Association of TLR2 and TLR4 non-missense single nucleotide polymorphisms with type 2 diabetes risk in a southern Chinese population: a case-control study

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ABSTRACT. Toll-like receptors (TLRs), the triggers of the innate and adaptive immune responses, are involved in the pathogenesis of type 2 diabetes mellitus (T2DM). Several studies have investigated the effects of genetic polymorphisms in TLR4 and TLR2, but they have yielded limited results. We investigated whether non-missense genetic
polymorphisms in the regulatory regions of TLR4 and TLR2 were related to T2DM in a southern Chinese population. Single nucleotide polymorphisms (SNPs) in TLR4 (rs1927911, rs11536889, rs1927907, rs1927906, rs1927914, rs7873784, and rs2149356) and TLR2 (rs1898830, rs3804099, rs4696480, and rs3804100) were genotyped in 552 T2DM and 552 unrelated age- and gender-matched controls by SNaPShot Multiplex assay. Genotypes GG (OR = 0.09, 95%CI = 0.01-0.83, P = 0.03) and CG (OR = 0.08, 95%CI = 0.01-0.74, P = 0.03) of the 3′-untranslated region (UTR) SNP rs7873784 in TLR4, and genotype AG (OR = 0.67, 95%CI = 0.46-0.97, P = 0.04) and allele G (OR = 0.88, 95%CI = 0.79-0.97, P = 0.01) of the intron SNP rs1898830 in TLR2 were identified as protective against the development of T2DM in southern Chinese people. In contrast, a meta-analysis of rs1927911 and rs1927914 showed no association. Haplotypes AGTT (OR = 0.34, 95%CI = 0.15-0.77, P = 0.01) and AATT (OR = 1.20, 95%CI = 1.01-1.44, P = 0.05) in TLR2 were significantly associated with susceptibility to T2DM. Our results suggest that the effects of non-missense polymorphisms located in the regulatory regions of TLR4 and TLR2 should not be neglected in T2DM association analysis.

**Key words:** Toll-like receptor 4; Toll-like receptor 2; Type 2 diabetes; Non-missense single nucleotide polymorphisms; Chinese