HIV Transmission in the United States: The Roles of Risk Group, Race/Ethnicity, and Geography

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BACKGROUND

- Studying HIV transmission networks provides insight into the spread of HIV and opportunities for intervention
- By identifying genetically similar HIV variants in large datasets, we can construct transmission networks
- Two persons infected with highly similar HIV variants likely have a direct or indirect epidemiologic connection and represent potential transmission partners
- Transmission dynamics between people who are similar or different with respect to race/ethnicity, risk characteristics, and geography are unclear

Objective

To identify demographic, risk, and geographic characteristics of potential transmission partners

METHODS

Inclusion Criteria

We analyzed HIV-1 *pol* sequences collected through the Molecular HIV Surveillance component of the U.S. National HIV Surveillance System during 2001–2012 (4–18 participating areas, depending on year)

- Aged ≥13y
- One sequence per person (longest and highest quality)
- Sequence length ≥ 500 nucleotides

We excluded potential contaminants (sequences ≤2.0% genetic distance from HXB2)

Analysis

Sequence and Network Analysis

- Aligned sequences to a reference sequence (HXB2)
- Performed pairwise Tamura-Nei 93 genetic distance calculations among all sequences
- Distance ≤1.5% considered evidence of possible linkage
- Constructed an HIV transmission network which included all sequences that had a possible linkage to at least one other sequence
- Transmission network constructed on a MacPro computer using a suite of software developed by the Viral Evolution Group at University of California, San Diego

Analysis of Characteristics of Pairs

- Analyzed data for pairs of potential transmission partners on
  - Transmission category, hierarchical (missing data were imputed)
    - Male-male sex
    - Male-male sex and injection drug use
    - Injection drug use (stratified by sex)
    - Heterosexual contact (stratified by sex)
      - Further stratified women with infection attributed to heterosexual contact by U.S. census region
  - Race/ethnicity
  - State of residency at diagnosis
- Unit of analysis was the dyad (a pair of persons with closely related sequences (distance ≤1.5%)

RESULTS

Table 1. Characteristics of persons with HIV-1 sequences

	n	%
Total	41294	100
Sex		
Male	32,276	78
Female	9018	22
Race/ethnicity		
Asian/NHOPI	778	2
Black/African American	19493	47
Hispanic/Latino	9247	22
White	10731	26
Other*	1045	3
Age group		
13-19 years	2282	6
20-29 years	13951	34
30-39 years	11507	28
40-49 years	8733	21
50-59 years	3749	9
≥60 years	1072	3
Transmission category		
Male-male sex	25141	61
Male-male sex and IDU	1621	4
IDU – males	2220	5
IDU – females	1692	4
Heterosexual contact – males	3259	8
Heterosexual contact – females	7306	18

NHOPI: Native Hawaiian or Other Pacific Islander
IDU: injection drug use
*Includes American Indian/Alaska Native, other race, multiple races, or unknown race

Description of network

- 12,910 sequences linked to at least one other sequence
- 29,493 pairs (dyads)

Table 2. Transmission category of potential transmission partners

	Partner Transmission Category: Male-male sex		Male-male sex and IDU		IDU		Male heterosexual		Female heterosexual		Total
For pairs containing at least one person with infection attributed to:	n	%	n	%	n	%	n	%	n	%	n
Male-male sex	22645	82%	1935	7%	853	3%	829	3%	1208	4%	27478
Male-male sex and IDU	1935	88%	101	5%	47	2%	42	2%	83	4%	2210
IDU – males	654	68%	28	3%	88	9%	48	5%	109	11%	957
IDU – females	199	33%	19	3%	121	20%	66	11%	203	33%	608
Heterosexual contact–males	829	54%	42	3%	114	7%	54	4%	486	32%	1524
Heterosexual contact–females	1208	44%	83	3%	342	13%	486	18%	597	22%	2718
HC-females: Northeast	156	41%	6	2%	58	15%	66	17%	96	25%	383
HC-females: South	404	33%	25	2%	137	11%	325	27%	315	26%	1207
HC-females: Midwest	488	54%	38	4%	125	14%	74	8%	182	20%	909
HC-females: West	159	66%	13	6%	23	9%	20	8%	26	11%	241

IDU: injection drug use; HC: heterosexual contact
Cells shaded in accordance with percentage of potential transmission pairs in that category (darker=higher percentage).

The majority of potential transmission partners connected to men who have sex with men (MSM) were also MSM

However, other risk groups were also commonly connected to MSM

For women with infection attributed to heterosexual contact, connections varied by U.S. region.

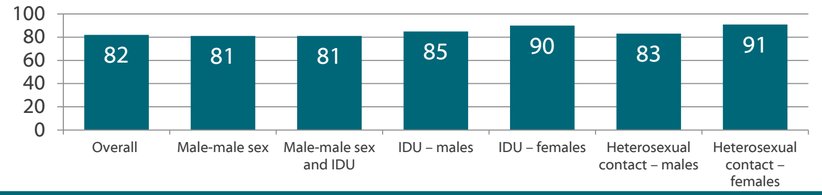
Table 3. Race/ethnicity of potential transmission partners

	Partner Race/Ethnicity: White		Black/ African American		Hispanic/ Latino		Asian/ NHOPI		Other*		Total
For pairs containing at least one person who is:	n	%	n	%	n	%	n	%	n	%	n
White	6892	47%	2790	19%	3951	27%	640	4%	536	4%	14809
Black/African American	2790	19%	9121	63%	1861	13%	95	1%	525	4%	14392
Hispanic/Latino	3951	45%	1861	21%	2382	27%	359	4%	220	3%	8773
Asian/ NHOPI	640	54%	95	8%	359	30%	65	5%	34	3%	1193
Other*	536	40%	525	39%	220	16%	34	3%	22	2%	1337

NHOPI: Native Hawaiian or Other Pacific Islander
*Other race includes American Indian/Alaska Native and multiple races
Cells shaded in accordance with percentage of potential transmission pairs in that category (darker=higher percentage).

Transmission pairs containing Blacks/African Americans were more racially homogeneous than other pairs

Figure 1. Percentage of potential transmission pairs consisting of two persons living in the same state at diagnosis



Most pairs, particularly those containing females, consisted of two persons living in the same state at diagnosis

LIMITATIONS

- Possible selection/sampling bias due to limited number of participating areas and differences in completeness of reporting
- Sequence results are from bulk sequencing
  - May miss some minority strains, and thus potential connections
- Partners represent potential partners
  - Cannot definitively draw a direct epidemiologic link between any two persons or establish direction of transmission
  - Can still gain insight into transmission dynamics from numerous potentially indirect links
- Analysis conducted at dyad level
  - People who have many transmission links are overrepresented
  - May not represent mixing among HIV-infected persons in general
- Geographic measure used was state of residence at diagnosis
  - May not reflect geographic moves or travel before or after diagnosis
- Percentage of in-state pairs likely overestimated
  - Many out-of-state connections likely missed due to limited number of participating areas

DISCUSSION

- This analysis is the first use of U.S. National HIV Surveillance System data to infer an HIV transmission network
- All risk groups were commonly connected to MSM
  - Interventions that reduce transmissions by MSM are likely to reduce HIV acquisition among other risk groups as well
  - This may be particularly true in the Midwest and West, where most dyads including heterosexual women showed links to MSM
- Racial/ethnic mixing in HIV transmission was present, although the extent varied by population
  - Blacks/African Americans were most commonly connected to other Blacks/African Americans
  - All other groups were most commonly connected to whites
- Transmission pairs were highly assortative by geography, although slightly less so for males than females
- These data are useful for understanding the spread of HIV

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