

MICROBIOLOGICAL STUDIES OF THE ORAL FLORA IN THE SHORT AND LONG-TERM FOLLOWING ORTHOPEDIC RESTORATION OF DENTAL IMPLANTS

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Abstract

On a patient with installed dental implants and having a system of implant-abutment connections using a fixing screw, the microbiological landscape of the oral cavity was studied in the dynamics of observation with and without the transition of the platform to the abutment. All patients were divided into 2 groups: group 1 consisted of 9 patients with an implant-abutment system without switches; 2 group made up 10 schemes with the transition of the platform to the abutment.

The material for the microbiological study was a biomaterial from the soft tissue mucosa around the abutment. The study of the dynamics of the microbial flora in patients with the transition of the platform to the abutment relative to the indicators before prosthetics, showing a decrease in the quantitative indicators of the representatives of both its stabilizing and aggressive components.

Introduction

The microflora of the oral cavity is formed through the evolutionary process between the human body and microorganisms, creating a unique, complex, and stable microbiocenosis that serves as a favorable environment for the growth and sustenance of microbial life (1, 3, 4).

The protective role of normal microbial flora against pathogenic and opportunistic bacteria is attributed to its synthesis of bactericidal substances (such as acidophilin, lactocidin, lactolin, and hydrogen peroxide) and organic acids (lactic, acetic, ketoglutaric, and succinic). During their life cycle, many microorganisms in the oral cavity produce organic acids that contribute to the development of dental caries. Furthermore, under certain conditions, some microorganisms can trigger profound pathological processes within the oral cavity (2, 5, 6).

Considering the foregoing, the study of the oral cavity's microbiocenosis during various orthopedic procedures is of great importance, as the failure rate resulting from such dental interventions remains high (7, 8, 9). When using a two-piece implant, the presence of a gap between the implant and the abutment is inevitable. Bacteria and their metabolic byproducts can colonize this space, potentially initiating an inflammatory reaction in the soft tissues surrounding the implant.



The objective of the study was to investigate the microbiological landscape of the oral cavity in individuals with and without the use of the platform-switching method during prosthetics on implants.

Materials and Methods

The study was conducted during the orthopedic stage of treatment at the Department of Orthopedic Dentistry of the Tashkent State Dental Institute on patients who had received two-stage dental implants (i.e., with an implant-abutment connection system using a fixation screw) manufactured by the IMPRO company. All patients were diagnosed with "Partial Secondary Edentulism" and were divided into 2 groups: Group 1 consisted of 9 patients with an implant-abutment system without platform switching; Group 2 included 10 patients with a platform-switched element on the abutment. The study was carried out by observing the patients over time - before the placement of the orthopedic structure, and then 3 and 6 months after its placement.

The material for the microbiological study was biomaterial taken from the mucosa of the soft tissues surrounding the abutment. The materials were delivered to the microbiology laboratory within 3 hours.

Results

In the biomaterial obtained from the mucosa of the soft tissues around the abutment, an almost complete list of microorganisms characteristic of the oral microbiocenosis was identified. A comparative analysis of the occurrence of microorganisms showed that the species of microorganism does not depend on the implant system, its connection type, or the size and duration of placement.

Almost half of the resident species of microorganisms are facultative and obligate anaerobic streptococci, represented by **S. mutans**, **S. sanguis**, **S. mitis**, **S. salivarius**, and peptostreptococci; the other half are represented by Veillonella and diphtheroids. The remaining oral microflora (staphylococci, lactobacilli, bacteroids, Neisseria, fungi) are detected in significantly smaller quantities than streptococci, Veillonella, and diphtheroids. These permanent representatives of the oral microflora have formed as a result of the mutual adaptation of macro- and microorganisms. An analysis of the bacterial association structure in the peri-implant cuff area, after implant placement but before prosthetics, reveals a relatively stable microflora composition. In all examined patients, microorganisms such as **S. mutans**, **S. salivarius**, **S. mitis**, Veillonella, peptostreptococci, and fusobacteria were detected in various concentrations (100%), while the incidence of staphylococci, mycobacteria, and anaerobic diphtheria was 30-40% (Table 1).

We initially assessed the microbial composition of the oral cavity in patients before prosthetics, which allowed us to conduct a comparative analysis of the changes in the quantitative composition of microorganisms in the first group of patients over time - before prosthetics, and at 3 and 6 months post-procedure.

After 3 months, a relative stabilization of the microflora composition was observed over time; that is, the representatives of the oral microflora we studied were detected with almost the same frequency and remained at nearly the same levels. Another important representative of the oral microbiocenosis is **Streptococcus salivarius**. Insignificant changes in its quantity were noted before prosthetics and after 3 and 6 months of observation. **Peptostreptococcus anaerobius**, a representative of anaerobic streptococci, was detected in quantities up to $6.2 \pm 0.21 \times 10^6$ CFU/g before prosthetics. After 3



months of observation, it decreased slightly to $4.1 \pm 0.20 \times 10^5$ CFU/g, but by the 6th month, an increase was noted, reaching $4.7 \pm 0.20 \times 10^5$ CFU/g. In this group of patients, an upward trend in the count of *Corynebacterium spp.* was observed, characterized by an increase during all observation periods compared to pre-prosthetic levels.

Table 1 Qualitative and quantitative composition of the primary oral microflora in individuals not switched to the platform (CFU/g)

Species of microorganisms	Periods of research		
	Before prosthetics	After 3 months	After 6 months
Streptococcus mutans	$(1,9 \pm 0,12) \times 10^4$	$(3,2 \pm 0,20) \times 10^{5*}$	$(3,6 \pm 0,19) \times 10^{5*}$
Streptococcus epidermidis	$(2,1 \pm 0,20) \times 10^5$	$(4,1 \pm 0,20) \times 10^{5*}$	$(4,5 \pm 0,21) \times 10^{5*}$
Streptococcus sanguis	$(4,2 \pm 0,21) \times 10^5$	$(4,1 \pm 0,21) \times 10^5$	$(5,2 \pm 0,19) \times 10^5$
Streptococcus salivarius	$(5,3 \pm 0,20) \times 10^6$	$(5,2 \pm 0,20) \times 10^6$	$(4,7 \pm 0,20) \times 10^6$
Neisseria spp.	$(4,4 \pm 0,21) \times 10^6$	$(2,6 \pm 0,21) \times 10^{5*}$	$(2,3 \pm 0,20) \times 10^{5*}$
Fusobacterium spp.	$(2,3 \pm 0,20) \times 10^4$	$(4,1 \pm 0,20) \times 10^{5*}$	$(4,5 \pm 0,21) \times 10^{5*}$
Staphylococcus aureus	$(5,1 \pm 0,20) \times 10^6$	$(4,8 \pm 0,21) \times 10^6$	$(4,2 \pm 0,20) \times 10^6$
Corynebacterium spp.	$(2,6 \pm 0,20) \times 10^5$	$(4,1 \pm 0,20) \times 10^{5*}$	$(4,5 \pm 0,21) \times 10^{5*}$
C.pseudodiphthericum	$(2,4 \pm 0,20) \times 10^6$	$(6,4 \pm 0,20) \times 10^5$	$(4,8 \pm 0,21) \times 10^5$
L.buccalis	$(1,8 \pm 0,20) \times 10^4$	$(5,6 \pm 0,20) \times 10^{4*}$	$(4,9 \pm 0,16) \times 10^{4*}$
V.parvula	$(8,6 \pm 0,19) \times 10^6$	$(3,0 \pm 0,20) \times 10^6$	$(3,2 \pm 0,22) \times 10^6$
B.gingivalis	$(5,8 \pm 0,11) \times 10^6$	$(6,6 \pm 0,18) \times 10^{4*}$	$(5,8 \pm 0,21) \times 10^{4*}$
Enterobacterium spp.	$(4,5 \pm 0,12) \times 10^6$	$(4,2 \pm 0,21) \times 10^{5*}$	$(4,5 \pm 0,20) \times 10^{5*}$
Peptostreptococcus anaerobius	$(6,2 \pm 0,21) \times 10^6$	$(4,1 \pm 0,20) \times 10^{5*}$	$(4,7 \pm 0,21) \times 10^{5*}$

Note: * - P < 0.05 difference is significant compared to the indicators before prosthetics.

We also identified representatives of aggressive microflora, among which it is necessary to identify Enterobacterium spp. It should be noted that their number decreased somewhat in the dynamics of observation. Identification of such nonspecific bacteria may indicate the presence of dysbiosis in the area of the implant-gingival contact. It is also necessary to note the presence of Staphylococcus aureus and the almost complete absence of dynamics during the observation period - $5.1 \pm 0.20 \times 10^6$ CFU/g at the beginning of the study and $4.2 \pm 0.20 \times 10^6$ CFU/g at the end of the observation period.

The study of the dynamics of microbial flora in patients who underwent prosthetics by the method of platform insertion in abutment showed that the quantitative indicators of representatives of its stabilizing and aggressive components were mainly reduced compared to pre-prosthetic indicators. Thus, at the 3rd month of observation, there is a slight increase in the number of S. mutans and S. epidermidis compared to the data before prosthetics. By the 6th month - a decrease in S. mutans and S. epidermidis is observed compared to the previous period, but remains slightly higher than the level of these indicators before prosthetics. Streptococcus sanguis before prosthetics decreased to $4.2 \pm 0.21 \times 10^5$ CFU/g, at 3 months to $3.2 \pm 0.16 \times 10^5$ CFU/g, and at the end of the study to $2.6 \pm 0.12 \times 10^5$ CFU/g.



Table 2 Qualitative and quantitative composition of the main microflora of the oral cavity in individuals with platform transition in abatment, CFU/g

Species of microorganisms	Periods of research		
	Before prosthetics	After 3 months	After 6 months
<i>S. mutans</i>	$(1,9\pm 0,12) \times 10^4$	$(2,8\pm 0,14) \times 10^4$	$(2,5\pm 0,15) \times 10^4$
<i>S.epidermidis</i>	$(2,1\pm 0,20) \times 10^5$	$(2,7\pm 0,21) \times 10^5$	$(2,4\pm 0,16) \times 10^5$
<i>S. sanguis</i>	$(4,2\pm 0,21) \times 10^5$	$(3,2\pm 0,16) \times 10^5$	$(2,6\pm 0,12) \times 10^5$
<i>S.salivarius</i>	$(5,3\pm 0,20) \times 10^6$	$(4,4\pm 0,23) \times 10^{5*}$	$(3,8\pm 0,16) \times 10^{5*}$
<i>Neisseria spp.</i>	$(4,4\pm 0,21) \times 10^6$	$(2,1\pm 0,18) \times 10^{5*}$	$(1,64\pm 0,23) \times 10^{5*}$
<i>Fusobacterium spp.</i>	$(2,3\pm 0,20) \times 10^4$	$(3,6\pm 0,17) \times 10^4$	$(2,8\pm 0,21) \times 10^4$
<i>S. aureus</i>	$(5,1\pm 0,20) \times 10^6$	$(3,8\pm 0,21) \times 10^{5*}$	$(3,2\pm 0,20) \times 10^{5*}$
<i>Corynebacterium spp.</i>	$(2,6\pm 0,20) \times 10^5$	$(5,4\pm 0,23) \times 10^5$	$(5,8\pm 0,21) \times 10^5$
<i>C.pseudodiphthericum</i>	$(2,4\pm 0,20) \times 10^6$	$(5,6\pm 0,20) \times 10^{5*}$	$(4,4\pm 0,18) \times 10^{5*}$
<i>L.buccalis</i>	$(1,8\pm 0,20) \times 10^4$	$(4,6\pm 0,20) \times 10^4$	$(3,8\pm 0,16) \times 10^4$
<i>V.parvula</i>	$(8,6\pm 0,19) \times 10^6$	$(4,0\pm 0,20) \times 10^{5*}$	$(2,8\pm 0,12) \times 10^{5*}$
<i>B.gingivalis</i>	$(5,8\pm 0,11) \times 10^6$	$(4,2\pm 0,14) \times 10^{4*}$	$(3,8\pm 0,21) \times 10^{4*}$
<i>Enterobacterium spp.</i>	$(4,5\pm 0,12) \times 10^6$	$(3,2\pm 0,21) \times 10^{5*}$	$(2,5\pm 0,20) \times 10^{5*}$
<i>P.anaerobius</i>	$(6,2\pm 0,21) \times 10^6$	$(3,1\pm 0,20) \times 10^{5*}$	$(2,7\pm 0,21) \times 10^{5*}$

Note: * - $P < 0.05$ difference is significant compared to the indicators before prosthetics.

For anaerobic streptococci *Peptostreptococcus anaerobius*, the quantitative indicator of patients in this group before prosthetics decreased by 3 months of observation and decreased to $2.7\pm 0.21 \times 10^5$ CFU/g by 6 months. Before prosthetics, the number of corynebacteria was at the level of $2.6\pm 0.20 \times 10^5$ CFU/g, and in the dynamics of observation, an increase in its level was noted by the 3rd and 6th months.

During their life cycle, corynebacteria actively reduce molecular oxygen and synthesize vitamin K, which contributes to the development of obligate anaerobes. Accordingly, it can be noted that the increase in the number of detected corynebacteria in subsequent observation periods positively characterizes the dynamics of oral microflora in these patients.

The quantitative indicator of enterococci, representatives of aggressive microflora, positively characterized the dynamics of the microbial landscape of the oral cavity at all stages of this observation, that is, if before prosthetics their number was $4.5\pm 0.12 \times 10^6$ CFU/g, then a decrease in their number was observed over 3 months, and at 6 months they were $2.5\pm 0.20 \times 10^5$ CFU/g.

Thus, the results of the study allow us to conclude that with the use of the platform transfer method in abatment, a positive microbiocenosis is formed in patients after 6 months of use of the prosthetic structure on implants, but a high level of representatives of all the microorganisms we studied remains valuable. At the same time, the microbial landscape is characterized by the distribution of stabilizing species (*Streptococcus salivarius*, *Streptococcus sanguis*, *Corynebacterium spp.*). At the same time, the proliferation of microorganisms, such as enterobacteria, enterococci, which are not characteristic of the oral cavity in the examined material, indicates the development of dysbiosis in the area of the implant-gingival connection.



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