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## **COMPREHENSIVE ASSESSMENT OF ORAL MICROBIOTA IN PEDIATRIC PATIENTS WITH PERIODONTAL INFLAMMATORY DISORDERS**

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### **Relevance**

It is known that the oral cavity serves as a favorable environment for the proliferation and biological activity of numerous microorganisms [1-3]. In this context, along with the positive symbiotic interactions with the soft tissues of the periodontal complex, the negative effects of representatives of the normal microflora are also observed [4-6].

### **The Aim of the Study**

To determine the frequency of occurrence and etiopathogenetic significance of key microbiota present in the oral cavity among healthy individuals (control group - CG) and patients with various forms of periodontitis.

### **Materials and Methods**

In the study, a targeted main group (MG-1) consisting of 112 patients with periodontitis and a control group (CG - Group II) of 40 healthy individuals aged 30-55 underwent comprehensive examinations to assess the condition of the oral cavity (OC). During patient evaluations, key clinical criteria for periodontal tissue (PT) assessment included hyperemia, swelling, hygiene status, coloration of the oral mucosa (OM), and other visual indicators of periodontal complex pathology. These parameters were assessed using traditional methods and included indices such as the Gingival Index (GI), Papillary-Marginal-Attached Index (PMA), Periodontal Index (PI), and Community Periodontal Index of Treatment Needs (CPITN).



### Results and its Discussion

The results show that pathogenic obligate anaerobes were more frequently isolated from group MG-1, with representatives of *Porphyromonas gingivalis* (58%/65%), *Actinobacillus actinomycetemcomitans/Aggregatibacter actinomycetemcomitans* (56%/63%), *Fusobacterium nucleatum* (24%/27%), *Prevotella* spp. (26%/29%), and *Peptostreptococcus* spp. (23%/26%). A large proportion of *Peptostreptococcus* micros were found to be associated with this group. On the other hand, *Peptostreptococcus* spp. (46%/18%), *Veillonella* spp. (18%/7%), and *Actinomyces* spp. (13%/5%) were more prevalent in the healthy individuals (CG) group. Additionally, among the obligate anaerobes, *P. gingivalis* and *T. denticola*, both with aggressive properties, were identified as playing an active role in periodontal bleeding and tissue destruction.

### Conclusions

The use of both classic and molecular-genetic methods enhances the diagnostic accuracy of identifying the mixed microbial composition of periodontal pocket microorganisms, revealing individual differences in the frequency of microorganism encounters. In this case, combining these two methods in laboratory practice provides the opportunity to gather regional data on major pathogens.

**Keywords:** Anaerobic and aerobic microbes, Oral microflora, Periodontitis, Periodontogenic microorganisms.

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