

Correlation between Hepatocellular Carcinoma and Hepatitis C genotypes and their role in Hepatocarcinogenesis

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Abstract

Background: Hepatitis C virus (HCV) is known to be a major risk factor for the development of hepatocellular carcinoma (HCC).

Aim of the work: to correlate HCV genotypes among HCV positive cases of HCC with the clinicopathological profiles of patients, and to assess if there is characteristic pattern of the virus that may accelerate oncogenesis.

Patients and methods: A prospective study; 60 patients; two groups: **Group I:** 30 patients: HCV with superadded HCC. **Group II:** 30 patients: HCV without superadded HCC (control); recruited from Alexandria University hospitals, Egypt. Confirmation of HCV infection and virus RNA extraction were done. The extracted HCV RNA was transformed to complementary DNA (cDNA) using reverse transcription PCR. INNO-LiPA HCV II was used to identify the genotype spectrum of the 60 samples.

Results: Most of HCC patients were in the 6th decade, males, of rural residence, in stage II (BCLC). Serum GGT was superior to AST and ALT in detecting deterioration in liver functions, suggesting that it could be used as a sensitive biochemical marker for development of HCC in patients with HCV. All 60 HCV-RNA positive samples (100%) were genotype 4. Sequence Analysis of 5-untranslated region of HCV (5UTR) was done to 8 RNA PCR extracts to check for a specific pattern of HCV genotype 4 in HCC patients. No mutations were detected in HCC group characterizing the virus. However; two different sequences (one from each group) were gathered in one ancestor and can be considered as a subgenotype from Genotype 4 in Egyptian patients.