Oral Microbiome Changes Associated with Periodontal Treatment: A Clinical and Microbiological Analysis

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Abstract

This study aimed to evaluate the changes in the oral microbiome following scaling and root planing (SRP) in patients with chronic periodontitis. Conducted at a tertiary hospital, the study involved adult patients aged 30-65 years. Plaque samples were collected at baseline and 6 weeks post-SRP and analyzed using next-generation sequencing (NGS). Significant improvements were observed in clinical parameters, including probing pocket depth (PPD), clinical attachment level (CAL), and bleeding on probing (BOP). Additionally, there was a marked reduction in the relative abundance of key periodontal pathogens, such as *Porphyromonas gingivalis*, *Tannerella forsythia*, and *Treponema denticola*, and an increase in beneficial microbial species. These findings suggest that SRP is effective in improving clinical outcomes and promoting a favorable shift in the oral microbiome, highlighting the importance of microbial dynamics in periodontal health.

Keywords: Periodontal Disease, Oral Microbiome, Scaling and Root Planing, Dysbiosis, Next-Generation Sequencing

Introduction

Periodontal disease is a complex inflammatory condition affecting the supporting structures of teeth and is largely driven by shifts in the oral microbiome. A healthy oral cavity hosts a diverse microbial community that maintains equilibrium through a delicate balance between beneficial and potentially pathogenic species. However, when this balance is disrupted, pathogenic microorganisms can proliferate, leading to the development and progression of periodontal disease (Hajishengallis, 2015). The role of the oral microbiome in periodontal health has received increasing attention as researchers seek to understand how shifts in microbial communities contribute to disease development and the effectiveness of treatment strategies.

Periodontal therapy aims to reduce pathogenic bacterial loads, alter microbial composition, and re-establish a healthy balance in the oral environment. Scaling and root planing (SRP), a standard treatment for periodontitis, has been demonstrated to reduce clinical signs of inflammation and improve periodontal health. However, the exact changes in the microbial profile following SRP and how these changes correlate with clinical outcomes remain a topic of active investigation (Slots, 2017). Recent advancements in molecular microbiology have provided deeper insights into these changes, allowing for a more comprehensive understanding of the oral microbiome and its response to treatment.

The concept of dysbiosis—an imbalance in the microbial community that favors pathogenic species—is crucial in understanding periodontal disease progression. By analyzing microbial shifts following periodontal therapy, it is possible to gain insights into the dynamics of dysbiosis and recovery in the oral environment (Griffen et al., 2012). This study aims to investigate changes in the composition of the oral microbiome in response to periodontal treatment, focusing on the shift from a dysbiotic to a more balanced microbial community. Understanding these microbial dynamics could offer valuable information for improving clinical outcomes and tailoring future periodontal interventions.

Literature Review

The oral microbiome is a dynamic and complex ecosystem that plays a crucial role in maintaining oral health and preventing disease. Numerous studies have demonstrated that a stable microbial community is essential for maintaining periodontal health, whereas shifts in this community can lead to the onset of periodontal disease (Wade, 2013). Specifically, periodontal disease has been associated with an increase in pathogenic bacteria, such as *Porphyromonasgingivalis*, *Tannerella forsythia*, and *Treponema denticola*, collectively known as the red complex, which are strongly implicated in disease progression (Socransky et al., 1998). These bacteria have been shown to possess virulence factors that promote tissue destruction and evade host immune responses.

Scaling and root planing (SRP) is the gold standard for treating periodontal disease, and it is well documented that SRP reduces the bacterial load and improves clinical parameters, such as pocket depth and bleeding on probing (Chapple et al., 2015). However, the changes in the composition of the oral microbiome post-SRP are still being explored, and studies have reported varied outcomes. For instance, research by Feres et al. (2015) demonstrated that SRP led to a significant reduction in red complex bacteria, while also promoting an increase in beneficial microbial species. Other studies have highlighted that although SRP can reduce pathogenic bacterial populations, complete eradication is rare, and some pathogenic species may persist or re-emerge over time (Sbordone&Bortolaia, 2003).

Recent advances in next-generation sequencing (NGS) technologies have enabled a more detailed characterization of the oral microbiome, providing valuable insights into the microbial shifts that occur in response to periodontal therapy. Studies using NGS have demonstrated that successful periodontal therapy is associated with a shift from a dysbiotic microbial community dominated by pathogenic species to a more diverse and balanced community (Griffen et al., 2012). Additionally, research has indicated that the resilience of the oral microbiome—that is, its ability to return to a healthy state after disruption—may be a key factor in determining the long-term success of periodontal treatment (Dabdoub et al., 2016).

Another important aspect of periodontal disease management is the role of host-microbial interactions. The host immune response plays a significant role in modulating the composition of the oral microbiome, and periodontal therapy aims not only to reduce pathogenic bacteria but also to modulate the host response (Hajishengallis& Lamont, 2012). Studies have shown that effective periodontal therapy can lead to a decrease in inflammatory mediators, such as interleukin-1β and tumor necrosis factor-α, which are typically elevated in periodontitis (Teles et al., 2013). These changes in the host immune response are thought to contribute to the restoration of a healthy oral microbiome.

The concept of dysbiosis is central to understanding the microbial etiology of periodontal disease. Dysbiosis refers to an imbalance in the microbial community that favors the proliferation of pathogenic species at the expense of beneficial ones (Hajishengallis, 2015). The microbial shifts observed in periodontitis are

characterized by an increase in Gram-negative anaerobes, which are associated with inflammation and tissue destruction. Research has shown that effective periodontal therapy can help restore microbial homeostasis by reducing the abundance of these pathogenic species and promoting a more balanced microbial community (Slots, 2017).

While SRP remains the cornerstone of periodontal therapy, adjunctive treatments have also been explored to enhance microbial and clinical outcomes. The use of antimicrobial agents, probiotics, and host-modulatory therapies has been investigated for their ability to further reduce pathogenic bacterial loads and promote a healthy oral microbiome (Teughels et al., 2008). For example, studies have shown that the use of locally delivered antimicrobials, such as chlorhexidine or minocycline, can enhance the effects of SRP by selectively targeting pathogenic bacteria (Rams et al., 2011). Similarly, probiotics have been suggested as a means of promoting beneficial microbial species, thereby contributing to the re-establishment of a healthy microbial balance (Gruner et al., 2016).

In conclusion, the literature highlights the importance of understanding the microbial changes that occur following periodontal therapy, as these changes are crucial for achieving and maintaining periodontal health. While SRP is effective in reducing pathogenic bacterial loads and improving clinical outcomes, the persistence of some pathogenic species and the variability in microbial shifts underscore the need for further research. Advanced molecular techniques, such as NGS, offer promising avenues for better understanding these microbial dynamics and tailoring periodontal interventions to improve long-term clinical success.

Methodology

This study was conducted at a tertiary hospital and involved adult patients diagnosed with chronic periodontitis. The study aimed to evaluate changes in the oral microbiome following scaling and root planing (SRP). Ethical approval was obtained from the ethics committee, and written informed consent was obtained from all participants prior to enrollment.

Study Population

Participants were recruited from the periodontal clinic of the tertiary hospital. Inclusion criteria included adults aged 30-65 years with a clinical diagnosis of chronic periodontitis, characterized by clinical attachment loss, probing pocket depth ≥5 mm, and radiographic evidence of alveolar bone loss. Exclusion criteria included individuals with systemic conditions affecting periodontal health (e.g., diabetes mellitus), those who had received antibiotics or periodontal treatment within the last three months, smokers, and pregnant or lactating women.

Study Design

This study employed a pre- and post-treatment observational design. Baseline clinical periodontal parameters, including probing pocket depth (PPD), clinical attachment level (CAL), and bleeding on probing (BOP), were recorded for each participant. Plaque samples were collected from the deepest periodontal pocket in each quadrant using sterile paper points. Participants then underwent SRP by a trained periodontist.

Sample Collection and Processing

Plaque samples were collected at baseline (prior to SRP) and at 6 weeks post-SRP. Sterile paper points were inserted into periodontal pockets for 30 seconds to collect subgingival plaque. The samples were immediately placed in sterile transport media and transported to the microbiology laboratory for analysis.

DNA was extracted from the plaque samples using a commercial DNA extraction kit, following the manufacturer's protocol.

Microbial Analysis

The composition of the oral microbiome was analyzed using next-generation sequencing (NGS) targeting the 16S ribosomal RNA gene. Sequencing was performed using the Illumina MiSeq platform, and the resulting sequences were processed and analyzed using QIIME2 software. Operational taxonomic units (OTUs) were assigned based on sequence similarity to reference databases. The relative abundance of key bacterial species, including *Porphyromonasgingivalis*, *Tannerella forsythia*, and *Treponema denticola*, was determined and compared between baseline and post-treatment samples.

Clinical Outcome Measures

The primary clinical outcome measures were changes in PPD, CAL, and BOP. These parameters were assessed at baseline and 6 weeks post-SRP to determine the effectiveness of treatment. The secondary outcome measure was the change in the composition of the oral microbiome, focusing on the reduction in pathogenic species and the increase in beneficial microbial diversity.

Statistical Analysis

Data were analyzed using SPSS software (version 25.0). Descriptive statistics were used to summarize the baseline characteristics of the study population. Paired t-tests were used to compare clinical parameters (PPD, CAL, BOP) and microbial abundance between baseline and post-treatment samples. A significance level of $p < 0.05$ was considered statistically significant.

Findings

The results of this study demonstrate significant changes in both clinical parameters and the composition of the oral microbiome following SRP. The findings are summarized in the tables below.

Clinical Outcomes

Clinical Parameter	Baseline (Mean ± SD)	Post-SRP (Mean ± SD)	p-value
Probing Pocket Depth (PPD)	5.8 ±1.2 mm	3.9 ±1.0 mm	< 0.001
Clinical Attachment Level (CAL)	6.2 ±1.3 mm	4.5 ±1.1 mm	< 0.001
Bleeding on Probing (BOP)	78%	32%	< 0.001

The data in Table 1 indicate a significant reduction in PPD, CAL, and BOP following SRP ($p < 0.001$), highlighting the effectiveness of SRP in improving clinical periodontal health.

Microbial Composition Changes

Bacterial Species	Baseline Relative Abundance (%)	Post-SRP Relative Abundance (%)	p-value
Porphyromonas gingivalis	12.3	4.5	< 0.001
Tannerella forsythia	8.9	3.2	< 0.001
Treponema denticola	7.1	2.9	< 0.001
Beneficial Microbial Species	20.4	35.7	< 0.001

Table 2 shows significant reductions in the relative abundance of key pathogenic species, including *Porphyromonasgingivalis*, *Tannerella forsythia*, and *Treponema denticola* ($p < 0.001$). Additionally, there was a significant increase in the relative abundance of beneficial microbial species, indicating a shift towards a more balanced and healthy oral microbiome.

These findings suggest that SRP is effective not only in improving clinical outcomes but also in promoting a favorable shift in the oral microbiome, reducing pathogenic bacteria, and enhancing microbial diversity.

Discussion

The findings of this study provide valuable insights into the impact of scaling and root planing (SRP) on both clinical outcomes and the composition of the oral microbiome in patients with chronic periodontitis. The significant reduction in probing pocket depth (PPD), clinical attachment level (CAL), and bleeding on probing (BOP) observed post-SRP demonstrates the clinical effectiveness of SRP in reducing the signs of periodontal disease. These results are consistent with previous studies that have highlighted the role of SRP as an essential non-surgical intervention for managing periodontal disease (Chapple et al., 2015).

One of the most noteworthy outcomes of this study is the significant shift in the oral microbiome composition following SRP. Specifically, there was a marked reduction in the abundance of key periodontal pathogens, including *Porphyromonasgingivalis*, *Tannerella forsythia*, and *Treponema denticola*, commonly known as the red complex bacteria. This reduction aligns with previous research that has demonstrated the ability of SRP to decrease pathogenic bacterial loads in the periodontal pocket (Feres et al., 2015). The significant decrease in these pathogenic species indicates that SRP can effectively disrupt the pathogenic biofilm and help restore microbial balance.

In addition to reducing pathogenic species, the study found a significant increase in the relative abundance of beneficial microbial species following SRP. This shift suggests that SRP not only reduces dysbiosis but also promotes the re-establishment of a healthier microbial community. This finding supports the concept that a successful periodontal treatment should aim not only to reduce the pathogenic load but also to enhance the presence of beneficial bacteria that contribute to maintaining periodontal health (Teughels et al.,

2008). The increase in beneficial microbial diversity is crucial, as it may enhance the resilience of the oral microbiome, reducing the likelihood of disease recurrence.

Despite these positive outcomes, it is important to acknowledge that the complete eradication of periodontal pathogens is challenging. Some studies have shown that pathogenic species can persist or re-emerge even after SRP (Sbordone&Bortolaia, 2003). The persistence of these bacteria may be due to their ability to invade periodontal tissues or form resistant biofilm structures. Therefore, while SRP is effective in reducing bacterial loads, adjunctive therapies, such as the use of locally delivered antimicrobials or host-modulatory agents, may be necessary to enhance treatment outcomes further and prevent recolonization by pathogenic species (Rams et al., 2011).

The findings of this study also highlight the role of advanced molecular techniques, such as next-generation sequencing (NGS), in characterizing the complex shifts that occur in the oral microbiome following periodontal therapy. NGS allowed for a detailed assessment of changes in microbial diversity, providing insights into how SRP influences the overall microbial ecosystem rather than focusing solely on a few specific pathogens. This approach aligns with the growing recognition that periodontal health is not determined by the presence or absence of specific pathogens but by the overall balance of the microbial community (Griffen et al., 2012).

Another important aspect of periodontal disease management is the host immune response. The significant reduction in bleeding on probing (BOP) observed in this study suggests a decrease in local inflammation, likely resulting from the reduction in pathogenic bacterial loads. Effective periodontal therapy not only reduces the microbial burden but also modulates the host immune response, leading to decreased production of inflammatory mediators (Teles et al., 2013). The decrease in inflammation is a positive outcome that contributes to the restoration of a stable and healthy periodontal environment.

While the findings of this study are promising, there are several limitations that should be considered. The study's sample size was relatively small, and all participants were recruited from a single tertiary hospital, which may limit the generalizability of the results. Additionally, the follow-up period was limited to 6 weeks post-SRP. Longer follow-up periods are needed to assess the long-term stability of the clinical and microbial changes observed. Future studies with larger sample sizes and extended follow-up durations are warranted to validate these findings and provide more comprehensive insights into the long-term effects of SRP on the oral microbiome.

In conclusion, this study demonstrates that SRP is effective in improving clinical outcomes and promoting a favorable shift in the oral microbiome in patients with chronic periodontitis. The reduction in pathogenic species and the increase in beneficial microbial diversity highlight the potential of SRP to restore microbial balance and support periodontal health. These findings underscore the importance of understanding microbial dynamics in the context of periodontal therapy and suggest that advanced molecular techniques, such as NGS, can provide valuable insights into the complex interactions between the oral microbiome and periodontal treatment. Further research is needed to explore adjunctive therapies that could enhance the effectiveness of SRP and to investigate the long-term stability of the observed microbial changes.

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