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GENES DIRECTLY REGULATED BY NF-KB IN HUMAN HEPATOCELLULAR CARCINOMA HEPG₂

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t has been well-known that over activation of NF-кВ has close relationship with hepatitis and hepatocellular carcinoma (HCC). However, the complete and exact underlying molecular pathways and mechanisms still remain not fully understood. By manipulating NF-KB activity with its recognized activator TNFa and using ChIP-seq and RNA-seq techniques, this study identified 699 NF-kB direct target genes (DTGs) in a widely used HCC cell line, HepG2, including 399 activated and 300 repressed genes. In these NF-kB DTGs, 216 genes (126 activated and 90 repressed genes) are among the current HCC gene signature. In comparison with NF-kB target genes identified in LPS-induced THP-1 and TNFa-induced HeLa cells, only limited numbers (24-46) of genes were shared by the two cell lines, indicating the HCC specificity of identified genes. Functional annotation revealed that NF-kB DTGs in HepG2 cell are mainly related with many typical NF-KB-related biological processes including immune system process, response to stress, response to stimulus, defense response, and cell death,

and signaling pathways of MAPK, TNF, TGF-beta, Chemokine, NF-kappa B, and Toll-like receptor. Some NF- κ B DTGs are also involved in Hepatitis C and B pathways. It was found that 82 NF- κ B DTGs code secretory proteins, which include CCL2 and DKK1 that have already been used as HCC markers. Finally, the NF- κ B DTGs were further confirmed by detecting the NF- κ B binding and expression of 14 genes with ChIP-PCR and RT-PCR. This study thus provides a useful NF- κ B DTG list for future studies of NF- κ B-related molecular mechanisms and theranostic biomarkers of HCC.

Biography

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