HEPATITIS B VIRUS MUTATIONS ASSOCIATED WITH HEPATOCELLULAR CARCINOMA IN BOTSWANA

#0615

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BACKGROUND

- Hepatitis B virus (HBV) resulted in 887,000 deaths in 2015 due to hepatocellular carcinoma (HCC) and cirrhosis.
- Mutations within the HBV core, precore, and X regions have been reported to lead to a rapid progression to HCC.
- Our aim was to identify HBV mutations associated with progression to HCC in HIV/HBV co-infected adults in Botswana.

METHODS

- This was a retrospective, cross-sectional study utilizing archived plasma samples from 100 HIV/HBV co-infected infected adults initiating HAART.
- The study was conducted at Botswana Harvard AIDS Institute Partnership utilizing samples from Bomolemo study.
- Twenty eight of 100 samples were hepatitis B surface antigen (HBsAg) positive, while 72 of the 100 samples had occult hepatitis B infection (HBsAg negative but HBV DNA positive).
- HBV regions (precore/core (276 kb) and X (465bp) regions) were amplified using a semi-nested polymerase chain reaction.
- Amplified sequences and a consensus sequence were aligned in clustal X and compared to identify clinically relevant mutations.

RESULTS

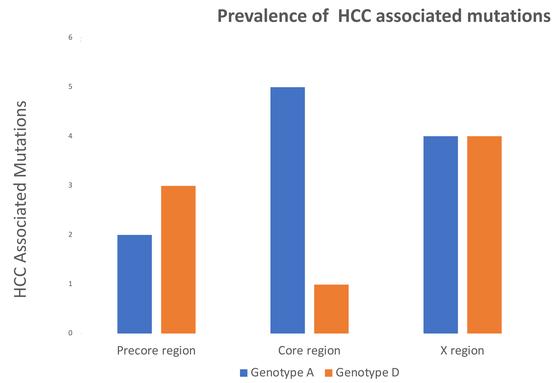


Table 1: HBV mutations associated with HCC in the precore, core and X regions

Region	Mutation	Genotype
Precore	M1L W28*	A
	V17F W28* G29D	D
Core	P50A E64D L65V T67N A131P	A
	P50H	D
X	T36A I127T K130M V131I	A
	H94Y I127L K130M V131I	D

*Stop codon

- Of the 100 samples, 60 could be amplified and sequenced. Thirty-six (60%) of 60 samples were infected with genotype D, while 24 (40%) of the 60 samples were infected with genotype A. Fifteen (25.0%) of 60 samples had 29 mutations which have been previously associated with HCC. Eleven HCC-associated mutations were detected in genotype A, while 18 HCC mutations were detected in genotype D samples. W28* mutation was seen in more than one participant and also occurred as a dual mutation. E64D and L65V were the most common mutations, occurring in 3 participants each.

CONCLUSION

- Some participants had HCC associated mutations hence might be prone to rapid disease progression and may require additional clinical monitoring.
- Other polymorphisms were also detected but have not been functionally characterized; thus, future in vitro studies on these mutations are warranted.

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