PHYLODYNAMIC EVIDENCE OF HIV TRANSMISSION BETWEEN AGE-DISCREPANT MSM IN KING COUNTY

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BACKGROUND

- Sexual mixing is typically age-assortative.
- Mathematical modeling studies suggest age-disassortative mixing has an important role in HIV transmission dynamics among men who have sex with men (MSM).[1]
- Younger MSM may acquire HIV from older partners.[2,3]

OBJECTIVES

Compare **molecular epidemiology** with **phylodynamic** methods to examine the frequency of HIV transmission between age discrepant MSM.

METHODS

Data:

- National HIV Surveillance System data from Public Health–Seattle & King County, including HIV-1 pol gene sequences.
- Results were nearly identical with and without inclusion of LANL reference sequences.

Study Population:

- MSM diagnosed with HIV in King County, Washington, USA from 2000-2018.

Molecular Epidemiology Methods:

- Identified genetic similarity clusters of 2+ individuals using TN93 pairwise genetic distance with a 0.015 threshold.
- Assessed correlates of clustering using multivariate logistic regression.

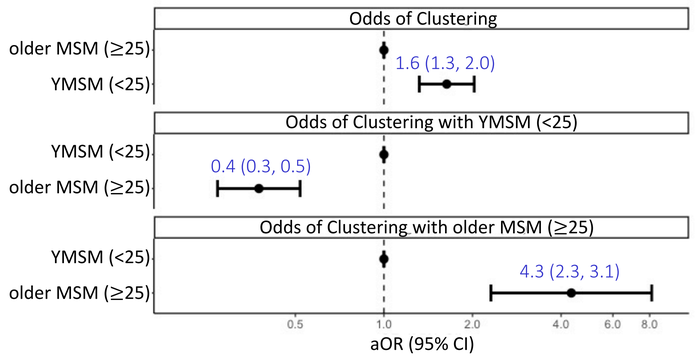
Phylodynamic Methods:

- Probabilistic phylodynamic modeling was conducted using methods developed by Volz and Frost. [4,5]
- Estimated transmission flows between Young MSM (YMSM) (age <25) and older MSM.

RESULTS

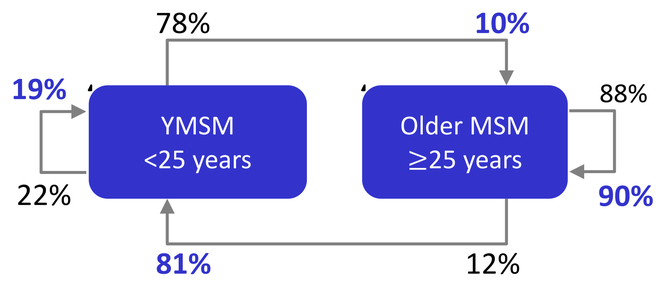
- YMSM had a higher odds of clustering, compared to older MSM, suggesting there were higher relative rates of HIV transmission among YMSM <25 years old (Fig. 1).
- 80% of HIV transmissions occurred exclusively among MSM age ≥25 years old (Fig. 3).
- 20% of transmission involve YMSM as either the recipient or transmitting partner (Fig. 3).
- Newman's assortativity coefficient was 0.08, suggestive of weak assortativity by age.
- YMSM acquire HIV from MSM with probability-weighted mean age of 11.2 years older (Fig. 4).
- Although modeling suggests YMSM frequently acquire HIV from older MSM (81%), older MSM have the highest probability of transmitting (88%) or acquiring HIV (90%) from older MSM, or clustering with older MSM (Figs. 1 & 2).

FIGURE 1. GENETIC CLUSTERING REGRESSION RESULTS



Logistic regression models were adjusted for early infection (defined as CD4 >500 cells/mm³ at diagnosis), race, mode of transmission (e.g. any injection drug use), and foreign-born status.

FIGURE 2. TRANSMISSION FLOWS BETWEEN OLDER AND YMSM ESTIMATED THROUGH PHYLODYNAMIC MODELING



Blue *is probability of acquiring HIV, and* black *is the probability of transmitting HIV.*

TABLE 1. MSM DIAGNOSED WITH HIV IN KING COUNTY, WA, USA 2000-2018

N	4,597
Age at diagnosis	
<25	654 (14%)
25-34	1,701 (37%)
35-44	1,413 (31%)
≥45	829 (18%)
Has an HIV sequence	2,851 (62%)
Clustered [a]	1,435 (50%)

[a] among individuals with a sequence, MSM clustered into 277 genetic similarity clusters using TN93 and 1.5% distance threshold

FIGURE 3. MIXING MATRIX OF THE PROPORTION OF OVERALL TRANSMISSIONS OF HIV AMONG MSM BY AGE

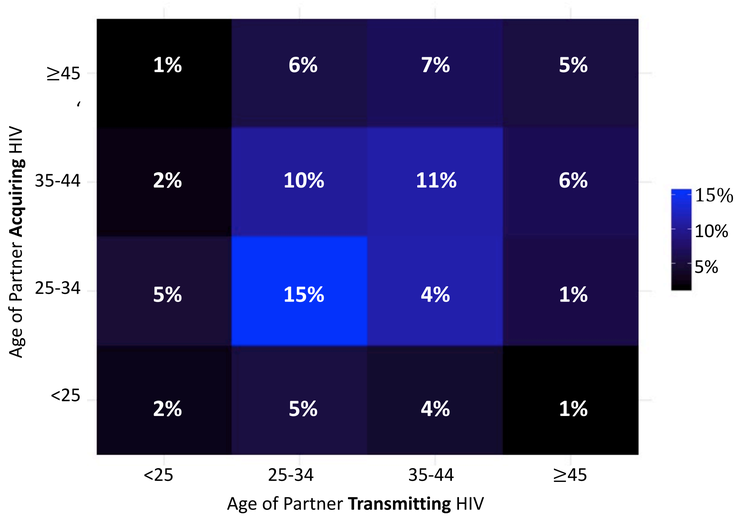
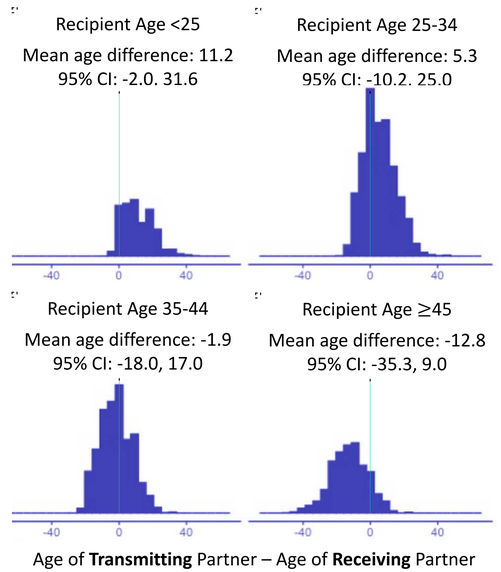


FIGURE 4. PROBABILITY-WEIGHTED AGE DIFFERENCE BETWEEN TRANSMITTING AND RECEIVING PARTNER



CONCLUSIONS

- Both molecular epidemiology and phylodynamic methods were suggestive of age-assortative mixing.
- However, YMSM frequently acquire HIV from older partners, suggesting that age-discrepant partnerships play an important role in HIV acquisition among YMSM.
- We obtained similar results to Le Vu, who examined transmission among MSM in the UK using identical methods.[6]

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