



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