



Associations between *INSR* and *MTOR* polymorphisms in type 2 diabetes mellitus and diabetic nephropathy in a Northeast Chinese Han population

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ABSTRACT. We explored the associations of *INSR* and *mTOR*, 2 key genes in the insulin signaling pathway, and the susceptibility to type 2 diabetes mellitus and diabetic nephropathy. Three single-nucleotide polymorphisms (SNPs) (rs1799817, rs1051690, and rs2059806) in *INSR* and 3 SNPs (rs7211818, rs7212142, and rs9674559) in *mTOR* were genotyped using the Sequenom MassARRAY iPLEX platform in 89 type 2 diabetes patients without diabetic nephropathy, 134 type 2 diabetes patients with diabetic nephropathy, and 120 healthy control subjects. Statistical analysis based on unconditional logistic regression was carried out to determine the odds ratio (OR) and 95% confidence interval (95%CI) for each SNP. Combination analyses between rs2059806 and rs7212142 were also performed using the χ^2 test and logistic regression. Among these 6 SNPs, 4 (rs1799817, rs1051690, rs7211818, and rs9674559) showed no

association with type 2 diabetes mellitus or diabetic nephropathy. However, rs2059806 in *INSR* was associated with both type 2 diabetes mellitus ($P = 0.033$) and type 2 diabetic nephropathy ($P = 0.018$). The rs7212142 polymorphism in *mTOR* was associated with type 2 diabetic nephropathy ($P = 0.010$, OR = 0.501, 95%CI = 0.288-0.871), but showed no relationship with type 2 diabetes mellitus. Combination analysis revealed that rs2059806 and rs7212142 had a combined effect on susceptibility to type 2 diabetes mellitus and diabetic nephropathy. Our results suggest that both *INSR* and *mTOR* play a role in the predisposition of the Han Chinese population to type 2 diabetic nephropathy, but the genetic predisposition may show some differences.

Key words: Diabetic nephropathy; *INSR*; *MTOR*; Polymorphisms; Type 2 diabetes mellitus