Guest Editorial

Oral Microbiome: The Microbial Gateway

The human mouth harbors one of the most diverse microbiomes in the human body, including viruses, fungi, protozoa, archea, and bacteria. The bacteria are responsible for the two commonest bacterial diseases of man: Dental caries (tooth decay) and the periodontal (gum) diseases. The oral microbiome is comprised of over 600 prevalent taxa at the species level, with distinct subsets predominating at different habitats. The oral microbiome has been extensively characterized by cultivation and culture-independent molecular methods such as 16S rRNA cloning as shown in Figure 1. Comparison of 16S rRNA gene sequences also provides a more accurate identification than phenotypic characterization. Advances in ancient DNA and paleoprotein technologies now allow detailed characterization of these ancient biomolecules, enabling direct comparisons between ancient and modern oral microbial communities. Cloning and sequencing of 16S rRNA genes offers several advantages for studying the stability of bacterial communities. Bacterial stability was greatest among healthy, clinically stable subjects and lowest for subjects whose periodontal status worsened. The measurement of microbial stability may be useful in clinical diagnosis and prognosis.

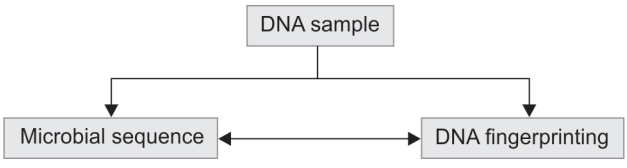

Fig.1: 16S rRNA sequencing

The link between oral health and systemic health seems undeniable. The US Surgeon General described the mouth as a "mirror of health or disease" and an early indicator of disease in other tissues and organs in the body. Periodontal diseases such as chronic gingivitis and periodontitis can result from an increase in the complexity and volume of biofilms located in the gingival crevice. Most of the conditions under which oral biofilms develop are tightly linked to the overall health and biology of the host. These biofilms are typically comprised mainly of Gram-positive facultative anaerobes (*Streptococcus anginosus and Actinomyces naeslundii*), but in the absence of proper hygiene, the percentage of Gram-negative species (e.g., *Porphyromonas, Campylobacterspecies, Tannerella forsythia, Treponema denticola, and Aggregatibacter actinomycetemcomitans*) in the biofilms increases, contributing to periodontal inflammation.

Many studies have indicated that bacteria present in biofilms have properties that are uniquely dependent upon such structures. This could have significant dental interest, since previous studies have documented the increased resistance of oral bacteria within dental plaque to antimicrobial agents relative to that in planktonic growth. Additional confirmation of these differences has been provided by numerous investigations examining gene expression and protein synthesis. This has revealed that some properties of oral bacteria grown within biofilms are distinct from those of comparable planktonic cultures. Advances in molecular techniques have led to a greater appreciation of the diversity of human microbiota, the extent of interactions with the human host, and the relation of individual variation.

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