HEPATITIS C VIRUS PHYLOGENETIC CLUSTERING AND LATENT CLASS ANALYSIS OF DRUG USE AMONG PEOPLE WHO USE DRUGS IN VANCOUVER CANADA

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Background: This study estimated latent classes (i.e., unobserved subgroups in a population) of people who use drugs in Vancouver, Canada and examined how these classes relate to phylogenetic clustering of hepatitis C virus (HCV) infection.

Methods: HCV antibody positive people who use drugs from two cohorts in Vancouver, Canada (1996-2012) with a Core-E2 sequence were included. Time-stamped phylogenetic trees were inferred and phylogenetic clustering was determined by time to most common recent ancestor. Latent classes were estimated and the association with the phylogenetic clustering outcome assessed using an inclusive classify/analyse approach.

Results: Among 699 HCV RNA positive participants (26% female, 24% HIV+), recent drug use included injecting cocaine (80%), injecting heroin (70%), injecting cocaine/heroin (e.g. speedball, 38%), and crack cocaine smoking (28%). Latent class analysis identified four distinct subgroups of drug use typologies: 1) cocaine injecting, 2) opioid and cocaine injecting, 3) crack cocaine smoking, and 4) heroin injecting and currently receiving opioid substitution therapy (OST). After adjusting for age and HIV infection, compared to the group defined by heroin injecting and OST, the odds of phylogenetic cluster membership was greater in the cocaine injecting group [adjusted OR (aOR): 3.05; 95% CI: 1.76, 5.27] and lower in the crack cocaine smoking group (aOR: 0.07; 95% CI: 0.01, 0.52).

Conclusions: Identifiable patterns of drug use in this cohort were associated with close HCV genetic relatedness. Combining latent class and phylogenetic clustering analyses provides novel insights into the complex dynamics of HCV transmission. Incorporating differing risk profiles associated with drug use may provide opportunities to further optimise and target HCV treatment and prevention strategies.

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