

Targeting new HIV prevention strategies through the combination of research and public health surveillance data

Ethan Morgan, PhD^{1,2}; Stephanie Masiello Schuette, PhD³; Richard D'Aquila, MD¹; Brian Mustanski, PhD^{1,2};

¹Northwestern University Feinberg School of Medicine; ²Northwestern Institute for Sexual and Gender Minority Health & Wellbeing; ³Chicago Department of Public Health
ethan.morgan@northwestern.edu

INTRODUCTION

- Phylogenetic analyses can be used to assess differences between genetic sequences of persons infected with HIV and to retrospectively construct transmission networks.¹
- These analyses can also be used to ascertain differences in HIV transmission risk by viral subtype,² drug resistance profile,³ and geographic location of sexual encounters.¹
- Past work has found that HIV transmission clusters are composed primarily of young Black men who have sex with men (MSM).¹
- These studies, however, have focused primarily on geographic differences,¹ basic demographic characteristics,^{4,5} or were conducted solely among young black men who have sex with men (MSM).⁵
- To better target and utilize research data, and to potentially prevent downstream transmission of HIV through sexual networks of YMSM, it is necessary to develop a better understanding of the risk environment in which study participants exist.

METHODS

- Data were collected as part of RADAR, an ongoing longitudinal cohort study of YMSM living in the Chicago metropolitan area.
 - Participants were recruited using a multiple cohort, accelerated longitudinal design.
 - Participants were between 16 and 29 years of age, assigned male at birth, and had a sexual encounter with a man in the previous year or identified as gay, bisexual or transgender.
 - HIV infection status, using fingerstick samples, was determined using the HIV1/2 Ab/Ag Combo 4th gen POC test
- Chicago Department of Public Health (CDPH) Data
 - All HIV genomic sequences from the PRRT *pol* region were obtained from CDPH electronic HIV surveillance records
- Genetic Sequencing
 - HIV DNA sequence generation utilized polymerase chain reaction and Sanger sequencing.
 - The protease and reverse transcriptase (PRRT) sections of the *pol* region of the viral genome were sequenced.
 - One sequence was obtained from each participant at either baseline or the visit in which they seroconverted (n = 150).
- Analyses
 - Sequences were aligned to the Consensus B HIV reference sequence using HIV-Trace.
 - Potential transmission events were defined as having a genetic distance ≤ 0.015 nucleotide substitutions per site.
 - A cluster was defined as ≥ 2 persons linked by ≥ 1 potential transmission event.
 - For the purposes of this analysis, CDPH data included: 1) ties to RADAR participants and 2) the ties of the individuals connected to RADAR participants

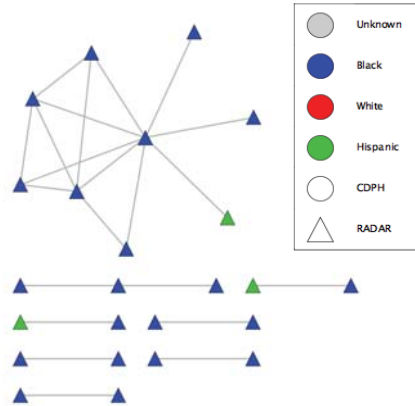


Figure 1. Inferred HIV transmission networks among HIV diagnosed RADAR participants, 2015-2017. Assessed using the *pol* region of the HIV genome where ties between nodes were inferred with a maximum genetic distance of 0.015 nucleotide substitutions per site.

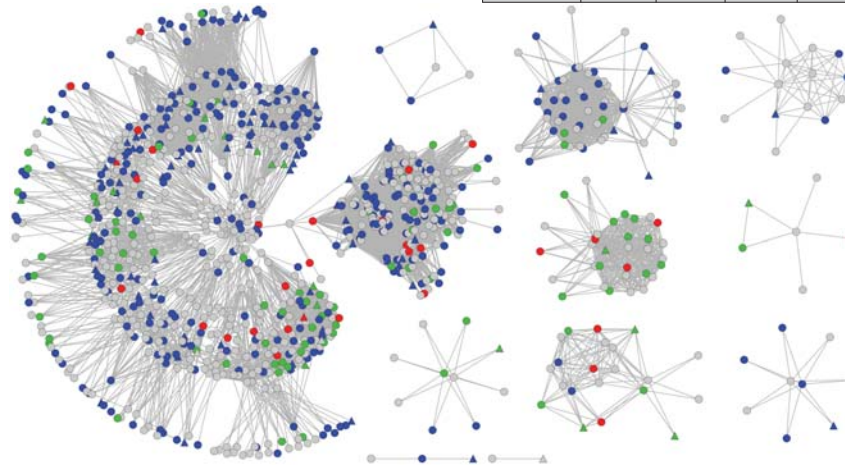


Figure 2. Inferred HIV transmission networks among HIV diagnosed Chicago residents, 2009-2017. Assessed using the *pol* region of the HIV genome where ties between nodes were inferred with a maximum genetic distance of 0.015 nucleotide substitutions per site. RADAR and CDPH eHARS, 2008-2017.

Table 1. Demographic characteristics of HIV diagnosed Chicago residents, RADAR and CDPH eHARS, 2008-2017 (N=451)

Race/Ethnicity	n	%
Black	289	64.1
White	58	12.9
Hispanic	82	18.2
Other	22	4.9
Age Category		
<20	33	7.3
20-29	271	60.1
30-39	85	18.8
>40	62	13.7

Table 2. Total number of ties between race/ethnicities among HIV diagnosed Chicago residents, RADAR and CDPH eHARS (N=3325)

	Black	White	Hisp.	Other
Black	1395	-	-	-
White	558	54	-	-
Hispanic	798	162	109	-
Other	174	30	38	7

RESULTS

- Among RADAR participants only:
 - 221 (21.4%) were identified as HIV-positive
 - 8 clusters existed with 22 ties between 24 participants
 - 150 sequences were available for analysis (the remainder were virally suppressed with amplification not possible)
 - Participants in an HIV transmission cluster:
 - Were significantly younger ($p < 0.001$),
 - Had more recent HIV diagnoses ($p < 0.001$),
 - And were less dependent on both marijuana and alcohol (both $p < 0.001$).
- Among RADAR and CDPH individuals:
 - 11 clusters existed with 3325 ties between 451 individuals
 - 93 (62%) RADAR participants clustered with CDPH data
 - The majority of individuals were black (289, 64.1%) and aged 20-29 (271, 60.1%)
 - By race, the majority of ties existed between black individuals (1395, 42.0%), while by age, the majority of ties existed between those who were aged 20-29 (1075, 32.3%)
 - Racial homophily was not a significant predictor of ties between individuals ($p = 0.302$) while age category homophily was a significant predictor ($p < 0.001$)
 - Compared to black individuals, Asian ($p < 0.001$) and other ($p = 0.022$) individuals had significantly fewer nodes.
 - Compared to those aged 20-29, those aged <20 ($p < 0.001$), 30-39 ($p < 0.001$), >40 ($p < 0.001$) had significantly few nodes in the transmission network.

DISCUSSION

- Fewer than expected RADAR participants cluster with city-wide data suggesting that non-clustering individuals are either being diagnosed with HIV outside the city limits or unexpectedly divergent sequences.
- Clusters consisted primarily of younger, black individuals, however, demographic characteristics differed by cluster.
- Combining research and surveillance data to re-construct transmission networks has the potential to provide a new method of analyzing data on new participants
- Future work should aim to assess survey data in the context of these larger transmission network structures.

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