PHYLOGENETIC CLUSTERING OF RECENT HEPATITIS C VIRUS INFECTION 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 ClusterPicker (90% bootstrap threshold, 5% genetic distance [GD] threshold). Pearson's chi-squared test was performed in STATA (version 14.1).

Results: In total, 352 participants were eligible for inclusion in this study from ATAHC (2004-2007, n=167), RAMPT-C (2009-2013, n= 70), ATAHC II (2011-2015, n=82), DARE-C I (2013-2015, n=14), and DARE-C II (2014-2015, n=19). The proportion with HIV/HCV co-infection was 43% (151/352). Core-E2 sequences were obtained from 274 participants. HCV genotype (GT) prevalence among sequences obtained was: GT1a/b: 64% (n=176), GT3a: 32% (n=89) and GT2/4/6: 3% (n=9). Overall, 30% of participants were in a pair or cluster (GT1a 44% [71/162], mean maximum GD [MMGD] = 3.0; GT1b 43% [6/14], MMGD = 0.26). Among HIV/HCV co-infected participants, 35% (48/138) were in a pair or cluster, compared to 21% (29/136, p=0.013) of participants with HCV mono-infection. Among those with GT1a/1b, 44% (42/96) and 35% (28/80) of HIV/HCV and HCV subjects were in a pair/cluster.

Conclusion: In this study of recent HCV infection in Australia from 2004-2015, a high proportion of participants demonstrated phylogenetic clustering. The greater proportion of clustering found among HIV/HCV co-infected participants 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.