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Association study of c.910A>G and c.1686C>G polymorphisms in *XRCC1* gene with risk of hepatocellular carcinoma in the Chinese population

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ABSTRACT. *XRCC1* (human X-ray repair complementing defective repair in Chinese hamster cell 1) gene is considered a potentially important gene influencing the risk of hepatocellular carcinoma (HCC). Our analyses detected two allelic variants of *XRCC1*, c.910A>G and c.1686C>G. We aimed to investigate whether these polymorphisms influence the risk of HCC. The association between the *XRCC1* polymorphisms and the risk of HCC was analyzed in 719 patients and 662 controls by polymerase chain reaction-restriction fragment length polymorphism. Our data suggested that the genotypes and alleles of c.910A>G and c.1686C>G polymorphisms were statistically associated with the risk of HCC. For c.910A>G, the GG genotype was associated with increased risk of developing HCC compared with the AA wild

genotype (OR = 1.95, 95%CI = 1.40-2.70, P < 0.0001). For c.1686C>G, the risk of HCC was significantly higher for the GG genotype compared with the CC wild genotype (OR = 1.89, 95%CI = 1.375-2.599, P < 0.0001). Significant differences in the risk of HCC were also found with other genetic models for these two SNPs. The G allele of both c.910A>G and c.1686C>G may contribute to the risk of HCC (G versus A: OR = 1.40, 95%CI = 1.20-1.64, P < 0.0001 and G versus C: OR = 1.38, 95%CI = 1.19-1.61, P < 0.0001, respectively). Our findings suggest that the c.910A>G and c.1686C>G polymorphisms of *XRCC1* are associated with the risk of HCC in the Chinese population.

Key words: Hepatocellular carcinoma; *XRCC1*; Molecular marker; Single nucleotide polymorphisms; Risk factors

