

ORT_24 - Identification of drug-related viral mutations in pregnant women infected with Hepatitis C virus

Kaio Callebe Pedro Ferreira²; Vinicius Motta Mello²; Giovana Guimarães Santos Nascimento²; Paulo Sergio Fonseca Sousa²; Aryele Raira Silva²; Poliana Fernandes²; Girleide Pereira Oliveira¹; Livia Melo Villar²; Barbara Vieira Lago²; Lia Laura Lewis Ximenez². ¹Secretaria Municipal de Saúde ²Instituto Oswaldo Cruz - Fiocruz

Introduction: It has been estimated that ~58 million people in the world are chronically infected with hepatitis C virus (HCV), of which an estimated 29,000 women of reproductive age, with approximately 8% being pregnant. HCV can be transmitted during pregnancy, especially when viral loads are \geq 600,000 IU/mL, and occurs more frequently during the second and third trimesters. Despite the existence of drugs with high cure rates for HCV, they cannot be used during pregnancy due to their teratogenic effects. Some studies show that certain mutations may be related to the vertical transmission of HCV and that previous drug resistance mutations can be transmitted from mother to baby.

Objectives: The aim of this study was to assess the genetic variability of HCV in pregnant women followed at a referral center in Rio de Janeiro between 2016-2022.

Methodology: Samples from pregnant women chronically infected with HCV and with viral loads of $\ge 3x10$ log were selected. After selecting the samples, the viral RNA was extracted, amplified by a qualitative RT-PCR for the HCV NS5B region, and further sequenced and analyzed to identify viral subtypes and possible clinical importance mutations.

Results: A total of 94 pregnant women with reactive anti-HCV were identified, 70 of whom had HCV RNA \geq 3x10 log. These pregnant women had a mean age of 32.9 ± 7.0 (18 to 45 years) and were mostly in the 2nd trimester of pregnancy (n=45; 47.9%). It was possible to amplify 53/70 (75.7%) and successfully sequence 33/53 (62.3%) samples, where the majority were subtype 1a (n=12/33; 36.4%), followed by 1b (n=17/33; 51.5%) and 3a (n=3/33; 9.1%). The results of the mutation analyses showed a low frequency of drug resistance mutations (n=6, 18.2%), such as V321L, V321IV and C316N.

Conclusion: Even though the mutations found related to drug resistance, were secondary and of low clinical relevance, future attention in treating these women in the postpartum period is required. Our results show the importance of identifying drug mutations in HCV pregnant women for epidemiological surveillance purposes.

Keywords: Hepatitis C; HCV; HCV mutations; Pregnant women; Vertical transmition