



Figure 1.

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### Complete genome sequence of Hepatitis C Virus isolated in Mexico

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**Introduction and Objective:** Death due to liver damage caused by the hepatitis C virus (HCV) represents one of the most frequent health threats in Mexico. However, the complete genome of HCV has not yet been sequenced. The aim of this study was to obtain the complete genome sequence of HCV isolated from patients in Mexico.

**Materials and Methods:** We evaluated patients with hepatitis C who sought medical care at the “Liver Unit” that belongs to the “Hospital Universitario Dr. José Eleuterio” in Monterrey, Mexico from May 2016 to August 2019. We extracted RNA from five samples and amplified the whole genome of HCV with tiled-PCR. Amplicons were sequenced with MinION, a third-generation sequencer technology. Obtained sequences were assembled with the Genome Detective program and posteriorly analyzed with IQtree platform.

**Results:** We obtained four partial and one complete VHC genome that corresponded to genotype 1b. The average coverage of the complete genome was 600X. The phylogenetic analysis of the complete genome showed that this sequence from Mexico was related to viruses isolated in the United States of America, Indonesia, and Japan. Because there is not a full HCV complete genome sequenced before in our country, we used the partial viral genomes reported before in Mexico to compare NS3 and NS5A genes with our reported sequences. The NS3 gene alignment showed that the newly sequenced viruses grouped in a clade different from the previously sequenced viruses. When NS5A gene was used, the newly obtained sequences grouped with the previously sequenced viruses in Mexico.

**Conclusion:** We were able to obtain the first complete and four partial HCV genomes from Mexican patients. This newly sequenced virus will improve the molecular epidemiology of HCV in Mexico.

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### Identification of resistance mutations to DAA's against Hepatitis C Virus in infected subjects in Mexico

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**Introduction and Objectives:** Death due to liver damage caused by hepatitis C virus (HCV), this agent represents one of the most frequent health threats in Mexico. Now direct-acting antiviral agents (DAA's) are available to treat HCV infections. Nevertheless, HCV has gained mutations that hinder the antiviral effect. The presence of these mutations in Mexico is unknown. The aim of this study was to identify resistance-associated substitutions (RAS) in subjects infected with HCV from Mexico.

**Materials and Methods:** We evaluated patients with hepatitis C who sought medical care at the “Liver Unit” that belongs to the “Hospital Universitario Dr. José Eleuterio” in Monterrey, Mexico from May 2016 to August 2019. We extracted RNA from five samples and amplified the whole genome of HCV with tiled-PCR. Amplicons were sequenced with MinION, a third-generation sequencer. Obtained sequences were assembled with the Genome Detective program and resistance-associated substitutions were identified with HCV-Glue software.

**Results:** We obtained four partial and one complete VHC genome. According to HCV-glu algorithm, we detected one virus with resistance to daclatasvir, and probable resistance to ledipasvir and velpatasvir. Another HCV with probable resistance to daclatasvir and ombitasvir and possible resistance to grazoprevir, peritaprevir and ledipasvir. Two HCV isolated had probable resistance to daclatasvir and possible resistance to grazoprevir and peritaprevir. Only one HCV had probable resistance to daclatasvir.

**Conclusion:** We detected one HCV with resistance to daclatasvir and four other viruses with probable antiviral resistance mutations. These findings are crucial to effectively managing the patient's treatment.

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### Hepatitis C virus NS5A and core proteins regulate epithelial-mesenchymal transition biomarkers in hepatoma cells

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**Introduction and Objectives:** Hepatitis C virus (HCV) NS5A and Core proteins play a key role in carcinogenesis development. Epithelial-mesenchymal transition (EMT) induced by HCV has been related to Snail and TGF $\beta$ 1 upregulation and E-cadherin downregulation. This study aimed to evaluate the effect of HCV NS5A and Core proteins in the regulation of Snail, TGF $\beta$ 1 and E-cadherin by transient transfection in the hepatoma cell system.