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Genetic variants in MIR3142HG contribute to the predisposition of IgA nephropathy in a Chinese Han population

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Objectives: The study aimed to evaluate the association of genetic variants in *MIR3142HG* with the predisposition of IgA nephropathy (IgAN) in a Chinese Han population

Methods: Six single-nucleotide polymorphisms (SNPs) in *MIR3142HG* were chosen for genotyping among 417 IgAN cases and 424 healthy controls using Agena MassARRAY technique. Logistic regression models adjusted for age and gender were used to calculate odds ratios (ORs) and 95% confidence intervals (CI). Haploview and multifactor dimensionality reduction (MDR) analysis were used to analyze the role of combined SNPs in IgAN risk

Results: Rs17057846-AA genotype (OR = 2.11, 95% CI: 1.04–4.27, $p = 0.039$) and rs58747524-CC genotype (OR = 1.89, 95% CI: 1.06–3.38, $p = 0.032$) had the higher risk for IgAN developing in the overall. Interestingly, rs7727115 had a reduced risk for IgAN in females, while rs17057846, rs2961920 and rs58747524 were related to the increased susceptibility to IgAN in females and the subjects with age £ 35 years; moreover rs17057846 and rs58747524 conferred to the higher risk for Lee's grade ≥ III IgAN ($p < 0.05$ for all). Besides, the combination of rs1582417, rs7727115, and rs2961920 was the best model (testing accuracy = 0.5468, CVC = 10/10, $p < 0.001$) to predict IgAN predisposition compared to the single SNP alone

Conclusions: Our study firstly indicated that rs17057846 and rs58747524 in *MIR3142HG* contributed to the elevated risk for IgAN in a Chinese Han population. These results might provide a new insight for the molecular mechanism in the progression of IgAN