

Abstract

ABSTRACT

BACKGROUND

The red complex bacteria which includes *Porphyromonas gingivalis*, and *Tannerella forsythia* (formerly *Bacteroides forsythus*), *Treponema denticola* are described as climax colonizers and are thought to play an important pathogen in progression of periodontal disease. These bacterial species are usually found together in periodontal pockets, suggesting that they may cause destruction of the periodontal tissue in a cooperative manner. Technological developments in sequencing and identifying DNA and powerful bioinformatics tools have helped in characterization of microbia of interest in relation to the total microbial load. The aim of our study was to evaluate the presence of the red complex bacteria in saliva using Next Generation Sequencing Technology in periodontal health and periodontitis.

MATERIALS AND METHODS

A total of 20 individuals seeking dental treatment in Ragas Dental College and Hospitals, Chennai, were involved in the present study, of which 10 were periodontally healthy individuals (control group) and 10 were periodontitis patients (test group). The salivary red complex was investigated with NGS

technology using Illumina MiSeq sequencing method. Amplicons from V3-V4 hypervariable regions of 16S rRNA gene were sequenced.

RESULTS

The results of our study suggest that the Red complex bacteria were significantly higher in periodontitis [*P. gingivalis* ($P = 0.020$), *T. forsythia* ($P = 0.005$), and *T. denticola* ($P = 0.033$)] when compared to healthy subjects and may therefore be used as microbial risk markers. However, a longitudinal study with a greater sample size will be required to confirm the findings of this study.

KEYWORDS

Illumina MiSeq Sequencing, Next Generation Sequencing, 16S rRNA, Periodontitis, Dysbiosis, salivary microbiome