Recent microbiome studies have shown that the human oral microbiome is composed of over 260 abundant bacterial species that predominantly live as polymicrobial biofilms accreted to the non-shedding hard surfaces of the teeth. In addition representatives of both Archaea and Fungi are found in the oral cavity and there is considerable colonisation of the soft tissues of the mouth. Most of these species are commensal and form complex biofilm communities that restrict the colonisation of the oral cavity by exogenous bacteria. Changes in the polymicrobial biofilm microenvironment such as those resulting from the effects of chronic inflammation for subgingival plaque, can lead to the emergence of opportunistic pathogens resulting in dysbiosis and the development of chronic diseases such as periodontitis in a susceptible host. The application of microbiomic studies to the analysis of these complex and dynamic communities in rigorously designed human clinical studies will provide valuable mechanistic insight into the bacterial succession and complex interactions involved in the development of dysbiosis and disease.

The human oral cavity is the entry point of the gastrointestinal tract and offers a number of microenvironments that enable the proliferation of a wide range of largely commensal bacteria, the vast majority of which are endemic to the human oral cavity. Considerable effort has been expended to identify the approximately 700 prokaryote species that compose the total human oral microbiome. Over one-third of these species remain uncultivated and less than half are officially named; however, draft genomes for approximately half of these taxa are now available from the Human Oral Microbial Database (www.homd.org)\(^1\).

16S rRNA gene sequence surveys are providing a cost effective means of studying microbiomes, identifying and enumerating a relatively unbiased set of the prokaryotic species present, including uncultivable species. This technique has been adopted for studying the oral microbiota; however, the results produced have not yet been definitive, with some studies finding huge variation across individuals and limited or no differences between healthy and diseased states. Many factors of the design and analysis of these experiments can make it difficult to compare results between the different studies, including pooling of samples, DNA extraction method, marker gene or region used, primer sets, PCR conditions, sequencing platform, choice of taxonomic classifier and level of classification, clustering of read data into microbial groups, and the statistical methods used for diversity analysis\(^2\). The composition of the healthy oral microbiota can certainly vary considerably across sites within the mouth, at the same site over time, and from person to person\(^3,4\). Although the 16S rRNA survey techniques are available most clinical studies to date have been cross-sectional and have investigated a limited number of bacterial species using either real time PCR, checkerboard DNA-DNA hybridisation, or more recently, the Human Oral Microbe Identification Microarray (HOMIM) techniques. To compound these limitations samples taken from a limited number of sites within the mouth are often pooled which can obscure comparative results and is not recommended for
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tooth can display varying degrees of disease severity, all undergoing periodontal disease progression at different rates. Therefore to conclusively determine the polymicrobial aetiology of chronic periodontitis and how opportunistic pathogens emerge and proliferate rigorously designed prospective human clinical trials coupled with microbiomic analyses are essential, followed by the testing of the bacterial species and communities identified in appropriate in vitro and animal models to determine their potential as polymicrobial biofilms to induce dysbiosis and disease.

References


Biographies

Stuart Dashper is a Professor in the Oral Health Cooperative Research Centre and The Melbourne Dental School, The University of Melbourne. Over the past 15 years he has developed a systems biology approach to the study of chronic oral diseases that incorporates the identification and characterisation of bacterial pathobionts, the composition and structures of the polymicrobial biofilm communities in which they dwell, the molecular characterisation of virulence-related traits and their interactions with other members of the bacterial community and the host.

Helen Mitchell is a researcher with the Oral Health CRC and Masters of Science student in Bioinformatics at The University of Melbourne. She is undertaking comparative genomics of the periodontal pathobiont *Porphyromonas gingivalis* to determine virulence characteristics and assist in vaccine development. She is using Next-Generation Sequencing techniques to determine bacterial biomarkers of early childhood caries in saliva.

Geoff Adams has over 30 years’ experience as a biostatistician and epidemiologist involved in consulting, teaching, and research. He has been employed by the Melbourne Dental School and the Oral Health CRC as a biostatistician and epidemiologist since 1999. Geoff manages the Oral and Systemic Disease program in the Oral Health CRC, which is investigating associations between periodontal disease and various systemic conditions.

Eric Reynolds AO PhD FICD FTSE FRACDS is a Melbourne Laureate Professor and CEO and Director of Research of the Oral Health CRC. He is also Head of the Oral Biology Section of the Melbourne Dental School. He has been researching and teaching for over 30 years on the aetiology and prevention of the two major oral diseases, dental caries and periodontal diseases, which are associated with polymicrobial biofilms.

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