



THE ROLE OF BACTERIA IN ACUTE AND CHRONIC RHINOSINOCYTETIOLOGY AND THEIR SENSITIVITY TO MODERN ANTIBIOTICS

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Annotation

A number of scientific studies aimed at the study of the etiology and pathogenesis of acute purulent geymoritis indicate that the study of the nature of this disease was complex, was associated with the biological state of the nasopharynx, hygienic properties and microbial factor.

At present, the main reason for the lack of a decrease in the trend of rhinosinocyte diseases is explained with the fact of the exchange of the causative agent circle in patients, increased importance of intracellular infections, the high resistance of the main etiological agents to antibacterial drugs, and the climbed number of weakened individuals with the immune system.

Keyword: rhinosinusitis, monoflora, assosiasia, anaerobes, Staphylococcus sp., Ps. aeruginosae + Streptococcus sp.

Relevance of the Topic

Today, One of the main problems of modern medicine is the treatment of acute and chronic inflammatory diseases that occur in the upper respiratory tract and the prevention of their complications [2,4,5,11].

The significance of the problems indicated during the practice of Otolaryngology is that inflammatory diseases of the nasal lateral cavities occupy a main place in the general structure of diseases of the upper respiratory tract. Many researchers also emphasize that the contribution of insulation of the mucous



membrane of the nasal cavities increases in the structure of the common Otolaryngological pathology (30-35%). [1,3,6, 7].

Separating microorganisms from pathological components of patients with acute rhinosinusitis and reptiliansinusitis, identifying species and their role in the etiology of the disease are important in the field of otolaryngological practice. By studying the resistance of alternatively isolated pathogens modern antibiotics, the doctor have the opportunity to treat the disease effectively on purpose and by reducing the patient's treatment days, it reduces the complications of the disease. In the case of these problems, we made the aim of our work to recommend. [3].

Otolaryngology polyclinics to use the drug as a primary antibiotic, a means of treatment by isolating bacterial flora from patients with acute and chronic sinusitis and determining the resistance of pathogens to antibiotics.

Material and Methods of Verification

48 patients aged from 17 to 50 and who are undergoing treatment in the Department and polyclinic of Otorhinolaryngology of the second clinic of TMA, 22 patients diagnosed with acute rhinosinusitis and 26 patients with chronic rhinosinusitis. From the patients diagnosed with rhinosinusitis biological material (grease) with a sterile tampon from the nasal cavity for bacteriological examination was obtained .Identification of isolated bacteria generation and species was conducted in the method of, Bergey's,. [8,9.]. It was noted that the etiological role of bacteria isolated from pathological cleavage plays a role in the disease, when the quantitative indicator in the ARS (Acute rhinosinusitis) is in the scale of (10^5 - 10^6) beign the excretion of the illness.

The results obtained and their analysis

In the process of analyzing the results, grease was taken from the nasal cavity and in the biological material was obtained from this biotope, we took into account the qualitative and quantitative composition of the microflora. Before the beginning of treatment with antibiotics, getting the biological extraction from the nasal cavity need to be carried out.

CRS (and chronic rhinosinusitis) made up this figure (86,4%) and microorganisms were separated from the detachments of 19 patients who were selected from 19 patients.

31 different microbial strains were distinguished from purulent strains in 19 patients with ARS 49 from 26 patients with CRS, a total of 85 different bacterial strains were distinguished.

From the presented literature reviews it is known that in the etiology of acute rhinosinusitis, it is natural that the arrival of associated bacterias cause some difficulties in the course and treatment of the disease. In this case, we also received the following results when we analyzed the role of microbial association in the etiology of ARS and CRS in the first diagram.

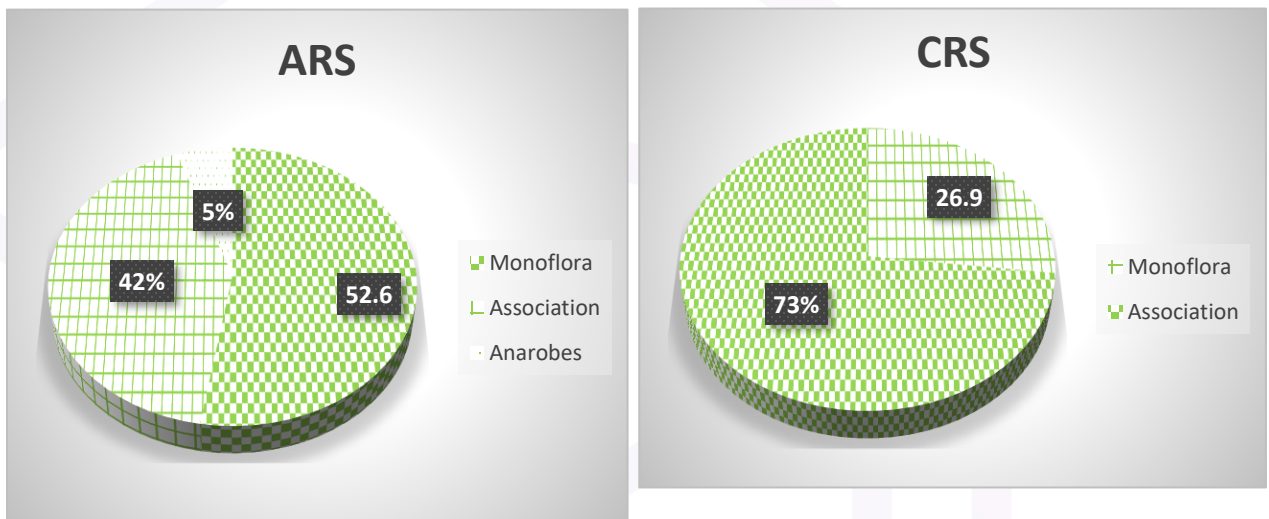


Diagramm-1- Changes in behavior of bacteria according to the samples collected in ARS and CRS.

ARS and CRS meet bacteria in monoflora and assosiasia in relation to the isolated strains.

As can be seen from the diagram, CRS monoinfection was observed in 10 patients and presented 52,6%. microbes can be seen in the form of association in 8 patients with the proportion of 42,1% In SRS, anaerobic bacteria were detected in the monoflora structure by 1 units (5,3%), while aerobic and elective were detected in 7 patients (87,5%). In the isolated associated structure, mainly aerobic+aerobic associations had a high rate (84,6%), while only 2 patients suffered from these associations (15,4%).

The occurrence of bacteria in mono-flora and association in CRS was differed from that in ARS. While CRS bacteria were found in 7 patients with mono-flora appearance and accounted for 26,9% their occurrence in the association was detected in 19 patients and accounted for 73,1% it was obvious that this result is more than 1,4 times than the oars's one. In the structure of SRS mono-flora,



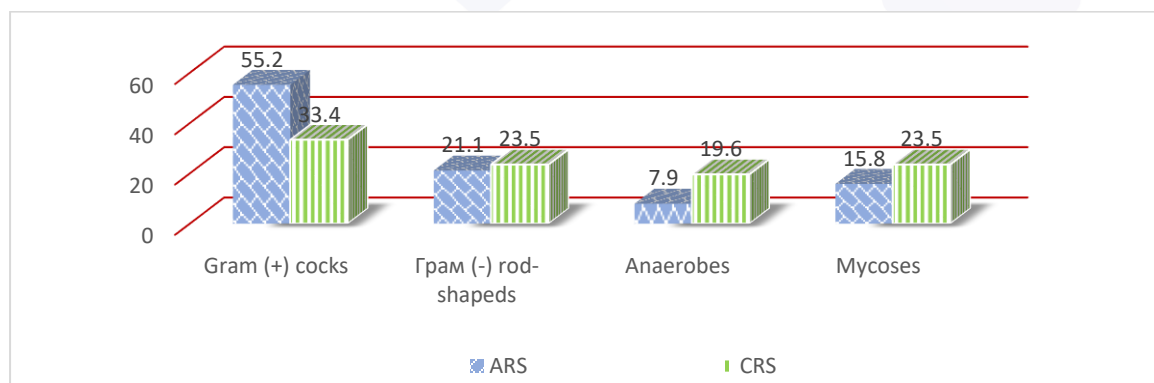
anaerobic bacteria were detected in 1 patient (14,3%), while aerobic and facultative were detected in 6 patients (85,7%). In the isolated association structure, aerobic +aerobic association index was found in 10 patients (52.6%), while anaerobic +aerobic association was found in 9 patients (47.4%).

In aerobic - aerobic associations, representatives of *Ps. aeruginosa* + *Staphylococcus* sp., *Ps. aeruginosa* + *Streptococcus* sp. ba *Ps. aeruginosa* + *Enterobacteriaceae* spp were observed in 2 cases. Whereas in anaerobic - aerobic associations, *Peptococcus* spp. (71,4%) can be seen in 5 patients (of 7 patients). It is interesting to note that in patients with SRS anaerobic bacteria mainly occur with representatives of fungal microorganisms (*Aspergillus* spp., *Penicillium* spp.) from the associations (62,5%). In the remaining cases, *Moraxella catarrhalis* (25%) and *Str.* came from the associations with pyogens (12,5%).

Ps. in the structure of aerobic - aerobic associations. *aeruginosa* + *Staphylococcus* sp., *Ps. aeruginosa* + *Streptococcus* sp. and *Ps. aeruginosa* + *Enterobacteriaceae* spp. representatives met in 2 cases. In the anaerobic-aerobic associations structure, 6 out of 8 patients had *Peptococcus* spp. (75%) and *Peptococcus* spp. in 2 patients. (25%) from. It is interesting to note that in patients with SRS anaerobic bacteria mainly occur with representatives of fungal microorganisms (*Aspergillus* spp., *Penicillium* spp.) from the associations (62,5%). In the remaining cases, *Moraxella catarrhalis* (25%) and *Str.* came from the associations with pyogens (12,5%).

It is clear from the results, the figure of aerobic +aerobic association decreased 1,3 times in the isolated associated structure CRS comparing to in ARS. Contrastly the trend of anaerobic and aerobic association grew 1,8 times in SRS than ARS.

Diagram 2. The appearance of pathogens from the detachment of patients with ARS (Acute rhinosinusitis) and CRS (chronic rhinosinusitis) relation to common isolated bacterial strains.





When the structure of 89 bacterial strains isolated from patients with Acute rhinosinusitis and chronic rhinosinusitis was studied (diag.2.) we observed the following results. If the rate of occurrence of gram-positive cocci at CRS decreased by 1.7 times compared to ARS, we can see that this indicator in gram-negative cocci is prone to increase. While Ars anaerobic bacteria accounted for 7,9% compared to the general isolated strains, CRS found that this indicator was convincingly high in 2,5 marotaba ($R < 0,05$).

It is interesting that in the etiology of CRS the role of piogen cocc. and Moraxella catarrhalis, Haemofillus influenzae 1,7; 1,3; and 2,2 times decreased respectively, and the role of Pseudomonas aeruginosae and E.coli from representatives of the intestinal noclostridial anaerobes increased accordingly (2,2; 2,9; 2,1).

It became known that fungi play a significant pathological role in the etiology of CRS. If you suffer from fungi 15,8% compared to the total isolated bacteria strain of ARS, this indicator increased to CRS in 1,5 times. Alternatively if representatives of fungi at Ars were detected in almost the same patients (5.2% respectively), CPC Candida spp. in addition to a decrease in the meeting of representatives of the generation, an increase in the share of representatives of mold fungi (Penicillium srr., Aspergillus srr. 1,5 and 2,3 times, respectively) was observed.

Consolations

In the etiological factors causing the patalogy, the main role was played by mainly 47,4% gram positive coccus (Staphylococcus sp., and Streptococcus sp.). The role of gram-positive (Penicillium srr., Aspergillus srr.) the etiological role was found to be more in marotaba (1,5-2,3; 2,2-2,5) respectively than in Ars. Alternatively the etiological role of CRS gram negative bacteria (Ps. aeruginosae, Enterobacteriaceae spp.), anaerobic cocci (Peptococcus srr. Peptococcus srr.) and fungi (Penicillium srr., Aspergillus srr.) was found to be 1,5- 2,2 -2,5 times more respectively than in ARS.

Of the isolated bacterial strains staphylococci, High sensitivity of staphylococci was noticed to cephalosporin and quinolin series antibiotics series (90%) and streptococcal bacteria representatives, except for the above groups, to tradision pentsillin series antibiotics (85-90%), to representatives of blue green pus sticks only from cephalosporin series antibiotics cefipam (80%)



and to levofloxacin and gatifloxacin (90-70%). While there was noticed sensitivity to some extent or no sensitivity at all in other groups of bacteria.

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