



e-ISSN: 2319-8753 | p-ISSN: 2347-6710

# IJRSET

International Journal of Innovative Research in  
**SCIENCE | ENGINEERING | TECHNOLOGY**

# INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN SCIENCE | ENGINEERING | TECHNOLOGY

Volume 10, Issue 12, December 2021

**ISSN** INTERNATIONAL  
STANDARD  
SERIAL  
NUMBER  
INDIA

Impact Factor: 7.569

 9940 572 462

 6381 907 438

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# Cases of Microbiotics in Chronic Rhinosinusitis

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**ABSTRACT.** Microbiota is an integral part of the human body, which is actively studied, incl. methods of mass parallel sequencing. However, the microbiomes of the lungs and sinuses have only come under scrutiny in the last decade.

For patients with cystic fibrosis, controlling airway microorganisms is important to preserve lung function. Elucidation of the role of sinuses and the presence of polyps in the formation of the microbiome of the respiratory tract became the goal of our study. We have shown that proteobacteria, also found in samples from the lower respiratory tract, are present in the sinuses already in childhood.

**KEYWORDS:** chronic rhinosinusitis, microbiome, nasal cavity, treatment, diagnosis.

## I.RELEVANCE

In the past 30 years, molecular biology techniques have allowed bacterial culture free studies of microbial communities, identifying microflora much more diverse than previously thought, including those in the upper respiratory tract. When available, studying the pathophysiology of the upper respiratory tract is necessary to establish the relationship between the microbiome and inflammatory patterns in order to find their clinical reflections as well as their possible causal relationships.

Such research could shed light on the path to therapeutic approaches when correcting an imbalanced microbiome. In this review, we summarize the methods used and current knowledge of the microbiome of upper respiratory tract diseases, limitations and pitfalls, and identified areas of interest for future research.

Microbes, which appeared about 3.5 billion years ago, are the oldest group of organisms currently existing on Earth. The ubiquity and total capacity of the metabolic potential of microorganisms determine their most important role in the circulation of substances, maintaining dynamic equilibrium in the Earth's biosphere. Man and microbes exist inseparably with each other, thousands of species of bacteria, archaea, fungi and viruses are found in the human body.

Considering their enormous influence on the vital activity of a macroorganism, modern science considers a person already as a superorganism, consisting not only of somatic cells, but also of a huge number of microorganisms. Thousands of years of interaction between microflora and the human body have taught a person with the help of the immune system not only to effectively defend against pathogens, but also to prevent autoimmune and allergic diseases - that is, they have developed the ability to immune regulation or modulation.

New views on the interaction of the immune system with normal microbiota as an independent phenomenon that establishes relationships with symbiotic microorganisms is a modern approach to understanding living systems, clarifying various types of multidimensional interactions and a more complete understanding of complex phenotypes of allergic and other immune-dependent diseases.

The growing availability of high-performance technologies has made it possible to carry out system-wide profiling of the genome, transcriptome, epigenome, microbiome and metabolome, has changed our understanding, providing the foundation for the study of asthma and allergy at a fundamentally different level, based on a new paradigm of complex interactions between the microbiome and its host, which can provoke or prevent the formation of respiratory disease.



Microbial changes have been associated with several human diseases. There is also evidence that, in the respiratory system, the composition of the respiratory microflora varies from healthy individuals to people with conditions such as asthma and cystic fibrosis (CF). Unfortunately, with limited research at this time, it cannot be contracted with the same degree of chronic rhinosinusitis (CRS). Investigation of the microbiome in the ABP Therefore, it is necessary to find out the pathophysiology of this disease, such as;

- 1) the relationship between the microbiome and inflammatory patterns,
- 2) possible causal relationships between the microbe and the CRS,
- 3) study of the microbiome of possible therapeutic properties. Dysregulation of interactions between the immune system and synanthropic bacteria is a factor contributing to the development and chronicity of a number of inflammatory diseases.

Microorganisms in the intestine may play an important role in the regulation of helper T cells (Th cells), regulatory T cells (Tregs) and dendritic cells, as well as the expression of the Toll-like receptor in the sentinel cell (macrophages and dendritic cells), which are related to respiratory diseases such as asthma and allergic diseases.

Diseases of the upper respiratory tract, including allergic rhinitis, chronic rhinosinusitis with or without polyps, and cystic fibrosis are characterized by significantly different inflammatory profiles. Traditionally, research on the relationship of specific bacterial specimens to inflammatory disease profiles has been dependent on bacterial culture.

**Purpose of the study.** Study of microbiotic conditions in chronic rhinosinusitis and prevention of pathological processes.

## II. RESEARCH METHODS

The main approaches to analyzing human microflora are: culture-dependent and culture-independent methods. Culture dependent methods include the isolation and cultivation of microorganisms prior to their identification according to morphological, biochemical or genetic characteristics. These methods are time-consuming due to culture and bias, as some media and growth conditions favor the growth of some bacteria over others.

## III. RESEARCH RESULTS

Summary of studies of chronic rhinosinusitis microflora; specimen type, technique used and genus determined Using culture independent (qPCR and 16S rRNA gene sequencing) methodology to identify the causative agent of chronic rhinosinusitis patients, including 57,407 pyrosequences were obtained. The most common ones were from Coagulase-negative staphylococci (100%), 21/21 specimens, *Corynebacterium* (spp specifically not *Corynebacteriumtuberculostearicum*) (85.7%) 18/21, *P. acne* (76.2%), 16/21, and *Staphylococcus aureus* (66.7%) 14/21.

Although these authors found significantly different distributions of 16S rRNA isolated from CRS versus non-CRS cases, neither the wealth nor the evenness indices showed statistically significant differences. In another approach using 16S rRNA genes clone sequences in a terminal fragment limiting polymorphism length assay (T-RFLP), bacteria present in 70 clinical samples from 43 CRS patients undergoing endoscopic surgery were characterized; a total of 48 separate groups were found.

Species belonging to 34 genera were identified as present by clone sequence analysis. Of the species found, those in the genera *Pseudomonas*, *Citrobacter*, *Haemophilus*, *Propionibacterium*, *Staphylococcus*, and *Streptococcus* are found to be numerically dominant, *Pseudomonas aeruginosa*, being the most frequently found species. Another prospective study collected mucosal biopsies from 18 patients undergoing endoscopic surgery for ASB and 9 control patients with healthy sinuses (indicator: pituitary adenoma) compared a swab culture with bTEFAP (bacterial FLX-encoded ampliconpyrosequencing tag).

Standard cultures mainly showed *Staphylococcus aureus* and coagulase-negative *Staphylococcus aureus*, while molecular analysis identified up to 20 predominant organisms on a sample of *Staphylococcus aureus* was nevertheless detected in about 50% .; In addition, they discovered anaerobic species with unknown yet effects in the inventory of *Diaphorobacter* and *Peptoniphilus*. Interestingly, *Diaphorobacter* is described as a strong biofilm creator.

Comparison of molecular analyzes shows that detection of microorganisms by fluorescence in situ hybridization (FISH) and culture is method dependent due to the abundance of the organism, in addition, cultivation tends to give the advantage of rapidly growing bacteria. Investigators use conventional culture, molecular diagnostics, and fish to detect *Staphylococcus aureus* as a standard. They found that the FISH assay had a sensitivity of 78% and a specificity of 93% when compared to molecular techniques.

Data from methods with high sensitivity show that healthy sinuses are clearly not sterile, but show a wide variety of resident microflora. The nasal microflora of healthy subjects is mainly composed of members of the phylum



actinobacteria (e.g. *Propionibacterium* spp. And *Corynebacterium* spp.), While the phylum Firmicutes (e.g. *Staphylococcus* spp.) And Proteobacteria (e.g. *Enterobacter* spp.) Are less common. It appears that the prevalence and abundance of organisms is critical in determining healthy conditions.

Thus, similar to CF, the data in the inventory indicated that the microbiome is unique to each individual patient and the microbial community is diversified. As a general principle, decreased bacterial diversity correlated with disease severity in CF, while CRS patients had an altered microbial composition and a greater abundance of *Staphylococcus aureus*. There has not been a single general microflora profile in patients with similar clinical conditions in the studies done so far, although *Staphylococcus aureus* has been prominent in most studies.

Thus, there is a clear need for a larger series of well-defined patients, selected and studied in an optimal way, as well as avoiding interference with recent antibiotic use in order to establish a link between the microbe and CRS disease. Limitations of Current Research Airway microbiome research has identified several important factors that may also affect CRS research. First of all, the inclusion of well-defined patients using pheno- and potentially endotypes of the upper respiratory tract disease, and the control group in significant numbers needs to draw well-founded conclusions.

Moreover, recent antibiotic treatment for 1 month prior to collection can significantly reduce the microbiome diversity in samples, and contamination of bacteria from other organs such as skin must be taken into account. Factors that may disturb the collection or assessment procedures contaminate host DNA or RNA, the presence of viruses such as bacteriophages in samples that can affect the number and genes of microbes, and technical issues such as extraction methods (for example, altered lysostaphin lysozyme a way to increase the isolation of *staphylococcus* DNA).

Currently, most publications in human microflora studies have highlighted 16S rRNA sequences in bacterial identification. Their results may underestimate the level of diversity and microbial composition, exacerbation of chimera and pseudogenes and / or inappropriate primer selection. The metagenomic shotgun method can avoid these problems by omitting amplification and allowing the detection of gene content of complex microflora and comparison of functional gene content between samples, but may still have limitations, as described above, and in samples with low levels of microbial burden.

#### IV. CONCLUSION

New molecular techniques increase our chance of identifying new bacteria inside the nose and nasal cavities; as a key function of the host has evolved into high microbial pressure, they will show a very complex network of microbes and thus microbe-host interactions.

On the host side, specific phenotypes and endotypes of CRS have been described as characterized by imbalances in Th1 and Th2 function. In CRSwNP patients, *Staphylococcus aureus* has been identified to unfold an effect on mucosal immune functions. The relationship between the microbiome and mucous membranes can be bidirectional, with pressure from bacteria and insufficient protection from the host. Research into how the specific effects of bacteria on the immune response, nasal and sinus mucosal lining may shed new light on the pathophysiology of CRS and may lead to new strategies for its treatment.

The manipulation of the microbiota, or the introduction of a particularly healthy microbiota, may prove beneficial in the treatment of inflammatory diseases. *Staphylococcus aureus* and *Pseudomonas aeruginosa* are major disruptors in the development of persistent severe airway disease in ASD and CF patients.

As bacterial resistance complicates the effectiveness of antibiotics, the use of probiotic bacteria as colonizers and antimicrobial agents that can inhibit the growth of pathogenic bacteria awaits further development.

#### REFERENCES

1. Lopatin, A.S. Acute and chronic rhinosinusitis: etiology, pathogenesis, clinical picture, diagnosis and treatment principles: textbook / A.S. Lopatin, V.P. Gamow. - M.: LLC "Medical Information Agency", 2011. - 72 p.
2. Morozova, O. V. Diagnostics and treatment of various forms of fungal sinusitis: abstract dissertation. ... Doctor of Medical Sciences. - SPb., 2012. - 42 p.
3. Piskunov, G.Z. Polypoid rhinosinusitis / G.Z. Piskunov. - M.: GEOTAR-Media, 2016. -- 96 p.
4. Shlyaga, I. D. Diagnostics and treatment of fungal sinusitis in modern conditions / I.D. Shlyaga // Medical journal. -2013. - No. 2. - S. 127-130.
5. European Position Paper on Rhinosinusitis and Nasal Polyps 2012 / W.J. Fokkens [et al.] // Rhinology Supplement. - 2012 Mar (23). - P. 1-298.
6. The sinonasal bacterial microbiome in health and disease [Electronic resource] / Vijay R. Ramakrishnan [et al.] // URL: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4751043/> (date accessed: 28.06.2017).



7. Microbiome Complexity and Staphylococcus aureus in Chronic Rhinosinusitis [Electronic resource] / Leah M. Feazel [et al.] // The Laryngoscope. - 2012. - Vol. 122, Issue 2. - P. 467-472.
8. Conditions Associated with the Cystic Fibrosis Defect Promote Chronic Pseudomonas aeruginosa Infection [Electronic resource] / Benjamin J. Staudinger [et al.]
9. The diagnosis and incidence of allergic fungal sinusitis / J.U. Ponikau [et al.] // Mayo Clin Proc. - 1999. - Vol. 74 (9). - P. 877-884.
10. Contribution of molecular tools for the diagnosis and epidemiology of fungal chronic rhinosinusitis / P. Comacle [et al.] // Vestnikotorinolaryngologii. - 2016. - N ° 5. - S. 98-99.
14. Dilshodov A.D., The name is quoted year of the main stages and features of the development of multimedia lectures in physics // Physics in the system of modern education (FSSO-15), 217-219 2015
15. Dilshodov A.D., Ways to strengthen individualization of students' training in the process of teaching the course of electrical engineering and electronics // Physics in the system of modern education (FSSO-15), 9-11 2015



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