Title: Subtype specific differences in transmission cluster dynamics of HIV-1 B and CRF01_AE in New South Wales, Australia

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Introduction:
The HIV-1 epidemic in New South Wales (NSW) is becoming more heterogeneous. NSW Health reported differences in drop in infections for Australian-born (41%) and non-Australian-born individuals (6%) since 2014. This suggests differences in transmission dynamics between risk groups that could be linked to an increase in non-B subtypes, which are more common in non-Australian-born individuals. We therefore sought to compare transmission dynamics between different subtypes and their associated demographic characteristics.

Methods:
We used *reverse transcriptase* sequences sampled from new HIV-1 notifications between 2004 – 2018 that classified as subtype B (n=2919) and CRF01_AE (n=473). We estimated maximum likelihood trees and identified NSW-specific clades as nodes with 100% NSW sequences. Sequence pairs contained only two sequences and clusters contained ≥3 sequences. All other NSW sequences were defined as singletons. Chi-Square statistics was used for comparison between demographic factors and sequences being associated with a cluster or not.

Results:
We identified 104 subtype B and 11 CRF01_AE growing clusters. For subtype B; sequences associated with clusters were more likely to be from individuals reporting men who have sex with men transmission, being Australian-born, and derived from the early stage of infection (p <0.01). For CRF01_AE sequences, only those derived from the early stage of infection were associated with clusters (p <0.05). We found 47 subtype B and seven CRF01_AE clusters that contained sequences sampled during the early stage of infection but with a large time gap in-between (>1 year) and did not have a close genetic

link. These are likely to be representing infections derived from intermediate transmission via undiagnosed individuals.

Conclusion:
We identified subtype specific transmission dynamics with subtype B being dominated by larger clusters and CRF01_AE by sequence pairs. We identified numerous active clusters potentially containing undiagnosed individuals that might play a major role in sustaining the ongoing epidemic.

Disclosure of interest statement
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