Effect of IL-32 polymorphism on viral clearance of hepatitis C virus infection

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Background and aim: Several host and viral factors affect the natural history of Hepatitis C Virus (HCV) infection. Interlukine 32 (IL-32), a proinflammatory cytokine, is increasingly recognized to be an important host-protective molecule against infectious diseases. This study aimed to evaluate any association between IL-32 polymorphism and HCV infection and its effect on viral clearance.

Methods: In a population-based study of 60 HCV patients and 75 healthy controls, IL-32 polymorphism was determined by RFLP-PCR. The mean age of the patients and controls was 38.32 ± 10.31 and 40.92 ± 3.026, respectively. Any association of IL-32 T/C polymorphism with viral clearance was also determined.

Results: There was a significant difference in IL-32 T/C genotypes distribution between HCV patients and controls (P=0.006). IL-32 TT genotype was more prominent in the patients compared to the controls (15% vs. 2.5%). The presence of C mutant allele was significantly increased HCV susceptibility risk up to 2.5 fold (95% CI; 1.35-4.8, p=0.00034). Interestingly, the patients harboring the favorable C allele had decreased HCV viral load. Moreover, no significant association in viral clearance was found when the study population was stratified by IL-32 genotype, possibly due to the low number of patients in each group.

Conclusion, in this study we found that the favorable IL-32 C allele seems to be related so as to achieve a good viral clearance in HCV-infected patients.

Keywords: IL-32, HCV, Polymorphism,