

A PHYLOGENETIC ANALYSIS OF HCV TRANSMISSION AMONG PWID ON OPIOID AGONIST THERAPY IN THE PREVAIL STUDY

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Background:

Understanding hepatitis C virus (HCV) transmission dynamics among people who inject drugs (PWID) is essential to public health intervention and prevention of new infections. Next-generation sequencing (NGS) allows for the detection of transmission between individuals using quasispecies sequencing. The goal of this study was to outline baseline transmission linkages and characterize reinfections in a cohort of 150 PWID from the PREVAIL study.

Methods:

We analyzed baseline (BL) and follow-up (FU) specimens from 150 PWID from 3 opioid treatment programs (OTP) in the Bronx, NY. The hypervariable region (HVR1) of HCV was amplified and the data acquired by NGS. Analysis was done by the Global Hepatitis Outbreak and Surveillance Technology (GHOST).

Results:

At BL, there were two linkages by transmission between study participants. Nine participants did not achieve sustained virologic response (SVR), and 4 were viremic following SVR. The 7 participants who did not achieve SVR with FU specimens had similar sequences to BL. Of the 4 participants who were viremic following SVR, 2 were reinfected with different phylogenetic strains, 1 had a late relapse with a similar strain, and one was only transiently viremic 17 months post-treatment with no specimen sent for NGS. One participant who achieved SVR was found to have a BL genotype 3a co-infection. Both BL transmission linkages were involved in intimate relationships. Among the 2 reinfections with NGS data, one occurred between two participants from the same OTP. This participant was also reinfected with an unrelated genotype 3a virus. The other participant was reinfected with multiple unrelated phylogenetic strains that differed from his BL sequence. All 3 reinfected participants reported ongoing high-risk behaviors.

Conclusion:

Our study demonstrates the utility of NGS in establishing linkages by transmission among PWID. It also reinforces the need for harm reduction among couples and those who report ongoing risk factors following SVR.

Figure. Baseline and follow-up sequences for PREVAIL participants who did not achieve SVR, had late relapse, or were reinfected following HCV treatment.

Disclosure of Interest Statement:

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