Combined Oligotyping and Metagenomic Approaches for a High-Resolution View of the Tongue Microbiome

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Studies of the oral microbiome, collectively those microbes that live within our mouths, have revealed their critical importance in oral health as they provide a range of services for the host. However, many oral bacteria cannot be grown, thus culture-independent approaches, such as sequencing regions of the 16S rRNA gene, are used to study community composition. However, current methods of analysis are not very sensitive for bacterial identification. Oligotyping, a new method for 16S sequence analysis, has revolutionized our ability to detect fine scale genetic structure of microbial communities. Oligotyping results are difficult to compare between studies as no suitable reference databases exist. Here we aim to create an Oligotype Database to complement and expand the Forsyth Institute's Human Oral Microbiome Database (HOMD). Oligotype analysis of tongue biofilms will be conducted, and oligotypes will be incorporated into the HOMD. Second, we aim to associate oligotypes to functional genetic information. Using the same samples as for oligotyping, community genomic (metagenomic) sequences will be obtained, partitioned into operational genomes, and associations with a subject's oligotypes determined. Finally, we will demonstrate this coupled approach by characterizing tongue bacterial communities involved in a putative symbiosis that processes dietary nitrate for the host. Expanding the HOMD to include oligotypes, and associating them with functional gene content, facilitates future comparative studies of oral microbiota measured between laboratories and human populations across the world, including the future use of 16S sequence analyses in detection of disease organisms, developing methods for early diagnoses and preventive intervention.