing factors are age, genetic predisposition, and environmental influences such as air pollution and smoking.

Microbial imbalance can lead to increased colonization by pathogens such as Staphylococcus aureus, Streptococcus pneumoniae, and Haemophilus influenzae, exacerbating inflammation and promoting recurrent sinusitis (De Boeck I. et al., 2020).

Recent studies indicate that restoring normal microbiota—through probiotics or limiting unnecessary antibiotic use—may reduce the risk of chronic ENT disorders and enhance mucosal immune responses (Ramakrishnan V.R. et al., 2019).

Microbiota and the Development of Chronic Sinusitis

The composition of the nasopharyngeal microbiota directly influences susceptibility to chronic sinusitis. Studies have shown that a reduction in the diversity of “beneficial” microorganisms is accompanied by an increase in pathogenic species, such as Staphylococcus aureus and Pseudomonas aeruginosa, which contribute to chronic mucosal inflammation (Abreu N.A. et al., 2012; Ramakrishnan V.R. et al., 2019).

Disruptions in microbiota balance can exacerbate local inflammation through activation of immune cells and increased production of proinflammatory cytokines. This establishes a vicious cycle: inflammation promotes further dysbiosis, while dysbiosis intensifies inflammation (De Boeck I. et al., 2020).

Clinical observations indicate that patients with chronic sinusitis often exhibit specific alterations in the microbiota, including reduced abundance of Corynebacterium and Dolosigranulum, which normally contribute to mucosal protection (Ramakrishnan V.R. et al., 2019). These changes are associated with more severe disease courses and higher recurrence rates.

Thus, the nasopharyngeal microbiota serves not only as a marker of mucosal status but also as a potential factor influencing the development of chronic sinusitis. Studying its composition offers opportunities for disease prediction and the development of preventive strategies.

Methods for Studying Nasopharyngeal Microbiota

Investigating the nasopharyngeal microbiota requires advanced methods that allow precise identification of microbial composition and abundance. Traditional culture-based techniques enable the detection of bacteria capable of growth on nutrient media, but they are limited and do not provide a complete picture of the microbiota (Abreu N.A. et al., 2012).

Modern molecular approaches, including 16S rRNA sequencing and metagenomic analysis, allow the identification of even hard-to-culture microorganisms and the assessment of microbial community diversity (De Boeck I. et al., 2020). These methods facilitate both quantitative and qualitative analyses of the microbiota, which are essential for detecting dysbiosis and predicting the risk of chronic sinusitis.

Additionally, emerging approaches such as metatranscriptomics and metabolomics enable the study of microbial activity and their interactions with the host immune system (Ramakrishnan V.R. et al., 2019). These techniques offer opportunities for the development of prognostic markers and novel preventive strategies.

Combining clinical data with molecular microbiota analyses not only allows the identification of compositional disturbances but also facilitates the prediction of chronic sinusitis progression, which is crucial for early diagnosis and disease prevention.

Clinical Prospects of Nasopharyngeal Microbiota Data

The study of the nasopharyngeal microbiota offers new opportunities for clinical practice, particularly in the prevention and early diagnosis of chronic sinusitis. Assessing microbiota composition may become an important tool for identifying patients at increased risk of disease recurrence and severe progression (Ramakrishnan V.R. et al., 2019; Man W.H. et al., 2017).

A promising approach is the use of microbiological data to develop personalized preventive strategies, including optimization of antibiotic regimens, probiotic interventions, and management of environmental factors (De Boeck I. et al., 2020).

Moreover, microbiota monitoring can aid in evaluating treatment efficacy and predicting disease outcomes. For instance, restoration of normal microbial balance following therapy may serve as an indicator of reduced risk of relapse (Abreu N.A. et al., 2012).

New microbiota analysis methods, combined with clinical data, enable prediction of chronic sinusitis development even before the onset of pronounced symptoms. In the future, this could lead to the creation of early-detection algorithms and individualized prevention strategies for ENT disorders.

Conclusion

The nasopharyngeal microbiota plays a crucial role in maintaining ENT health and protecting the mucosa from pathogenic microorganisms. Dysbiosis, or disruption of microbiota balance, increases susceptibility to chronic sinusitis by exacerbating inflammatory processes and promoting disease recurrence.

Modern research methods, including 16S rRNA sequencing and metagenomic analysis, allow detailed characterization of the microbiota, identification of imbalances, and prediction of the risk of chronic inflammatory processes. These insights offer opportunities for early diagnosis, individualized prevention, and the potential use of microbiota as a prognostic marker.

Therefore, systematic investigation of the nasopharyngeal microbiota represents a significant avenue in contemporary clinical practice, with the potential to enhance understanding of the mechanisms underlying chronic sinusitis and improve the effectiveness of its prevention.

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