Association between the c.1564A>T genetic polymorphism of the \textit{MDR1} gene and hepatocellular carcinoma in Chinese population

Y.Y. Wan, X.W. Wang, H.X. Hui and L. Wan

Department of Oncology, The Huai’an First People’s Hospital, Nanjing Medical University, Huai’an, Jiangsu, China

Corresponding author: Y.Y. Wan
E-mail: yiyuan_wan@sina.com

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ABSTRACT. The objective of this study was to evaluate the influence of c.1564A>T genetic polymorphisms in the multidrug resistance 1 gene (\textit{MDR1}) on hepatocellular carcinoma (HCC) susceptibility through association analysis. A total of 632 HCC patients and 645 cancer-free controls were enrolled in this study. The c.1564A>T genetic polymorphisms were genotyped by created restriction site-polymerase chain reaction (CRS-PCR) and confirmed using DNA sequencing methods. The potential associations of c.1564A>T genetic polymorphisms with the risk of HCC were analyzed by different genetic models. Statistically significantly increased risks of HCC were detected in the homozygote comparison (TT versus AA: OR = 1.70, 95%CI = 1.17-2.45, \(\chi^2 = 7.99, P = 0.005\)), recessive model (TT versus AT/AA: OR = 1.64, 95%CI = 1.15-2.33, \(\chi^2 = 7.66, P = 0.006\)), and allele contrast (T versus A: OR = 1.23, 95%CI = 1.04-1.45, \(\chi^2 = 6.09, P = 0.014\)). Our data suggest that the genotypes/alleles from c.1564A>T genetic polymorphisms are...
statistically associated with HCC risk. The allele-T and genotype TT may contribute to susceptibility to HCC in the Chinese Han population.

**Key words:** *MDRI* gene; Genetic polymorphisms; Susceptibility; Hepatocellular carcinoma; Risk factors