

## ABSTRACT

**Background:** Oral microbiome and chronic inflammation are known to influence carcinogenesis. Many studies are ongoing to ascertain the relationship between oral microbiome, inflammation and oral cancer. This study was done to ascertain the oral microbiome in the saliva of Oral Squamous Cell Carcinoma (OSCC) and healthy individuals using 16S rRNA gene sequencing.

**Aim and objectives:** To ascertain the oral microbiome in saliva samples of OSCC patients and healthy individuals using 16S rRNA gene sequencing of bacteria with BLAST(Basic Local Alignment Search Tool) analysis in NCBI( National Centre for Biotechnology Information) database and to quantify the concentration of DNA extracted from bacterial cells using QUBIT™ Fluorometer.

**Materials and Methods:** Saliva from ten OSCC patients and ten healthy individuals (controls) were collected. DNA was extracted from the saliva samples and then subjected to 16S rRNA gene sequencing to assess the oral microbiome between the two groups.

**Results:** A total of 19 phyla were identified of which Proteobacteria(39%), Firmicutes(22%), Actinobacteria(15%) and Bacteroidetes(12%) were the major phyla. The most prevalent bacteria present in OSCC patients were Bacillus, Bacterium, Buchnera, Caulobacter, Clostridium, Corynebacterium, Desulfotomaculum, Enterococcus, Flavobacterium, Gemmata, Hymenobacter, Lactobacillus, Listeria, Lysinibacillus, Marinifilum, Ruminococcus, Streptococcus, Streptomyces, Thermoanaerobacter. In healthy individuals the prevalent bacteria were Bacillus, Enterococcus, Lactobacillus, Massilia, Paenibacillus, Streptococcus. The predominant bacteria

that were common in OSCC patients and in healthy individuals are Bacillus, Enterococcus, Lactobacillus and Streptococcus.

**Conclusion:** The oral microbiome is complex and our study shows that there are differences in the microbiome of OSCC subjects and healthy individuals. The data from this study will help us to identify the species which need to be studied further to ascertain their role in oral carcinogenesis.

**Keywords :** Microbiome, 16S rRNA gene sequencing, OSCC.