

New method helps determine effectiveness of interventions in reducing spread of HIV

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Using genetic sequencing to understand the evolutionary relationships among pathogens, an international team of researchers—including several from the Center for Drug Use and HIV/HCV Research (CDUHR) at New York University—has developed a new method to determine how effective interventions are against the spread of infectious diseases like HIV.

The study, published in the *American Journal of Epidemiology*, describes how the new method establishes the source of a disease and whether its [transmission](#) in the community can be traced back to individuals who were or were not part of an [intervention](#).

Over the last decade our understanding of how pathogens spread has improved, but preventing the transmission of infectious diseases still remains a challenge. The introduction and spread of pathogens now occur more easily than ever due to the ease of international travel and people living in densely populated areas.

"Given globalization and other social phenomena, controlling the spread of infectious diseases is an imperative public health priority," said Gkikas Magiorkinis of the National and Kapodistrian University of Athens in Greece, the study's lead author.

For scientists and public health practitioners, it can be difficult to determine whether an intervention—such as a needle exchange program or treatment with antiretroviral therapy—is actually effective in reducing

[disease transmission](#) in the community. Evaluating the effectiveness of interventions that can mitigate the spread of pathogens is expensive, and in many circumstances unrealistic.

Importantly, most evaluations only measure those directly involved in an intervention but neglect the community effect, or the ability of the intervention to minimize the spread of disease from people directly involved to other community members.

"Our research seeks to understand if an intervention has a community effect and can reduce disease transmission not only by the recruited individuals, but also by the contacts in their risk networks," said Samuel R. Friedman, director of the Institute for Infectious Disease Research at National Development Research Institutes (NDRI), associate core director and senior theoretician at CDUHR, and the study's senior author.

To better measure the community effect of an intervention, the research team developed a new method to evaluate an intervention for reducing HIV transmission. In order to examine the transmission of the virus from already-infected people to those newly infected, the researchers use phylogenetics, or the evolutionary relationships among organisms, to understand the evolutionary dynamics of HIV.

The method involves collecting blood samples from three groups of people: individuals with HIV who participate in an intervention study, others with HIV who are not part of the intervention (the control group), and—at a later date—individuals who are newly infected with HIV.

Performing genetic sequencing of HIV, they can then compare characteristics of the virus to determine the source of transmission and whether new infections can be linked to individuals who did or did not participate in the intervention.

"Due to the inability of traditional methods to trace infections back to a source, there are major gaps in our understanding on how to best reduce the spread of HIV within a community. This new method enables us to quantify the flow of transmissions within a community, evaluate whether an intervention reduces new transmissions in comparison to a control condition, and thus estimate the relative decrease in new infections in the community due to the intervention," said Magiorkinis.

The researchers provide proof of concept through simulating an intervention to prevent HIV transmission among people who inject drugs. Comparing transmission from those with HIV who did or did not participate in the intervention, they calculated fewer people contracting HIV from individuals in the intervention, suggesting that the simulated intervention reduces [disease](#) transmission.

The researchers note that a key advantage of their method is that it can assess the wider community effect of an intervention without having to follow up with study participants. A one-time collection of blood samples is much easier than tracking participants long-term, especially in communities for which follow-up is a challenge, such as people who inject drugs. In addition, the method can be applied to evaluate interventions to reduce transmission of other [infectious diseases](#) beyond HIV.

More information: Gkikas Magiorkinis et al, An innovative study design to assess the community effect of interventions to mitigate HIV epidemics using transmission-chain phylodynamics, *American Journal of Epidemiology* (2018). [DOI: 10.1093/aje/kwy160](https://doi.org/10.1093/aje/kwy160)

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