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Correlation between genetic variations and serum level of interleukin 28B with virus genotypes and disease progression in chronic hepatitis C virus infection

Mohammed N Al Ahdal[1,3], Ahmed Al-Qahtani[1,2,4], Mashael Al-Anazi[1], Ayman A Abdo[4,5], Faisal M Sanai[5,6], Hamad I Al-Ashgar[7], Mohammed Q Khan[7] and Nisreen Khalaf[1]

[1]King Faisal Specialist Hospital and Research Center, Saudi Arabia
[2]Alfaisal University School of Medicine, Saudi Arabia
[3]King Faisal Specialist Hospital and Research Center, Saudi Arabia
[4]Liver Disease Research Center, King Saud University, Saudi Arabia
[5]College of Medicine, King Saud University, Saudi Arabia
[6]King Abdulaziz Medical City, Saudi Arabia
[7]King Faisal Specialist Hospital and Research Center, Saudi Arabia

Hepatitis C virus (HCV) is a leading cause of chronic liver disease worldwide. Recent studies have demonstrated polymorphisms near the interleukin 28B (IL-28B) gene could predict the response to Peg-IFN-a/RBV combination therapy in HCV-infected patients. The aim of the study was to correlate the serum level of IL28B in HCV-infected patients with virus genotype/subgenotype and disease progression. IL28B Serum level was detected using IL28B-specific ELISA kit. Variations at five single nucleotide polymorphisms (SNPs) (rs8105790, rs8099917, rs7248668, rs12980275 and rs12979860) in IL28B gene region were studied and they were found to be strongly associated with HCV infection when healthy control group was compared to HCV-infected patients with all p values <0.0001. Functional analysis revealed that subjects carrying rs8099917-GG genotype had higher serum level of IL28B than those with GT or TT genotypes (p = 0.04). Also, patients who were presented with cirrhosis (Cirr) only or with cirrhosis plus hepatocellular carcinoma (Cirr+HCC) had higher levels of serum IL28B when compared to chronic HCV-infected patients (P=0.005 and 0.003, respectively). No significant association was found when serum levels of IL28B were compared to virus genotypes/subgenotypes. In conclusion, this study indicates that variation at SNP rs8099917 could predict the concentration serum levels of IL28B in HCV-infected patients. Furthermore, IL28B serum level might be useful as a marker for the development and progression of HCV-associated diseases.

drahdal@gmail.com