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PHYLOGENETIC PATTERNS OF HIV TRANSMISSION AMONG TRANSGENDER WOMEN IN LOS ANGELES

Epidemiology/Public Health: (R) Epidemiology

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Background: Transgender women (TGW) are among the groups at highest risk for HIV infection, with a prevalence of 22% in the US. Despite this high risk, TGW have documented a high rate of undiagnosed HIV infection. We propose that this disparity can be addressed by characterizing TGW in a molecular transmission network to inform a targeted public health response.

Methods: Since 2005, Los Angeles County (LAC) has collected HIV pol sequences from drug resistance testing along with demographics and transmission risk factor data (including transgender status). We reconstructed a molecular transmission network using HIV-TRACE (pairwise genetic distance threshold of 0.015 substitutions/site) from the earliest pol sequences of 22,398 unique individuals in LAC, including 412 (2%) self-identified TGW. We examined the epidemiological predictors of clustering (a proxy for transmission risk) in the network using multivariate logistic regression (diagnosis age, race/ethnicity, transmission risk factor, gender, and country of birth were included as covariates) and calculated assortativity-the tendency for nodes to link to other nodes with the same attributes-for each transmission risk group.

Results: We found 1,722 molecular transmission clusters, and 36% of individuals (8,133/22,398) clustered in the network. TGW who indicated a sexual risk factor were the most likely to cluster in the network: 147/345 (42.6%) linked to at least one other person (AOR 2.20, $p < 0.001$, reference group: cis-men reporting IDU). MSM also had high clustering odds (AOR 2.05, $p < 0.001$); TGW who reported IDU did not have significantly elevated odds of clustering. Both MSM and TGF were highly assortative in the network (0.17 and 0.08, respectively; $p < 0.001$), indicating that MSM and TGW tended to cluster with members of their own risk groups. TGW were distributed across 126 clusters, and the presence of one TGW in a cluster increased the odds of there being another TGW in the same cluster 9-fold.

Conclusion: TGW in LAC were more likely to cluster than other risk groups, suggesting high transmission rates-despite low representation of TGW in the database. TGW tended to be part of the same clusters, indicating shared risk activities (i.e. linked directly or through shared partners). This assortativity demonstrates the potential to use molecular epidemiology to both identify transmission clusters likely to include undiagnosed or undisclosed HIV-infected TGW and improve the targeting of public health prevention and treatment activities to TGW.