



Comprehensive Evaluation of Microbials in Continuing Periodontal Pockets Related To Endodontic Pathologies: An Original Research Study

Dr. Apoorva Sharma,¹ Dr. Jyoti Sarin,² Dr. Nikita Sharma,³ Dr. Pulkit Arora,⁴ Dr. Megna Bhatt,⁵ Dr. Deeksha Tomar⁶

¹*Senior Lecturer, Department of Conservative and Endodontics, Shree Bankey Bihari Dental College and Hospital, Ghaziabad, Uttar Pradesh, India*

²*Reader, Department of Periodontics, I.T.S Dental College & Hospital, Greater Noida, Uttar Pradesh, India*

³*Senior Lecturer, Department of Conservative and Endodontics, Shree Bankey Bihari Dental College and Hospital, Ghaziabad, Uttar Pradesh, India*

⁴*Senior Lecturer, Department of Conservative and Endodontics, Shree Bankey Bihari Dental College and Hospital, Ghaziabad, Uttar Pradesh, India*

⁵*Senior Lecturer, Department of Conservative and Endodontics, Shree Bankey Bihari Dental College and Hospital, Ghaziabad, Uttar Pradesh, India*

⁶*Reader, Department of Conservative and Endodontics, Shree Bankey Bihari Dental College and Hospital, Ghaziabad, Uttar Pradesh, India*

Corresponding Author: Dr. Apoorva Sharma, Senior Lecturer,
Mail id: drapoorvasharma07@gmail.com

Abstract

Background and Aim: Dental therapy encompasses various aspects of supporting structures, including preventing and addressing lesions in the gingival sulcus. In contrast, endodontics primarily addresses pulp and periapical tissue-related conditions. The effectiveness of both periodontal and endodontic treatments relies on successfully eliminating these disease processes, whether they occur independently or as a combined lesion. The connection between periodontal and endodontic diseases has long been a topic of interest. **Materials and Methods & Results:** This paper aims to provide a comprehensive review of various facets of peri-endo lesions. Periodontal and endodontic diseases are diseases associated with biofilms. The presence of microorganisms in the canal (RC) and the complex microbiota of the periodontal pocket (PP) contribute to development of endodontic and periodontal diseases. This study performed a systematic analysis using state-of-the-art sequence data to assess the microbial composition of infected RC and PP in order to further evaluate the microbiome and check for possible cross-contamination between these sites. **Conclusion:** Within the limitations of the study authors concluded that the RC microbiota was less complex and assorted than PP and moreover there were intuitive between the microbial communities.

Keywords: Classification, Combined Lesions, Perio-Endo Lesion

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Introduction

Endodontic-periodontal diseases refer to the presence of both pulp and periodontal disease affecting the same tooth.^[1] When an infection occurs within the pulp tissue and is left

untreated, it can advance to pulpal necrosis and often results in the breakdown of periodontal tissues, leading to apical periodontitis. Conversely, severe periodontal disease can initiate or worsen the inflammatory processes within the pulp tissue. However, a pulp lesion develops when periodontal disease progresses from the root's apex to the main foramen.^[1-5] The most common diseases of the oral cavity are caused by bacterial biofilms formation and adhesion on tooth surfaces, such as caries and periodontitis.^[6-9] Highly pathogenic infectious biofilms are difficult to detect with diagnostic routine and inherently tolerable as recurrent host antibiotic therapies.^[10] In addition, biofilms propagate antibiotic-resistant fibers from a horizontal plane gene transfer process. Considering the relationship between microorganisms as an etiological factor in endodontic and periodontal diseases as well as the fact that microbial communication between these sites is implicated in disease progression, This study was performed to evaluate the bacterial composition of RC and infected periodontal pockets (PP) and check for the possibility of cross-contamination between these sites.

Materials and Methods

Study Population: Twelve patients with mixed endodontic and periodontal diseases were selected for this study. Physical examination revealed necrotic pulp and clinical signs of periodontal disease showed the lesion parameters described by Gomes et.al. (2015). Pulp condition is assessed using thermal endurance tests and cavity tests. Condition was assessed based on the presence or absence of clinical signs or symptoms during percussion and palpation. Periodontal disease assessed using periodontal probes at six sites of affected teeth and x-rays.^[11]

Sample Collection

Periodontal pocket and canal samples were obtained prior to initiation of both treatments. Samples were collected according to the protocol established by Gomes et al.(2015). Three consecutive sterile paper dots were held in place for 60 s, then added to a sterile tube containing 1 mL of VMGA III transport medium, and then frozen at $-70\text{ }^{\circ}\text{C}$ until processing.

Evaluation of the RC and PP Microbiomes

Research to evaluate the interrelationship (communication) of RC and PPs was performed using metagenomic methods and next-generation sequencing. DNA extracted from 12 RCs and PPs using the QI-Aamp DNA Micro Kit. Raw sequence data were punched for pre-processing and deletion. Statistical and comparative analyzes were performed using the Microbiome Analyst resources.^[12-14]

The readings submitted for analysis were filtered by the following criteria setting:

- (i) The minimum number is four;
- (ii) Count filters with a prevalence of 10%.

For comparative studies, a low variance filter was applied, based on the interregional range and features less than 10% were removed. Data were normalized against the minimum library size and normalized to the total value of reads obtained before any statistics comparison.^[15]

Statistical studies were performed including Venn diagrams, clustering, correlation, co-occurrence and calculation of diversity indices among observed OTUs for phylum, genus and species.

Results

Microbiome of the RCs and PPs: The RC microbiome showed the presence of eight bacterial strains, including: Firmicutes (75.68%), Proteobacteria (10.5%), Actinobacteria (7.96%), Bacteroidetes (4.03%), Synadystetes (1.43%), Spirochetes (0.2%), Chloroflexi (0.14%) and Fusobacteria (0.07%).^[16] A total of 68 bacterial genera were identified in the RC, of which 37 genera were OTU percentage is over 0.1%. The microbiomes of the PPs showed the presence of nine phyla, including Firmicutes (57.86%), Proteobacteria (24.8%), Actinobacteria (5.62%), Saccharibacteria (TM7) (3.72%), Fusobacteria (3.13%), Bacteroidetes (2.96%), Synergistetes (1.29%), Spirochaetes (0.39%) and Chloroflexi (0.23%).

Comparative Studies of RC and PPs Microbiomes: The Venn diagram of the phyla observed for RCs and PPs showed the presence of eight common taxa among the studied sites (Figure a). In contrast, a similar study conducted for genus revealed 68 common taxa between RCs and PPs. A total of five genera were identified only in PPs, including Bacteroidales [G-2], Saccharibacteria (TM7) [G-1], Lachnoanaerobaculum, Aggregatibacter and Lachnospiraceae G (Figure b).

Table 1: Basic Statistical Explanation with Level Of Significance Evaluation Using Pearson Chi-Square Test [For Root Canal Samples (RC)]

Group	Mean	Std.	Std.	95%	Pearson	df	Level of
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		Deviation	Error	CI	Chi-Square Value		Significance (p value)
RC	1.62	0.948	0.647	1.96	1.324	1.0	0.02*
*p<0.05 significant							

Table 2: Basic Statistical Explanation with Level Of Significance Evaluation Using Pearson Chi-Square Test [For Periodontal Pocket (PP)]

Group	Mean	Std. Deviation	Std. Error	95% CI	Pearson Chi-Square Value	df	Level of Significance (p value)
PP	1.31	0.637	0.466	1.96	2.152	2.0	0.08
*p<0.05 significant							

Table 3: Comparison Among The 2 Study Groups Using One-Way Anova [For RC & PP]

Variables	Degree of Freedom	Sum of Squares Σ	Mean Sum of Squares $m\Sigma$	F	Level of Significance (p)
Between Groups	3	2.751	1.238	2.1	0.001*
Within Groups	22	5.303	0.118		-
Cumulative	121.43	11.001	*p<0.05 significant		

Discussion

Over 700 species of bacteria have been identified in the oral cavity.^[25] It can lead to pulp and RC contamination.^[26] Many of these microorganisms are Potential agent of infection in RC and PP.^[2,17] Our study confirmed a large body of research on RC microbial populations, including Eubacteria, Fusobacteria. The genera Peptostreptococcus, Porphyromonas, Prevotella and Streptococcus^[2,17-18]. However, other extremely important genera have been identified among the most common in RC, namely, Enterococcus, Parvimonas, Stomatobaculum, Peptoniphilaceae [G-1], Mogibacteria, Olsenella, Bacteroidaceae [G-1], Filifactor, Oribacteria and Pseudomonas, among others. Statistical methods were used to evaluate the relationship between the RC and PP bacterial communities, observing a correlation between the endodontic and periodontal microbiota, although large numbers of bacteria were visible than the single expenditure for PP. Anti-microbial treatment was a major progress without noteworthy decrease in possibly fatalities, starting a modern period of irresistible illness treatment.^[19] Long time after this pharmaceutical advancement with anti-

microbial treatment, it brought extreme causes with respect to developmental reactions to the specific weight applied by anti-microbials, coming about in microbial species safe to for all intents and purposes all known drugs (antibiotics), which strengthens the comes about gotten in this investigate since numerous markers for anti-microbial resistance qualities were found.^[20] Fortifying the writing showing that bacteremia may be related with bacterial endotoxins from tainted canals, showing dangers for systemic complications.

Conclusions

Within the limitations of the study authors concluded highly remarkable inferences. The RC microbiota was less complex and assorted than PP. There were intuitive between the microbial communities. Shared species can signalize communication between the endodontic and periodontal microbiomes. We too emphasize that microorganisms related to endodontic-periodontal illnesses have a solid relationship with systemic maladies. Authors expect some other studies to be performed with larger samples size and comprehensive analysis.

Conflicts of Interest: The authors deny any conflicts of interest.

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