

Effect of Oral Microbe in Human Health

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Editorial

The human microbiome, like the numerous terrestrial biomes that make up the Earth, is made up of a variety of bacteria, fungi, viruses, archaea, protists, and other microbes whose compositions are influenced by environmental factors. Varied parts of the human body might be thought of as distinct biomes, each with significantly diverse conditions and nutrition availability, promoting different populations.

Even within a single body location, the microbiome composition might vary dramatically across people in different stages of health, with different lifestyles, or for a variety of other reasons. The human oral microbiome, as well as strategies for addressing its investigation and delineating its normal makeup as we presently know it, as well as its variations under atypical settings, will be the topic of this paper.

The mouth cavity has one of the most varied and distinct populations of bacteria in the human body, but it is understudied in comparison to the gut—a PubMed search for "oral microbiome" yielded 746 articles, compared to 5605 for "gut microbiome" at the time of writing this study. A millilitre of saliva includes roughly 108 microbial cells, and studies have shown up to 700 different prokaryotic taxa, with a normal healthy microbiome containing between 100 and 200 different bacterial species.

The introduction of next-generation sequencing technology has opened up new possibilities for large-scale metagenomic investigations in a variety of populations, allowing for the definition of microbiome structure as well as, in some cases, functional roles and implications for health. The mouth as a biome is home to a variety of distinct habitats, each with its own microbial community.

Multiple studies have examined the microbiomes of the saliva, tongue, buccal mucosa, teeth surfaces, gums, palate, subgingival and supragingival plaque, as well as the throat and tonsils, finding overall similarities but minor differences, such as higher levels of the genus *Corynebacterium* in both types of plaque or higher levels of the phylum Firmicutes in both saliva and buccal mucosa when compared to plaque.

While some metagenomics research focus on each of these habitats independently, an oral rinse is frequently used as a sample collection method to gather a representative sample of the whole oral microbiome. Regardless of

the biome or habitat being studied, the current trend in microbiome research is to use culture-independent NGS methods, which are becoming more affordable in terms of both money and computing power, as databases of microbial genomic sequences continue to grow.

Only 57% of oral bacterial species have been formally recognised, 13% have been grown but remain nameless, and 30% are uncultivated, according to the enlarged Human Oral Microbiome Database. As a result, not only have NGS approaches made studies reasonably rapid and straightforward, but they have also greatly increased our knowledge of unculturable and uncommon microbiota.

Periodontitis, gingivitis, and dental caries are just a few of the diseases that may impact the mouth, and they've all been linked to changes in the oral microbiome. However, because the mouth is an access site for the respiratory and digestive systems and is highly vascularized, the oral microbiota may have consequences in other systemic disorders. Indeed, a rising number of studies have found links between alterations in the oral microbiota and other disorders. This shows that the oral microbiota might be used as biomarkers in the detection of some systemic disorders [1-5].

Conflict of interest

None

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