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Original Research

Assessment of periodontal pathogens in persisting periodontal pockets of endodontic origin

[1]Aftab Nawab, [2]Uzma Talath, [3]Vinay Kumar M B, [4]Sumati Patel, [5]Hiya Datta, [6]Dikshita Das

[1,3]Assistant Professor, Dept of Periodontics and Implantology, College of Dental Sciences, Davanagere, Karnataka, India;
[2]Assistant Professor, Dept of Biochemistry, SS Institute of Medical Science and Research Center, Davanagere, Karnataka, India;
[4,5,6]Postgraduate, Department of Periodontology, Babu Banarasi Das College of Dental Sciences, Lucknow, Uttar Pradesh, India

ABSTRACT:
Background: Porphyromonasgingivalis (Pg) and Tannerella forsythia (Tf) have been implicated as major pathogens in the etiology of periodontitis. The present study was conducted to assess periodontal pathogens in persisting periodontal pockets of endodontic origin. **Materials & Methods:** 60 patients of endodontic–periodontal lesion of both genderswere selected and subgingival plaque samples were collected and analyzed for quantification using the real-time polymerase chain reaction (RT-PCR).The cycle threshold (Ct) was recorded. The clinical parameters assessed were probing pocket depth, clinical attachment loss, plaque index, extent of destruction in the furcal region, and tooth mobility. **Results:** Pg, Pi, Th, Tf, Pm and Ef showed score 1 in 40%, 45%, 15%, 76%, 67% and 10%, score 2 in 56%, 55%, 85%, 14%, 33% and 90% and score 3 in 4% respectively. The difference was significant (P< 0.05). The mean cycle threshold levels forP gingivaliswas37.5, P intermedia was 37.9, T. denticola was 33.2, T. forsythia was 38.5, E. faecalis was 34.2 and for P. micra was 37.8. The difference was non- significant (P> 0.05). **Conclusion:** Ef and Td were found to be most prevalent. Porphyromonasgingivalis and Tannerella forsythia were in minimal to non-existent levels.
Key words: Bacteria, Periodontium, real-time polymerase chain reaction

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Corresponding author: Aftab Nawab, Assistant Professor, Dept of Periodontics and Implantology, College of Dental Sciences, Davanagere, Karnataka, India

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INTRODUCTION

Bacterial migration between the endodontium and periodontium may occur via dentin as well as via lateral and accessory root canals.[1] Controlled studies of this process are hampered by problems in sampling and in cultivation of periodonto-pathogenic bacteria. Infections of the two structures can find clinical expression in a therapy-refractory course of endodontic and/or periodontal diseases, since the untreated structure may form a pool for re-infection of the treated one.[2]

The environmental dynamics of these differing ecologic niches determine the dominant microorganisms and their capability to modulate the persistence of disease.[3] Porphyromonasgingivalis (Pg)and Tannerell a forsythia (Tf) have been implicated as major pathogens in the etiology of periodontitis and are commonly isolated together, implying the existence of an ecological relationship between them.[4] Treponema denticola (Td) has also been considered as a major pathogen in periodontitis and is correlated with chronic periodontitis. These three bacteria, which were categorized together as the red complex have also been frequently isolated from infected dental pulps.[5]

While certain key pathogens and bacterial groups play a dominant role in various forms of marginal periodontitis, in case of pulpo-periapical disease a correlation of groups of bacteria and the clinical course of an infection proves to be very difficult.[6]The present study was conducted to assess periodontal pathogens in persisting periodontal pockets of endodontic origin.

MATERIALS & METHODS

The present study comprised of 60 patients of endodontic–periodontal lesion of both genders.

All gave their written consent for the participation in the study.

Data such as name, age, gender etc. was recorded. Subgingival plaque samples were collected and analyzed for quantification using the real-time polymerase chain reaction (RT-PCR).he cycle threshold (Ct) was recorded. The clinical parameters assessed were probing pocket depth, clinical attachment loss, plaque index, extent of destruction in the furcal region, and tooth mobility. Radiographically acceptable obturation was assessed by a radiodense, root canal filling. Data thus obtained were subjected to statistical analysis. P value < 0.05 was considered significant.

RESULTS

Table I Quantitative assessment of organisms in plaque samples

Scores	Pg	Pi	Th	Tf	Pm	Ef	P value
Score 1	40%	45%	15%	76%	67%	10%	0.04
Score 2	56%	55%	85%	14%	33%	90%	0.02
Score 3	4%	0	0	0	0	0	0.05

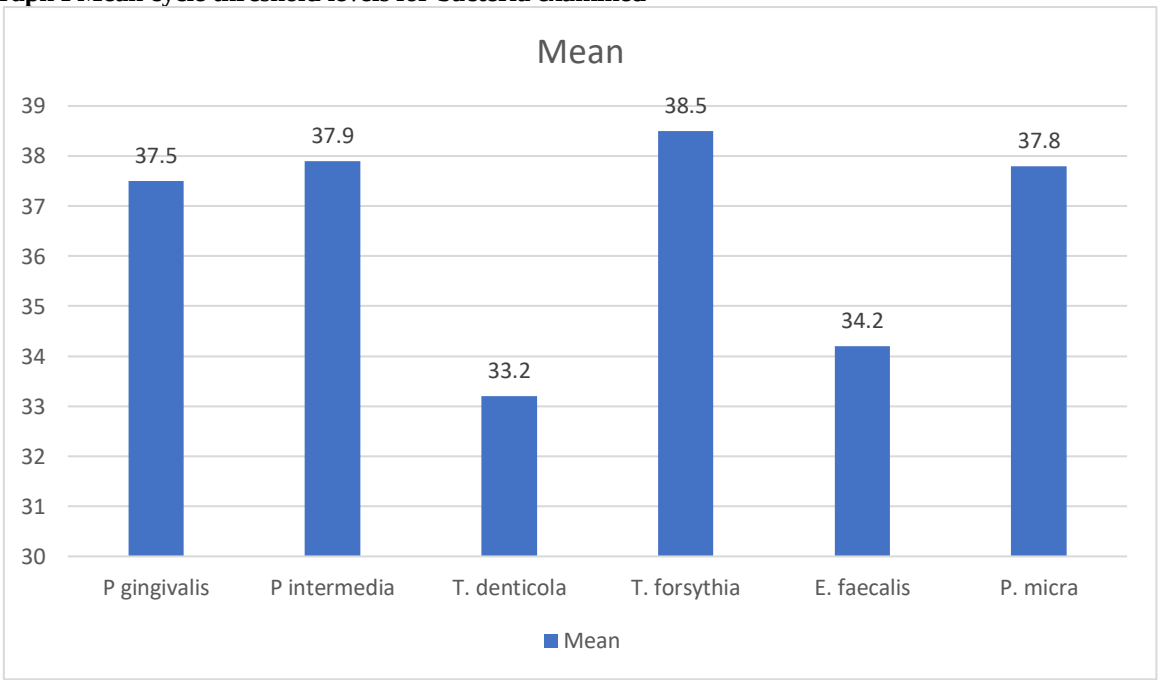
Table I shows that Pg, Pi, Th, Tf, Pm and Ef showed score 1 in 40%, 45%, 15%, 76%, 67% and 10%, score 2 in 56%, 55%, 85%, 14%, 33% and 90% and score 3 in 4% respectively. The difference was significant (P< 0.05).

Table II Mean cycle threshold levels for bacteria examined

Bacteria	Mean	P value
P gingivalis	37.5	0.81
P intermedia	37.9	
T. denticola	33.2	
T. forsythia	38.5	
E. faecalis	34.2	
P. micra	37.8	

Table II shows that mean cycle threshold levels for P gingivalis was 37.5, P intermedia was 37.9, T. denticola was 33.2, T. forsythia was 38.5, E. faecalis was 34.2 and for P. micra was 37.8. The difference was non-significant (P> 0.05).

Graph I Mean cycle threshold levels for bacteria examined



DISCUSSION

The challenges for a modern endodontology expand in proportion with the knowledge about the systemic importance of periodontal pathogens.[7] Adequate diagnostic methods are in the focus of present research.[8] Over the last decade PCR has been facilitating oral bacterial diagnostics substantially due to its rapidity, cost-effectiveness, independence of particular cultivation equipment and low demands on sample transportation and storage conditions.For the

detection of oral pathogens, PCR is an established method.[9] Once its specificity has been tested, it has low demands on sampling and sample transportation, since neither living nor cultivable bacteria are required. The total number of bacteria can be determined by means of a competitive quantitative polymerase chain reaction.[10]The present study was conducted to assess periodontal pathogens in persisting periodontal pockets of endodontic origin.

We found that Pg, Pi, Th, Tf, Pm and Ef showed score 1 in 40%, 45%, 15%, 76%, 67% and 10%, score 2 in 56%, 55%, 85%, 14%, 33% and 90% and score 3 in 4% respectively. Victor et al[11] in their study subgingival plaque samples were collected from fifty patients diagnosed with a primary endodontic and a secondary periodontal lesion that persisted even after completion of the root canal treatment. Clinical parameters such as probing pocket depth, clinical attachment level, plaque index, furcation, and tooth mobility were recorded. Real-time polymerase chain reaction was used to determine the possible association between six bacteria, which are frequently associated with periodontal and endodontic lesions.The mean cycle threshold value for Treponema denticola (Td) was found to be 33.74, and for Enterococcus faecalis (Ef), it was 34.39. With regard to clinical attachment loss, Td ($P < 0.04$) and Parvimonas micra ($P < 0.05$) had a significant correlation.

We found that mean cycle threshold levels forP gingivalis was 37.5, P intermedia was 37.9, T. denticola was 33.2, T. forsythia was 38.5, E. faecalis was 34.2 and for P. micra was 37.8.Rupf et al[12] found that periodontal pathogens often accompany endodontic infections and concluded that periodontic and endodontic pathways are critical in determining whether the cases will be refractory to conventional endodontic or periodontal therapy.The inflammatory by-products of pulpal origin may permeate through the apex or through smaller canals in the apical third of the root canal system and exposed dentinal tubules which in turn trigger an inflammatory vascular response in the periodontium. Among those are certain strains of bacteria and viruses which are encountered in periodontal inflammatory disease as well.

Ef is frequently found in association with unresolving lesions following endodontic treatment. It grows as a part of the biofilm on root canal walls and is also implicated in monoinfection in treated canals without synergistic support from other bacteria.[13] These factors make it highly resistant to antimicrobial agents. It also possesses many survival mechanisms to live in unfavorable conditions such as low oxygen, high pH, or poorly nutrient environment.[14]

The limitation the study is small sample size.

CONCLUSION

Authors found that Ef and Td were found to be most prevalent. Porphyromonasgingivalis and Tannerella forsythia were in minimal to non-existent levels.

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