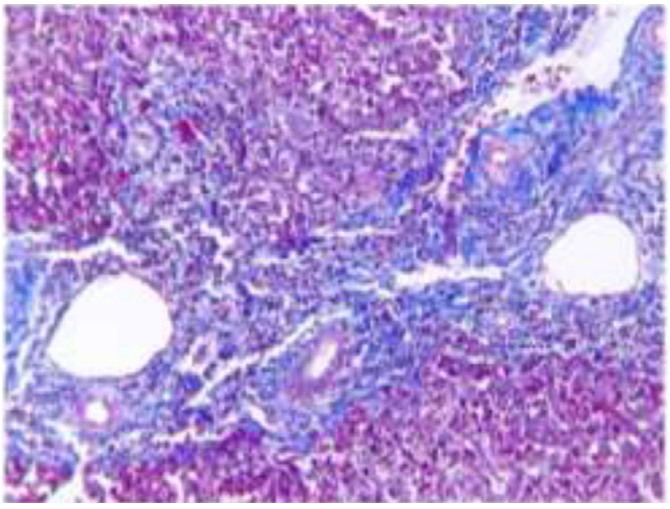

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Post-infantile giant cell hepatitis, management, six-year follow-up and re-transplantation, a successful case report during the pandemic

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Introduction and Objectives: HCG is a relatively common histological finding in newborns. In children, it presents with cholestasis, hyperbilirubinemia and inflammation; in the adult population, it remains poorly defined, with only 100 cases published in the literature during the last three decades.

Materials and methods: We present the case of a 20-year-old female patient with a history of herbal medicine and valproate, debuting six years ago with pain in the right hypochondrium, jaundice and fever with progression to liver failure, hepatotropic virus infections and autoimmunity were ruled out. Start liver transplant protocol with incompatible ABO organ, with induction with rituximab, immunoglobulin and basiliximab with post-surgical complications with resolved hemoperitoneum and pulmonary hemorrhage, with subsequent discharge and histopathological report of giant cell hepatitis explant, continuing immunosuppression for six years until readmission due to pruritus with liver biopsy that reported acute cellular rejection and ERCP with choledocho-choledochoanastomosis stenosis with endoscopic rehabilitation, with subsequent biochemical deterioration, starting basiliximab, steroids, plasma exchanges and MARS without improvement, subsequent ABO compatible retransplantation without complications. Currently no rejection data.

Discussion: HCGPI is a progressive, often fatal, disease process with a 50% survival rate without liver transplantation. The high mortality rate is caused by liver failure or sepsis as a result of immunosuppressive therapy.

Conclusion: HCGPI in our patient manifested acutely with rapid evolution toward liver failure. The use of valproate and herbal medicine were factors. Thanks to the possibility of using MARS as a bridge for the transplant, the result was optimal.

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Autoimmune hemolytic anemia as a paraneoplastic syndrome in hepatocarcinoma, case report

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Introduction and Objective: Hemolytic anemia can be associated with various types of solid tumors; however, in hepatocarcinoma, it is extremely rare.

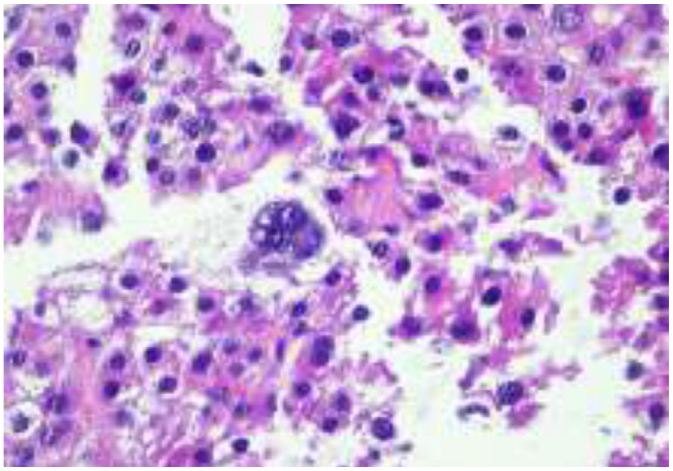
Case Summary: Man 74 years old. Symptoms of two months with dyspnea, asthenia and adynamia. On physical examination, generalized pale skin and sclera, normal heart and lung area, soft, depressible abdomen, with peristalsis present, palpation of the liver edge 5 cm below the costal margin. Laboratories with leukocytes 6.1 103/Al, neutrophils #4.1, lymphocytes #1.3, HB 6.2 g/dL, HTC 16.8%, MCV 103fL, HCM 38pg, platelets 395.00 103/Al; BD 0.5 mg/dL, BI 2.80 mg/dL, BT 3.30 mg/dL, DHL 403 IU/L. Direct Coombs is performed positive dilution 1:128. FSP with anisocytosis, red blood cell agglutination, macrocytosis and macroplatelets, reticulocytes 1.48%, alpha-fetoprotein 12.7 IU/mL. Warm antibodies (IgG) attached to the erythrocyte membrane were documented. Simple and contrast-enhanced abdominopelvic tomography, with images suggestive of multifocal cellular hepatocarcinoma. Liver biopsy, which reports findings of hepatocarcinoma. Management with oral steroid drugs was initiated jointly, reversing the hematological alterations without requiring blood products.

Discussion: There are few cases in the medical literature on hematological alterations associated with solid tumor metastases. In this case, the hematological involvement of the patient was not due to metastasis but to a paraneoplastic syndrome since the first manifestation found was anemia with jaundice secondary to hemolysis.

Conclusion: The diagnosis must be reached by exclusion, ruling out other causes such as primary hematological alterations, metastases, or vascular processes.

Funding: The resources used in this study were from the hospital without any additional financing

Declaration of interest: The authors declare no potential conflicts of interest.



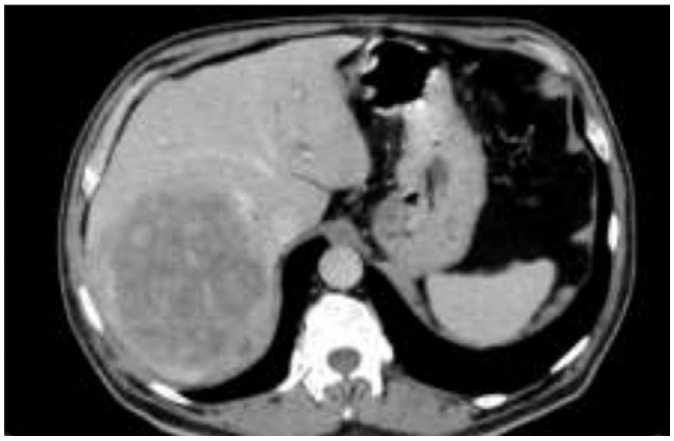


Figure 1.
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Complete genome sequence of Hepatitis C Virus isolated in Mexico

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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.

Funding: The resources used in this study were from the hospital without any additional financing

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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-glue 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 TGFβ1 upregulation and E-cadherin downregulation. This study aimed to evaluate the effect of HCV NS5A and Core proteins in the regulation of Snail, TGFβ1 and E-cadherin by transient transfection in the hepatoma cell system.