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STAT3 gene polymorphisms and susceptibility to non-small cell lung cancer

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ABSTRACT. Signal transducer and activator of transcription protein 3 (STAT3) has been implicated in cancer development and is recognized as a type of oncogene. However, association studies of single nucleotide polymorphisms (SNPs) in the *STAT3* gene with cancer risk are rare and not available for lung cancer. We examined whether *STAT3* polymorphisms are associated with the risk of non-small cell lung cancer (NSCLC). Eight SNPs in the *STAT3* gene were genotyped by TaqMan assays in 326 NSCLC cases and 432 controls in a Chinese population. Significant decreased risk of NSCLC was observed for carriers of minor alleles rs4796793 (odds ratio (OR) = 0.68, 95% confidence interval (CI) = 0.51-0.92), rs7211777 (OR = 0.67, 95%CI = 0.50-0.90), rs12949918 (OR = 0.73, 95%CI = 0.54-0.97), rs744166 (OR = 0.69, 95%CI = 0.51-0.92), rs9912773 (OR = 0.75, 95%CI = 0.55-0.98), and rs3869550 (OR = 0.70, 95%CI = 0.53-0.94). The GGCGGC haplotype, comprised of minor alleles of the six NSCLC-associated SNPs,

had a 0.78-fold (95%CI = 0.62-0.97) significantly decreased risk of NSCLC, as compared to the most common haplotype of CATACT. Stratification analyses by clinical stage showed that the trend for the association between *STAT3* polymorphisms and NSCLC risk was present both for stage I/II and stage III/IV, and appeared moderately stronger for stage III/IV. We conclude that polymorphisms in the *STAT3* gene may have a protective role in the development of NSCLC, particular of stage III/IV NSCLC.

Key words: Non-small cell lung cancer; Polymorphisms; STAT3

