Medical Xpress

HIV transmission networks mapped to reduce infection rate

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Researchers at the University of California, San Diego School of Medicine have mapped the transmission network of human immunodeficiency virus (HIV) in San Diego. The mapping of HIV infections, which used genetic sequencing, allowed researchers to predictively model the likelihood of new HIV transmissions and identify persons at greatest risk for transmitting the virus.

The findings are published online in the June 5 issue of the journal *PLOS ONE*.

"The more we understand the structure and dynamics of an HIV transmission network, the better we can identify 'hot spots' of transmission," said Susan Little, MD, professor of medicine at the UC San Diego AntiViral Research Center and lead author of the study.

"Not everyone who is HIV-infected is equally likely to transmit the infection to others. There are clusters of more active disease transmission. We can use this information to target treatment interventions to those most likely to transmit the virus to others and markedly reduce the number of new infections."

The researchers analyzed the HIV-1 sequence data from recently HIV-1 infected persons and their sexual and social contacts in San Diego, between 1996 and 2011. Sequence data were collected as part of routine HIV genetic testing used to determine if a virus is resistant to certain classes of HIV medications. Genetic similarities between viral sequences

infecting different people were compared. Viruses from two people with a high degree of genetic similarity were suggestive of a transmission link. The scientists noted that viral similarity does not independently prove that a transmission occurred, only that the individuals are part of a closely connected transmission network.

Within the observed HIV transmission network, researchers calculated a transmission network score (TNS) to estimate the risk of HIV transmission from a newly diagnosed individual to a new partner. Participants with a high TNS were significantly more likely than those with low TNS to develop a close linkage to another person within their first year of HIV infection, suggestive of onward transmission.

Through network modeling, investigators showed that using this information to deploy antiretroviral therapy (ART) to individuals with the highest TNS resulted in a significantly greater likelihood of reduced new HIV-1 transmissions than providing ART to the same number of randomly selected individuals.

"Focusing our prevention and treatment resources to the populations at greatest risk of transmission could dramatically reduce the number of new infections associated with these populations," said Little. "Used in conjunction with traditional partner services, TNS-guided treatment and prevention interventions could markedly lower rates of new HIV infection in our community."

Provided by University of California - San Diego