

Original Paper

## Hepatitis B virus x protein coding sequence variation in chronically infected patient

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### Abstract

**Background and Objective:** Chronic infection with Hepatitis B virus (HBV) is one of the main causes of cirrhosis and hepatocellular carcinoma (HCC). The pathogenicity of the virus is determined by the multi-functional protein x (HBx). Changing the sequence of the gene encoding this protein causes the regulation of transcription and pathogenicity factors. This study was done to analyze the genetic dynamics of the HBx coding gene in a person with chronic HBV.

**Methods:** In this descriptive laboratory study, an infected person with chronic hepatitis B virus infection was first amplified and cloned into complete sequence of HBx encoder. Then, the reference sequences of genotypes, serotypes and different virus subtypes of the GenBank database were matched by CLC Sequence Viewer software. The comparative result was used to plot the phylogenetic tree by T-rex server and population genetic analysis using DnaSP software. Natural selection at the nucleotide and protein level was performed by the Tajima's D test.

**Results:** No known mutation at the level of the protein was found in the chronic sequence of the HBx encoder. The results of natural selection indicated neutral mutations in the HBx gene. The phylogenetic results showed that the HBx encoding sequences in the chronic infected individual had a genetic affinity with genotype D and ayw2 subtype.

**Conclusion:** Neutrality polymorphism takes place in HBx coding region. Also, the phylogenetic results of the present study are consistent with the previous findings of Golestan province and Iran which have reported the prevalence of genotype D and subspecies ayw2.

**Keywords:** Hepatitis B virus, HBx, Population genetics, DnaSP, Genotype D, Serotype ayw2

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