

SUBGINGIVAL MICROBIOTA IN SEVERE CHRONIC PERIODONTITIS

Christina Popova¹, Velitchka Dosseva-Panova¹, Angelina Kisselova-Janeva², Vladimir E. Panov³

1) Department of Periodontology, Faculty of Dental Medicine, Medical University, Sofia, Bulgaria

2) Department of Imaging and Oral Diagnostics, Faculty of Dental Medicine, Medical University, Sofia, Bulgaria

3) Department of Conservative Dentistry and Oral Pathology, Faculty of Dental Medicine, Medical University, Varna, Bulgaria

SUMMARY

Literature data relate certain Gram-negative anaerobe microorganisms with advanced destructive periodontal lesion. There are some references which reported higher levels of periodontal pathogens by the red and orange complex in deep periodontal pockets. The aim of this study is to determine the presence of most important periodontal pathogens and *Candida spp.* in deep periodontal pockets in patients with severe chronic periodontitis. The results of this study indicate the presence of high levels of periodontal pathogens in a strong connection with periodontal disease in deep periodontal pockets of patients studied.

Key words: chronic periodontitis, periodontal pathogens, *Candida spp.*

BACKGROUND:

Studies have shown the presence of certain Gram-negative anaerobes in periodontal environment in chronic periodontitis and their involvement in the processes of progressive destruction of soft tissue and bone [1 -7] For some unidentified microorganism as periodontal pathogens such as viruses (cytomegalovirus, Epstein-bar), *Escherichia coli*, *Candida spp.*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* is also reported to be found in periodontal pockets in patients with periodontitis [8 - 14]. There are some references which reported higher levels of periodontal pathogens by the red and orange complex in periodontal pockets with a depth greater than 6mm [1, 2, 6, 7, 15, 16]. Elimination of pathogenic species of subgingival environment and the control of bacterial load leads to periodontal health and lack of clinical, microbiological and biochemical evidences for continued attachment loss during periodontal maintenance therapy.

OBJECTIVE:

To evaluate the pathogenic subgingival microbiota in periodontal pockets with probing depths > 6 mm. by Real time PCR (PET plus and CAT test) in patients with severe chronic periodontitis.

MATERIAL AND METHODS:

The study included 20 patients with advanced chronic periodontitis, selected free of systemic diseases and periodontal or any antibiotic treatment in last 6 months, aged 47,55 +/- 6,42 (average value). Subgingival samples were taken with sterile paper pins from the deepest periodontal pockets (PD>6 mm) in each patient. Standard commercially available tests are used for assessing the qualitative and quantitative composition of the subgingival microbiota by Real time PCR (PET plus and CAT test) (MIP Pharma GmbH). The study detects the presence and quantity of following periodontal pathogens: *Aggregatibacter actinomycetemcomitans*, *Porphyromonas gingivalis*, *Treponema denticola*, *Tannerella forsythia*, *Prevotella intermedia*, *Peptostreptococcus /Micromonas/ micros*, *Fusobacterium nucleatum*, *Eubacterium nodatum*, *Capnocytophaga gingivalis*, as well as *Candida spp.*: *Candida albicans*, *Candida glabrata*, *Candida krusei*, *Candida tropicalis*, *Candida parapsilosis*.

RESULTS:

The results of this study indicate the presence of high levels of periodontal pathogens in a strong connection with periodontal disease in deep periodontal pockets of patients studied (Fig.1. and Fig. 2.). Outcomes of the detection of fungal species did not indicate any presence of *Candida spp.* in deep periodontal pockets. Recorded few positive samples are not statistically significant (Fig.3.).

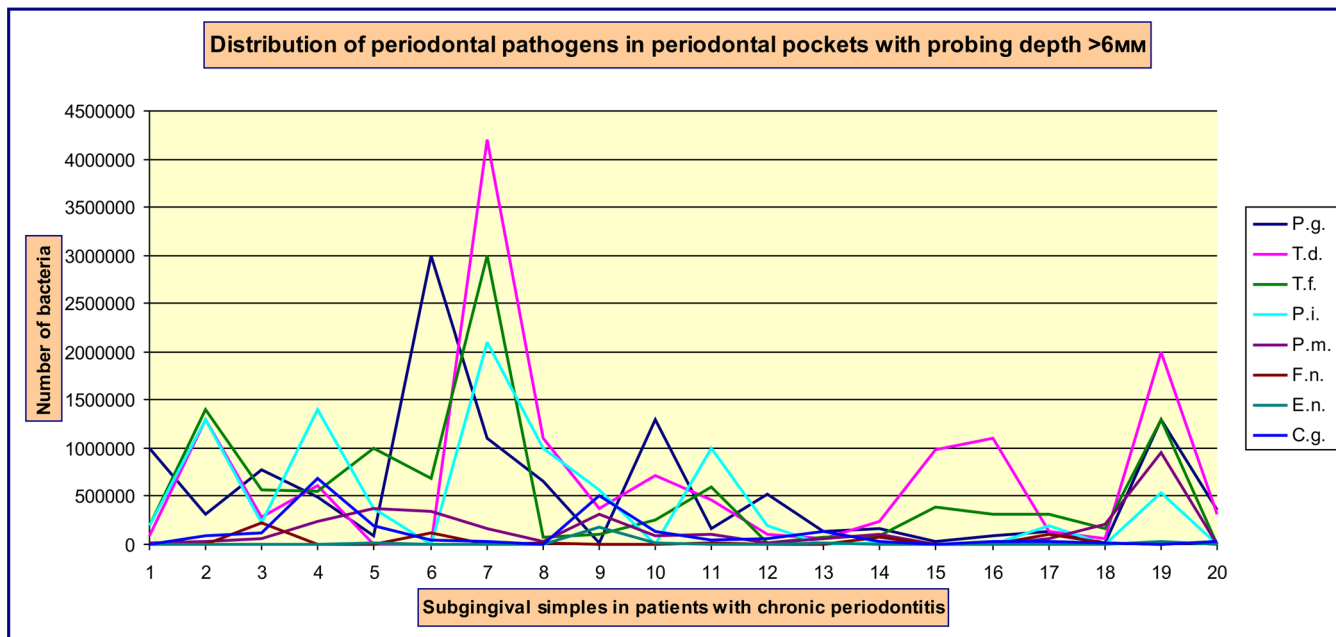


Fig. 1. Presence of periodontal pathogens in deep periodontal pockets.

The total number of microorganisms show a significant correlation only with *Tannerella forsythia* ($R = 0,46$) and a strong inverse correlation with the percentage of *Porphyromonas gingivalis* ($R = -0,71$) and *Peptostreptococcus micros* ($R = -0,60$). In patients with small total number was observed a small number of *Tannerella forsythia* and an increased percentage of *Porphyromonas gingivalis* and *Peptostreptococcus micros*.

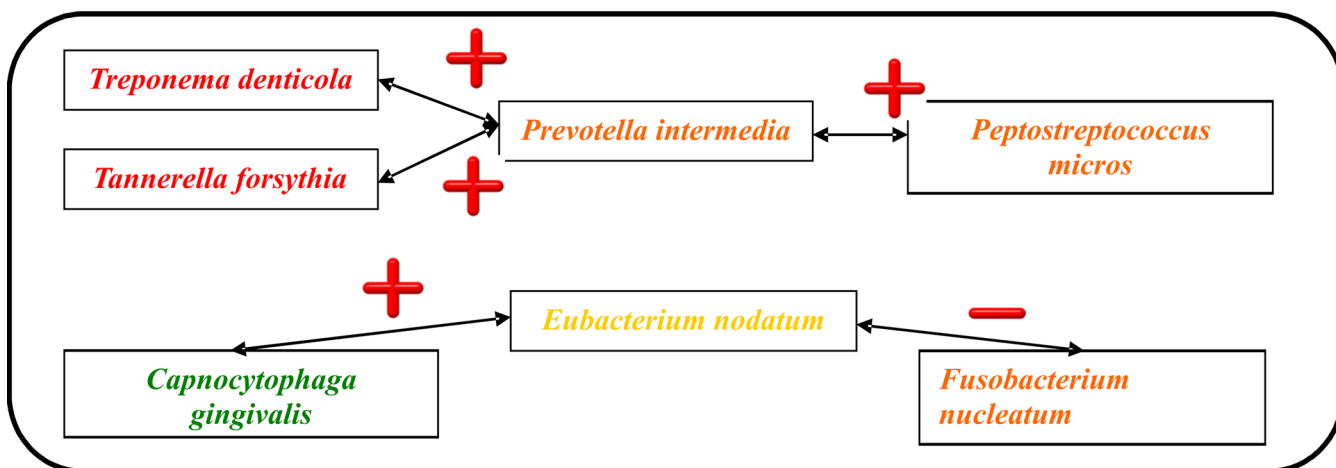


Fig.2. Relationship between detected bacteria - significant correlation is established between the amounts of the studied species of bacteria held at Spearman correlation analysis. The figure shows that in our study we established (presented with (+) and (-)) positive and negative correlation coefficients between different microorganisms.

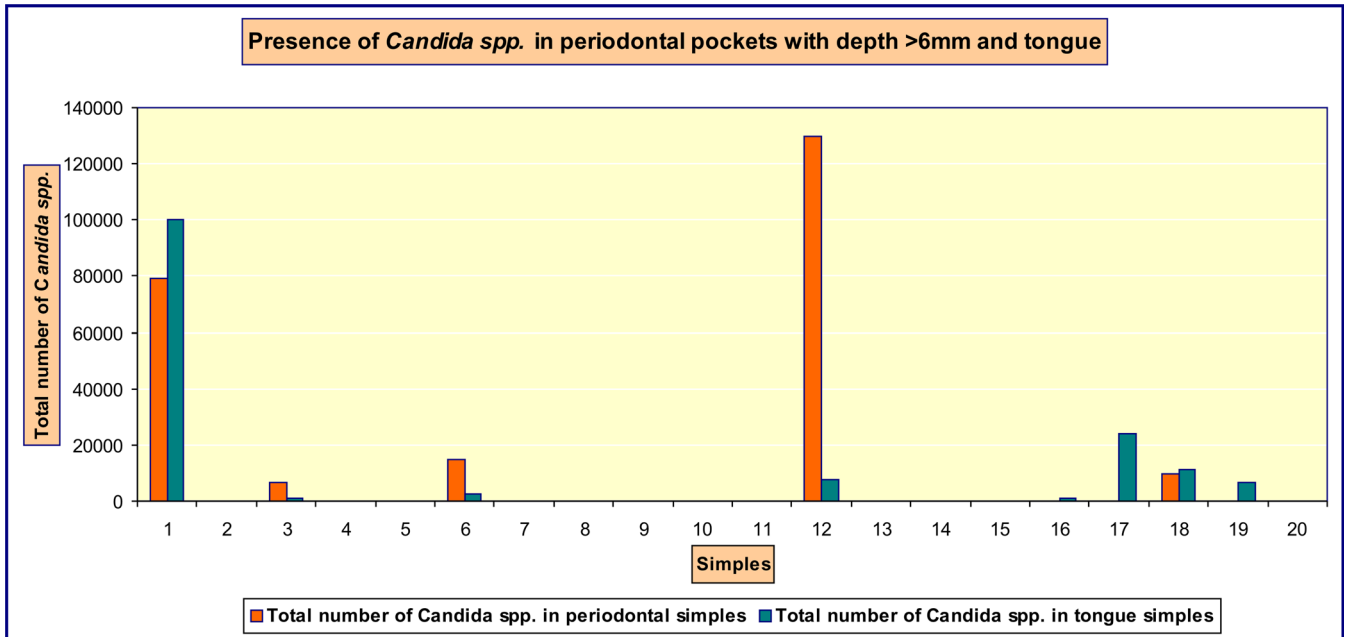


Fig. 3. Presence of *Candida* spp. in deep periodontal pockets in patient with chronic periodontitis.

DISCUSSION:

The analysis of subgingival microbiota in investigated patients with severe chronic periodontitis confirms data from the literature on the significance of key pathogens in the etiology and pathogenesis of periodontal diseases.

In recent years a great interest of *Candida albicans* has shown in conjunction with the severity of periodontal disease [7, 10, 11, 13, 16]. In dentistry this result from the fact that this is the most founded fungal microorganism in the human oral cavity. Many researchers have shown that *Candida albicans* lives in conditions of anaerobiosis [8, 9, 11, 17]. They detected *C. albicans* in several oral niches such as periodontal pockets, abscesses, apical periodontitis, root canals, radicular dentinal walls [10 - 15, 18, 19]. For this reason was the interest in our study to confirm or reject these suggestions. In result of present study we may confirm the data of the literature that show the presence of *Candida*

strains in deep periodontal pockets in low levels. In this study there is no correlation of *Candida* spp. presence and periodontal disease and consequently with pathogenesis of periodontitis. Although these results are not statistically verifiable to suggest any relation in cases with chronic periodontitis in generally healthy patients the detection of *Candida* spp. levels may be useful in cases with different systemic diseases and conditions considering the risk of *Candida* infection [12, 20].

CONCLUSION:

The results of this study did not show any presence of *Candida* spp. in periodontal pockets in patients with chronic periodontitis. At the same time there is a confirmation of the literature data for the strong association of chronic periodontitis with the main periodontal pathogens.

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Address for correspondence:

Professor Christina Popova, PhD, DM;
Department of Periodontology, Faculty of Dental Medicine,
1, Georgi Sofiiski str, 1431 Sofia, Bulgaria
E-mail: hrpopova@yahoo.com;