

Role of tumor necrosis factor β polymorphism in Hepatitis C virus related chronic liver diseases

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Background: Tumor necrosis factor gene polymorphisms are suggested to affect the [Hepatitis C virus](#) (HCV) infection natural course. TNF family includes Lymphotoxin- α (LTA) as a pro-inflammatory cytokine and is an important mediator of hepatic fibrogenesis. LTA gene polymorphisms are shown to play a role in different inflammatory and immunomodulatory diseases including cancers.

Aim: Study the contribution of LTA gene polymorphism in different stages of chronic Hepatitis C viral (CHC) infection and risk of primary hepatocellular carcinoma (HCC) in these patients.

Patients and Methods: Our study included 108 chronic HCV patients grouped according to the disease clinical stage. Group (A): CHC, Group (B): Liver Cirrhosis (LC), Group (C): LC with HCC and Group (D): Healthy Controls. Routine laboratory investigations, Polymerase Chain Reaction (PCR) for quantification of HCV, abdominal ultrasonography and Liver Stiffness Measurement (LSM) were done. Child-Turcotte-Pugh, Model for End-stage Liver Disease (MELD) and Fibrosis index based on 4 (FIB-4) scores were calculated. We used the PCR-restriction fragment length [polymorphism technique](#) for Lymphotoxin- α genotyping.

Results: A/A genotype was the most frequent one in the control group (50%) and the A/G genotype was the predominant variant in all patients groups. In HCC patients, G/G genotype was more frequent (31.8%) than in the LC group (19.4%), CHC group (17.8%) and healthy controls (4.17%). No significant association was found between the three genotypes and LSM, FIB 4 and viral load. A significant association was found between LTA genotypes and the Child classes in HCC but not in LC patients. HCC patients carrying A/G genotype had higher MELD scores than other genotypes. There was no statistically significant difference between the three genotypes regarding liver cancer stages, ultrasonography findings or alpha-fetoprotein levels in patients group with HCC. Multivariate binary logistic regression analysis confirmed that LTA G/G genotype and low platelet count were independent predictors for HCC development in patients with HCV-related LC.

Conclusion: Detection of LTA G/G genotype in patients with HCV-related chronic liver diseases could help to recognize high-risk patients for disease progression and HCC development.

Biography

Amr Mohamed Zaghloul is an Associate Professor of Tropical Medicine and [Gastroenterology](#) Sohag University, Egypt.

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