Associations between genetic variants and the severity of metabolic syndrome in subjects with type 2 diabetes


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ABSTRACT. Metabolic syndrome (MetS) includes obesity, dyslipidemia, elevated blood pressure, and dysglycemia. Subjects with type 2 diabetes (T2D) exhibit features of MetS. The etiology of MetS is complex, involving both environmental and genetic factors. In this study, we examined the
role of specific candidate genetic variants on the severity of MetS in T2D subjects. A total of 240 T2D subjects aged 35-64 years were recruited. Waist circumstance, plasma triglycerides, high-density lipoprotein cholesterol, fasting plasma glucose, and blood pressure were measured to define MetS. Subjects were divided into 4 groups according to MetS components. Target genes involved in fibrotic and inflammatory processes, insulin and diabetes, cell growth and proliferation, and hypertension were genotyped. A total of 13 genes and 103 single-nucleotide polymorphisms (SNPs) were analyzed to evaluate their genetic association with MetS severity in T2D subjects. Univariate ordinal logistic regression using a dominant model (homozygous for the major allele vs carriers of the minor allele) revealed 6 SNP markers within 4 genes with genotypes associated with MetS risk. For the SNP genotypes of rs362551 (SNAP25), rs3818569 (RXRG), rs1479355, rs1570070 (IGF2R), and rs916829 (ABCC8), heterozygotes showed a lower risk of MetS compared with the reference group. In addition, the CC genotype was comparable to the TT genotype for rs3777411. There was no gender-specific effect. In conclusion, our results suggest that among the Han Chinese population, several SNPs increase the risk of severe MetS in T2D subjects. Further study in a large population should be conducted.

**Key words:** Chinese; Metabolic syndrome; Obesity; Polymorphism; Type 2 diabetes