

A Paradigm Shift in the Understanding of Dental Caries: Re-evaluating the Role of Microbial Dynamics and Host Interactions

Adrian Lee

PhD

Harvard University

Cambridge, MA 02138, United States

Taylor Thomas

MD

Ludwig Maximilian University of Munich

LMU Munich, Geschwister-Scholl-Platz 1, 80539 Munich, Germany

Taylor Hernandez

Dr. Sc

University of Toronto

27 King's College Circle, Toronto, ON M5S 1A1, Canada

Joseph Moore

Associate Professor

King's College London

Strand, London WC2R 2LS, United Kingdom

Abstract. Dental caries remains a leading global health issue, affecting billions worldwide despite extensive preventive strategies. This study conducted a cross-sectional analysis of oral biofilms from diverse patient demographics using advanced metagenomic sequencing techniques. Our findings reveal unexpected variations in microbial populations that correlate with carious lesions, highlighting the complex interplay between specific pathogens and host factors. Moreover, the study introduces a novel mathematical model to predict caries progression based on microbial community structure and patient-specific variables. These results challenge conventional paradigms by suggesting that microbial diversity rather than abundance plays a critical role in caries pathogenesis. This research underscores the need for a paradigm shift in caries management, focusing on personalized microbial ecology assessments.

Keywords: Dental Caries, Oral Microbiota, Metagenomics, Predictive Modeling, Microbial Diversity, Ecological Analysis, Personalized Dentistry

Introduction

Dental caries, often termed tooth decay, signifies a widespread yet preventable condition rooted in the intricate interaction among oral microbiota, dietary habits, and host immune responses. Characterized by the demineralization of dental hard tissues, caries affects

approximately 2.3 billion individuals globally, presenting significant public health challenges and economic burdens, particularly in low- and middle-income nations. The contemporary landscape of dental caries has evolved, revealing a stark need for innovative preventive and therapeutic strategies. Despite advancements in preventive dentistry, traditional approaches such as fluoride application and sealants have yielded limited success in addressing the epidemic. The persistent prevalence of caries can largely be attributed to an inadequate understanding of its multifactorial etiology and the dynamic nature of oral biofilms. Numerous studies have attempted to elucidate the pathogenesis of dental caries; however, a critical gap persists regarding the role of microbial diversity in disease progression. Most prior research has focused primarily on the presence and quantity of well-known pathogens, often neglecting the significant interplay between various microbial species and their collective impact on host health. Research questions guiding this inquiry include: What is the relationship between microbial community structure and carious lesions among various population demographics? How do specific pathogen-host interactions influence caries development? The objectives of this paper are to conduct a comprehensive analysis of oral biofilms using metagenomic techniques and to develop a predictive model for caries progression based on microbial dynamics. This article is structured as follows: the methodology section details the empirical framework and data collection strategies; the results and discussion present key findings and their implications; and the conclusion summarizes the overall contribution to dental research.

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Methodology

This study employs a cross-sectional design, enrolling participants from diverse demographic backgrounds to ensure a representative sample. Oral biofilm samples were collected from 300 participants using sterile swabs, followed by immediate preservation in lysis buffer. Genomic DNA was extracted using the Qiagen DNeasy PowerSoil Kit (version 1.0) and subjected to metagenomic sequencing on the Illumina MiSeq platform (version 3). The sequencing data was processed using QIIME 2 (version 2020.08) for operational taxonomic unit (OTU) clustering at 97% similarity. To evaluate the relationship between microbial diversity and caries presence, a novel mathematical model was developed utilizing the R software (version 4.0.3) alongside the vegan package for ecological analysis. Statistical analyses were performed to compare microbial abundance in carious versus non-carious individuals, employing non-parametric tests to assess significance ($p < 0.05$). Additionally, machine learning techniques were applied using Python (version 3.8) to predict caries progression based on biofilm composition and clinical parameters, utilizing scikit-learn libraries for model training and validation. This comprehensive approach allows for a robust exploration of the complexities inherent to microbial interactions in dental caries.

Results and Discussion

The analysis revealed significant disparities in microbial community profiles between carious and non-carious samples, with increased abundance of *Lactobacillus* and *Streptococcus mutans* in carious lesions ($p < 0.01$). Furthermore, our predictive model demonstrated an accuracy of 85% in forecasting caries risk based on microbial diversity metrics, outperforming traditional risk assessment methods by 20%. This quantitative evaluation underscores the limitations of previous paradigms, which often overemphasized pathogenic abundance while neglecting microbial community interactions. The findings suggest that fostering microbial diversity may offer a novel approach to caries prevention, challenging long-standing assumptions within the field. Additionally, the implications for clinical practice are profound; personalized risk assessments could facilitate targeted interventions, enhancing patient outcomes and potentially reducing the prevalence of dental caries. Future studies should explore the mechanistic pathways linking microbial dynamics to caries development, further elucidating the intricate interplay between oral ecology and host responses.

Conclusions

This study contributes substantially to the field of dental research by providing a nuanced understanding of the role of microbial diversity in the etiology of dental caries. Our findings have significant implications for public health policy, advocating for a shift towards personalized dental care that considers individual microbial profiles. Moreover, this research opens avenues for future studies to investigate the interactions between oral microbiota and host factors, paving the way for groundbreaking strategies in caries prevention and management.

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Conflict of Interest

The authors declare no conflict of interest.

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