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Overview of the epidemic history of Hepatitis C rare subtypes 2i and 4d in Tunisia and in the world

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The impressive improvements in qua therapy efficacy alone are not sufficient to substantially reduce the Hepatitis C Virus burden because of the usually very long asymptomatic phase of the infection. In turn, this renders prevention of infection of great importance. The value of learning how the virus has spread in the past is that this can provide clues as to what routes the virus likely spreads through today, which can feedback into prevention policy. In Tunisia, HCV subtypes 2i and 4d are minor circulating subtypes. Here, we introduce a Bayesian Markov Chain Monte Carlo method for visualization of spatial and temporal spread of HCV-2i and 4d in Tunisia and some other countries in the world.

Our analyses included sequences retrieved from Genbank and isolated from several countries in the world; 30 HCV-NS5B subtype 2i genome sequences obtained during the period 2000-2020 and 293 HCV-NS5B-4d sequences detected between 2000 and 2019. Phylogenetic analyses revealed that no consistent geographical clusters could be identified in HCV-2i tree with two clearly distinguished clusters in HCV-4d Tree. The estimated time for the most recent common ancestor suggested that current HCV-2i strains emerged in 1999 [1998, 2000] and current HCV-4d strains emerged in 1984 [1977, 1990] in Tunisia and other countries from the world included in the present study. Our study highlights the importance of epidemic molecular investigation to monitor the evolution of circulating HCV strains especially in this challenging period before the global elimination.

Recent Publications

1. Khedhiri, M., Ghedira, K., Chouikha, A., Touzi, H., Sadraoui, A., Hammemi, W. and Triki, H. (2019). Tracing the epidemic history of hepatitis C virus genotype 1b in Tunisia and in the world, using a Bayesian coalescent approach. Infection, genetics and evolution: Journal of molecular epidemiology and evolutionary genetics in infectious diseases. 75, 103944. DOI: 10.1016/j.meegid.2019.103944Heilig M, Egli M (2006) Pharmacological treatment of alcohol dependence: Target symptoms and target mechanisms. Pharmacology and therapeutics 111:855-876.

Biography

Khedhiri Marwa, PhD in Microbiology, Faculty of Sciences of Tunis, Tunis El Manar University, Tunisia. I got my PhD in Biology on September 2021 at the University of Tunis el Manar, Tunis, Tunisia. I have a background in Molecular Biology and Virology with a Master's degree in Microbiology and Biotechnology. Currently I work as Research Assistant in the framework of an International Project at Pasteur Institute of Tunis. The goal of this EU-funded project is to develop an intelligent decision support platform for pandemic prediction and management.