KSN 2017 Abstract

KSN-17-O079

Determination of IL-1B (rs16944) and IL-6 (rs1800796) genetic polymorphisms in IgA nephropathy in a northwest Chinese Han population

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Objectives : IgA nephropathy (IgAN) is the most common form of primary glomerulonephritis worldwide, but etiology and pathogenesis are still poorly understood. Polymorphisms in the cytokine genes may play a role in the etiology and pathogenesis of IgAN. The incidence of different between different ethnic groups suggested important genetic influences on its pathogenesis.

Methods : We genotyped 10 single nucleotide polymorphisms (SNPs) in IL-1B and IL-6 gene using Sequenom Mass-ARRAY technology from 417 IgAN patients and 463 healthy controls of Chinese Han population. We evaluated these SNPs associated with IgAN using the chi-square tests and genetic model analysis.

Results : We identified that the minor alleles of rs16944 ("A"), rs1800796 ("G") in IL-1B, IL-6 were associated with a increased risk of IgAN in allelic model analysis, respectively ($P < 0.05$). The rs16944 in IL-1B and rs1800796 in IL-6 were associated with 1.23-fold (95% CI, 1.02-1.48, $P = 0.031$) and 1.33-fold (95% CI, 1.11-1.66, $P = 0.003$) increases in the risk of developing IgAN, respectively. There was only rs1800796 still correlated with IgAN in the allelic model after adjustment by age and gender and Bonferroni correction. In addition, Haplotype G rs1800796A rs2069837G rs2069840 and G rs1800796A rs2069837C rs2069840 in IL-6 were found to be associated with increased IgAN risk ($P < 0.05$).

Conclusions : This study verified the IL-6, IL-1B genetic variants polymorphisms contributed to IgAN susceptibility in a Chinese Han population. Although we identified SNPs susceptibility, however, replication studies and functional research are required to confirm the genetic contribution in IgAN.

Keywords : IgA nephropathy ; genetic polymorphism ; IL-1B ; IL-6