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## Hepatitis B virus genotype D sub genotype D1 circulating in Pakistan, China and India: An *In-Silico* analysis

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Heve genotype D subgenotype D1 predominates in Pakistan and India. It is more than 80% among all genotypes of HBV in these two regions. However, it is less dominant in China where genotype B and C predominates. In this study, we present a computational analysis of HBV genotype D subgenotype D1 in Pakistan, India, and China. For this purpose, 25 complete genome sequences of HBV genotype D subgenotype D1 were collected. Four complete genome sequences were obtained from Pakistan 8 from China and 13 from India. Sequence alignment showed less than 4% divergence in reported sequences from Pakistan, India, and China. C and X genes showed the divergence of less than 3%. While comparison over the S gene showed a similarity ratio of 97–98% of genotype D subgenotype D1. The phylogenetic analysis highlighted that Pakistan HBV complete genome isolate has the closest evolutionary relationship with the HBV complete genome isolate prevailing in its neighbor countries China and India. Gene structure analysis showed that exons of 'P' gene were the longest; about 75% of the gene size while gene 'S' had 2nd longest coding regions with two exons and one intron with the size ratio of 40% and 60% respectively.

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