The diversity of microbiome profiles in periodontal subgingival pockets

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Background and Aims

The oral microbiota contains over 700 microbial species, with an average of 250 species per person. The oral environment consists of micro-environments with distinct microbiome compositions. In this project, we characterized the microbiome profile in two periodontal environments, 'Shallow' and 'Deep' pockets, to see if the microbiota composition differed.

Methods

The samples were collected from 1287 participants from a population based study with extensive dental examination as HUSK-T (HUSK Dental Health) in Western Norway. All Participants were born in 1950-1951. Subgingival plaque was collected from individuals with shallow (<5 mm) and deep (\geq 5 mm) pockets, as well as individuals with only shallow (<5 mm) pockets. Shotgun metagenomics was used to profile taxonomic composition and diversity of microbial communities.

Results

We visualized the relative abundance of microbial taxa in periodontal pockets, showcasing differences between 'Shallow' and 'Deep' pockets (Figure 1).

We conducted microbiome composition analysis in periodontal pockets, specifically focusing on the association with pocket depth (Figure 2). The resulting plot visually represents the top 50 species identified as significantly associated with pocket depth. Positive values (greater than 0) indicate a positive association with "Deep" pockets, and negative values (less than 0) indicate a positive association with "Shallow" pockets. The magnitude of the coefficient indicates the strength of this association.



Figure 1. Microbial composition in Deep vs. Shallow Periodontal Pockets



Conclusions

Our analysis of the oral microbiome composition in periodontal pockets has provided valuable insights into the relationship between microbial communities and pocket depth. We observed distinct patterns of microbial abundance associated with 'Shallow' and 'Deep' pockets, shedding light on potential microbial markers for periodontal health.



