

PHYLOGENETIC CLUSTERING AMONG PEOPLE WITH RECENT HEPATITIS C VIRUS INFECTION IN AUSTRALIA BETWEEN 2004-2015

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Background: Little is known about hepatitis C virus (HCV) transmission among people with recent infection and in particular among gay and bisexual men with HIV co-infection. Phylogenetic methods can provide useful insights into transmission. The aim of this study was to identify phylogenetic pairs and clusters among people with recent HCV infection in Australia.

Methods: Data and specimens from five studies of recent HCV in Australia recruited between 2005 and 2015 were used for this study. Viral RNA was extracted from samples and HCV Core-E2 region sequenced. Phylogenetic trees were inferred using maximum likelihood analysis and 1000 bootstrap replicates. Clusters were identified using 5% genetic distance [GD] threshold and logistic regression performed in STATA 14.1.

Results: In total, 352 participants were eligible for inclusion in this study and the proportion with HIV/HCV co-infection was 43% (151/352). Core-E2 sequences were obtained from 237 participants. HCV genotype (GT) prevalence among sequences obtained was: GT1a/b:55% (n=141), GT3a: 38% (n=89) and GT2/4/6: 3% (n=6). Overall, 50% of participants were in a pair or cluster. Among HIV/HCV co-infected participants, 60% (74/123) were in a pair or cluster, compared to 30% (34/113, p=0.013) of participants with HCV mono-infection. Among those with GT1a, 21% (18/85) and 60% (27/45) of HCV and HIV/HCV subjects were in a pair/cluster respectively. Clusters displayed homogeneous characteristics, such as exclusively containing individuals from one city, with HIV/HCV co-infection, or route of acquisition of HCV.

Conclusion: This study of recent HCV infection in Australia found a high proportion of participants demonstrated phylogenetic clustering. Clusters' exclusively containing individuals with particular characteristics suggests that HCV transmission occurs through discrete networks, particularly among HIV/HCV co-infected individuals. The greater proportion of clustering found among HIV/HCV co-infected participants also highlights the need to provide broad DAA access and rapid uptake, together with ongoing monitoring of the phylogeny.

Disclosure of Interest Statement: None to declare.