



Sociedad de Investigación y Docencia en Virología e Infectología.

Congreso SIDVI 2.0

“Innovación Educativa e Investigación en Virología”

22 al 18 de agosto de 2018 en la Ciudad de México.

Presence of rare hepatitis C virus subtypes, 2j, 2k and 2r, in Mexico City as identified by sequencing.

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Objetivo: Determine the molecular epidemiology of the HCV GTs in CHC patients naive to treatment living in Mexico City. **Metodos:** From 2015-2016, 50 CHC patient samples were collected at Hospital de Infectología. Diagnosis was established by NAT. For sequencing and phylogenetic analysis of the 5'UTR, Core/E1 and NS5B regions, HCV RNA was extracted from plasma, cDNA was obtained by RT-PCR. The studied regions were amplified by nested PCR. Sequencing was performed on a 3500 Genetic Analyzer. Phylogenetic reconstruction by a maximum likelihood tree was performed on the three regions using a General Time Reversible model. Robustness was estimated from 1000 bootstrap replicates, and branches with >70% support were considered significant. **Resultados:** The HCV 5'UTR, Core/E1 and NS5B regions of samples from fifty patients infected with the hepatitis C virus (HCV) were analysed. Seventeen patients were identified with genotype (GT) 1b, eleven with GT-1a, nine with GT-2b and four with GT-3a. Two rare subtypes were detected: GT-2j in two patients and GT-2r in one patient. Three patients had mixed infections: one with GT-2k+2j and two with GT-1b+2b. This work identifies HCV GTs, 2j, 2k and 2r for the first time in Mexico. **Conclusión:** The genotyping based on sequencing and phylogenetic analysis of several HCV regions is useful for understanding the molecular epidemiology of this virus in a specific population, considering that variants can be modified by population movement. Continuous vigilance is a key strategy for eradicating HCV in the new era of DAA-based treatment. These rare subtypes should be analysed in considering CHC pathophysiology and treatment response.

Palabras clave: HCV; genotype; epidemiology; phylogenetic analysis.

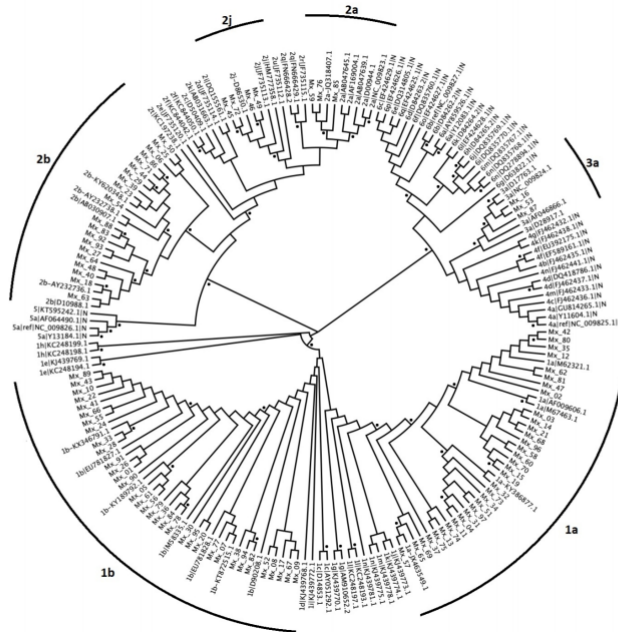


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Maximum likelihood phylogenetic tree of 0.03 the HCV NS5B region. The tree was constructed using Mega v.7 software, using the maximum likelihood method. tree was inferred using a GTR+G+I model for nucleotide substitutions.

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