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THE EFFECT OF THE COMPOSITION OF MICROORGANISMS IN THE ORAL CAVITY ON THE LEVEL OF PROTECTION AGAINST COLONIZATION BY PARODONTAL INFLAMMATORY PROCESSES IN PATIENTS WITH GASTROINTESTINAL DISEASES: AN ANALYSIS OF THE RELATIONSHIP

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ABSTRACT

The study conducted at the Department of Dentistry of the Bukhara State Medical Institute in the period from 2020 to 2023 covers the analysis of the relationship between pathologies of the gastrointestinal tract and the characteristics of the oral microbiome. 138 patients with chronic generalized parodontitis took part, with special attention paid to patients with gastrointestinal diseases using non-removable prostheses. The study revealed significant changes in the oral microflora, highlighting the link between the state of the microbiome and overall human health. The results of the study demonstrate the importance of an integrated approach in diagnosis and treatment, pointing to the interaction between oral and systemic diseases.

Key words: oral microbiome, chronic generalized parodontitis, gastrointestinal tract, non-removable prostheses, integrated approach, inflammatory diseases, oral microflora, Bukhara State Medical Institute, dental research, human health.

INTRODUCTION

The research presented in this article is highly relevant in the field of medical science, especially in understanding the complex relationships between the oral microbiota and human systemic health. The main attention is paid to significant changes in the microbiome of the oral cavity in patients with inflammatory parodontal diseases, including those suffering from diseases of the gastrointestinal tract. This study highlights the importance of an integrated approach in the diagnosis and treatment of oral and systemic diseases, recognizing the close relationship between them.

The findings of the study emphasize the need for further study of this area, which can lead to improved diagnostic, preventive and therapeutic strategies in medical practice. The study draws attention to the dynamics of changes in the microflora of the oral cavity, which may be not only the result of local pathologies, but also a reflection of more extensive changes in the body associated with the functioning of the gastrointestinal tract. This opens up new perspectives for understanding the mechanisms of interaction between the oral microbiota and general health, offering new approaches to the prevention and treatment of diseases.

In general, the results of this study can have a significant impact on the development of new diagnostic and treatment methods, linking the state of the oral microbiome and general health, which is important for a wide range of medical professionals, including dentists, gastroenterologists and therapists.

The aim of the study was to analyze the effect of the composition of microorganisms in the oral cavity on the level of protection against parodontal inflammatory processes in patients with diseases of the gastrointestinal tract.

Research materials and methods:

The study was conducted at the Department of Dentistry of the Bukhara State Medical Institute in the period from 2020 to 2023. 138 patients, divided by age and sex categories, aged from 18 to 60 years, took part in it. The distribution of participants by gender and age is shown in table 1. All participants were diagnosed with chronic generalized parodontitis of varying severity.

The main selection criteria for participation in the study were the presence of diseases of the digestive system in patients and their use of non-removable prostheses. Of the total number of participants, 108 people suffered from diseases of the gastrointestinal tract (GI tract) in the acute stage. In this group, 52 patients used metal bridges, 28 used metal–ceramic prostheses, and another 28 had dentures on dental implants.

The control group consisted of 30 patients, among whom 12 used metal bridges, 10 – dentures on dental implants, and 8 – metal-ceramic prostheses. This made it possible to conduct a comparative analysis of the oral microflora between the main and control groups, taking into account the differences in the types of prostheses.

The results of the study and their discussion. The human oral microbiota is a complex, constantly changing ecosystem formed during the evolutionary process of interaction between the host and microbial populations. Empirical studies demonstrate a continuous dynamic balance between the commensal and pathogenic microflora in the human oral cavity. It is important to emphasize that any generalized pathological processes can disrupt this balance, leading to a decrease in the number of resident microorganisms.

Activation of pathogenic microflora often correlates with certain predisposing factors that contribute to their increased adhesion and reproduction. Such factors include extensive caries, occlusion anomalies, structural abnormalities in the maxillofacial region, as well as the presence of parodontal pockets and improperly installed dentures. In these situations, the state of local immunity in the oral cavity is of particular importance.

During our study, microbiological assessments of the oral cavity of participants from the first and second groups, as well as in healthy subjects from the control group, were performed. Special attention was paid to the study of the level of colonization resistance in various segments of the oral cavity, including the tongue, palate, inner surface of the cheeks and gums.

According to current literature, the human oral microbiome consists of more than 800 diverse microorganisms classified into 7 families, 10 genera and 26 species. Healthy individuals are characterized by relative stability in both qualitative and quantitative aspects of the microflora.

The presence of lactobacilli was recorded in the following concentrations: 1.8±0.2 CFU/cm2 on the gums, 1.08±0.02 CFU/cm2 on the inside of the cheeks, 1.6±0.1 CFU/cm2 on the tongue and 1.0±0.1 CFU/cm2 on the palate. Meanwhile, Streptococcus mutans concentrations were detected in higher amounts on the gums (2.04±0.1 CFU/cm2) and tongue (2.18±0.4 CFU/cm2), while on the inner surfaces of the cheeks and palate their levels were lower, amounting to 1.04±0.3 CFU/cm2 and 1.02±0.1 CFU/cm2, respectively.

As part of the microbiological analysis of the oral cavity, it was found that Escherichia coli microorganisms were identified exclusively in the tongue, where their concentration was 1.2±0.1 colony-forming units (CFU) per square centimeter. The absence of these bacteria was observed in the rest of the oral cavity. In contrast, bacteria of the genus Staphylococcus demonstrated a significant predominance in the gum area, with a concentration of 4.83±0.6 CFU/cm2. These microorganisms were also present in noticeable amounts on the cheeks and tongue with concentrations of 3.9±0.2 CFU/cm2 and 3.5±0.4 CFU/cm2, respectively.

Streptococcus salivarius was detected in high concentrations on the gums (4.18±0.4 CFU/cm2) and on the tongue (2.83±0.1 CFU/cm2), while its presence on the cheeks and palate was significantly lower. Streptococcus mitis, in turn, also demonstrated variability in distribution over different areas of the oral cavity, reaching a maximum concentration on the gums (3.22±0.2 CFU/cm2).

Bacteria of the genus Klebsiella were not found in any of the studied areas of the oral cavity. At the same time, Candida fungi were present on the gums and on the tongue, where their concentrations reached 2.07±0.2 CFU/cm2 and 3.11±0.2 CFU/cm2, respectively, while their absence was noted on the cheeks and palate.

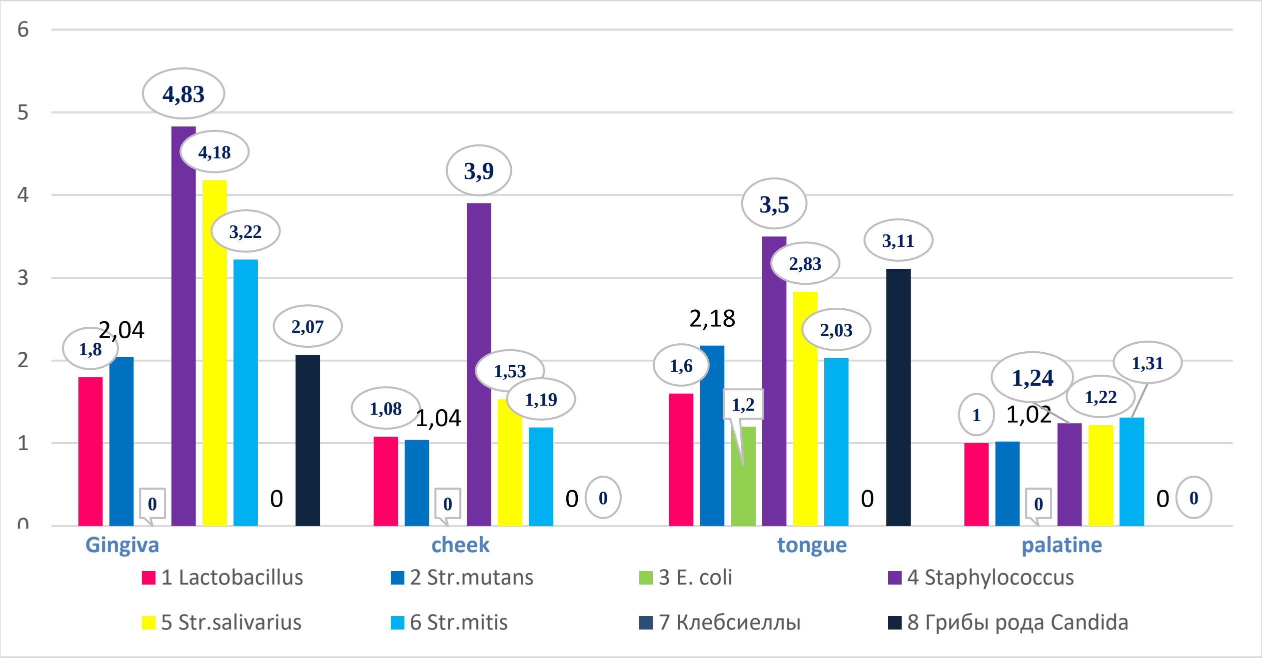

Fig. 1. Measurement of microbial population density in various areas of the oral cavity in healthy individuals of the control group (M±m, CFU/cm2)

In the course of our study, a detailed study of the quantitative and qualitative aspects of changes in the oral microflora in patients with inflammatory parodontal diseases using non-removable prostheses was performed. The key point of the study was taking samples of biological material in the form of smears from various sections of the oral mucosa. The analyses revealed the presence of 387 aerobic and 95 anaerobic microorganisms. Gram-positive bacteria (788 species) turned out to be the predominant group, while gram-negative microorganisms (95 species) and yeast-like fungi (83 species) were also identified. 12 species of opportunistic microorganisms were also identified, including 5 species from the family Micrococcae, 5 species from the family Enterobacteriaeae and 2 species of fungi of the genus Candida.

An important part of the study was the study of changes in the colonization density of microorganisms in the oral mucosa. A significant increase in this indicator was recorded, on average by 3-5 times compared with the control group of healthy individuals. A particularly pronounced increase in colonization was observed among yeast-like fungi, in particular Candida albicans, Candida pseudotuberculosis, Candida krusei and Candida tropicalis species. A marked increase in the number of these fungi was noted on the mucous membrane of the cheeks and gums, which is atypical for the normal microflora of the oral cavity in healthy individuals (Table 1).

These scientific results strengthen the theory of a significant correlation between gastrointestinal pathologies and the characteristics of the oral microbiome. The revealed increase in the number of opportunistic and pathogenic microorganisms, in particular yeast-like fungi, may be an indicator of an imbalance in the gastrointestinal microbiome caused by various gastroenterological diseases. Consequently, destabilization of the microflora of the gastrointestinal tract can stimulate shifts in the microbiological profile of the oral cavity. This, in turn, can contribute to the activation of inflammatory processes in parodontal tissues. Such conclusions emphasize the need for an integrated approach in the treatment and diagnosis of gastrointestinal and oral diseases, as well as the importance of taking into account the interaction of these systems when developing therapeutic plans.

Table 1

The density of the microbial population in different areas of the oral cavity in patients with non-removable prostheses and inflammatory periodontal diseases (M±m, CFU/cm2)

№	Groups of microorganisms	Localization			
		gingiva	cheek	tongue	palate
1	Lactobacillus	1,12±0,15	0	0,9±0,02	0
2	E.coli	2,23±0,10	1,42±0,10	2,12±0,10	0
3	Str.mitis	2,12±0,09	1,38±0,10	1,41±0,11	1,12±0,10
4	Str.salivarius	2,32±0,30	1,08±0,20	1,9±0,1	0
5	Staphylococcus	4,23±0,25	2,42±0,10	3,59±0,45	1,58±0,15
6	Str.mutans	1,35±0,10	2,08±0,10	2,59±0,08	0
7	Klebsiella	2,45±0,12	1,1±0,1	1,65±0,15	1,1±0,1
8	Fungi genera Candida	4,45±0,35	3,42±0,27	2,55±0,2	3,15±0,15

The presence of lactobacilli with a concentration of 1.12±0.15 CFU/cm2 was observed in the gingival tissues, whereas their level in the tongue was 0.9±0.02 CFU/cm2. The absence of these bacteria was noted on the inner surface of the cheeks and in the palate area. The observed concentration of E.coli bacteria was significantly higher in the gums (2.23±0.10 CFU/cm2) and on the tongue (2.12±0.10 CFU/cm2), while on the cheeks it reached 1.42±0.10 CFU/cm2.

Streptococcus mitis bacteria showed balanced distribution throughout the oral space, including gums (2.12±0.09 CFU/cm2), cheeks (1.38±0.10 CFU/cm2), tongue (1.41±0.11 CFU/cm2) and palate (1.12±0.10 CFU/cm2). In the context of Streptococcus salivarius, high concentrations were detected in the gums (2.32±0.30 CFU/cm2) and on the tongue (1.9±0.1 CFU/cm2), while their presence on the cheeks and in the palatine region was minimal or not detectable.

Staphylococcus is registered as one of the predominant microorganisms, especially in the gums (4.23±0.25 CFU/cm2) and on the tongue (3.59±0.45 CFU/cm2), with lower values on the cheeks (2.42±0.10 CFU/cm2) and palate (1.58±0.15 CFU/cm2). Streptococcus mutans showed predominant presence on the tongue (2.59±0.08 CFU/cm2) and cheeks (2.08±0.10 CFU/cm2), but it was not found in the palatine region.

Klebsiella were also recorded in all the studied areas of the oral cavity, with the highest values in the gums (2.45±0.12 CFU/cm2) and the lowest in the palate and cheeks (1.1±0.1 CFU/cm2). In addition, fungi of the genus Candida revealed a high degree of colonization, especially pronounced in the gums (4.45±0.35 CFU/cm2) and on the cheeks (3.42±0.27 CFU/cm2), as well as on the tongue (2.55±0.2 CFU/cm2) and palate (3.15±0.15 CFU/cm2). The average detection rate of Candida fungi was 1.29±0.2 CFU/cm2 in the first group and 3.39±0.15 CFU/cm2 in the second group.

These studies confirm significant differences in the composition of the oral microflora in people using non-removable prostheses and suffering from inflammatory periodontal pathologies. An increase in the level of colonization of both normal inhabitants of the microflora and microorganisms, which are usually conditionally pathogenic, has been observed.

In the course of a comprehensive analysis aimed at studying the relationship between inflammatory parodontal diseases in people with gastrointestinal pathologies and changes in the microbiome of the oral cavity, significant results were revealed. These data indicate significant quantitative and qualitative shifts in the composition of the oral microbiome in such patients.

In particular, there was an increase in colonies of bacteria of the genus Klebsiella in various biotopes, especially on the mucous membrane of the gums, where the concentration reached lg 2.45±0.12 CFU/ml, which is significantly higher compared to other microorganisms. A similar increase was also recorded for E.coli bacteria, which are usually found on the surface of the tongue in healthy people, but in patients with inflammatory parodontal diseases were also found on the gums and cheeks, with an average of lg 2.23±0.10 CFU/ml.

The study revealed a significant decrease in the number of microorganisms of the genus Streptococcus and Lactobacillus in all studied regions of the oral cavity in patients with inflammatory periodontal diseases. This indicates the destabilization of the normal microbiological balance and a decrease in the level of colonization resistance. Populations of Str.salivaruis, Str.mutans, and Str.mitis have noticeably decreased, and their number has almost halved.

As part of this study, a comparative analysis of the oral fluid microflora was also performed in patients with inflammatory periodontal pathologies and in healthy participants from the control group. A decrease in the functions of the protective barrier of colonization resistance was found, which manifested itself in an increase in the number of colonies of Staphylococcus, Peptostreptococcus and Escherichia, as well as the appearance of colonies of Proteus and Staphylococcus aureus with a frequency of 65%, which is unusual for healthy oral microflora and is not found in healthy people.

Table 2

Qualitative and quantitative composition of oral fluid in the control group and in patients with parodontal inflammatory processes against the background of gastrointestinal diseases (lg M±m, CFU/ml)

№	**Groups of microorganisms**	**The number of microbes in 1 ml of saliva**			
		Control group n=30		**Patients of groups 1 and 2 n=108**	
		Detection frequency, %	**Quantity in 1 ml**	**Detection frequency, %**	**Quantity in 1 ml**
1	Lactobacillus	90	4,55±0,11	8	2,01±0,15
2	Peptostreptococci	100	2,65±0,15	100	3,82±0,1
3	Staph.aureus	0	0	65	4,37±0,08
4	Staph.epidermidis	48	4,02±0,15	25	4,51±0,15
5	Str.salivarius	100	4,21±0,15	35	3,32±0,1
6	Str.mutans	67	2,07±0,10	45	4,40±0,15
7	Str.mitis	90	2,52±0,11	17	4,28±0,8
8	Escherichia LP	12	0,74±0,01	38	2,33±0,1
9	Proteus	3	0,21±0,01	20	2,09±0,10
10	Klebsiella	3	0,82±0,02	39	1,93±0,02
11	Veillonella	100	2,32±0,10	100	3,94±0,03
12	Fungi of the genus Candida	45	2,03±0,18	82	4,38±0,20
13	Total number of aerobes	-	5,25±0,12	-	7,90±0,28
14	Total number of anaerobes	-	5,61±0,14	-	3,66±0,15

The control group of healthy people was dominated by Str.salivaruis, Veillonella and Peptostreptococcus (100%), followed by Str.mitis (90%) and Str.mutans (67%). Average occurrence rates were recorded for Staphylococcus epidermidis (48%) and fungi of the genus Candida (45%). The lowest occurrence was noted for Gram-negative bacteria, including Escherichia coli (12%), proteus and Klebsiella (3%).

Conclusion. In conclusion, a thorough analysis of the data obtained from both study groups revealed a surprising degree of similarity and identity in the results. This fact is reflected in table 12, where information from both groups was synthesized and presented as a single information unit.

Such results not only highlight significant changes in the microbiome of the oral cavity in patients with inflammatory parodontal diseases against the background of diseases of the gastrointestinal tract, but also open up new horizons for understanding the complex relationships between oral microflora and the general state of human health. Our study clearly shows that the imbalance of the oral microbiome may not only be a consequence of local pathologies, but may also reflect more global changes in the body associated with impaired functioning of the gastrointestinal tract. This highlights the need for an integrated approach to the study of interactions between systemic and local diseases, which can make a significant contribution to the development of new strategies for diagnosis, prevention and treatment.

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