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Linking Periodontal Diseases and Ulcerative Colitis Through Subgingival-Gut Mucosal Microbiome

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Objectives To characterize the subgingival and gut mucosal microbiome compositions in ulcerative colitis (UC) patients with different periodontal statuses by comparing them with age- and gender-matched non-UC controls and explore the subgingival-gut mucosal microbial signatures in this relationship.

Methods Thirty newly-diagnosed active UC patients and 30 non-UC controls from the Gastroenterology Department at Gazi University Hospital were included. Patients were categorized based on their periodontal status as healthy (n=10), gingivitis (n=10), and periodontitis (n=10). Multiple colonic mucosa biopsies were obtained from inflamed areas, and simultaneously, subgingival plaque samples were collected from the teeth with the deepest probing depths before any medication or therapy related to UC. All samples underwent analysis using 16S ribosomal RNA gene amplicon sequencing. Periodontal parameters were assessed on the same day as sample collection.

Results There was no statistical difference found in periodontal parameters between UC patients and non-UC controls. In subgingival plaque samples, the non-UC group showed significantly higher bacterial abundance and diversity than the UC group, as demonstrated by alpha-diversity indicated by the Shannon index. In gut mucosal biopsy samples, periodontal health exhibited significantly higher bacterial abundance and diversity than gingivitis and periodontitis in the non-UC group, as indicated by alpha-diversity (Chao index) ($p < 0.05$). In UC patients, a higher abundance of *Streptobacillus* for periodontal health, *Campylobacter rectus*, and *Prevotella stercorea* for gingivitis, and *Streptococcus anginosus* and *Bifidobacterium* for periodontitis were identified in subgingival plaque samples. A significant association of *Bacteroides vulgatus, Prevotella copri, Bacteroides fragilis*, and *Parabacteroides*

merdae was found in both colonic mucosal and subgingival plaque samples of UC patients (p<0.05).

Conclusions In both subgingival and gut mucosal biopsy samples, UC patients diagnosed with gingivitis presented the highest abundance and diversity of microbial compositions. In UC patients, subgingival and gut microbiome profiles share some common microorganisms, such as *Prevotella copri* and *Bacteroides fragilis*.