

ABSTRACT

Background:

Periodontal disease is a chronic inflammatory condition which is of microbial origin resulting in destruction of the supporting structures of the 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 is to evaluate the orange complex bacteria in saliva in periodontal health and periodontitis

Materials and methods:

In this study, Subjects were periodontally evaluated and allocated into two groups as healthy controls (ten subjects) and periodontitis patients (ten subjects).orange complex microbiome was evaluated from periodontally healthy and periodontitis individuals using NGS technology with Illumina sequencing. Amplicons from V3-V4 hypervariable regions of 16S rRNA gene were sequenced.

Results:

Fusobacterium nucleatum vincentii was present in all the 20 samples examined including periodontal health and disease.

There was a statistically significant increase in frequency distribution of *Campylobacter gracilis* $P=0.020$ in periodontitis when compared to health.

Fusobacterium nucleatum nucleatum ($P=0.033$), *Fusobacterium nucleatum periodonticum* ($P=0.000$), *Prevotella intermedia* ($P=0.011$) was present in periodontitis and not in health with a statistically significant difference between the two.

Streptococcus constellatus ($P=0.474$) was present in periodontitis not in health, but without any statistically significant difference.

Conclusion:

Some members of the orange complex seem to be suitable candidates for use as microbial risk markers in periodontal diseases.

Keywords:

Salivary microbiome, Illumina Sequencing, Next Generation Sequencing, 16S rRNA, Periodontitis, Dysbiosis.