Genetic variability of hepatitis C virus in South Egypt and its possible clinical implication.


Abstract:

Egypt is one of the countries with very high rates of hepatitis C virus (HCV) related morbidity and mortality. However, little is known about geographical and clinical differences in genetic variability of HCV in Egypt. Using direct sequencing and phylogenetic analysis of partial core/E1 and NS5B regions of the HCV genome, HCV genotype/subtype was determined in 129 HCV-infected patients residing in three governates in south Egypt: Assuit, Sohag, and Qena. According to clinical stage of infection, patients were categorized into four groups: asymptomatic carriers, n = 16; chronic hepatitis C patients, n = 36; liver cirrhosis, n = 54; and hepatocellular carcinoma (HCC), n = 23. Genotype 4a was detected in 80.6%, whereas 1g, 4l, 4n, 4o, 4f, and 4m were identified in 7.7%, 4.7%, 3.9%, 1.6%, 0.8%, and 0.8% of cases, respectively. The prevalence of 4a differed regionally; from 88.5% (in Sohag) to 64% (in Assuit, P = 0.002). Genotypes 4l and 4n had a higher prevalence in Assuit (12.8%, 10.3%) than Sohag (0%, 0%; P

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