

13th International Conference on**CLINICAL GASTROENTEROLOGY, HEPATOLOGY AND ENDOSCOPY**

November 13-14, 2017 | Las Vegas, USA

Epidemiological and clinical evaluation of Hepatitis B, Hepatitis C, and Delta H viruses in Tajikistan Hepatitis**Khakimova Zebinniso**

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The implication of genotypes is recognized increasingly in the clinical course of *Hepatitis B virus* (HBV) and in response to anti-viral drugs of *Hepatitis C virus* (HCV). Genotypic prevalence of both etiological agents varies geographically and no data are available for Tajikistan. To investigate the epidemiology and clinical significance of HBV and HCV genotypes in chronic hepatitis (group 1) and liver cirrhosis/hepatocellular carcinoma (HCC) (group 2) patients in Tajikistan, 124 patients with chronic liver disease (group 1=84 and group 2=40) were enrolled. Genotypes of HBV, HCV, and delta hepatitis virus (HDV) were determined by sequencing. The overall prevalence of anti-HCV, HCV core antigen (HCVcAg) and HBsAg was 46% (57/124) and 41.1% (51/124), respectively. Coinfection of HCV/HBV, HBV/HDV, and HCV/HBV/HDV was found in 4.8% (6/124), 11.2% (12/124), and 0.8% (1/124) of cases, respectively. HDV genotype 1 was found in 19.6% (10/51) of HBsAg-positive patients. The HBV/HDV coinfection was relatively high in group 2 compared to group 1 (15% vs. 7.1%). HCV/1b detected in 84.6% (44/52) of HCV RNA-positive patients, followed by 3a (7.6%), 2a (5.7%), and 2c (1.9%). HBV/D was detected in 94.1% (48/51) of HBsAg-positive patients, followed by HBV/A [5.8% (3/51)]. T1762/A1764 double mutation was associated with liver cirrhosis/HCC in HBV-infected patients ($P=0.0004$). This is the first study on the molecular epidemiology of Hepatitis viruses among chronic liver diseases patients in Tajikistan. Among HBV-infected patients, the T1762/A1764 mutation was associated with liver cirrhosis/HCC.

Biography

Khakimova Zebinniso at the age of 37 years graduated from Institute of Gastroenterology of the Republic of Tajikistan. She works at the Department of Virology, Institute of Gastroenterology of the Republic of Tajikistan. She has published more than 5 papers in reputed journals.

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