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From subgingival to saliva: microbial signatures and differential genes reflect changes according to periodontal disease severity

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Periodontal disease is a highly prevalent chronic inflammatory disorders, leading to tooth loss and significant systematic health implications. Its pathogenesis is driven by a microbial dysbiosis in the subgingival plaque. While the subgingival microbiota represents a primary etiological agent, the salivary microbiota does not directly cause disease but instead reflects microbial shifts in the subgingival niche, offering a potential source of non-invasive biomarkers. In this study, we examined microbial changes according to the severity of periodontal disease using two different cohorts, both of which were stratified into four groups: healthy controls (H), gingivitis (G), moderate periodontitis (MP), and severe periodontitis (SP). To compare microbial biomarkers and differential gene functions of saliva reflecting subgingival plaque, the first cohort was analyzed using distinct paired sets with two sampling sites (subgingival plaque and saliva) and two sequencing methods (16S rRNA gene and whole metagenome). The results revealed that microbial composition was primarily influenced by the sampling site, followed by the sequencing method, and lastly by periodontal health status. In addition, periodontitis-enriched species and pathway identified in saliva were also detected in subgingival plaque. For detailed investigation of the salivary microbiome, the second cohort focused on the severe periodontitis. The same periodontitis-enriched species, gene, and pathway found in first cohort were confirmed, and further SP-subgroup were discovered. Analysis of this subgroup with clinical data suggested that microbial heterogeneity within SP corresponds with gradations in periodontal disease severity.