

Study of Association Between 3' Non-coding Region Polymorphism of Interleukin-16 Gene and Chronic Hepatitis B Infection

Abbas Behelgardī*

Research Center for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran,, Iran

a.behelgardī@yahoo.com

Background & Objectives: IL-16 activates T-cells, macrophages, monocytes and dendritic cells by binding to CD4 molecules and it can also stimulate the production of other cytokines such as IL-6, IL-15 and tumor necrosis factor. Thus, IL-16 plays a key role in protection against immune system related infections such as Hepatitis B infection. This study was undertaken to investigate the association between IL-16 gene polymorphism rs1131445 and susceptibility to chronic Hepatitis B infection.

Methods: In a case-control study, we analyzed 100 chronic HBV patients along with 100 healthy controls, using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) Methods. To make sure that the results are correct, 15 samples were subject to direct sequencing.

Results: Allele frequency among healthy controls and patients was determined (T: 68.5%, C: 31.5% for healthy controls and T: 69.5%, C: 30.5% for patients). Genotype frequencies TT, TC and CC among healthy controls were 49%, 39% and 12% and among patients were 47%, 45% and 8% subsequently. There was no significant association between genotype and allele frequencies and susceptibility to chronic HBV infection.

Conclusion: Genotypes of rs1131445 from IL-16 gene were not associated with chronic HBV infection in Iranian population of this study. So rs1131445 gene polymorphism cannot be a prognostic factor for Iranian patients with chronic Hepatitis B infection.

Keywords: Genotype; Allele Frequencies