KIR2DL4/HLA-G polymorphisms were associated with HCV infection susceptibility among Chinese high-risk population

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Abstract

Background: Killer-cell immunoglobulin-like receptors 2DL4 (KIR2DL4) and the human leukocyte antigen class I-G (HLA-G) display vital parts in immune responses against HCV infection. We select four potentially functional SNPs of KIR/HLA to explore the associations between KIR2DL4/HLA-G genetic variants and HCV infection results. Methods: In the present case-control investigation, KIR2DL4-rs660773, KIR2DL4-rs660437, HLA-G-rs9380142, and HLA-G-rs1707 SNPs were sorted as genotype in a total of 2225 high-risk subjects, involving 1778 paid blood donors and 447 drug users. The SNPs were functionally annotated using bioinformatics analysis. Results: Following adjusting by age, sex, ALT, AST, IFNL4-rs12979860, IFNL4-rs8099917, and the infection route, the logistic regression analysis (LRA) discovered that KIR2DL4-rs660773 and HLA-G-rs9380142 were correlated with vulnerability to HCV infection (all P <0.05). In a locus-dosage way, compared with subjects carrying the rs9380142-AA or rs660773-AA genotypes, subjects with rs9380142-AG or rs660773-AG/GG (all P <0.05) were more vulnerable to HCV infection; the overall impact of their risk genotypes (rs9380142-AG-rs660773-AG/GG) was correlated with an elevated incidence of HCV infection (P trend<0.001). In the Haplotype analysis, patients with haplotype AG were more likely to contract HCV compared to those with the highest common AA haplotype (P = 0.002) were higher in susceptibility to infect HCV.

The SNPinfo web server estimated that rs660773 is a transcription factor binding site (TFBS), whereas rs9380142 is a potential microRNA-binding site. Conclusion: In the Chinese high-risk population, KIR2DL4 rs660773 and HLA-G rs9380142 polymorphisms are related to HCV susceptibility.

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