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Of Microbiological Study In Patients With Acute Odontogenic Puscular Inflammatory Diseases

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Abstrak. Relevance of the study. The prediction of the course of purulent-inflammatory diseases of the maxillofacial region in odontogenic inflammatory diseases is becoming an urgent problem due to its widespread prevalence and the possibility of developing severe complications. According to a number of authors, the relative weight of purulent-inflammatory diseases in the general structure of diseases in maxillofacial hospitals is 60% and has a tendency to increase. According to many researchers, the situation is associated with the following factors. Many works have been devoted to studying the composition of cytokines in the blood and oral fluid of patients with purulent-inflammatory diseases of the maxillofacial region , but the impact of instability on the clinical course and prognosis of the disease has not been fully studied. One of the leading directions in predicting the course of the inflammatory process is the study of gene expression in various factors of immunity. For example, much attention is being paid to searching for associations between cytokine gene variants that determine the stability of immune reactivity.
The purpose of the study. Study of the results of microbiological studies in patients with acute odontogenic purulent-inflammatory diseases.
Results and analyses. In order to determine the composition of the microflora in patients with acute odontogenic purulent-inflammatory diseases and the correlation between the study groups of patients , a microbiological analysis was conducted. When purulent exudate obtained during surgery in 15 1 children with acute odontogenic purulent-inflammatory diseases was studied, it was determined that 62.5 % of the 8 species studied from colony-forming microorganisms were obligate anaerobic bacteria, among which Neisseria spp. , Bacillus sp. , E. cloacae, Proteus spp., Cl. perfringens were detected in the largest number. The concentration of microorganisms in the purulent exudate was 3.71*10 3 from 2.71*10 5 Changed to KOE/ml (colony forming units in 1 ml). Facultative-anaerobic microorganisms consisted mostly of gram-positive species (staphylococci, streptococci, corynebacteria). The concentration of these microorganisms in the pus center varied from 2*10 3 to 1*10 6 KOE/mld, that is, their amount is 10-100 times less than the amount of obligate anaerobes. this information is the domain of most researchers confirms the opinion about the dominance of anaerobic microflora in odontogenic inflammatory diseases.

Keywords: Odontogenic infection, Microbiology, Anaerobic bacteria, Oral microflora, Maxillofacial disease

Our analysis showed that the composition and structure of the microflora differed in different age groups. The smallest number of species was detected in children aged 2 to 3 years. Streptococci and corynebacteria dominated in this age group. It is noteworthy that the associations included 2-3 species, while the ratio of facultative and obligate anaerobes was almost the same (from 2*10 4 to 1*10 6

CFU/ml). The total concentration of microorganisms was one to two times lower compared to other groups. A similar rate was observed in children aged 4-6 years. However, non-spore-forming anaerobic microorganisms appeared in the associations (bacteroids, fusobacteria). From 2 to 4 species were detected in the associations. In the presence of anaerobes, they dominated the associations and were expressed in very high concentrations (1.8*10 8 CFU/ml). In the 7-11 age group, both a sharp increase in the number of microbial associations and a predominance of non-spore-forming anaerobes were observed, the frequency of bacteriological isolation of streptococci, staphylococci, corynebacteria decreased. Fusobacteria, peptostreptococcus, bacteroids were more common among anaerobes. It should be noted that the number of isolated staphylococci in this age group was only 7.6%, while in the literature there are no reports of inflammatory diseases of the maxillofacial region in children The observation group also noted a significant increase in the number of these microorganisms. A pronounced tendency towards a further predominance of the association of strict anaerobes was also detected in the 12-17 age group. An increase in both gram-negative (bacteroids, fusobacteria) and gram-positive bacteria was observed. The frequency of isolation of anaerobes exceeded 60.0%, i.e. the microbial “landscape” approached that observed in adults. At the same time, the percentage of streptococci remained at a sufficiently high level, which is not observed in adults. Another characteristic feature of this age group was a further decrease in the percentage of isolated corynebacteria and staphylococci (4.0%). The concentration of microorganisms in this group ranged from 2*10 6 to 4*10 8 CFU/ml, with obligate anaerobes isolated in higher concentrations than facultative anaerobes.

Different groups of children with acute odontogenic purulent-inflammatory diseases, in our opinion, is primarily associated with the peculiarities of the oral microbiocenosis of patients, which, undoubtedly, in the observation group is associated with the weakening of the child's organism due to concomitant diseases, the weakening of the immune system, early loss of primary and permanent teeth , and the deterioration of the hygienic condition of the oral cavity . The above allows us to conclude that in the formation of acute odontogenic purulent-inflammatory diseases in patients of the observation group, there is not only an odontogenic route of entry of microflora , but also an endogenous one. On the day of presentation of patients with acute odontogenic purulent-inflammatory diseases, the purulent focus was opened using an emergency surgical method and a culture was taken from the exudate released from the purulent focus for microbiological examination.

From the data in the table above, it can be seen that in the analysis of research materials obtained from patients in the observation group (n=122), S. aureus was observed in 75 (61.47 %) of the total patients , with an average of 4.83± 0.17 x 10 5 If the CBC Log/ml was detected, S. pyogenes was detected in 49 (40.16 %) patients with an average of 4.21 ± 0.26x105 CKD Log/ml was detected. The next place in the occurrence of bacterial environment in patients of the observation group was occupied by E. coli, which was found in 42 (34.43%) of the total patients with an average of 2.33 ± 0.14 x10 4 CFU Log / ml . Cl . perfringens was found in 32 (26.23%) patients with an average of 2.27 ± 0.21 x10 4 CFU Log / ml , Proteus spp. was found in 25 (20.49%) patients with an average of 2.71 ± 0.21 x10 5 CFU Log/ml . With similar indicators, E. cloacae was found in 23 (18.85%) patients with an average of 2.34 ± 0.19 x10 4 CFU Log / ml and Neisseria spp. The average was 3.71 ± 0.21 x10 3 CBC Log/ml. The lowest number of Bacillus sp. was detected in only 6 (4.91%) patients in the bacterial environment, with an average of 1.08 ± 0.19 x10 5 The CRP showed a Log/ml value.

Conclusion.

In the control group (n=29) with acute odontogenic purulent-inflammatory diseases, a significant difference in the composition of associations was also observed. In this case , S. aureus was detected in 22 (75.86%) patients with an average of 3.32 ± 0.18 x10 5 CFU Log/ml , S. pyogenes in 13 (44.82%) patients with an average of 2.87 ± 0.42 x10 5 CFU Log /ml , E. coli in 4 (13.79%) patients with an average of 6.75 ± 0.21 x10 3 CFU Log/ml. Only 1 (3.45%) of the control group patients had Cl. perfringens in 8.91 x10 2 CFU Log/ml , while Proteus spp. was detected in 2 patients. and E. cloacae were detected at 4.28 ± 0.19 x10 3 CFU Log/ml and 4.54 ± 0.22 x10 3 CFU Log/ml, respectively. Neisseria spp. was detected in 3 (10.34%) patients of the group at an average of 8.20 ± 0.28 x10 2 CFU Log/ml. Bacillus sp. was not detected in the patients of the control group.

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