



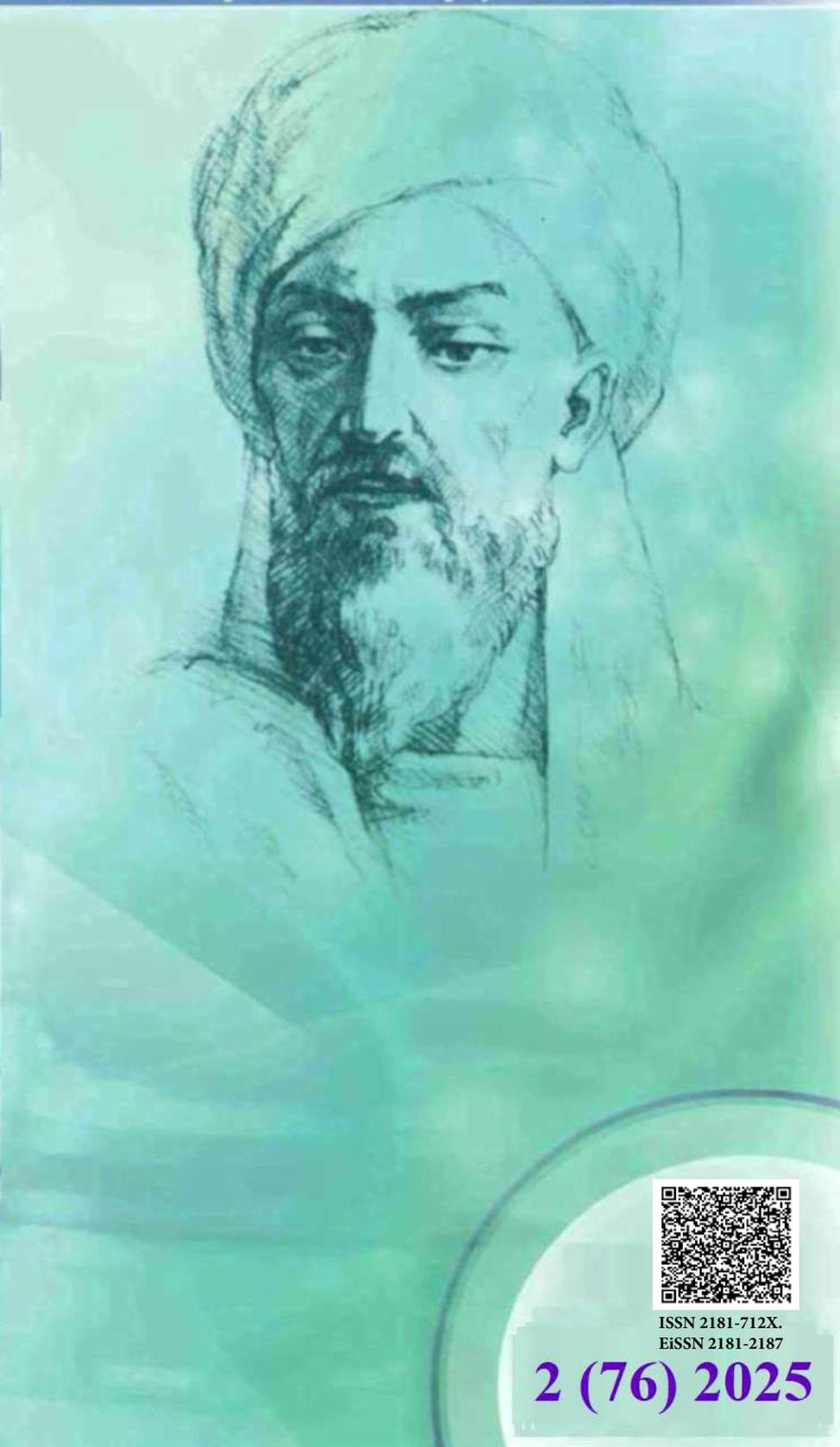
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**ТИББИЁТДА ЯНГИ КУН
НОВЫЙ ДЕНЬ В МЕДИЦИНЕ
NEW DAY IN MEDICINE**

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ВЛИЯНИЕ МИКРОБНОЙ ПОПУЛЯЦИИ РОТОВОЙ ПОЛОСТИ НА УРОВЕНЬ ЗАЩИТЫ ПЕРЕД ЛИЦОМ ПАРОДОНТАЛЬНЫХ ВОСПАЛЕНИЙ У ПАЦИЕНТОВ С ЗАБОЛЕВАНИЯМИ ЖЕЛУДОЧНО-КИШЕЧНОГО ТРАКТА

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✓ Резюме

В рамках исследования в Бухарском Государственном Медицинском Институте с 2020 по 2023 год было проведено изучение связи между патологиями желудочно-кишечного тракта и состоянием микробиома в ротовой полости. В исследовании участвовали 138 пациентов с хроническим пародонтитом, особенно среди носителей несъемных протезов и пациентов с ЖКТ-заболеваниями. Исследование подчеркнуло значимость изменений микрофлоры, связывая состояние микробиома с общим здоровьем человека и подтверждая необходимость комплексного подхода в диагностике и лечении.

Ключевые слова: микробиом ротовой полости, пародонтит, желудочно-кишечный тракт, несъемные протезы, микрофлора, здоровье человека, воспалительные процессы, комплексное лечение.

O'G'IZ BO'SHLIG'IDAGI MIKROORGANIZMLAR TARKIBINING OSHQOZON-ICHAK KASALLIKLARI BILAN OG'RIGAN BEMORLARDA PARODONT YALLIG'LANISH JARAYONLARIGA QARSHI HIMOYA DARAJASIGA TA'SIRI

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✓ Резюме

2020 yildan 2023 yilgacha Buxoro Davlat Tibbiyot Institutida o'tkazilgan tadqiqot oshqozon-ichak trakti kasalliklari bilan bog'liq holda og'iz bo'shlig'i mikrobiomasining xususiyatlarini o'rganishga qaratilgan edi. Tadqiqotda surunkali parodontit bilan aziyat chekuvchi 138 bemor ishtirok etdi, ayniqsa, olib tashlanmaydigan protezlar foydalanuvchilar va oshqozon-ichak trakti kasalliklariga chalingan bemorlar diqqat markazida edi. Tadqiqot og'iz mikroflorasidagi o'zgarishlarni ta'kidlab, mikrobioma holati va umumiy sog'liq o'rtasidagi bog'liqlikni ko'rsatib, diagnostika va davolashda integratsion yondashuv zarurligini tasdiqladi.

Kalit so'zlar: og'iz mikrobiomasi, parodontit, oshqozon-ichak trakti, olib qo'yilmaydigan protezlar, mikroflora, inson salomatligi, yallig'lanish jarayonlari, kompleks davolash.

INFLUENCE OF ORAL MICROBIOME ON DEFENSE AGAINST PARODONTAL INFLAMMATION IN PATIENTS WITH GASTROINTESTINAL DISEASES

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✓ *Resume*

The research conducted at the Department of Dentistry at the Bukhara State Medical Institute from 2020 to 2023 focused on analyzing the relationship between gastrointestinal tract pathologies and the state of the oral microbiome. It involved 138 patients suffering from chronic parodontitis, particularly those using non-removable prostheses and those with gastrointestinal ailments. The study highlighted significant changes in the oral flora, linking the microbiome's condition with overall human health and affirming the necessity for a comprehensive approach in diagnosis and treatment.

Key Words: oral microbiome, parodontitis, gastrointestinal tract, non-removable prostheses, microflora, human health, inflammatory processes, comprehensive treatment.

Relevance

The research presented in this article is highly relevant in the field of medical science, especially in understanding the complex relationships between oral microbiota and human systemic health. The main focus is on significant changes in the oral microbiome of patients with inflammatory periodontal diseases, including those with gastrointestinal diseases. This study emphasizes the importance of an integrated approach in the diagnosis and treatment of oral and systemic diseases, recognizing their close interrelationship.

The research findings highlight the need for further research into this area, which can lead to improved diagnostic, preventive, and therapeutic strategies in medical practice. The study focuses on the dynamics of oral microflora changes, which can be not only the result of local pathologies, but also a reflection of more extensive changes in the body related to the functioning of the gastrointestinal tract. This opens up new perspectives for understanding the mechanisms of interaction between oral microbiota and overall health, offering new approaches to disease prevention and treatment. Overall, 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 to the general health status, which is important for a wide range of medical professionals, including dentists, gastroenterologists, and therapists [1.3.5.7.9].

Purpose of the study: to study the relationship between pathologies of the gastrointestinal tract and the state of the microbiome in the oral cavity.

Materials and research methods

The study was conducted at the Department of Dentistry of the Bukhara State Medical Institute from 2020 to 2023. The study included 138 patients aged 18 to 60, divided by age and gender. The distribution of participants by gender and age is presented in Table 1. All participants were diagnosed with chronic generalized periodontitis of varying severity.

The main selection criteria for participation in the study were the presence of digestive system diseases in patients and the use of non-removable prostheses. Of the total number of participants, 108 people suffered from gastrointestinal diseases (GIC) in the acute phase. In this group, 52 patients used metallic bridge prostheses, 28 patients used metal-ceramic prostheses, and 28 patients had dental implants.

The control group consisted of 30 patients, of whom 12 used metallic bridge prostheses, 10 used dental implants, and 8 used 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 dentures.

The research results and their discussion

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 commensal and pathogenic microflora in the human oral cavity. It is important to note that any generalized pathological processes can disrupt this balance, leading to a decrease in the number of resident microorganisms.

The activation of the pathogenic microflora often correlates with certain predisposing factors, which contribute to their increased adhesion and reproduction. These factors include extensive caries, occlusion anomalies, structural disorders in the maxillofacial region, as well as the presence of

periodontal pockets and improper dental prostheses. In these situations, the state of local immunity in the oral cavity becomes particularly important.

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

According to current literature, the human oral microbiome consists of over 800 different 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 at 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 found in higher quantities in the gums (2.04 ± 0.1 CFU/cm²) and tongue (2.18 ± 0.4 CFU/cm²), while their levels were lower on the inner surfaces of the cheeks and palate, reaching 1.04 ± 0.3 CFU/cm² and 1.02 ± 0.1 CFU/cm², respectively.

As part of the microbiological analysis of the oral cavity, *Escherichia coli* microorganisms were identified only in the tongue, where their concentration was 1.2 ± 0.1 colony-forming units per square centimeter. The absence of these bacteria was observed in the remaining parts of the oral cavity. In contrast, *Staphylococcus* bacteria showed a significant predominance in the gums, with a concentration of 4.83 ± 0.6 CFU/cm². These microorganisms were also present in significant amounts on the cheeks and tongue at concentrations of 3.9 ± 0.2 CFU/cm² and 3.5 ± 0.4 CFU/cm², respectively.

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

No *Klebsiella* bacteria were found in any of the studied areas of the oral cavity. At the same time, *Candida* fungi were present on the gums and 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.

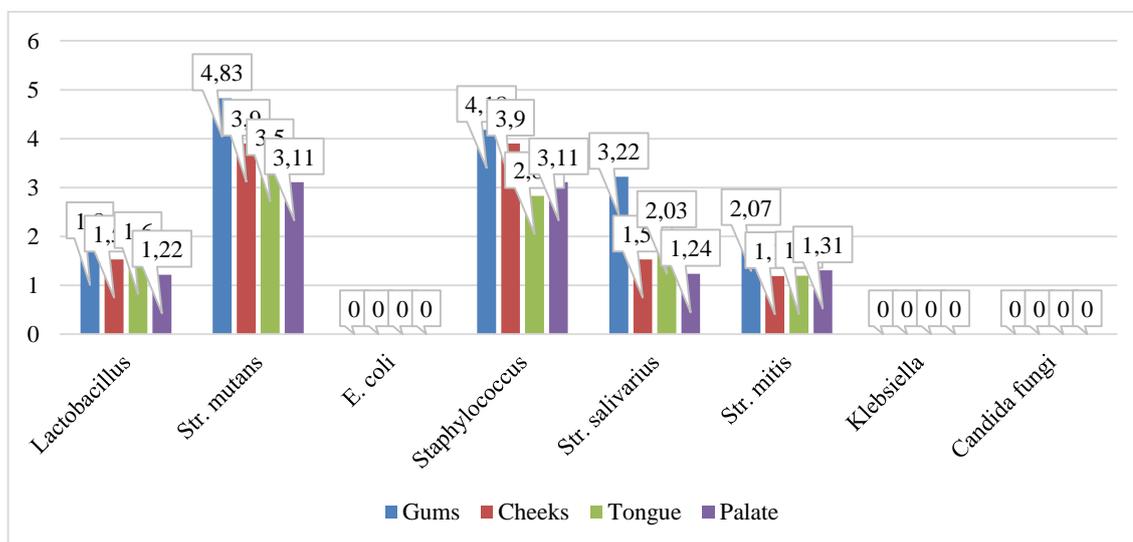


Figure 1. Measurement of microbial population density in different zones of the oral cavity in healthy individuals of the control group ($M \pm m$, CFU/cm²)

Our research thoroughly examined the quantitative and qualitative aspects of oral microflora changes in patients with inflammatory periodontal diseases who use non-removable dentures. The key point of the study was the collection of biological material samples in the form of ointments from various sections of the oral mucosa. Analysis revealed the presence of 387 aerobic and 95 anaerobic microorganisms. Gram-positive bacteria (788 species) were the dominant 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 Micrococcae family, 5 species from the Enterobacteriaceae family, and 2 species from the Candida genus.

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 noted, averaging 3-5 times, compared to the control group of healthy individuals. A particularly pronounced increase in colonization was observed among yeast-like fungi, particularly *Candida albicans*, *Candida pseudotuberculosis*, *Candida krusei*, and *Candida tropicalis*. A marked increase in the number of these fungi was noted in the mucous membrane of the cheeks and gums, which is atypical for normal oral microflora in healthy individuals (Table. 1).

These scientific findings confirm the theory of significant correlation between gastrointestinal tract pathology and oral microbiome characteristics. The identified increase in the number of opportunistic and pathogenic microorganisms, particularly yeast-like fungi, can be an indicator of the imbalance in the microbiome of the gastrointestinal tract caused by various gastrointestinal diseases. Therefore, the destabilization of the gastrointestinal tract microflora can stimulate shifts in the microbiological profile of the oral cavity [2.4.6.8.10]. This, in turn, can contribute to the activation of inflammatory processes in the periodontal tissues. These conclusions highlight the need for an integrated approach to the diagnosis and treatment of gastrointestinal diseases, as well as the importance of taking into account the interaction of these systems in the development of therapeutic plans.

Table 1

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

№	Groups of microorganisms	Location			
		jaw	cheek	tongue	sky
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	Clebsiella	2,45±0,12	1,1±0,1	1,65±0,15	1,1±0,1
8	Candida fungi	4,45±0,35	3,42±0,27	2,55±0,2	3,15±0,15

In the gingival tissue, lactobacilli with a concentration of 1.12±0.15 CFU/cm² were observed, while their level on 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 area of the palate. The observed concentration of *E. coli* bacteria was significantly higher in the gums (2.23±0.10 CFU/cm²) and tongue (2.12±0.10 CFU/cm²), while in the jaws it reached 1.42±0.10 CFU/cm².

Streptococcus mitis bacteria showed a balanced distribution throughout the oral cavity, including the 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 found in the gums (2.32±0.30 CFU/cm²) and tongue (1.9±0.1 CFU/cm²), while their presence in the cheeks and in the temple area was minimal or not detected.

Staphylococcus was registered as one of the dominant microorganisms, especially in the gums (4.23±0.25 CFU/cm²) and tongue (3.59±0.45 CFU/cm²), with lower indicators in the cheeks (2.42±0.10 CFU/cm²) and palate (1.58±0.15 CFU/cm²). *Streptococcus mutans* was predominantly present on the tongue (2.59±0.08 CFU/cm²) and cheeks (2.08±0.10 CFU/cm²), but it was not detected in the parietal region.

Clebsiella were also observed in all studied areas of the oral cavity, with the highest values in the gums (2.45±0.12 CFU/cm²) and the lowest values in the temple and cheeks (1.1±0.1 CFU/cm²). In addition, *Candida* fungi exhibited a high degree of colonization, particularly pronounced in the gums (4.45±0.35 CFU/cm²) and faces (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 incidence 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 oral microflora composition in individuals who use non-removable prostheses and suffer from inflammatory periodontal pathologies. There is an increase in the colonization rate of both normal microflora inhabitants and microorganisms, which are usually opportunistic. A comprehensive analysis aimed at studying the relationship between inflammatory periodontal diseases in individuals with gastrointestinal pathology and changes in the oral microbiome revealed significant results. These data indicate significant quantitative and qualitative shifts in the oral microbiome composition in such patients [7.9.11].

Specifically, an increase in the number of Klebsiella bacteria colonies was observed in different biotopes, especially in the mucous membrane of the gums, where the concentration reached $\lg 2.45 \pm 0.12$ CFU/ml, which is significantly higher compared to other microorganisms. Similar growth was also recorded for E. coli bacteria, which are usually found on the surface of the tongue in healthy individuals, but in patients with inflammatory periodontal diseases, they were also found on the gums and cheeks, with an average of $\lg 2.23 \pm 0.10$ CFU/ml.

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

This study also included a comparative analysis of oral fluid microflora in patients with inflammatory periodontal pathologies and healthy participants from the control group. A decrease in the function of the protective barrier of colonization resistance was found, which manifested in an increase in the number of Staphylococcus, Peptostreptococcus, and Escherichia colonies, as well as the appearance of Proteus and Staphylococcus aureus colonies with a frequency of 65%, which is not characteristic of healthy oral microflora and is not found in healthy individuals.

Table 2

The qualitative and quantitative composition of oral fluid in the control group and in patients with inflammatory processes of the periodontium against the background of gastrointestinal diseases ($\lg M \pm m$, COE/ml)

№	Groups of microorganisms	Number of microbes in 1 ml of saliva			
		Control group n=30		Patients of Groups 1 and 2 n=108	
		Detection frequency, %	Number in 1 ml	Detection frequency, %	Number in 1 ml
1	Lactobacilli	90	4,55±0,11	8	2,01±0,15
2	Pepto Streptococcus	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.salivaruis	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 coli	12	0,74±0,01	38	2,33±0,1
9	Proteus	3	0,21±0,01	20	2,09±0,10
10	Clebsiella	3	0,82±0,02	39	1,93±0,02
11	Veillonella	100	2,32±0,10	100	3,94±0,03
12	Candida fungi	45	2,03±0,18	82	4,38±0,20
13	Total number of aerobics	-	5,25±0,12	-	7,90±0,28
14	Total anaerobes	-	5,61±0,14	-	3,66±0,15

In the control group of healthy individuals, Str.salivaruis, Veillonella, and Peptostreptococcus (100%) dominated, followed by Str.mitis (90%) and Str.mutans (67%). The average incidence rates were recorded for Staphylococcus epidermidis (48%) and Candida (45%). The lowest frequency was observed for gram-negative bacteria, including escherichia (12%), proteus, and clebsiella (3%).

Conclusion

In conclusion, a thorough analysis of the data obtained from both study groups revealed an amazing degree of similarity and identity in the results. This fact was reflected in Table 12, where the 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 periodontal diseases against the background of gastrointestinal diseases, but also open up new horizons for understanding the complex relationships between the oral microflora and the general state of human health. Our research clearly shows that the disbalance of the oral microbiome can be a consequence not only of local pathologies, but also can reflect more global changes in the body associated with disorders of the gastrointestinal tract. This highlights the need for an integrated approach to studying the interaction between systemic and local diseases, which can significantly contribute to the development of new diagnostic, prevention, and treatment strategies.

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