

## NEXT-GENERATION SEQUENCING (NGS) IN HUMAN ORAL MICROBIOME RESEARCH: A SYSTEMATIC REVIEW

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### ABSTRACT

Human oral microbiome research has been conducted using different methodologies. One of them is next-generation sequencing (NGS), which is the state-of-the-art methodology that allows more comprehensive analysis than the traditional Sanger sequencing to characterise the constituents of human diverse microbial communities. However, no systematic reviews have been conducted to discuss the advantages of this methodology in relation to genetic richness of human oral microbiome and the benefits of this data for human health and diseases. Therefore, this systematic review was conducted to systematically learn the trends in using NGS with regards to human oral microbiome since its very first publication until the most recent ones. Literature related to oral microbiome and NGS were searched on Scopus and Web of Science (WOS), resulting in a total of 42 unique, open-access original articles, 29 from Scopus and 13 from WOS, published since 2009 until 2019. The microbiome in the studies was characterised on the basis of V1, V2, V3 and V4 hypervariable region of the 16S rRNA gene by using paired-end sequencing on Illumina MiSeq platform. The sequencing method, specifically NGS, was able to give insights about the diversity and uniqueness of oral microbiomes of individuals, in health and in diseased states such as caries, carcinoma, coronary artery disease (CAD), and atherosclerosis. Firmicutes, Proteobacteria, Fusobacteria, Bacteroidetes, and Actinobacteria were some of the common phyla detected using NGS, as reported in the literature. NGS is the most recent technology that opens the door to better characterise the oral microbiome in human for better diagnostics and prognostics in cases of diseases and to find ways to maintain human health.

**Keywords:** Next-Generation Sequencing (NGS), Human Oral Microbiome Research, A Systematic Review