HIV-1 cluster dynamics in the era of ongoing public health-associated PrEP intervention in NSW, Australia

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Background

Australia's successful, rapid roll-out of PrEP from 2016 was followed by steep declines in new HIV diagnoses. Routinely reported surveillance data shows that declines are uneven across the population, with a greater decline observed in inner-Sydney. We estimated transmission clusters using protease and reverse transcriptase sequences from newly diagnosed individuals in New South Wales, Australia between 2011- 2021 and assessed the impact of PrEP on these clusters.

Methods

A total of 3,366 diagnoses were made between 2011-2021. We selected a total of 2,174 sequences that represented the earliest sequences with available metadata. We inferred a maximum-likelihood tree in IQTree and defined transmission clusters using ClusterPicker with distance threshold of 3.0%. We estimated the reproductive number (*Re*) for large clusters (>10 sequences) with the Birth-Death Skyline model in BEAST2 to determine changes in cluster growth dynamics over time.

Results

Overall, 1,080 sequences (49.7%) were singletons, and 1,094 sequences (50.3%) were found in 170 sequence pairs and 150 clusters. The latter included 143 sequences in 11 large clusters. Individuals in large clusters were predominantly MSM (95.1%) with subtype B (92.3%) and C (7.7%) infections and were diagnosed during early-stage infection (diagnosis within 12 months of infection; 73.4%). The 5-year average proportion of early-stage infections in any cluster increased to 69% in 2017-2021 from 66% in 2011-2016. *Re* remained >1 for large clusters past 2016, except for one where *Re* declined after 2016 to epidemiological threshold (*Re*=1). We identified two rapid growing clusters that emerged after 2016.

Conclusion

These results suggest the prevention impact of PrEP is unevenly distributed and may be greater among sub-populations with higher awareness of prevention measures, whom frequent testing facilitates earlier diagnosis and linkage to care. Further analysis is needed to effectively evaluate these outcomes due to the impact of COVID-19 lockdowns on HIV testing and sequencing.

Disclosure of Interest Statement:

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