

# SPECIFIC FEATURES OF ORAL CAVITY MICROBIOCENOSIS IN CHILDREN USING NON-REMOVABLE ORTHODONTIC APPLIANCES

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## INTRODUCTION

In modern Orthodontics, which is viewed as an integral part of dentistry, non-removable appliances are the most widespread approach as they allow moving and keeping under control the teeth position in the sagittal, frontal and transversal planes [2, 7]. Growing fundamental knowledge, extensive clinical experience, and advanced technology have led to the development of bracket systems that meet not functional requirements alone yet also aesthetic ones [1, 10]. Experts have proven that orthodontic treatment comes along with a high level of microbial contamination on the teeth surface, dental systems and the tongue, which can trigger the development of the oral cavity dysbacteriosis [3, 4, 5, 6, 8, 9]. Studying the oral cavity microflora in patients undergoing orthodontic treatment is of great interest not only for researchers but for practicing experts as well since it allows preventing the development of complications associated with a sharp increase in the potentially pathogenic microorganisms titer.

### *Aim of study:*

to evaluate the qualitative and quantitative composition of aerobic microorganisms representing the oral microbiota in patients with dental issues through their orthodontic treatment with bracket-based appliances.

To complete the objectives, a study was carried out focusing on the range and quantity, as well as on the presence of microorganisms' pathogenicity fac-

tors in the gingival groove contents, dental plaque, in scraping from the tongue back mucosa and in saliva. The study involved 86 school students aged 12–18 with various occlusion issues. The children were examined prior to, and through the orthodontic treatment (treatment course – 8–18 months). The control group included children of the same age undergoing a routine examination and who did not require orthodontic treatment. The sampling and the microbiological study were performed employing the respective classical methods. The work was carried out at the Microbiology Department, Stavropol State Medical University. The data were processed with the STATISTICA (Stat Soft Russia) and BIOSTAT application software.

## RESULTS

When the non-removable orthodontic appliances were installed, reliable qualitative changes in the microorganism status were identified in children in two biotopes — saliva and dental plaque. In the saliva of adolescents aged 12–18, 93% of the cases were found to have streptococci; in 71% of the cases — lactobacilli; in 56% — staphylococci (including *Staphylococcus aureus*); less than 48% were yeast-like fungi of the *Candida* genus, and enterobacteria. The prevalence of these microorganisms was 8–43% lower, compared to similar rates in healthy children.

In 73% of the cases the dental plaque was found to contain streptococci, which is 34% above the normal value. Less than 49% were yeast-like fungi of the *Candida* genus, staphylococcus and lactobacillus; the prevalence of these microorganisms was 18–32% lower compared to the normal values. Besides, *Staphylococcus aureus* was identified, which is not to be found in the healthy participants.

From the point when the non-removable orthodontic appliances were installed and for one year into the treatment, there were dynamic quantitative changes going on in terms of the oral aerobic microflora. The saliva, for instance, developed a higher concentration of *Candida* yeast-like fungi increased by 2 logs (from 3 to 4.9 lg CFU/ml) and lactobacteria by 1.6 logs (from 4.2 to 5.8 lg CFU/ml). The enterobacteria concentration went down from 4 to 3 lg CFU/ml. The streptococci and staphylococci

concentration was comparable to that of healthy people. *Staphylococcus aureus* and enterobacter were detected, which were not found in healthy adolescents. The dental plaque, when compared with the normal values, had a higher concentration of *Candida*, which increased by 1 log (from 2 to 3 lg CFU/g); besides, *Staphylococcus aureus* was found to appear. The staphylococcus and enterobacteria concentration was comparable with the normal range values. The gingival groove had a concentration of bacilli and *Candida* similar to that in healthy people. The amount of enterobacteria went down from 3 to 1.9 lg CFU/g, whereas the staphylococci level went up from 1.2 to 2.1 lg CFU/g. Enterobacter, diphtheroids and *Staphylococcus aureus* appeared, though, which had not been there in the healthy school students. The scraping from the back of the tongue were shown to have Enterobacter and *Staphylococcus aureus*, as well as an increased amount in the enterobacteria contents (by 4 logs — from 2 to 6.3 lg CFU/g) and streptococci (by 1 log — from 5 to 6 lg CFU/g) if compared to healthy children. The concentration values for *Neisseria* and *Staphylococcus* were comparable with the normal ones. The *Candida* concentration fell from 2.5 to 1.5 lg CFU/g, lactobacilli — from 3.1 to 2.1 lg CFU/g.

The systematic analysis of the obtained data suggests that orthodontic treatment is associated not only with changes in the oral aerobic microflora range leaning towards a lower prevalence of normal flora and a higher level of potentially pathogenic microflora, yet also entails specific quantitative changes. Besides, such changes in the microbial pattern can trigger dental complications in patients undergoing treatment with non-removable orthodontic appliances.

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