GENOTYPE IDENTIFICATION OF HBV AND HDV IN PATIENTS WITH CHRONIC VIRAL HEPATITIS B+D IN SAMARKAND REGION

Voseeva D.Kh.– Assistant of the

Department of Infectious Diseases,

Samarkand State Medical University,
Samarkand, Uzbekistan.

Abstract

Chronic hepatitis B virus (HBV) and hepatitis D virus (HDV) co-infection remains one of the most severe forms of viral liver disease, contributing to rapid progression of fibrosis, cirrhosis, and hepatocellular carcinoma. Genotype identification of HBV and HDV is critical for understanding viral epidemiology, disease severity, and treatment outcomes. In Uzbekistan, particularly in the Samarkand region, where viral hepatitis is highly prevalent, recent molecular studies have revealed that HBV genotype D dominates in the majority of patients, with subtypes D1–D3 identified in those with advanced liver disease. HDV genotype 1 is the most frequent in Central Asia, correlating with aggressive clinical outcomes. Advances in molecular diagnostic technologies, including PCR-based assays, sequencing, and phylogenetic analysis, have facilitated more precise genotyping. This review summarizes global and regional data on HBV and HDV genotypes, highlights studies conducted by Uzbek researchers, and discusses their epidemiological and clinical implications for patient management in Samarkand .

Keywords: chronic hepatitis B, hepatitis D virus, HBV genotype, HDV genotype, Samarkand region, molecular epidemiology, Uzbekistan.

Introduction

Chronic viral hepatitis remains a major cause of liver-related morbidity and mortality worldwide. Among these, HBV and HDV co-infection represents the most aggressive form, accelerating progression to cirrhosis and hepatocellular carcinoma compared to HBV monoinfection [1]. In Uzbekistan, viral hepatitis continues to be an urgent public health problem. Despite mass vaccination programs, HBV remains endemic, and HDV co-infection is frequently observed in clinical practice. Genotype analysis is essential for understanding local epidemiology and guiding therapeutic strategies [2].

Global and regional epidemiology. HBV is classified into at least ten genotypes (A–J), while HDV has eight genotypes (HDV-1 to HDV-8). HBV genotype D is common in the Mediterranean, Middle East, and Central Asia, whereas HDV genotype 1 is distributed worldwide and associated with severe disease [3].

In Uzbekistan, several molecular epidemiological studies have provided valuable insights into HBV genotype distribution. A large cohort analysis demonstrated that 96.5% of patients carried HBV genotype D, while 3.5% had genotype A [4]. Another study confirmed similar findings, with 87% of patients infected with genotype D and 13% with genotype A [5]. Additional research among patients with fibrosis and cirrhosis revealed exclusively HBV genotype D, predominantly subgenotypes D1, D2, and D3, highlighting its role in advanced liver disease [6]. A pediatric study also reported HBV/D in 69% of children, HBV/A in 23%, and HBV/C in 8%, indicating some genetic diversity and possible influence of transmission routes [7].

Molecular methods for genotype identification. Modern techniques for HBV/HDV genotyping include PCR with restriction fragment length polymorphism (RFLP), S-gene sequencing, and next-generation sequencing (NGS). These approaches allow precise identification of subgenotypes and mixed infections. In Uzbekistan, PCR-based diagnostics are widely used, but sequencing remains limited to research centers in Tashkent and Samarkand.

Integration of NGS into regional laboratories could significantly improve molecular surveillance.

Clinical implications in Samarkand region. The predominance of HBV genotype D and HDV genotype 1 in Uzbekistan has important therapeutic consequences. Genotype D is associated with poorer response to interferon-based therapy compared to genotype A, while HDV-1 infection is linked to more aggressive disease and limited treatment success. For Samarkand region, where co-infection is common, genotype identification may guide clinicians in predicting treatment response, planning long-term monitoring, and considering new therapeutic approaches.

Conclusion

Genotype identification of HBV and HDV is crucial for understanding the molecular epidemiology and clinical outcomes of chronic hepatitis B+D. Data from Uzbek studies confirm that HBV genotype D and HDV genotype 1 are predominant in the region, with implications for treatment efficacy and prognosis. Expanding molecular diagnostic capacity in Samarkand will contribute to improved patient management and strengthen regional contributions to global hepatitis research.

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