hTERT promoter gene polymorphism and the risk of hepatocellular carcinoma (HCC) in patients with chronic hepatitis B

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Background and Aim: Telomerase plays an important role in carcinogenesis and tumor progression and human telomerase reverse transcriptase (hTERT), a subunit of telomerase, is crucial for the regulation of telomerase activity. In this study, we evaluated the association of hTERT promoter gene polymorphism with the development of HCC in patients with chronic hepatitis B. **Methods:** A total of 290 HBV-related HCC patients (HCC group) and 277 chronic hepatitis B patients (control group) were recruited. We analyzed the upstream 800 bp of the hTERT promoter DNA sequence, especially transcription binding site (c-Myc, SP1, Ets2 or GC-box), by direct sequence method. Also, we investigated the effects of a -245 T or C polymorphism within the hTERT promoter region on the hTERT promoter activity in HCC cell lines (HepG2 and Huh7). **Results:** A single nucleotide polymorphism (SNP) –245kb upstream (Ets2 binding site, rs2853669) of the hTERT promoter was significant associated with an increased risk of HCC. In the HCC group, the proportions of the T/T, T/C and C/C genotypes were 46.2, 41.8 and 12%, respectively, which were significantly different from those in control group (35.7%, 39.7%, 24.6%, P<0.001). The promoter activity in the T/T was significantly higher than that in the C/C (p<0.001) in luciferase assay. The T-allele in the -245 upstream of the hTERT promoter was associated with the development of HCC in patients with chronic hepatitis B. **Conclusion:** The polymorphism of hTERT promoter contributes to the development of HCC in patients with chronic hepatitis B.

색인단어: Hepatocellular carcinoma, Chronic hepatitis B, hTERT promoter, polymorphism