

Microbiome in periodontitis patients and healthy individuals show differences in the use of metabolic pathways in spite of ecologic similarity.

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Abstract.

The bacterial community associated with periodontitis and healthy individuals show differences in both ecological and functional aspects. Microbiomes from periodontitis patients and healthy individuals from a Colombian population were studied to analyze their ecological and functional characteristics. We collected subgingival plaque from three patients with a clinical diagnosis for periodontitis, with periodontal pockets  $\geq 3$ mm and two individuals without a diagnosis for periodontitis. The DNA extraction was performed from the subgingival plaque. This DNA was used to sequence the V3-V4 region in the subunit 16S in the ribosomal RNA gene. The sequencing data was analyzed to establish the composition of the bacterial community, diversity, richness, and evenness for each group. The DNA sequences also were used to identify the presence of metabolic pathways in each microbiome. It was not observed significant differences in richness and diversity between periodontitis patients and periodontally healthy individuals. However, each microbiome exhibited taxa exclusively. Microbiome associated with periodontitis showed a high expression of metabolic pathways associated with fatty acid lipid biosynthesis, fermentation, and nucleic acid processing. Meanwhile, in the microbiome associated with periodontal health pathways such as amine and polyamine degradation, metabolic regulator biosynthesis, fatty acid, and lipid degradation were most frequent. In this study, the microbiome associated with periodontal health and periodontitis did not show differences in diversity or richness of species. However, these microbiomes presented differences in the use of metabolic pathways, which would indicate functional modification of the communities in responding to subtle changes in environmental conditions.