Targeting new HIV prevention strategies through the combination of research and public health surveillance data
Ethan Morgan, PhD1,2; Stephanie Masiello Schuette, PhD3; Richard D’Aquila, MD1; Brian Mustanski, PhD1,2;
1 Northwestern University Feinberg School of Medicine; 2 Northwestern Institute for Sexual and Gender Minority Health & Wellbeing; 3 Chicago 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 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 HIV-1/2 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 22 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.

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 fewer 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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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. RADAR and CDPH eHARS, 2008-2017.

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

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<th>Race/Ethnicity</th>
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</tr>
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<tbody>
<tr>
<td>Black</td>
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<td>Hispanic</td>
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<td>18.2</td>
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<tr>
<td>Other</td>
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</table>

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

<table>
<thead>
<tr>
<th></th>
<th>Black</th>
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<th>Hisp.</th>
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<tbody>
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<td>Black</td>
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<td>Other</td>
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