Abstract
ABSTRACT

BACKGROUND

Periodontal disease is a chronic inflammatory condition which is of microbial origin resulting in destruction of the supporting structures of the teeth leading to loss of teeth. While earlier studies focused on a small number of periodontal pathogens, it is now accepted that the whole bacterial community may be important. The application of open ended methods in bacterial identification has expanded the horizon of understanding of the oral microbiome.

The aim of this study was to evaluate the sub-gingival microbiome from plaque samples of periodontally healthy individuals and in patients with gingivitis using NGS technology and to compare the subgingival microbiome of gingivitis with that of periodontal health.

MATERIALS AND METHODS

A total of 8 subgingival samples were collected from 4 periodontally healthy individuals and 4 gingivitis patients who reported to the outpatient of the department of Periodontics of Ragas Dental College and Hospital. It was then subjected to 16sRNA sequencing using the NGS technology in a Illumina Solexa Sequencer.
RESULTS

A total of 6 phyla, 21 genera and 37 species were found in the health samples and 7 phyla, 32 genera and 59 species were found in the gingivitis samples. Synergistetes was found only in the gingivitis groups. The comparison of abundance of the top 20 species between periodontal health and disease revealed no significant difference between them, which could be suggestive of a microbiome that is predominantly commensal in nature at this stage of biofilm. Hence no distinct microbiome was identified in gingivitis.

CONCLUSION

Within the limitations of this study, the very presence of this microbial profile could suggest that further environmental changes could lead to dysbiosis and disease progression.

KEYWORDS

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