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Analyzing the association between *XRCC1* c.1804C>A genetic variant and lung cancer susceptibility in the Chinese population

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ABSTRACT. Lung cancer is the most common cancer occurring worldwide. The human X-ray repair complementing group 1 (*XRCC1*) gene is one of the most important candidate genes that influence the susceptibility to lung cancer. The objective of this study was to analyze the potential association between the c.1804C>A genetic variant of *XRCC1* and lung cancer susceptibility. A total of 703 subjects were recruited for this study. Genotyping of c.1804C>A genetic variant was performed using the created restriction site-polymerase chain reaction. Statistically significant differences in allele frequencies and genotype were found between lung cancer patients and cancer-free controls. The genotype AA was statistically associated with the increased risk of lung cancer when compared to the wild genotype, CC, and the carrier genotype, CA/CC (AA *vs* CC: OR = 2.71, 95%CI = 1.57-4.67, P < 0.001; AA *vs* CA/CC: OR = 2.54, 95%CI = 1.50-4.29, P < 0.001). The allele A likely contributes to the susceptibility to lung cancer (A *vs* C: OR = 1.47, 95%CI = 1.17-1.84, P = 0.001). Our data indicates that the

c.1804C>A genetic variant of *XRCC1* is statistically associated with the susceptibility to lung cancer in the Chinese population.

Key words: Lung cancer; *XRCC1*; Genetic variant; Risk factor; Molecular marker

