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Protein-protein interaction network and mechanism analysis of hepatitis C

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ABSTRACT. We predicted potential genes and identified pathways associated with hepatitis C. The gene expression profiles of GSE40184 from blood samples and GSE38597 from liver biopsy samples were downloaded from the GEO database. Differentially expressed genes (DEGs) were recognized using the Limma Package. The Pearson correlation test was used to construct the co-expression network of DEGs. Gene set enrichment analysis was used to define significant functions and pathways for DEGs. A total of 165 DEGs in blood samples and 523 DEGs in liver biopsy samples were identified. Eight DEGs were common between these samples. Gene Ontology enrichment analysis showed that 165 DEGs in blood samples were significantly enriched regarding the response to protein binding, receptor binding, G-protein coupled receptor binding, cytokine receptor binding, and cytokine activity. The most significant term of the Kyoto Encyclopedia of Genes and Genomes pathway was the cytokine-cytokine receptor

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interaction. Protein-protein interaction network analysis indicated that three subnetworks with more nodes and edges were involved in these interactions. We used robust biomarkers that were differentially expressed in hepatitis C and determined their relevance in the biological function, signal pathways, protein-protein interaction network, and co-expression network of hepatitis C.

Key words: Co-expression network; Differentially expressed genes; Hepatitis C; Pathway

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