Association between *IL18*-607C/A and -137G/C polymorphisms and susceptibility to non-small cell lung cancer in a Chinese population

W.Y. Gan, H.M. Li, Y.G. Zhang, C.M. Li and Y. Wang

The Second Breathing and Intensive Care Ward,
Zhumadian City Center Hospital, Zhumadian, China

Corresponding author: W.Y. Gan
E-mail: wenyungangw@163.com

Genet. Mol. Res. 15 (4): gmr15048822
Received May 18, 2016
Accepted October 11, 2016
Published December 19, 2016
DOI http://dx.doi.org/10.4238/gmr15048822

ABSTRACT. Lung cancer is one of the main causes of cancer-related mortality in males and females worldwide. A pleiotropic effect has been observed in the interleukin 18 gene (*IL18*); its effects include the activation of natural killer cell cytotoxicity and the promotion of the Th1 immune response through the alteration of the expression of interferon-γ and TNF-α in humans. IL18 is therefore involved in the elimination of tumor cells in the human body. We recruited 357 patients with non-small cell lung cancer (NSCLC) and 414 controls to evaluate the correlation between two genetic variations (*IL18*-607C/A and *IL18*-137G/C) and the pathogenesis of NSCLC. We used polymerase chain reaction-restriction fragment length polymorphism to genotype *IL18*-607C/A and *IL18*-137G/C. Statistical analysis revealed that individuals harboring the AA genotype of *IL18*-607C/A had an increased risk of NSCLC compared to those harboring the CC genotype (OR = 2.20, 95%CI = 1.30-3.74). Individuals expressing the A allele of *IL18*-

607C/A had an elevated risk of developing NSCLC compared to those expressing the C allele (OR = 1.31, 95%CI = 1.06-1.62). In summary, our analysis shows that the *IL18*-607C/A genetic variation is related to the risk of NSCLC, whereas the *IL18*-137G/C variation is not. Therefore, the *IL18*-607C/A variation is related to the pathogenesis of NSCLC in the Chinese population studied.

Key words: Non-small cell lung cancer; IL18; *IL18*-607C/A; *IL18*-137G/C; Polymorphism