Abstract
ABSTRACT

BACKGROUND

The role of microbial antigens in the initiation of the chronic inflammatory responses and the importance of plaque in the initiation and progression of periodontal disease are well documented. Technological developments in sequencing and identifying DNA and powerful bioinformatics tools have helped in characterization of the subgingival microbiome. Wide variations in the oral microbiome are known to exist across population and ethnicity due to various dietary and lifestyle patterns. The subgingival microbiome in Indian population is yet to be characterized.

The aim of this study is to characterize the subgingival microbiome in periodontal health and disease using NGS technology and compare the subgingival microbiome of chronic periodontitis with health.

MATERIALS AND METHODS

A total of 8 subgingival samples, 4 each from healthy individuals and from chronic periodontitis patients were analyzed. The subgingival microbiome was investigated with the NGS technology using the Illumina sequencing method.


RESULTS

A total of 27 phyla, 626 genera and 1278 species were identified from all the samples that have been collected. Novel subgingival species belonging to genera Zhouia, Alkaliphilus, Pectinatus, Chryseobacterium, Leptotrichia were identified. The traditional periodontal pathogens including Porphyromonas gingivalis, Tannerella forsythia, Treponema denticola and recently reported periodontal pathogens such as Filifactor alocis, Dialister invisus showed no significant difference between health and disease.

CONCLUSION

The health and disease associated microbiome showed distinct microbial profiles including many previously unreported bacteria.

KEYWORDS

SUBGINGIVAL MICROBIOME, ILLUMINA SEQUENCING, NEXT GENERATION SEQUENCING, 16S RRNA, CHRONIC PERIODONTITIS, DYSBIOSIS.