



Gibbs Sampling Method Identifies Disrupted Pathways and Genes in Periodontitis

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ABSTRACT Periodontitis is a chronic inflammatory disease triggered by the host immune response. The aim of this study is to explore the disturbed pathways and genes in periodontitis. Transcriptome data of healthy and diseased gingival tissues and human pathway data were recruited from public available database. Then, Gibbs sampling and Markov chain Monte Carlo (MCMC) algorithm were implemented to identify disturbed pathways and key genes. Disturbed pathways and key genes were identified under adjusted posterior value > 0.8. The researchers identified two disturbed pathways (cytokine-cytokine receptor interaction and hematopoietic cell lineage) and two key genes (TNFRSF17 and CXCL6). Gene expression analysis showed that all the disturbed pathways and key genes had increased expression levels in diseased gingival samples compared with healthy samples. The identified pathways and genes may play important role in periodontitis and could be considered as potential biomarkers for early detection and therapy for periodontitis.