

PHYLOGENETIC CLUSTERING PATTERNS AMONG PEOPLE LIVING WITH HIV AND HEPATITIS C IN AUSTRALIA

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Introduction: In the move towards hepatitis C (HCV) infection elimination among people living with HIV in Australia, understanding HCV transmission patterns may provide key insights to guide ongoing initiatives. The aim of this study was to identify phylogenetic transmission clusters among HIV/HCV co-infected adults in the Control and Elimination of HCV from HIV-infected individuals within Australia (CEASE-D) study.

Methods: RNA was extracted from dried blood spot (DBS) samples collected between 2014-2016 at CEASE enrollment and HCV Core-E2 region sequenced (HCV genotype [GT] 1a H77 position 347–1750). Maximum likelihood phylogenetic trees (1000 bootstrap replicates) were used to identify clusters (3% genetic distance threshold). STATA 14.1 was used for statistical analysis.

Results: Among 288 HCV RNA positive participants 242 sequences were obtained, with GT prevalence: GT1: 65% (n=159), GT3: 28% (n=68) and GT2/4/6: 6% (n=15). Overall, 33% (80/242) of sequences clustered (≥ 2 participants) (GT1: 31% [50/159], GT3: 44% [30/68], $p=0.023$). Among gay and bisexual men (GBSM) (n=196), of those in a cluster, 71% (54/76) reported unprotected anal intercourse (UAI) during last month and 47% (36/76) reported group sex, compared to 44% (53/120, $p=0.001$) not clustered reporting UAI and 21% (25/120, $p<0.001$) group sex. Time from HCV diagnosis to study enrolment was shorter, at 2 years (interquartile range [IQR] 1, 7) among those clustered, compared to 12 (IQR 6, 2) among those not clustered (Cox hazard ratio 2.01, 95% confidence interval 1.46 to 2.79).

Conclusion: This study found a high proportion of HCV phylogenetic clustering, predominantly amongst GBSM. Reporting UAI or group sex was more common among clustered participants, suggesting sexual networks play an important role in HCV transmission among GBSM. Shorter time from diagnosis among those in

clusters may suggest infections in these networks are more recently acquired. These findings highlight importance of rapid DAA treatment initiation, together with ongoing monitoring of the phylogeny.

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