Genetic Analysis of HIV Is Potent Surveillance Tool Even In Low-Infection-Rate States

The CDC is expanding its use of molecular surveillance of recent HIV infections to identify clusters of infections.

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Molecular surveillance of HIV is likely as promising a means of combating the spread of HIV in states with a low infection rate as it is in high-impact states.

The Centers for Disease Control and Prevention (CDC) is expanding its use of this tool, in which genetic analyses of recent cases of the virus are conducted to identify infection clusters. Subsequently, clinicians and public health workers can make contact with members of such clusters and conduct partner services, in which the newly diagnosed individuals can help identify other sexual or needle-sharing partners that may be at risk for HIV or living with an undiagnosed infection.

Publishing their findings in the Morbidity and Mortality Weekly Report, workers at the Wisconsin Division of Public Health (DPH) and CDC researchers studied genetic analysis of new cases of HIV reported in Wisconsin between 2014 and 2017. Wisconsin has a relatively low diagnosis rate, at 4.6 new diagnoses per 100,000 people in 2016. Pairs of new cases that were similar genetically were considered linked, and two or more links formed a cluster. (Currently, it is not possible to determine the direction of infection.)

The researchers identified 1,401 people whose HIV was analyzed genetically, with results reported to the Wisconsin DPH during the study period. A total of 433 (30.9 percent) of the viruses had a genetic link to those of at least one other person, and between them there were 703 unique pairings of cases and 119 clusters (which ranged between two and 20 people per cluster). Of the 433 people, 88.5 percent were male, 57.3 percent were Black, 80.8 percent were men who have sex with men (MSM) and 50.3 percent were in their 20s.

The investigators compared these clusters to information gathered from partner services that had been conducted with newly diagnosed individuals independent of the molecular surveillance. The patterns they identified were similar to those observed in states with a high HIV diagnosis rate.

Most of the linkages between new HIV cases were between people of the same race. Blacks were linked to other Blacks 78.2 percent of the time, while whites and Latinos were linked to people of their own race 54.5 percent and 31.7 percent of the time, respectively.

MSM were linked with other MSM 90.2 percent of the time. MSM who injected drugs were linked to other MSM 88.3 percent of the time.

The largest age bracket represented in the analysis was 20 to 29 years old. Members of this group were linked with other twentysomethings 59.2 percent of the time. People ages 13 to 19 years old were linked with individuals 20 to 29 years old 58.2 percent of the time.

A total of 33.8 percent of the partners identified through partner services were plausibly transmission partners according to molecular surveillance.

“Analysis of HIV sequence data is a useful tool for characterizing transmission patterns not immediately apparent using traditional public health interview data, even in a state with lower HIV morbidity,” the study authors concluded. “Prevention recommendations generated from national data (e.g., targeting pre-exposure prophylaxis [PrEP] for HIV-negative persons at high risk and implementing measures to maintain viral suppression among persons with HIV infection) also are relevant in a lower HIV-morbidity [meaning less illness associated with the virus] state.”

To read a POZ feature article about molecular surveilance, click here.

To read the CDC report, click here.

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