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SALIVARY miRNA AS A POTENTIAL BIOMARKER OF SUSCEPTIBILITY TO PERIODONTITIS

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AUTHOR'S DECLARATION

I declare that the work in this thesis was carried out in accordance with the regulations of Universiti Teknologi MARA. It is original and is the results of my own work, unless otherwise indicated or acknowledged as referenced work. This thesis has not been submitted to any other academic institution or non-academic institution for any degree or qualification.

I, hereby, acknowledge that I have been supplied with the Academic Rules and Regulations for Post Graduate, Universiti Teknologi MARA, regulating the conduct of my study and research.

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ABSTRACT

Introduction: Salivary transcriptome is increasingly recognised as a highly potential and futuristic diagnostic fluid since it is readily available, non-invasive and may be used to elucidate the disease susceptibility, including periodontitis. Acknowledging this, salivary microRNA (miRNA), part of the transcriptomic biomarkers, may present as the source of a potential biomarker in periodontitis patients. **Objective**: The general aim of this study is to elucidate the expression of miRNA from the saliva of periodontitis and healthy participants. Specifically, this study aimed to ascertain the feasibility of salivary miRNA as a biomarker in participants susceptible to periodontitis Stage III and IV and compare the expression of novel miRNA in periodontitis and healthy participants. **Materials and Methods**: A total of 21 research participants (thirteen localised or generalised periodontitis Stage III and IV and eight healthy participants) participated in this study. Whole saliva samples were collected using the unstimulated saliva collection technique. Total RNA, including small RNA, was extracted and purified from the whole saliva using miRNeasy Micro kit from Qiagen. Based on the minimal concentration for library preparation, nine out of 21 purified miRNA samples were converted into complementary DNA (cDNA) from the single-stranded RNA using the reverse transcription-polymerase chain reaction (RT-PCR). Library preparation was prepared, and each sample was given an index for identification before sequencing. Only two samples from healthy (H6) and periodontitis (D12) met the criteria for sequencing with the NextSeq 500/550 from Illumina. Known and novel miRNA expression from the NGS were later subjected to small RNA sequencing analysis. **Result**: After sequencing with the NGS, 814 novel and 338 known miRNAs identified from D12, while 1035 novel and 365 known miRNAs identified from H6. Based on small RNA sequencing analysis, 16 novel miRNAs were upregulated in the periodontitis group, while 15 novel miRNAs were upregulated in the healthy group. novelMiR_48 was expressed in both groups wherein D12 was upregulated but downregulated in H6. MITF, one of the targeted genes of novelMiR_48, is speculated to be responsible for osteoclast differentiation via the RANK-RANKL-Calcium signaling pathway, hence initiate alveolar bone loss, which is the hallmark for periodontitis. **Conclusion**: From this study, it can be concluded that novel miRNA expression differs between periodontitis and healthy participants. In addition, salivary miRNA is feasible to be use as a biomarker in patients susceptible to periodontitis Stage III and IV.

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