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Microarray analysis in acute and chronic hepatitis B virus infection

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Background

Different genes are involved in the pathogenesis of acute and chronic hepatitis B virus (HBV) infection, although little is known about these genes.

Materials and methods

A full length HBV genome was cloned and sequenced from serum of a chronic hepatitis B (CHB) patient. The genome and sterilized Milli-Q water were transfected to HepG2 and HepG2.2.15 cells, respectively, by lipofectamine 2000. The prior cell line was named HepG29BL. The two cell lines were collected post transfection 48 hours. Differential genes were examined using Affy Human U133 2.0A gene chip; Real time polymerase chain (RT-PCR) was performed to confirm the expression of lumican in six human hepatoma carcinoma cell lines.

Results

Of 50,000 transcripts and variants on the gene chip, 4860 genes were significantly altered between the two cell lines. Pro-inflammatory and interferon associated molecules (e.g, IL-6, IFNAR2, IFNA17, etc.) were up regulated in HepG29BL, while down regulated in HepG2.2.15. The ratio of lumican was significantly high between the two cell lines. The levels of lumican were showed in six cell lines as follows: HepG29BL> HepG2>7402> Alexander>MHCC-97 >HepG2.2.15 ($P < 0.05$, but the comparsion between MHCC-97 and HepG2.2.15 was not statistically significant).

Conclusion

The result of this study provides a foundation for future investigations of genes involved in the pathogenesis of HBV infection. Lumican, as reported in CHB [1] and in other organs cancer pathogenesis study [2], may play an role in liver fibrosis and carcinogenesis.

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