



Short Communication

The genetic variant rs401681C/T is associated with the risk of non-small cell lung cancer in a Chinese mainland population

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ABSTRACT. Although lung cancer (LC) is a highly environmentally associated disease, genetic factors are also thought to play a role in this disease. In recent years, genome-wide association studies have identified various susceptible genetic regions for LC. Herein, we used high-resolution melting analysis to genotype 2 significant single nucleotide polymorphisms previously reported in Caucasians, that is, rs401681 at 5p15.33 and rs8034191 at 15q25, in a case-control study with 492 LC cases and 486 cancer-free controls in a Chinese population. We found

that the rs401681C/T allele in the *TERT-CLPTMIL* gene was associated with the risk of non-small cell lung cancer [NSCLC; P = 0.012, odds ratio (OR) = 1.29, 95% confidence interval (95%CI) = 1.09-1.50], but was not associated with the risk of small cell lung cancer (P = 0.571, OR = 1.15, 95%CI = 0.82-1.47). However, no significant association was found between rs8034191T/C and LC risk. These results suggest that genetic variants in the *TERT-CLPTMIL* gene may predispose individuals to be susceptible to LC, particularly NSCLC, in the Chinese population.

Key words: Lung cancer; Single nucleotide polymorphism; Risk factor; Non-small cell lung cancer; High-resolution melting analysis