

CAN HEPATITIS C VIRUS (HCV) REINFECTION BE PREDICTED AND PREVENTED AMONG PEOPLE WHO CURRENTLY INJECT DRUGS (PCID)? THE POTENTIAL IMPORTANCE OF UNDERSTANDING AND INTERVENING UPON INJECTION NETWORKS TO ACHIEVE SUSTAINED AVIREMIA.

Authors:

Eckhardt BJ^{1,2}; Davis L³; Edlin BR^{2,3}; Marks KM²

¹ New York University Medical Center Weill Cornell Medicine

² Weill Cornell Medicine

³ National Development and Research Institutes

Background:

Limiting reinfection remains a challenge when treating active PCID for HCV. Modeling suggests that a network treatment strategy which involves treating HCV-infected injection partners concurrently may reduce rates of reinfection and consequently community HCV prevalence. Using viral phylogenetic as well as quantitative and qualitative injection network data, we sought to explore whether a network treatment strategy could have prevented HCV reinfection.

Methods:

Beginning in June 2014, PCID recruited in a syringe service program (SSP) were offered on-site treatment for HCV. Pre- and on-treatment quantitative data was collected on participants' injection networks and sharing behavior. Next-generation sequencing (NGS) was performed on virus from most participants to provide a background library. Individuals with viremia post treatment participated in a qualitative interview about their injection practices, including names of others who injected near them ("proximity partners"). Global Health Outbreak and Surveillance Technology (GHOST), was used to compare viral sequences with the background library to evaluate for linked transmission pairs.

Results:

Eighty HCV-infected SSP participants were seen by an HCV provider, and 53 participants started treatment. Pre-treatment virus from 31 were analyzed by NGS. None had infection with mixed genotypes. Forty-eight (91%) achieved a sustained virologic response 12 weeks after treatment completion, while 3 patients had post-treatment viremia. Standardized surveys of the three patients captured no sharing events pre-, or on-treatment. Two of three samples could be sequenced. Both clustered phylogenetically with virus from the library suggesting transmission links. In both of these cases, post-treatment qualitative interview failed to capture sharing events, but did identify the transmission network seen in GHOST results, through proximity partner naming.

Conclusion:

In an HCV treatment program in a SSP, proximity partner naming aligned with phylogenetic transmission links. Further study is warranted to determine if a network treatment strategy will prevent HCV reinfection in high risk PWID.

Disclosure of Interest Statement: See example below:

This project was partially funded by a research grant from BMS. Dr. Eckhardt has received research grants to New York University from Gilead Sciences Inc and to Weill Cornell from BMS. Dr. Marks has received research grants to Weill Cornell from Gilead Sciences Inc, Merck, and BMS.