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Pathogenetic Feature Of The Microflora Of The Nasal Cavity In Patients With Polyposis Rhinosinusitis

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Abstract— *Polypoid rhinosinuitis is one of the widespread chronic diseases of the nasal cavity and paranasal sinuses. Bacterial and fungal infections are considered as potential pathogenetic factors of this disease; anatomical abnormalities of the nasal cavity and ostiomeatal complex; ciliary dysfunction; atopy, defects of systemic and local immunity.*

Keywords— polyposis rhinosinuitis, mass spectrometry, microflora, humoral immunity.

1. INTRODUCTION

The problem of polyposis rhinosinuitis remains relevant, since the main aspects of this pathology (etiological, pathogenetic, immunological, therapeutic) have not been fully resolved all over the world. The disease is accompanied by a violation of the basic functions of the nose and a decrease in the patient's quality of life.

2. MAIN PART

According to the latest position papers on rhinosinusitis and nasal polyps of the European Academy of Allergology and Clinical Immunologe (EAACI Position Paper on Rhinosinusitis and Nasal Polyps - EPOS, 2007; 2012), the prevalence of chronic polypous rhinosinuitis in the population ranges from 1 to 4%, while men get sick more often [2]. Disease
occurs at the working age - at 25-35 years. Nasal polyps are a manifestation of the so-called special form of chronic rhinosinusitis, caused by a bacterial or fungal infection, with the formation of chronic eosinophilic inflammation. Clinically, chronic polypous rhinosinusitis is characterized by a year-round course with nasal congestion, difficulty in nasal breathing until it is completely absent. Factors predisposing to the development of CPMS are allergies, aspirin intolerance, vasomotor rhinitis, chronic and recurrent rhinosinusitis, to a lesser extent genetic factors and environmental pollution. In 50-60% of patients with chronic polypous rhinosinusitis, bronchial asthma develops.
Leading importance among bacterial infections is given to Staphylococcus aureus streptococcus and the theory of the superantigen. According to the authors, superantigens induce polyclonal activation of T and B cells, increase eosinophilic inflammation and the formation of local edema. In a series of studies by C. Bachert et al. [3] set an increased
the content of specific IgE to Staphylococcus aureus in the tissue of nasal polyps, suggesting that enterotoxin Staphylococcus aureus may play the role of a superantigen that provokes a hyperimmune reaction and causes rapid growth of nasal polyps, as well as the development of concomitant bronchial asthma. In recent years, the etiological role of bacterial microflora in polyposis rhinosinuitis remains the subject of heated debate. With polypous rhinosinitis, microbial associations are more often distinguished, represented by a wide variety of aerobic and anaerobic pathogenic and saprophytic microorganisms:
Peptostreptococcus spp., Bacteroides spp., Veillonella spp., Prevotella spp., Fusobacterium spp., Corynebacterium spp., Staphylococci, streptococci, Haemophilus influenzae Helicobacter pylori and other gram-positive and gram-negative bacteria. Recent studies have shown that the seeding of Staphylococcus aureus in the middle nasal passage in patients with chronic polypous rhinosinusitis is significantly higher (63.6%) than in patients with chronic rhinosinusitis (27.3%) [4].
P. Gevaert [5], H. Riechelmah [6] indicate the possibility of intraepithelial location of Staphylococcus aureus during its colonization from 70 to 90% in patients with chronic polypous rhinosinusitis. Recently, it has become known that, in addition to obligate intracellular parasites - chlamydia and mycoplasma, many other microbes are capable of penetrating into cells and persisting in them [7]. The frequency of detection of chlamydia, according to the literature, varies within significant limits - from 3 to 52% [8].
The ability to penetrate the epithelial cells of the respiratory tract was noted in pyogenic streptococcus [9, 10]. An important role in the development of polyposis rhinosinusitis belongs to the endotoxin of gram-negative microflora, which is in contact with almost all components of cellular immunity, causing cascade disturbances in the process of the immune response. There are reports in the literature on the identification of
Chlamydia pneumoniae and Mycoplasma pneumoniae in CPMS patients in the study of discharge from the mucous membrane of the inferior turbinates by direct immunofluorescence [11]. In recent years, the question of the importance of mycotic infection in the development of polyposis rhinosinusitis has been actively discussed [12, 13]. At the same time, J. Ponikau, E. Kern [14] believe that the development of eosinophilic inflammation may be a manifestation of innate immune defense against "extramucous" fungi, similar to the well-known role of eosinophils in protecting the body from non-goocytic parasites.
Thus, the study of the microflora vegetating in the nasal cavity and paranasal sinuses with nasal polyposis remains a very urgent task.

The aim of the study was to compare the indicators of microbiological examination of the nasal mucus with the data on the functional state of the nose and humoral immunity.

Material and methods:

We examined 110 patients with polypous rhinosinuitis aged 17 to 60 years with a disease duration of 1 to 11 years. All patients underwent an in-depth clinical and functional examination of the nasal cavity as well as a study of the nasal microbiota using the method of mass spectrometry of microbial markers (MSMM)

All patients, in addition to general clinical and microbiological examination, underwent a study of the state of the immune status, i.e. the content of IgA, IgM, IgG. determination of the total number of eosinophils in the blood; microbiological examination of mucus from the nasal cavity with the isolation, identification and counting of colonies of bacterial and fungal flora;

results

Using the MSMM method, it was possible to establish the presence of markers of microorganisms by smears extracted from the deep parts of the nose. Along with the cultivated flora, the method makes it possible to identify uncultivated
microorganisms of the nasal mucosa. According to the results of the analysis of markers of the microbial community in relation to the duration of the disease, a significant dependence of the qualitative and quantitative composition of the microbiota on the duration of the disease was found. When analyzing the mean values in a shorter period of the disease, the minimum colonization by microbes was determined with the least species diversity in the mucous membrane. Among them were aerobes Streptococcus spp., Str. pneumoniae, Moraxella cat., Nocardia, Pseudomonas aeruginosa, Bacillus megaterium, Stenotrophomonas maltophilia, Corineform CDC-group XX, Staphylococcus, Nocardia asteroids and anaerobes Clos tridium propionicum, Lactobacillus, Cl. difficile, Eubacterium / Cl. coccoides, Bifidobacterium, Clostridium perfringens, Eubacterium, / Cl. subterminale, Propionibacterium acnes, Ruminicoccus, Actinomycetes, Actinomyces viscosus. With a long period of the disease, the fungi actinomycetes, Pseudonocardia, Streptomyces, Mycobacterium / Candida, and the Herpes virus were determined. As it turned out, the greatest total number of microorganisms and their significant diversity were characteristic of patients who had been ill for more than 5 years, when the nasal mucosa is a "vaccine laboratory" and has a significant effect on the formation of adaptive immunity. At the same time, Streptococcus spp., Bacillus cereus, Str.pneumoniae, Moraxella cat., Nocardia, Pseudomonas aeruginosa, Bacillus megaterium, Stenotrophomonas maltophilia, Alcaligenes, Rhodococcus, Staphylococter Enterococcus, Nocardia asteroides, and among anaerobes - Peptostreptococcus anaerobius, Porphyromonas, Lactobacillus, Cl. difficile, Prevotella, Eubacterium / Cl. Coccoides, Clostridium perfringens, Eubacterium, Propionibacterium / Cl. Subterminale, It is interesting that in patients with long-term illness, a wide variety of microorganisms was identified with a relatively small total number. Among them were Staf / aurens aerobes Streptococcus spp., Bacillus cereus, Str. pneumoniae, Bacillus megaterium, Stenotrophomonas maltophilia, Alcaligenes, Rhodococcus, Staphylococcus, Enterococcus, Nocardia asteroides and anaerobes Peptostreptococcus anaerobius, Clostridium propionicum, Selenomonas, Lactobacilllla / coccoides, Clostridium perfringens, Eubacterium, Propionibacterium / Cl. subterminale, Propionibacterium acnes, Actinomyces viscosus.

In addition, in all children of this group, the fungi actinomycetes, Pseudonocardia, Streptomyces, Rhodococcus, Mycobacterium / Candida and the Herpes minicoccus virus, Actinomycetes Actinomyces viscosus were detected.

Mass spectrometry results demonstrate in one analysis the presence of both resident (Actinomyces, Clostridium spp., Candida, Lactobacillus spp., Mycobacterium spp., Neisseria spp., Peptococcus spp., Peptostreptococcus spp., Pseudomonas spp., Staphyloccus spp., Pseudomonas spp., Saphyloccus spp. Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus spp., Treponema spp.) And facultative microflora (Alcaligenes, Bacillus cereus, Bacillus megaterium, Bacteroides fragilis, Bifidobacterium, Eubacterium / Cl. , Clostridium propionicum, Clostridium ramosum, Cl.difficile, Clostridium perfringens, Enterococcus, Flavobacterium, Eubacterium, Herpes, Helicobacter pylori, Prevotella, Porphyromonas, Propionibacterium / Cl. Subterminale, Streptomyces).

From the data obtained, it can be seen that markers of some microorganisms are determined only in individual patients, therefore, they must be individually taken into account when analyzing the microbial passport. At the same time, we were able to identify a number of microorganisms that demonstrate a single trend of changes depending on the duration of the disease: Streptococcus spp., Bacillus cereus, Alcaligenes, Lactobacillus, Lactobacillus, Mycobacterium / Candida, Cl. difficile, Prevotella, Eubacterium / Cl. coccoides, Staphylococcus, Helicobacter pylori, h18, Enterococcus, Herpes, Ruminicoccus, Actinomycetes 10Me14, Actinomyces viscosus

When these microorganisms are participants in the infectious process (Clostridium, Eubacterium, Enterobacteriaceae, Lactobacillus, Helicobacter pylori), they have high pathogenetic activity, and the diseases they cause are difficult to treat and the polyposis process can spread outside the nose.

The data obtained on the functional state of the nasal cavity upon admission indicate that the respiratory function of the nasal cavity is 22.52 ± 2.44, the motor function of the ciliated epithelium decreases by 67%, and the absorption function of the nasal cavity increases by 14.7%, which significantly differs from control ($P < 0.001$).

The data obtained on the functional state of the nasal cavity upon admission indicate that the respiratory function of the nasal cavity is 22.52 ± 2.44, the motor function of the ciliated epithelium decreases by 43%, and the absorption function of the nasal cavity increases by 16.7%, which significantly differs from control ($P < 0.001$).

There was also a pathological shift in the indices of humoral immunity, i.e. decrease in IgA, increase in IgG, no significant change in IgM was observed).

3. CONCLUSION

The data obtained show that a violation of the functional state of the nasal cavity with a decrease in humoral immunity leads to a change in the microflora of the nasal cavity, which has a certain value in the pathogenesis of nasal polyposis and paranasal sinuses. The state of the nasal microbiota makes it possible to assess the pathogenesis of pollipous rhinosinuitis and the severity of the course with the study of the function of the nasal cavity with the immunological parameters of the blood on the one hand and choose the tactics and control of treatment. Proceeding from this, we used the pathological microflora of the nasal cavity and sensitivity to antibiotics to select drugs for the treatment of patients with polypous rhinosinuitis.

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