Screening Hub Genes in Microbial Keratitis Based on Gibbs Sampling Analysis

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ABSTRACT This study aimed to identify potential key pathways and hub genes. The enrichment pathways were chosen through merging the gene expression data from microarray data with KEGG pathways. Gibbs sampling was performed to screen out significant pathways and the pathway gene set was determined. Finally, hub genes were identified using Gibbs sampling and statistics. A total of 278 pathways were chosen according to gene overlap greater than 5. Markov chain (MC) was established based on the enrichment of the gene expression profile in each pathway using Gibbs sampling and then 26 significant pathways were determined judging by $adj\_á_{pi}$ greater than 0.8. Additionally, 1167 pathway gene sets were found out. Finally, 26 pathways were chosen as key pathways and 5 hub genes were identified on basis of their importance, which will contribute to elucidating potential molecular mechanism of microbial keratitis. We identified potential key pathways and hub genes in microbial keratitis.