10th World Congress on
Control and Prevention of HIV/AIDS, STDs & STIs
54th International Conference on
Nursing Leadership and Management
31st World Congress on Nursing
July 20-21, 2022
WEBINAR

Hepatitis B Virus sub-genotype A1 evolutionary dynamics in Botswana

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Background: Hepatitis B virus (HBV) infection is a major global health problem. Botswana has an intermediate HBV prevalence of 3.1–10 %. The predominant genotypes are A, D and E with a prevalence of 80%, 18.6% and 1.4%, respectively. No studies have investigated the origins and evolutionary history of the HBV genotypes in Botswana. We sought to investigate the Time to Most Common Recent Ancestor (tMRCA) and spread of the predominant HBV subgenotype, A1 (HBV/A1) in the population of Botswana. We also aimed to determine the diversity of HBV/A1 open reading frames (ORFs) in Botswana HBV sequences.

Method: A retrospective study was conducted utilizing 24 near-full length HBV sequences sequenced in Botswana from 2009 and retrieved from NCBI sequence database. Additional 130 HBV near full-length sequences were included as references. Bayesian coalescent analyses were used to study the population dynamics of the 154 HBV/A1 sequences. The temporal signal was estimated through the root-to-tip method using node density in tempest. Correlation coefficient was used to indicate the amount of variation in genetic distance explained by sampling time and used as a measure of the clockliness of the data. Skyline plots were used to estimate the effective HBV infections in Botswana population over time. Botswana sequences were partitioned into 7 HBV ORFs and used to calculate nucleotide diversity based on pairwise distances analysis implemented in MEGA.

Results: We estimated the tMRCA of HBV/A1 to be 1959 (1920–1980), 95% Highest Posterior Density (HPD) in Botswana. Skyline plot analysis showed an increase in the size of the HBV/A1 infected population around 1985 and 1990 which is over the last 30–40 years. Pre-core region had highest median diversity of 1 (IQR, 0.0115–1) and the surface region was relatively conserved with median diversity of 0.0075 (IQR, 0.0029–0.0135) $p < 0.01$.

Conclusion: Study provides baseline subgenotype-based phylodynamic information by predicting the tMRCA of HBV/A1 sequences revealing the evolutionary dynamics of HBV/A1 thus aiding in theoretical, clinical prevention and treatment of HBV/A1 in Botswana. Statistically significant mean diversity was observed between the different HBV/A1 ORFs that should be taken into consideration in future treatments and vaccine designs of HBV/A1.

Biography

Doreen Ditshwanelo MSc student at (BIUST)/graduate student at Botswana Harvard Aids Partnership with close to 4 years' experience of biomedical research.

Received: April 22, 2022; **Accepted**: April 25, 2022; **Published**: July 20, 2022