

Hepatitis C Virus (HCV) Genotyping in Infected Patients From Albaha Region

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ABSTRACT

Background: Hepatitis C virus (HCV) is a significant public health issue in Saudi Arabia, with an estimated prevalence of 1.4% in the general population. The preponderance and distribution of HCV genotypes varies globally, and in Saudi Arabia. Genotypes 1a, 1b, and 4 are most commonly found. HCV genotype is predictive of the response of HCV-infected patients to antiviral therapy. Thus, the genotype should be determined so that the patient can receive the most appropriate therapy regimen.

Objective: To examine the distribution of HCV genotypes in infected patients from Albaha region.

Setting: Medical Laboratory Department, Central laboratory and blood bank, Albaha.

Design: A retrospective cross-sectional study.

Method: Forty suspected cases of HCV collected from Central laboratory and blood bank at Albaha from January 2020 to April 2020 were included in the study. All samples were analyzed with real-time RT- qPCR for HCV RNA detection as described previously. HCV RNA positive samples were further analyzed. The HCV genotype-specific multiplex PCR was performed using Abbott RealTime HCV Genotype II assay.

Result: Between January 2020 to April 2020, 40 suspected cases of HCV were analysed; 21(52.5%) were HCV RNA negative and 19 (47.5%) were HCV RNA positive. Genotype 1a was the most prevalent among all the genotypes observed followed by 1b and genotype 2. Genotype 4 and 5 were found in 5% of our samples.

Conclusion: HCV genotype 1a is highly prevalent in Albaha region. These findings will help medical professionals to prescribe more appropriate treatment for the HCV infection, and they will also develop plans for more efficient disease control.

Keywords: Prevalence, Genotype, Hepatitis C Virus

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