ABSTRACT

Periodontitis is a chronic polymicrobial disease that causes destruction of the periodontium. It may ultimately lead to tooth loss if no treatment is done. There is a need for improved diagnostic tools to curb the disease progression. The current diagnosis that is based on physical examination is time-consuming, low in sensitivity and specificity, and limited as information on current disease status is unavailable. Since the gene expression of the polymicrobial community changes according to the health status of the periodontium, specific genes can be used as biomarkers for diagnosis of the disease. Therefore, the aim of this study is to identify possible periodontitis-specific biomarkers from metatranscriptomics data of healthy and periodontitis patients. The dental plaque RNA extraction was optimized using several methods. The RNA samples were sequenced, and differential expression analysis was performed using R package DESeq2. The differentially expressed genes were functionally annotated using automated annotation server, KEGG GhostKOALA. Spin-column method was found to be the best RNA extraction procedure in terms of quality and yield. A total of 7,012 and 74 genes were found to be upregulated and downregulated, respectively in periodontitis patients. These genes, which are involved in various pathways, were found to act synergistically in mediating cellular motility, adhesion, biofilm formation and virulence of the disease. In particular, *fliC*, *susD*, *mcp*, *gingipain*, *GroEL*, *fldA* and *korB* genes were found to be potential periodontitis-specific biomarkers. In conclusion, differentially expressed genes in periodontitis were analysed and disease-specific markers were successfully identified. Further analysis on a larger sample size is required to validate the use of these genes for periodontitis diagnosis.