

ONWARD TRANSMISSION OF HEPATITIS C VIRUS INFECTION AMONG YOUNGER AND OLDER PEOPLE WHO INJECT DRUGS IN VANCOUVER, CANADA

Jacka B¹, Applegate T¹, Poon AF^{2,3}, Raghwani J⁴, Harrigan PR^{2,3}, DeBeck K^{2,5}, Milloy M-J^{2,6}, Krajden M⁷, Olmstead A⁷, Joy JB², Marshall BDL⁸, Hayashi K², Pybus O⁴, Lima VD^{2,3}, Magiorkinis G^{4,9}, Montaner J^{2,3}, Lamoury F¹, Dore GJ¹, Wood E^{2,3}, and Grebely J¹

1 Viral Hepatitis Clinical Research Program, The Kirby Institute, UNSW Australia, Sydney NSW, Australia, 2 BC Centre for Excellence in HIV/AIDS, St Paul's Hospital, Vancouver BC, 3 Division of AIDS, Department of Medicine, Faculty of Medicine, University of British Columbia, Vancouver, BC, Canada, 4 Department of Zoology, University of Oxford, Oxford, UK, 5 School of Public Policy, Simon Fraser University, Vancouver, BC, Canada, 6 Department of Family Practice, Faculty of Medicine, University of British Columbia, Vancouver, BC, 7 BC Centre for Disease Control, Vancouver BC, 8 Department of Epidemiology, Brown University, Providence, RI, USA, 9 Virus Reference Department, Public Health England, London, United Kingdom

Background: Understanding factors influencing transmission of HCV among people who inject drugs (PWID) is important for the design of treatment as prevention strategies. Phylogenetic co-clustering among younger participants and those with recent HCV seroconversion were evaluated among a cohort of PWID in Vancouver, Canada.

Methods: Participants HCV antibody positive at enrolment or during follow-up (1996-2012) were tested for HCV RNA and sequenced (Core-E2). Time-stamped phylogenetic trees were inferred using BEAST with a Bayesian Skyline tree prior and SRD06 substitution model. Phylogenetic segregation (Association Index) was assessed by BaTS, and factors associated with clustering (maximum cluster age: 5 years) were identified using logistic regression.

Results: Among 655 participants with HCV subtype 1a, 2b and 3a infection (26% female, 23% HIV+): 22% were younger (<27 years), and 11% had recent HCV seroconversion. When inferred cluster age was limited to <5 years, 15% (n=100) were in clusters/pairs. Younger age (vs. ≥ 40 , AOR: 2.47, 95% CI: 1.26, 4.83) and HIV infection (AOR: 1.74, 95%-CI: 1.08, 3.77) were independently associated with clustering. Phylogenetic segregation of younger participants was significant across subtypes, suggesting younger participants are more likely to co-cluster with other young participants than randomly among remaining participants by chance, and vice versa. There was no significant segregation related to recent HCV seroconversion. Most participants were in clusters containing only those aged ≥ 27 years (61/100), while 52% (14/27) of younger participants clustered only with other young participants.

Conclusion: In this cohort of PWID from Vancouver, phylogenetic clustering was associated with younger age and HIV co-infection. Age was associated with phylogenetic segregation, although younger participants co-clustered equally between themselves and older participants. These data suggest that HCV transmission among PWID is complex, with transmission occurring between both older and younger PWID. As such, treatment as prevention strategies will likely require broad scale-up across the PWID population.