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Periodontal Therapy, Oral Microbiome and Respiratory Health: an Intervention Study

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Objectives To evaluate whether change in the oral microbiome impact respiratory health.

Methods Periodontitis patients (n=57), never-smokers and free from any other medical conditions, received periodontal therapy with full-mouth disinfection protocol. At baseline (T0) and six weeks following therapy (T1), subgingival plaque and airway resistance (Rrs) by Forced Oscillation Technique (Tremoflo C-100, Thorasys Medical Systems, Canada) were collected. Plaque was sampled from the deepest pocket from each quadrant and pooled before freezing.

Shotgun sequencing was used for microbiome analyses. Alpha-diversity was analysed with Wilcoxon rank test and beta-diversity by Bray-Curtis dissimilarity and PERMANOVA. Differential abundance testing was performed with Analysis of Compositions of Microbiomes with Bias correction adjusted for sex.

Results Mean age was 35.8 years; 21% had stage I periodontitis, 66% Stage II and 13% had Stage III. Rrs at 11 and 19Hz decreased with 4.7% and 5.4%, respectively ($p < 0.05$). The alpha-diversity was significantly reduced from T0 to T1, and the beta-diversity also changed significantly (both $p < 0.001$). The alpha- and beta-diversity did not differ by change in Rrs.

Patients with improved airway resistance had significantly higher abundance of *Neisseria*, *Actinomyces*, *Collinsella*, and *Gemella spp.* at T1, whereas patients with no Rrs-improvement showed significant reduction in *Peptostreptococcus*, *Tannerella*, *Treponema*, *Saccariamonas*, *Selenomonas* and increased abundance of *Ottowia spp.*, which was not observed in the Rrs-improvement group.

Conclusions Following periodontal therapy, a significant decrease in Rrs was observed alongside significant changes in alpha- and beta-diversity for the subgingival plaque samples. The airway resistance improvement vs the no improvement group differed in the types of bacteria showing significant increase or decrease in abundance following therapy.