Association between the *TRAIL* single nucleotide polymorphism rs1131580 and type 2 diabetes mellitus in a Han Chinese population

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**ABSTRACT.** Tumor necrosis factor (TNF)-related apoptosis-inducing ligand (*TRAIL*) is expressed in different tissues and cells, including the pancreas and lymphocytes, and it can selectively induce apoptosis in tumor cells but not in most normal cells. *TRAIL* plays critical roles in type 1 diabetes mellitus, and is involved in type 2 diabetes mellitus (T2DM). We recently discovered the association of nonalcoholic fatty liver disease, a risk factor for T2DM, with a single nucleotide polymorphism (SNP) in the *TRAIL* (*TNFSF10*) gene at site 1595C/T (rs1131580), indicating the possible association of T2DM with this *TRAIL* polymorphism. The aim of this study was to investigate the
relationship of the TRAIL SNP at site 1595C/T (rs1131580) with T2DM susceptibility and the biometabolic parameters of T2DM in a Han Chinese population. The polymerase chain reaction-restriction fragment length polymorphism method was used to genotype SNP rs1131580 in 292 patients with T2DM and 266 healthy controls. We found that the frequency of the CC genotype and that of the C allele of rs1131580 were significantly higher in T2DM patients than in the control group. Additionally, the triglyceride and serum creatinine levels of T2DM patients with the CC genotype were significantly higher than those of patients with the TT genotype. Thus, the CC genotype of the TRAIL SNP at 1595C/T (rs1131580) confers increased susceptible to T2DM in a Han Chinese population from Shandong Province. These data suggest that the CC genotype at this SNP is related to diabetic severity and it might be a candidate for the prognostic assessment of T2DM.

**Key words:** Tumor necrosis factor-related apoptosis-inducing ligand; Polymerase chain reaction-restriction fragment length polymorphism; Type 2 diabetes mellitus; Single nucleotide polymorphism