

Prevalence of HCV Genotypes in Correlation with Viral Load in Northern Region of Iraq

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ABSTRACT

Background: Hepatitis C virus (HCV) is a globally prevalent pathogen with a diverse genotype distribution. The purpose of this study was to determine the prevalence of HCV genotypes and their relationships to sociodemographic traits and viral loads in patients from Iraq's northwestern areas.

Methods: 212 patients from six governorates in Iraq who had been sent to the Genome Diagnosis Laboratory after receiving positive findings for anti-HCV antibody and HCV-RNA tests participated in a cross-sectional study (GDL). Only samples with a positive result for HCV- RNA were selected for detection of HCV genotypes and viral load.

Results: Most of the cases were from Erbil, Kirkuk and Sulaimania, with the highest prevalence being genotype 1a (29.2%) followed by genotypes 4 and 1b (23.6% and 22.7%, respectively). Genotype distribution was not significantly different among various age groups ($P= 0.067$). The overall high viral load was observed in younger age groups particularly in males. The overall distribution of viral load among genotypes in relation to patient age and gender did not, however, show any statistically significant variations ($P= 0.86$ and 0.3 , respectively).

Conclusion: The genotypes 1a, 4 and 1b were more prevalent among the HCV patients. High viral load was observed in younger age groups particularly in males.

Keywords: Hepatitis C infection, Genotyping, Viral load

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