

FULL-LENGTH SEQUENCING OF HIV PROVIRUSES IN HIV-HBV CO-INFECTED INDIVIDUALS FROM THAILAND

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Background:

HIV-hepatitis B virus (HBV) co-infected individuals experience higher rates of liver disease than mono-infected individuals. Previous studies have found that HIV co-infection can impact the natural course of HBV infection, but the reverse has not been confirmed. We aimed to determine the frequency of intact provirus in HIV-HBV co-infected individuals prior to ART initiation and whether this frequency was associated with any clinical parameters.

Methods:

HIV-HBV co-infected individuals naïve to ART were recruited in Thailand as part of a prospective observational cohort study (n=39). Single near full-length HIV subtype AE proviruses were amplified using Full-Length Individual Proviral Sequencing (FLIPS) assay and sequenced using Next Generation Sequencing. Proviruses were then characterised as defective or genetically intact, and quantified to determine the proportion of infected cells.

Results:

To date, a total of 347 HIV sequences have been sequenced and analysed from 12 individuals. When all sequences were pooled, 32.9% of HIV proviruses were genetically intact. These intact sequences were genetically unique and had genetic diversity ranging from 0.2 to 1.4%. Extremely large variation in the proportion of genetically intact HIV proviruses were observed between participants (17%-66%), which did not correlate to any clinical or laboratory parameters including plasma HBV DNA or HIV RNA, HBeAg status and ALT levels. The proportions of genetically intact provirus from these untreated participants were much greater than those found in a different cohort of participants on suppressive ART previously analysed by our laboratory (genetically intact: 1-10%).

Conclusion:

Genetically unique and intact HIV proviral sequences were commonly identified in untreated HIV-HBV co-infected participants. The frequency of intact virus was far higher than previous studies of on-therapy participants. Future work will focus on whether these findings are a result of HBV co-infection or whether intact virus is commonly found in all untreated HIV-infected individuals.