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Identifying significant pathways of hepatitis B virus-related hepatocellular carcinoma based on crosstalk and network pathways

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ABSTRACT. This study aims to identify significant pathways in hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC) based on the pathway network strategy. We proposed a pathway network where a protein-protein interaction (PPI) network was integrated with the crosstalk of pathways. Pathway data were first obtained from background PPI network, Reactome pathway database, and common genes between mRNA differentially expressed genes (DEGs), and miRNA target genes of HBV-related HCC. Pathway interactions were subsequently randomly extracted based on gene-gene interactions, and a weight value was assigned to each crosstalk using the Spearman correlation coefficient. Finally, pathways and crosstalk were visualized via Cytoscape to construct the final pathway network. A total of 9 common genes were identified between 396 mRNA DEGs and

400 miRNA target genes, and 17 pathways were identified based on background pathways and common genes. In addition, we constructed a pathway network that included 136 interactions and 17 pathways. The weight value of netrin-1 signaling and regulation of Frizzled proteins (FZD) by ubiquitination was the largest, at 0.228. In conclusion, we identified 17 significant pathways that might act as potential biomarkers of HBV-related HCC. This information may offer some insight into treatment and detection of HBV-related HCC.

Key words: Hepatocellular carcinoma; Hepatitis B virus; Pathway; Network; Crosstalk

