

Abstract



ABSTRACT

BACKGROUND

Periodontal disease is a microbially induced chronic inflammatory disease resulting in the destruction of the attachment apparatus of the tooth and is one of the most common causes of tooth loss. The microbiota in the periodontal environment initiates the disease process, but is the host response which eventually does the damage. Dental calculus is nothing but mineralized dental plaque which serves as a primary plaque retentive factor and is always covered with a layer of unmineralized plaque. The study hypothesizes that the plaque covering the supragingival calculus could have an influence on the subgingival microbiota which is seen as a characteristic pattern of periodontal disease that which is associated with gingival recession in our population.

The aim of this study was to evaluate the microbiome of plaque covering supragingival calculus and to compare it with that of periodontally healthy individuals using Next Generation Sequencing (NGS) Technology.

MATERIALS AND METHODS

A total of 8 supragingival plaque samples were collected from 4 periodontally healthy subjects and 4 patients with plaque covering supragingival calculus who reported to the outpatient department of Periodontics at Ragas Dental College and Hospital, Chennai. It was then

subjected to 16s rRNA sequencing using the NGS technology in an Illumina Solexa sequencer. V3– V4 regions were sequenced and for each of the 8 plaque samples, bacterial phyla, genera and species were identified and their relative abundance was quantified via taxonomic assignment against reference database.

RESULTS

A total of 7 phyla, 30 genera and 54 species were found in the healthy samples and 9 phyla, 30 genera and 52 species were found in the plaque covering the calculus samples. At the phyla level, there was a similar microbial profile in both the groups. At the genus level, increased presence of newer periodontal pathogens viz. *Dialister* and *Aggregatibacter* was observed in the plaque that covered supragingival calculus, which points to a microbial shift. *Veillonella tobetsuensis* along with the unclassified were the most abundant species in both the groups. There was an increase in *Dialister invisus* and *Aggregatibacter segnis* in the calculus group. At phylum, genus and species level, the comparison of overall abundance in between the disease/calculus and periodontal health group was not statistically significant.

CONCLUSION

As determined by NGS, the microbiome of the plaque that covers the supragingival calculus did not present a distinct microbial profile when compared to that of periodontal health, but points to a microbial shift that

could contribute to the disease process. Further studies with a larger sample size and a longitudinal study design would help to draw meaningful clinical implications.

KEYWORDS: PLAQUE, SUPRAGINGIVAL CALCULUS, MICROBIOME, 16s rRNA SEQUENCING, NGS TECHNOLOGY.