

TITLE: MODELLING THE EFFECTS OF TARGETED DAA HEPATITIS C VIRUS TREATMENT STRATEGIES USING A MOLECULAR TRANSMISSION NETWORK OF PEOPLE WITH RECENT INFECTION

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Background: Molecular data can be used to reconstruct pathogen transmission networks and identify characteristics of individuals who may be more likely to transmit pathogens, enabling targeted treatment and prevention strategies. This study reconstructed a hepatitis C virus (HCV) transmission network to identify factors associated with higher network connectivity among three studies of people with recently acquired HCV infection in Australia recruited from 2006–2013.

Methods: HCV sequence data (Core-E2) from participants at the time of HCV detection were analysed to infer a molecular transmission network by connecting pairs of sequences whose divergence was ≤ 0.03 substitutions/site. Directionality of transmission was based on estimated date of infection of participants. Logistic regression was used to identify factors associated with being connected in the network. The impact of targeting HCV direct acting antivirals (DAAs), assuming 90% treatment efficacy, at both HIV co-infected and random nodes was simulated (1 million replicates).

Results: Among 236 participants, 57% had recently injected drugs (within last 6 months) and 15% had HIV co-infection. All those with HCV/HIV (n=36) were male and acquired infection through homosexual exposure. Overall, 21% (n=49) were connected in the network. HCV/HIV co-infected participants (47%) were more likely to be connected compared to HCV mono-infected participants (16%) (OR 4.56; 95%CI; 2.13–9.74). Simulations targeting DAA HCV treatment to HCV/HIV co-infected individuals prevented 2.5 times more onward infections than providing DAAs to random individuals. By curing one HIV co-infected node, an average of 0.35 follow-on HCV infections were prevented, compared with 0.14 follow-on infections prevented by curing a random node.

Conclusion: These findings demonstrate that sequence data from people with recent HCV infection can be used to characterise highly connected transmission networks. Targeted interventions of DAA HCV therapy to networks of people with HCV/HIV co-infection may be useful to prevent onward transmission in treatment as prevention strategies.