Injecting networks influence hepatitis C transmission

Genetic signatures of the hepatitis C virus demonstrate the important role of injecting networks in its transmission amongst people who inject drugs.

THE ISSUE

Hepatitis C is a viral infection that can lead to liver cirrhosis and liver cancer. In high-income countries, including Australia, people who inject drugs (PWID) are at the greatest risk of hepatitis C infection[1], with transmission occurring through unsafe injecting. It is thought that a PWID's social and injecting networks play an important role in viral transmission. Importantly, even after a person's hepatitis C is cured with treatment, or they spontaneously clear their infection, they can be reinfected with hepatitis C multiple times if re-exposed to the virus.
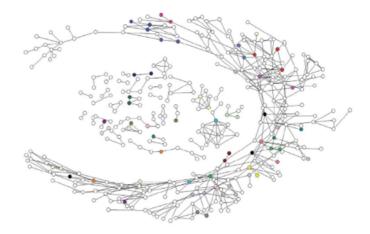
WHAT OUR WORK FOUND

This study followed a cohort of PWID in Melbourne, Australia to better understand hepatitis C transmission dynamics amongst PWID. Molecular phylogenetics, which relies on the genetic signature of viruses, was used to identify pairs and clusters of infection. The researchers studied the association of self-reported social-injecting networks with the genetic signatures of the hepatitis C viruses found in PWIDs' blood samples.

▸ Of the 376 PWID included in the study, 204 were infected with hepatitis C at study enrolment (54%), and 20 became infected for the first time during the study (approx. 5%).

▸ 20 reinfections and 15 viral strain switches were observed during the study period.

▸ 26 separate genetic clusters were detected in this study. These clusters included 25% of hepatitis C infections at enrolment, 48% of first infections, 29% of reinfections, and 43% of new viral strains.

▸ Genetic signatures were used to identify groups of people among whom hepatitis C virus may have been transmitted; these 'genetic' groups were significantly correlated with the injecting relationships reported by the study.

CONCLUSION

This is the first study to show that the genetic signature of a particular hepatitis C virus is associated with an individual's injecting network. This finding suggests that injecting networks significantly influence hepatitis C transmission amongst PWID. Given that the majority of new infections were linked to infections among the few close contacts that were reported to study investigators, this also implies that treating the close contacts of one network member would result in a considerable reduction of risk of hepatitis C infection for the individual.

Example of a network diagram with phylogenetic clusters identified in the Networks 2 study. A circle represents an individual and a line represents an injecting relationship. Each colour represents a genetic cluster, identified using phylogenetic analysis.

Policy Implications

▸ Genetic analysis can provide meaningful information regarding hepatitis C transmission dynamics.

▸ Targeted interventions for injecting networks are an important opportunity to reduce hepatitis C transmission.

▸ Eliminating hepatitis C from an individual's contact network is likely to result in a considerable reduction in risk for the individual.

▸ Simultaneous treatment of injecting partners may reduce post-treatment reinfection risk.

References

1. Degenhardt et al., *Lancet Global Health*. 2017; 5(12): e1195 – e1207

Burnet Institute
Medical Research. Practical Action.