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Association of suppressor of cytokine signaling 3 polymorphisms with liver fibrosis progression in Moroccan patients with chronic hepatitis C

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Context: Infection with hepatitis C virus (HCV) is one of the most important risk factors of hepatocellular carcinoma (HCC). HCV is suspected to induce HCC primarily through chronic inflammation and promotion of cirrhosis. However, the pathogenesis of insulin resistance (IR) in hepatitis C infection is a very intriguing problem. In fact, the HCV is now recognized responsible for direct interference with the insulin signaling pathway. In addition, HCV-related IR has been shown to have a remarkable clinical impact on the progression of hepatic fibrosis and development of HCC. In the liver, HCV core protein up-regulates suppressor of cytokine signaling (SOCS-3) and (SOCS-1), which are known to inhibit insulin signaling by causing ubiquitination of insulin receptor substrate (IRS-1) and (IRS-2) proteins. Genetic variations affecting this gene can induce insulin resistance and decrease the response to interferon, both can accelerated the process of liver carcinogenesis.

Objective: This study aims to evaluate the association between SOSC-3 polymorphisms and progression liver fibrosis in chronic hepatitis C infected patients.

Materials & Methods: In this study, 208 patients chronically infected with HCV (92 patients with moderate fibrosis and 116 patients with advanced fibrosis) were genotyped for 4874 A/G (rs4969170) and A+930-->G (rs4969168) variants using the real time PCR.

Results: A significant difference in genotype distribution of rs4969168 and rs4969170 were detected between mild and advanced fibrosis group. Although these results of SNP genotyping showed that the AA and GA genotypes are increased in advanced fibrosis patients compared to mild fibrosis patients for both SNPs.

Conclusion: These findings indicated that recipient genetic factors play a role in HCV-related fibrosis progression. Molecular studies of these pathways may elucidate the pathogenesis of fibrosis progression and provide risk prediction markers.

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