

The Role of Periodontal Microbes in Disease Pathogenesis: A Narrative Review

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ABSTRACT

Periodontal disease reflects a disturbed interaction between a polymicrobial biofilm and a susceptible host. Contemporary models emphasize community-level shifts (dysbiosis), biofilm architecture, interspecies interactions and host-microbe immune crosstalk as core drivers of disease development and progression. Advances in molecular approaches (16S rRNA sequencing, shotgun metagenomics, metatranscriptomics) have revealed greater microbial diversity, functional potential and ecological dynamics than classical culture-based paradigms. Clinically relevant areas include the ecological/keystone-pathogen framework, limitations and evolving roles of microbial diagnostics, and microbiome-informed therapeutic strategies (mechanical therapy, antimicrobials, host modulation, probiotics/prebiotics and emerging ecological interventions). Key research priorities remain establishing causal, function-level links between microbial states and outcomes, developing clinically translatable diagnostics, and designing interventions that restore a durable healthy microbiome. This narrative review synthesizes major concepts, clinical implications and future directions.

Keywords: Periodontal microbiota, dysbiosis, biofilm, keystone pathogens, periodontitis

INTRODUCTION

The oral cavity is a highly dynamic environment hosting one of the most diverse microbial ecosystems in the human body. Over 700 bacterial species have been identified, many of which colonize the subgingival environment¹. These microorganisms exist in a delicate balance with the host, contributing to oral health by preventing colonization by exogenous pathogens and participating in immune system modulation². Periodontal health is therefore defined as a state of symbiosis between the host and resident microbiota, whereas periodontal disease arises when ecological shifts favor pathogenic communities².

Historically, periodontitis was attributed primarily to *Porphyromonas gingivalis*, considered the central etiologic agent of disease³. However, contemporary evidence supports a polymicrobial synergy and dysbiosis model, in which the disease results from cooperative interactions among a complex microbial community rather than a single pathogen³. This paradigm shift emphasizes that changes in microbial composition and activity, rather than the mere presence of specific bacteria, drive periodontal tissue destruction.

Composition of the Periodontal Microbiome Advances in culture-independent molecular techniques, including 16S rRNA sequencing and metagenomics, have revealed that periodontal pockets harbor highly complex microbial consortia⁴. In health, subgingival biofilms are dominated by Gram-positive facultative bacteria, including *Streptococcus*, *Actinomyces*, and *Rothia* species⁵. These commensals contribute to microbial homeostasis, inhibit pathogenic colonization, and modulate host immunity⁴.

In contrast, periodontitis-associated biofilms are enriched in Gram-negative anaerobes such as *P. gingivalis*, *Tannerella forsythia*, *Treponema denticola*, and *Fusobacterium nucleatum*^{6,7}. These pathogens are often grouped into complexes based

on co-occurrence patterns and pathogenic potential. The 'red complex', comprising *P. gingivalis*, *T. forsythia*, and *T. denticola*, is strongly correlated with clinical parameters such as pocket depth, bleeding on probing, and attachment loss⁸. The microbial shifts in disease represent not just a change in species composition but also in gene expression profiles, metabolic activity, and interspecies interactions, which collectively enhance virulence.

Pathogenic Mechanisms of Key Periodontal Microbes

P. gingivalis functions as a keystone pathogen capable of modulating the host immune response and altering microbial community composition⁹. Its virulence factors, including gingipains (cysteine proteases), degrade host structural proteins and immune effectors, disrupting tissue integrity and promoting chronic inflammation¹⁰. *T. forsythia* expresses an S-layer protein that facilitates adhesion, biofilm formation, and immune evasion¹¹. *T. denticola* possesses motility, chemotaxis, and proteolytic enzymes, enabling tissue invasion and the degradation of extracellular matrix proteins¹².

The synergy among these organisms amplifies inflammatory responses, creating a self-perpetuating cycle of tissue destruction¹³. Cross-feeding relationships, quorum sensing, and metabolic interdependencies further enhance community virulence. This polymicrobial collaboration demonstrates that periodontitis is not a result of single pathogens but the outcome of complex microbial consortia.

Ecological Shifts and Dysbiosis

Periodontal disease represents an ecological shift from a symbiotic to a pathogenic microbial community¹⁴. Dysbiosis occurs due to factors such as altered nutrient availability, inflammation-induced environmental changes, and host immune modulation¹⁵. Keystone pathogens, including *P. gingivalis*, trigger dysbiosis by manipulating complement and Toll-like receptor pathways, promoting a pathogenic community that extends beyond their own abundance¹⁵.

Metatranscriptomic analyses reveal that microbial gene expression in disease states favors virulence factors, proteolytic activity, and inflammatory mediator production¹⁶. These ecological shifts create a feed-forward cycle, wherein inflammation provides nutrients for pathogenic species, which in turn exacerbate tissue destruction and further alter the microbial environment¹⁷. Understanding dysbiosis at the molecular level is crucial for developing interventions that restore microbial homeostasis.

Host-Microbe Interactions

The host immune response plays a dual role in periodontal disease. While protective against infection, it also mediates collateral tissue damage through pro-inflammatory cytokines, complement activation, and recruitment of polymorphonuclear neutrophils^{18,19}. Host susceptibility is further influenced by genetic polymorphisms, systemic conditions such as diabetes, and lifestyle factors including smoking²⁰.

Microbes exploit these responses to establish chronic infection. For instance, *P. gingivalis* can subvert complement C5a-R1 signaling, modulating neutrophil function and suppressing microbial clearance²¹. Similarly, bacterial virulence factors can interfere with T-cell responses, osteoclastogenesis, and epithelial barrier integrity, leading to persistent inflammation and progressive attachment loss.

Emerging Concepts and Therapeutic Implications

Next-generation sequencing and multi-omics approaches have uncovered previously uncultivable taxa, such as *Filifactor alocis* and members of the Synergistetes phylum, that are associated with advanced periodontitis²². These discoveries highlight the limitations of traditional culture-based diagnostics and suggest novel microbial targets for therapy.

Current interventions informed by the ecological-plaque-hypothesis include probiotics, prebiotics, host-modulation therapies, and precision microbiome-targeted approaches²³. Personalized periodontal care increasingly integrates microbial, immunological, and genetic biomarkers to guide treatment planning and predict therapeutic outcomes^{24,25}. The future of periodontology lies in strategies that restore symbiotic microbial communities while modulating host inflammatory responses.

CONCLUSION

Periodontal microbes exist in a dynamic equilibrium with the host. Disease emerges when ecological shifts and keystone pathogens disrupt this balance, leading to dysbiosis and chronic inflammation. A comprehensive understanding of microbial ecology, interspecies interactions, and host-microbe signaling is essential for developing effective diagnostics, preventive strategies, and personalized therapeutics in periodontology.

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Conflicts Of Interest

The authors reported no conflict of interest.

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