Association between -1082G/A, -819C/T, and -592C/A genetic polymorphisms in IL-10 and risk of type 2 diabetes mellitus in a Chinese population


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ABSTRACT. Type 2 diabetes mellitus is the most common form of endocrine disease in humans; genetic factors are known to contribute to the development of this disease. In this case-control study, we investigated the relationship between the -1082G/A, -819C/T, and -592C/A polymorphisms in interleukin 10 (IL-10) and the pathogenesis of type 2 diabetes mellitus in a Chinese population. Patients with type 2 diabetes mellitus (N = 228) and control subjects (N = 240) were recruited from the Department of Endocrinology at the People’s Hospital of Linyi City, between September 2013 and April 2015. The IL-10 -1082G/A, -819C/T, and -592C/A polymorphisms were genotyped by polymerase chain reaction-restriction fragment length polymorphism. Multivariate logistic regression analyses revealed that patients carrying the AA genotype of IL-10 -592C/A were at a higher risk of developing type 2
diabetes mellitus compared to those carrying the CC genotype [adjusted odds ratio (OR) = 1.74; 95% confidence interval (CI) = 1.03-2.95]. In addition, individuals carrying the A allele of \(IL-10\) -592C/A showed a 1.34-fold higher risk of developing type 2 diabetes mellitus compared to those carrying the C allele (adjusted OR = 1.34; 95%CI = 1.03-1.75). There was no significant correlation between the \(IL-10\) -1082G/A and -819C/T polymorphisms and risk of type 2 diabetes mellitus. In conclusion, this study shows that the -1082G/A polymorphism of \(IL-10\) contributes to the onset of type 2 diabetes mellitus, and may be considered a biomarker for early screening of type 2 diabetes mellitus in the Chinese population studied here.

**Key words:** \(IL-10\); Polymorphism; Type 2 diabetes mellitus