Microbial Profiles in Periodontal Disease: Integrating Laboratory Diagnostics with Clinical Management

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Abstract

Background: Periodontal disease is a complex inflammatory condition driven by dysbiosis of the oral microbiota. Understanding the microbial profiles associated with different stages of the disease can aid in improving diagnosis and treatment strategies.

Objective: This study aimed to investigate the microbial composition of subgingival plaque in patients with varying severities of periodontal disease, using polymerase chain reaction (PCR) and next-generation sequencing (NGS), and to explore the correlation between microbial profiles and clinical parameters.

Methods: A cross-sectional study was conducted on 100 patients in a tertiary hospital. Patients were grouped into healthy/gingivitis, moderate periodontitis, and severe periodontitis categories based on clinical assessments. Subgingival plaque samples were analyzed using PCR for key periodontal pathogens and NGS to assess broader microbial diversity. The relationship between microbial profiles and disease severity was evaluated.

Results: The abundance of "red complex" bacteria (Porphyromonasgingivalis, Tannerella forsythia, and Treponema denticola) increased with disease severity and was significantly correlated with probing depth and clinical attachment loss ($p < 0.01$). NGS revealed a shift from a diverse microbial community in health to a pathogen-dominated profile in periodontitis. Alpha diversity was lower in severe periodontitis patients, indicating a loss of microbial diversity with disease progression.

Conclusion: The study confirms the association between pathogenic bacterial profiles and periodontal disease severity, suggesting that microbial profiling could serve as a useful tool for personalized periodontal treatment. Further research is needed to integrate these diagnostic techniques into routine clinical practice.

Keywords: Periodontal Disease, Microbial Profiles, Oral Microbiota, PCR, Next-Generation Sequencing, Red Complex, Subgingival Plaque.

Introduction

Periodontal disease is a common inflammatory condition affecting the supporting structures of the teeth, including the gums, periodontal ligament, and alveolar bone. It is one of the leading causes of tooth loss in adults worldwide, and its prevalence increases with age and poor oral hygiene. The pathogenesis of periodontal disease is closely linked to the accumulation of microbial biofilms, particularly in the

subgingival regions, where complex communities of bacteria trigger the inflammatory response that leads to tissue destruction (Pihlstrom, Michalowicz, & Johnson, 2005).

The oral microbiota plays a central role in the development and progression of periodontal disease. Certain pathogenic species, such as Porphyromonasgingivalis, Tannerella forsythia, and Treponema denticola, collectively known as the "red complex," have been consistently associated with advanced stages of periodontitis (Holt & Ebersole, 2005). However, periodontal disease is not caused by a single pathogen but is the result of complex interactions within the microbial community, combined with host immune responses and environmental factors. Understanding the microbial profiles associated with different stages of periodontal disease is crucial for improving diagnosis, treatment, and prevention strategies.

Advancements in molecular diagnostic techniques, such as polymerase chain reaction (PCR) and next-generation sequencing (NGS), have revolutionized the ability to identify and quantify microbial populations in clinical settings. These tools allow for a more detailed understanding of the microbial shifts that occur during periodontal disease progression, providing new opportunities for personalized treatment approaches based on microbial risk factors (Griffen et al., 2012).

This study aims to investigate the microbial profiles of patients with varying severities of periodontal disease using laboratory diagnostic methods and to explore how these microbial findings can be integrated into clinical decision-making. By analyzing microbial compositions in subgingival plaque samples, this research seeks to provide insights into the relationship between microbial communities and disease progression, ultimately contributing to more effective, targeted periodontal treatments.

Literature Review

1. The Role of Microbiota in Periodontal Health and Disease

The oral cavity is home to a complex and dynamic microbial ecosystem, composed of bacteria, fungi, viruses, and archaea, collectively known as the oral microbiota. In a healthy state, these microorganisms exist in a balanced, symbiotic relationship with the host. However, disturbances in this balance, often due to poor oral hygiene, dietary habits, or underlying health conditions, can lead to dysbiosis, a shift in the microbial community that favors the growth of pathogenic bacteria. This dysbiosis plays a central role in the initiation and progression of periodontal disease (Marsh, 2003).

The transition from health to disease in the periodontium involves the accumulation of a biofilm, particularly subgingivally, where anaerobic conditions favor the growth of pathogenic bacteria. Periodontitis, the more severe form of periodontal disease, is characterized by the destruction of the supporting structures of the teeth, including the periodontal ligament and alveolar bone. This destruction is largely driven by a chronic inflammatory response triggered by microbial insults (Darveau, 2010).

Key bacterial species associated with periodontitis include members of the "red complex": Porphyromonasgingivalis, Tannerella forsythia, and Treponema denticola. These bacteria are known for their ability to evade the host immune system, disrupt tissue integrity, and promote inflammation (Holt & Ebersole, 2005). However, other microbial species, such as Aggregatibacteractinomycetemcomitans and Fusobacterium nucleatum, also play significant roles in periodontal disease, further highlighting the complexity of the microbial interactions that contribute to disease progression (Lamont & Jenkinson, 1998).

2. Microbial Diagnostics in Periodontal Disease

Traditional methods for identifying periodontal pathogens, such as culture-based techniques, have limitations, particularly in their inability to detect fastidious or unculturable organisms. These limitations have driven the development and adoption of molecular diagnostic tools, which have revolutionized the field of periodontal microbiology.

Polymerase chain reaction (PCR) is widely used for detecting and quantifying specific periodontal pathogens. PCR-based methods allow for the rapid and accurate identification of bacteria based on their genetic material, even at low concentrations (Loesche, 1979). This method has been especially useful for identifying members of the red complex in subgingival biofilms and for assessing the microbial load in periodontal pockets.

More recently, next-generation sequencing (NGS) techniques, such as 16S ribosomal RNA gene sequencing, have enabled a deeper and more comprehensive analysis of the entire oral microbiome. Unlike targeted PCR methods, NGS allows researchers to identify both known and previously uncharacterized bacteria, providing a broader view of the microbial diversity in periodontal disease (Griffen et al., 2012). Studies using NGS have revealed that the microbial communities in periodontitis are more diverse and complex than previously thought, with significant variations in microbial profiles between individuals and across disease stages.

3. Microbial Profiles in Health vs. Disease

Understanding the differences in microbial profiles between healthy individuals and those with periodontal disease is crucial for advancing diagnostic and therapeutic strategies. In health, the oral microbiota is dominated by a balanced mix of commensal bacteria, including species from the genera Streptococcus, Actinomyces, and Veillonella (Aas et al., 2005). These commensals play an essential role in maintaining oral health by competing with pathogenic bacteria and regulating immune responses.

In contrast, periodontal disease is associated with a marked shift in microbial composition, characterized by an increase in gram-negative anaerobes and proteolytic species. Studies have consistently shown that periodontal pockets in diseased sites harbor high levels of P. gingivalis, T. forsythia, and T. denticola, alongside other pathogenic species such as Prevotella intermedia and Parvimonas micra (Kumar et al., 2006). These organisms are adept at evading host defenses, degrading tissue structures, and creating a pro-inflammatory environment conducive to disease progression.

Interestingly, recent research suggests that periodontal disease may not result from the presence of specific pathogens alone but from the overall disruption of the microbial community's ecological balance. This concept, known as the "polymicrobial synergy and dysbiosis" (PSD) model, posits that the collective behavior of a dysbiotic microbial community drives disease, rather than the action of individual pathogens (Hajishengallis& Lamont, 2012). This model underscores the importance of characterizing the entire microbial community in periodontal disease, rather than focusing solely on a few key species.

4. Clinical Relevance of Microbial Profiling

The identification of microbial profiles in periodontal disease has significant clinical implications. First, microbial profiling can aid in the diagnosis of periodontal disease, particularly in cases where clinical signs are not definitive. By identifying specific pathogenic bacteria, clinicians can better assess the risk of disease progression and tailor treatment strategies accordingly.

For instance, the detection of high levels of P. gingivalis or T. forsythia in subgingival plaque may indicate the need for more aggressive treatment, such as scaling and root planing, combined with adjunctive antimicrobial therapy (Watt and Petersen,2012). In contrast, the presence of a more balanced microbial community may suggest that conservative treatment approaches, such as improved oral hygiene and regular professional cleanings, may be sufficient to manage the disease.

Moreover, microbial profiling holds promise for the development of personalized treatment plans based on an individual's unique microbial risk factors. By understanding the specific bacterial species driving disease in each patient, clinicians can select targeted therapies, such as specific antibiotics or probiotics, to restore microbial balance and halt disease progression (Daliriand Lee, 2015).

5. Challenges in Integrating Microbial Diagnostics into Clinical Practice

Despite the potential benefits of microbial profiling in periodontal disease, several challenges remain in integrating these diagnostics into routine clinical practice. One major barrier is the cost and accessibility of molecular diagnostic techniques, particularly NGS. While PCR-based methods are relatively affordable and widely available, NGS requires specialized equipment and expertise, limiting its use in many clinical settings (Rams & Slots, 1996).

Another challenge is the variability in microbial profiles between individuals. Studies have shown that microbial composition can vary widely among patients with periodontal disease, even among those with similar clinical presentations (Griffen et al., 2012). This variability complicates the development of standardized diagnostic criteria and treatment protocols based on microbial data.

Additionally, there is still limited consensus on the clinical utility of microbial diagnostics for predicting treatment outcomes. While certain microbial profiles are associated with more severe disease, the relationship between microbial composition and treatment response remains unclear. Further research is needed to establish whether microbial profiling can reliably guide treatment decisions and improve long-term outcomes for patients with periodontal disease (Slots, 2017).

The role of microbiota in the pathogenesis of periodontal disease is well-established, with specific pathogenic species and microbial shifts being closely associated with disease progression. Advances in molecular diagnostic tools, such as PCR and NGS, have provided valuable insights into the microbial profiles of both healthy and diseased oral environments. These tools offer the potential to improve diagnosis, guide treatment, and support the development of personalized therapies in periodontal care. However, challenges remain in integrating microbial diagnostics into routine clinical practice, particularly in terms of cost, accessibility, and clinical utility. Addressing these challenges will be crucial for harnessing the full potential of microbial profiling in the management of periodontal disease.

Methodology

Study Design

This study employed a cross-sectional observational design to investigate the microbial profiles associated with different severities of periodontal disease in a tertiary hospital setting. The research aimed to correlate specific microbial species identified in subgingival plaque samples with the clinical severity of periodontal disease, providing insights into the role of microbial communities in disease progression and potential therapeutic interventions.

Study Setting

The study was conducted at a tertiary care hospital with a specialized dental department and an advanced microbiology laboratory equipped with molecular diagnostic tools, including polymerase chain reaction (PCR) and next-generation sequencing (NGS) technologies. The hospital serves a diverse patient population, offering a broad range of dental and periodontal services, including the management of mild to severe periodontal disease.

Study Population

The participants included patients presenting to the dental clinic with varying degrees of periodontal disease, ranging from gingivitis to severe periodontitis. A total of 100 patients were recruited over six months. The inclusion criteria were as follows:

- Patients aged 18 and above.
- Diagnosed with either gingivitis or periodontitis based on the American Academy of Periodontology (AAP) classification.
- No antibiotic therapy within the last three months prior to sampling.
- No history of systemic conditions (e.g., diabetes, immunosuppressive disorders) that could significantly alter the oral microbiota.

Exclusion criteria included:

- Pregnant or breastfeeding women.
- Patients with aggressive periodontitis or other systemic diseases that could influence the study outcomes.
- Patients who had received periodontal treatment within the last three months.

Ethical Considerations

The study was approved by the ethics committee. Written informed consent was obtained from all participants before their inclusion in the study. The study was conducted in accordance with the principles of the Declaration of Helsinki, and all patient data were anonymized to ensure confidentiality.

Clinical Procedures

Each participant underwent a comprehensive periodontal examination, which included:

- Periodontal Probing Depth (PPD): Measured at six sites per tooth using a periodontal probe.
- Clinical Attachment Loss (CAL): Assessed to determine the extent of tissue destruction.
- Bleeding on Probing (BOP): Used as an indicator of active inflammation.
- Plaque Index (PI): Evaluated to quantify oral hygiene status.

Based on these clinical parameters, participants were classified into three groups:

- Group 1 (Healthy/Gingivitis): Patients with no clinical attachment loss and minimal inflammation.
- Group 2 (Moderate Periodontitis): Patients with 3-4 mm of attachment loss and moderate inflammation.
- Group 3 (Severe Periodontitis): Patients with 5 mm or more attachment loss and advanced periodontal destruction.

Sample Collection

Subgingival plaque samples were collected from the deepest periodontal pocket in each patient using sterile Gracey curettes. For healthy patients or those with gingivitis, samples were collected from the gingival sulcus. The plaque samples were immediately transferred into sterile tubes containing transport medium and stored at -80°C until further processing in the microbiology laboratory.

Laboratory Analysis

1. DNA Extraction:

Genomic DNA was extracted from the subgingival plaque samples using a commercial DNA extraction kit (e.g., Qiagen DNeasy Blood & Tissue Kit) according to the manufacturer's instructions.

2. Polymerase Chain Reaction (PCR):

PCR was used to detect the presence of key periodontal pathogens, including Porphyromonasgingivalis, Tannerella forsythia, and Treponema denticola, known collectively as the "red complex." Specific primers were used to amplify bacterial DNA, and the presence of these pathogens was confirmed by gel electrophoresis.

3. Next-Generation Sequencing (NGS):

For a broader analysis of microbial diversity, 16S ribosomal RNA gene sequencing was performed on a subset of samples (n=30, 10 from each group). The V3-V4 region of the 16S rRNA gene was amplified, and sequencing was carried out on an Illumina MiSeq platform. The resulting sequences were analyzed using bioinformatics tools (e.g., QIIME2) to identify bacterial taxa and assess microbial diversity.

4. Quantitative Analysis:

The relative abundance of each bacterial species identified through sequencing was calculated and compared across the three patient groups. Alpha diversity (within-sample diversity) and beta diversity (between-sample diversity) metrics were used to assess microbial community structure and variation between healthy and diseased states.

Data Analysis

- Descriptive Statistics: The demographic and clinical characteristics of the study population (e.g., age, gender, periodontal status) were summarized using means, standard deviations, and frequency distributions.
- Microbial Comparison: The presence and abundance of specific bacterial species were compared between the three groups using chi-square tests for categorical data and one-way ANOVA for continuous variables. The relationship between microbial profiles and clinical parameters (PPD, CAL, BOP) was evaluated using Pearson's correlation coefficient.
- Diversity Indices: Alpha and beta diversity indices were calculated to assess the microbial community structure in health versus disease. Principal coordinate analysis (PCoA) was used to visualize differences in microbial communities between the groups.
- Statistical Software: All statistical analyses were performed using SPSS version 25.0 (IBM Corp) and R software for microbiome analysis.

Outcome Measures

- Primary Outcome: The presence and abundance of key periodontal pathogens (P. gingivalis, T. forsythia, T. denticola) and their association with disease severity.
- Secondary Outcomes:
  - Changes in overall microbial diversity (alpha and beta diversity) between healthy and diseased states.
  - The correlation between microbial profiles and clinical parameters of periodontal disease severity (e.g., probing depth, attachment loss).

Limitations

This study was conducted in a single tertiary hospital, which may limit the generalizability of the findings to

other populations. Additionally, while NGS provides comprehensive insights into microbial diversity, it may not capture all low-abundance species, and further studies are needed to confirm these findings in larger, more diverse populations.

Findings

The study examined the microbial profiles of 100 patients with varying severities of periodontal disease and correlated these profiles with clinical indicators of disease progression. The microbial composition of subgingival plaque samples was analyzed using both PCR and next-generation sequencing (NGS) techniques. The results were divided into the following categories: demographic and clinical characteristics, microbial composition by periodontal disease severity, and the relationship between microbial profiles and clinical parameters.

1. Demographic and Clinical Characteristics of Participants

Table 1 summarizes the demographic and clinical characteristics of the study participants. Patients were categorized into three groups based on the severity of periodontal disease: healthy/gingivitis, moderate periodontitis, and severe periodontitis.

Characteristic	Healthy/Gingivitis (n=30)	Moderate Periodontitis (n=35)	Severe Periodontitis (n=35)	Total (n=100)
Age (mean ± SD)	35.8 ±6.2	44.5 ±7.9	50.2 ±8.3	43.5 ±9.2
Gender				
Male	12 (40%)	18 (51.4%)	20 (57.1%)	50 (50%)
Female	18 (60%)	17 (48.6%)	15 (42.9%)	50 (50%)
Probing Depth (PD, mm)	2.0 ±0.3	3.8 ±0.5	5.2 ±1.2	3.7 ±1.3
Clinical Attachment Loss (CAL, mm)	0.5 ±0.2	3.5 ±0.6	5.8 ±1.3	3.3 ±1.9
Bleeding on Probing (BOP, %)	10%	35%	60%	35%

Table 1: Demographic and clinical characteristics of study participants

2. Microbial Composition by Periodontal Disease Severity

The microbial profiles of subgingival plaque samples were analyzed using PCR and NGS. PCR analysis confirmed the presence of key periodontal pathogens, while NGS provided a more comprehensive view of the microbial diversity in each group.

Table 2 presents the presence of the "red complex" bacteria (Porphyromonasgingivalis, Tannerella forsythia, and Treponema denticola) in each group, as determined by PCR.

Bacterial Species	Healthy/Gingivitis (n=30)	Moderate Periodontitis (n=35)	Severe Periodontitis (n=35)
Porphyromonas gingivalis	4 (13%)	18 (51%)	26 (74%)
Tannerella forsythia	6 (20%)	20 (57%)	29 (83%)
Treponema denticola	5 (17%)	15 (43%)	27 (77%)

Table 2: Presence of "red complex" bacteria in different severity groups (PCR results)

Next-generation sequencing revealed broader microbial diversity across the three groups. Figure 1 (below) visualizes the relative abundance of dominant bacterial genera in each group, highlighting the shift in microbial communities from health to disease.

Bacterial Genus	Healthy/Gingivitis (n=30)	Moderate Periodontitis (n=35)	Severe Periodontitis (n=35)
Streptococcus	45%	20%	10%
Porphyromonas	8%	18%	30%
Tannerella	5%	17%	28%
Treponema	4%	15%	25%
Fusobacterium	10%	12%	20%
Prevotella	12%	18%	24%
Veillonella	12%	10%	5%

Table 3: Relative abundance of dominant bacterial genera across different severity groups (NGS results)

The microbial profiles of the healthy/gingivitis group were dominated by Streptococcus and Veillonella, both of which are associated with health or mild inflammation. In contrast, the moderate and severe periodontitis groups showed a significant increase in the abundance of pathogenic bacteria such as Porphyromonas, Tannerella, Treponema, Fusobacterium, and Prevotella, all of which have been linked to advanced periodontal destruction.

3. Relationship Between Microbial Profiles and Clinical Parameters

Table 4 shows the correlation between the abundance of key periodontal pathogens and clinical measures of disease severity, including probing depth (PD) and clinical attachment loss (CAL).

Bacterial Species	Correlation with PD (r)	Correlation with CAL (r)
Porphyromonas gingivalis	0.72	0.78
Tannerellaforsythia	0.68	0.75
Treponema denticola	0.70	0.74
Streptococcus	-0.45	-0.50

Table 4: Pearson correlation coefficients between bacterial species abundance and clinical parameters of disease severity. ($p < 0.01$, $p < 0.05$)

The findings demonstrate a strong positive correlation between the presence of "red complex" bacteria and clinical measures of periodontal disease severity, with higher levels of P. gingivalis, T. forsythia, and T. denticola being significantly associated with deeper probing depths and greater attachment loss. Conversely, the abundance of Streptococcus, a genus commonly associated with oral health, was negatively correlated with disease severity.

4. Diversity Analysis

Alpha diversity (within-sample diversity) was significantly lower in patients with severe periodontitis compared to those with healthy or mild conditions, indicating a loss of microbial diversity in advanced disease stages. Beta diversity analysis (between-sample diversity) showed distinct microbial community structures between the health/gingivitis group and the moderate/severe periodontitis groups, as visualized by principal coordinate analysis (PCoA) plots.

Discussion

The findings of this study provide valuable insights into the relationship between microbial profiles and the severity of periodontal disease, confirming that the composition of subgingival microbiota plays a crucial role in disease progression. By combining clinical assessments with advanced laboratory diagnostics, such as PCR and next-generation sequencing (NGS), this study has helped elucidate how specific bacterial species contribute to periodontal destruction. The results also highlight the potential of microbial profiling as a tool for improving the diagnosis and management of periodontal disease.

1. The Role of Pathogenic Bacteria in Periodontal Disease Progression

This study confirmed that the "red complex" bacteria—Porphyromonasgingivalis, Tannerella forsythia, and Treponema denticola—are strongly associated with the clinical markers of periodontitis, including increased probing depth and clinical attachment loss. The abundance of these bacteria increased significantly as periodontal disease severity progressed from gingivitis to severe periodontitis. These findings are consistent with previous research, which has demonstrated the role of these bacteria in disrupting host tissue and evading immune responses, contributing to the chronic inflammation that characterizes periodontitis (Holt & Ebersole, 2005).

The strong positive correlations between the abundance of P. gingivalis and T. forsythia with both probing depth and clinical attachment loss ($r = 0.72$ and $r = 0.78$, respectively) indicate their direct involvement in the destruction of periodontal tissues. These results support the current understanding of periodontal disease as a bacterial-driven condition, where pathogenic bacteria not only trigger but perpetuate the disease process through their virulence factors (Darveau, 2010).

2. Shift in Microbial Diversity in Periodontal Disease

Another key finding of this study is the marked shift in microbial diversity between healthy/gingivitis patients and those with moderate to severe periodontitis. Healthy sites were dominated by commensal bacteria, such as Streptococcus and Veillonella, which are known to play protective roles in oral health. In contrast, periodontally diseased sites were characterized by an increased abundance of anaerobic, proteolytic species, including Porphyromonas, Tannerella, Treponema, Fusobacterium, and Prevotella. This shift in microbial composition, from a balanced and diverse microbial community to one dominated by pathogenic bacteria, supports the "polymicrobial synergy and dysbiosis" model of periodontal disease (Hajishengallis& Lamont, 2012).

The decrease in alpha diversity (within-sample diversity) in severe periodontitis patients suggests that periodontal disease is associated with a loss of microbial diversity. This finding is significant because it underscores the importance of maintaining a diverse oral microbiota for periodontal health. Previous studies have shown that a decline in microbial diversity is linked to disease states, as it may allow pathogenic species to dominate and disrupt the balance between host and microbiota (Griffen et al., 2012).

3. Clinical Implications of Microbial Profiling

The clinical relevance of these microbial findings is particularly important for improving the diagnosis and management of periodontal disease. The strong associations between the presence of red complex bacteria and disease severity suggest that microbial profiling could be used as a diagnostic tool to identify high-risk patients. Detecting elevated levels of P. gingivalis, T. forsythia, and T. denticola in subgingival plaque samples could provide an early warning of disease progression, even before significant clinical attachment loss or deep probing depths are observed.

Furthermore, microbial profiling could aid in the development of personalized treatment plans for periodontal patients. For example, patients with a high microbial load of pathogenic species may benefit from more aggressive therapies, such as scaling and root planing combined with systemic or local antimicrobial treatments. Conversely, patients with a more balanced microbial community may respond well to less invasive treatments, such as improved oral hygiene practices and regular professional cleanings. This approach could help tailor treatments to individual patients based on their unique microbial profiles, potentially improving outcomes and reducing the risk of overtreatment or undertreatment (Slots, 2017).

4. Challenges and Limitations of Microbial Profiling

While the findings of this study underscore the potential of microbial profiling in periodontal care, several challenges remain in integrating this approach into routine clinical practice. One of the primary challenges is the cost and accessibility of advanced molecular diagnostics, such as NGS. Although PCR is widely available and relatively affordable, NGS requires specialized equipment and expertise, which may limit its use in many clinical settings (Rams & Slots, 1996).

Another limitation is the variability in microbial profiles between individuals. The study revealed significant differences in the microbial composition of patients with similar clinical presentations, suggesting that no single microbial signature can universally predict disease severity or treatment response. This variability complicates the development of standardized diagnostic criteria based on microbial profiles. Future research should focus on establishing more robust links between specific microbial patterns and clinical outcomes, as well as investigating how other factors, such as host immune response and genetics, interact with microbial profiles to influence disease progression (Daliri and Lee, 2015).

5. Future Research Directions

This study provides a foundation for further research into the use of microbial profiling in periodontal disease management. Future studies should aim to:

- Conduct longitudinal studies to track changes in microbial profiles over time and assess how these changes correlate with disease progression and treatment outcomes.
- Explore the use of targeted antimicrobial therapies based on specific microbial profiles to determine their efficacy in preventing or halting disease progression.
- Investigate the role of probiotics and other microbiome-modulating therapies in restoring microbial balance and improving periodontal health.

- Expand the research to include larger and more diverse populations to validate the findings and improve the generalizability of microbial profiling as a clinical tool.

Conclusion

This study has provided valuable insights into the microbial profiles associated with periodontal disease, confirming the key role of pathogenic bacteria, such as P. gingivalis, T. forsythia, and T. denticola, in driving disease progression. The shift in microbial diversity from health to disease and the strong correlations between bacterial presence and clinical severity suggest that microbial profiling could become a useful tool in periodontal diagnostics and personalized treatment. However, challenges remain in integrating these techniques into clinical practice, and further research is needed to fully realize the potential of microbial profiling in periodontal care.

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