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Genetic variants of IL-1R1 and IL-1R2 genes and IgA nephropathy risk in the Han Chinese population

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Objectives : IgA nephropathy (IgAN), as the most common primary glomerulonephritis in the world, is the major cause of end-stage renal disease(ESRD) in Asia and its pathogenesis is influenced by both genetic and environmental factors. Single nucleotide polymorphisms (SNPs) in IL1R1 and IL-1R2 may be associated with susceptibility to IgAN. In this study, we study the association between genetic variants of IL-1R1 and IL-1R2 and IgA nephropathy risk in the Chinese Han population.

Methods : A case-control study was conducted including 426 nephropathy patients and 463 healthy controls. Chi-squared tests and genetic model were used to evaluate associations.

Results : In the allelic model analysis, the rs10490571 and rs3917225 were associated with a 1.40-fold (95%CI: 1.10-1.78; P = 0.006),and 1.31-fold (95%CI:1.08-1.59; P= 0.06) increased risk of IgA nephropathy, respectively. In the genetic model analysis, the rs10490571 in IL1R1 was associated with increase 1.46-fold risk of IgAN in the dominant model and increase 1.36-fold risk in the Log-additive model, respectively. In addition, the rs12712127 in IL1R1 and rs3917225 in IL1R2 were associated with an increased risk. However, the rs3218977 in IL1R2 was associated with decrease 0.71-fold risk of IgAN in the dominant model and 0.71-fold risk in the over-dominant model, respectively.

Conclusions : These findings suggest that IL-1R1 and IL-1R2 polymorphisms may contribute to the development of IgAN.

Keywords : IgA nephropathy ;Genetic variants; Interleukin 1 Receptor Type I ;Interleukin 1 Receptor Type 2