

## HETEROGENEITY FEATURES GENOMIC HEPATITIS B VIRUS MOROCCO

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**Introduction.** Viral hepatitis B is a major public health problem around the world. According to the WHO about 50 million people worldwide are infected with hepatitis B each year, 325 million live with chronic infection. Deaths from hepatitis B is comparable to the mortality rates of tuberculosis and HIV infection. According to WHO, in Morocco, approximately 850,000 people are infected with the hepatitis B virus, and 400,000 – simultaneously with hepatitis B virus and hepatitis C virus 15 to 45% of those infected with hepatitis B virus in people spontaneously get rid of the virus within 6 months after infection without treatment-or, as in 55-85% of those infected develop chronic infection.

**Aim.** The aim of the work was to analyze the characteristics of genomic heterogeneity of the hepatitis B virus in Marokkko.

**Materials and methods.** The peculiarities of the phylogenetic analysis of the nucleotide sequences of isolates of hepatitis B virus in Morocco.

**Results and its discussion.** The development and use of modern molecular genetic techniques allowed to expand the understanding of the biology of hepatitis B. The genetic variability of the viral genome of hepatitis B virus has led to the emergence of 10 different geographical distribution of genotypes, genotypes identified within subgenotypy, differ from each other by 4-8% of the total genome sequences. The regularities of the geographical spread of the different genotypes of hepatitis B virus in the world. So genotypes B and C are associated with the population of Asian countries, genotypes A and D are common among the European countries and in the United States. In the African region, including Morocco revealed the presence of genotype A and three subgenotipov – A1, A2, A3, dominated by genotype D and identified five subgenotipov (D1-D5).

**Conclusions.** It is found that the geographic distribution of genotypes of hepatitis B virus is closely associated with endemic regions and indigenous population living in them, which is essential in understanding the relationship between mutant HBV and a broad spectrum of clinical and pathologic states associated with HBV infection.

On the example of the causative agent of hepatitis B revealed the possibility and prospect of using molecular genetic approaches to study the characteristics of the epidemic process in this infection.