



DNA methyltransferase 3B -149C/T polymorphism and the risk of laryngeal squamous cell carcinoma: a case-control study

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ABSTRACT. A variety of molecular epidemiological studies have been conducted to examine the association between the *DNMT3B* -149C/T polymorphism and cancer susceptibility; however, there has been no study investigating the association between the *DNMT3B* -149C/T polymorphism and the risk of laryngeal squamous cell carcinoma (LSCC) until now. To determine the role of the *DNMT3B* -149C/T polymorphism in LSCC, we genotyped 113 patients with LSCC and 110 controls from a Chinese population using polymerase chain reaction-restriction fragment length polymorphism analysis. The chi-square test was used to examine differences in the distributions of genotypes studied between patients and controls. The association between the *DNMT3B* -149C/T polymorphism and the risk of LSCC was estimated using ORs and their 95% CIs. Genotypic frequencies in the patients with LSCC were not similar to those of the controls, with the differences being statistically significant ($P =$

0.001). When the *DNMT3B* -149 CC genotype was used as the reference group, the CT genotype was not associated with LSCC risk (adjusted OR, 2.12; 95%CI = 0.89-5.19; P = 0.07), but the TT genotype was associated with significantly increased risk for LSCC (adjusted OR = 3.27; 95%CI = 1.79-10.66; P = 0.009). Under the recessive model of inheritance, the TT genotype was associated with significantly increased risk for LSCC (adjusted OR = 1.98; 95%CI = 1.12-5.95; P = 0.012), compared with other genotypes. These results suggested that the *DNMT3B* -149C/T polymorphism is associated with a genetic susceptibility for developing LSCC in a Chinese population.

Key words: *DNMT3B* -149C/T polymorphism; Genetic susceptibility; Risk; LSCC