

Molecular Determining of HIV-1 with the Presence of Hepatitis B Virus and Hepatitis C Virus Co-infections

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Background: Because of the similar modes of transmission (include unsterile medical injection, blood transfusion, sexual intercourse and injecting drug use), co-infection with viral hepatitis and HIV is increasingly seen as a major public health problem. In addition to that, co-infection with HIV and certain other infections, such as HBV or HCV infection, increases the urgency of starting ART (1). On the other hand, increasing the demographic mass movements, may be changed the virus transmitted trends and may have a potential effect for HIV and co-infection surveillance in the future. In this study, we aimed to determine the molecular characteristics HIV-1 in the presence of hepatitis B virus (HBV) and hepatitis C virus (HCV) co-infections in Turkey.

Material & Methods: The present study was conducted between March 2010 and March 2017. HIV-1 RNA was detected and quantified by a commercial real-time PCR assays. Subtyping and genotypic resistance analysis were performed by population sequencing of the viral protease and rt regions of HIV-1 pol gene. Drug resistance mutations were defined according to the Surveillance Drug Resistance Mutation list as recommended by the World Health Organization.

Results: We detected totally 3896 HIV-1 positive patients whose molecular laboratory tests were completed in Turkey. The viral hepatitis co-infections were detected in 4.3% (n=170) of all HIV-1 infected patients in this study. HBV and HCV co-infections were observed as 3.2% and 0.5% in HIV-1 positive patients, respectively. Major HIV-1 subtypes were detected as a group M, subtype B (67.5%). We observed 13.5 % drug resistance mutation motifs in HIV-1 genomes which included this study. NRTI, NNRT and PI resistance mutations have been investigated in a detailed manner and the mutation rates were determined 9.4%, 5.3% and 1.8%, respectively.

Conclusion: HBV and HCV co-infections can be seen more frequent in HIV positive patients because of similar transmission routes. However, the ART drug resistance mutation pattern are observed similar. The molecular characterisation of HIV-1 genome for ART resistance is not different from noncoinfecting. In the light of increasing demographic mass movements and their potential to affect of infection transmission trends, patients with HIV-1 and their viral hepatitis co-infections should be recommended an carefully surveillance.

Reference

A Working Group of the Office of AIDS Research Advisory Council (OARAC). Guidelines for the Use of Antiretroviral Agents in Adults and Adolescents Living with HIV. <https://aidsinfo.nih.gov/guidelines> on 1/18/2018.