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Comparative transcriptome analysis of periodontitis and peri-implantitis in human subjects

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Background: Peri-implantitis is similar to periodontitis, but there are some differences. For the effective control of peri-implantitis, it is necessary to clarify its similarities and differences with periodontitis in terms of gene expression. Methods: This cross-sectional study included 20 participants (10 healthy subjects and 10 patients with periodontitis and peri-implantitis). Gingival tissue samples (10 healthy, 10 periodontitis, and 10 peri-implantitis tissues) were collected, RNAs were extracted, and RNA sequencing and analysis were performed. Results: Differentially expressed gene (DEG) analysis identified 757 upregulated and 159 downregulated genes common between periodontitis and peri-implantitis. Periodontitis tissues uniquely showed 186 overexpressed and 22 suppressed genes compared with peri-implantitis and healthy tissues, while peri-implantitis had 1974 and 642, respectively. Each common and unique differential gene set showed distinct enriched biological features between periodontitis and peri-implantitis after the pathway enrichment analysis. The expression pattern of selected DEGs focused on the representability of the disease was validated by RT-qPCR. Conclusions: Although periodontitis and peri-implantitis showed common gene expression that was clearly differentiated from healthy conditions, there were also unique gene patterns that were differentially expressed only in peri-implantitis. These findings will help elucidate the mechanisms involved in the progression of peri-implantitis.