#214

Risk Factor Predicts Geographic Spread Within New York City HIV-1 Transmission Network and Beyond

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Background

- HIV transmission networks inferred from sequence data can be used to identify risk groups for targeted intervention
- Transmission clusters spread over larger geographic areas may require different methods of intervention than geographically localized clusters

Network Construction/Information

- 39,135 individuals' earliest *pol* sequence was reported to NYC-DOHMH through routine laboratory surveillance between 2005 and 2012
- Geography based on aggregate zip codes (UHF) at diagnosis
- Align sequences to HXB2 reference; screen for potential contaminants
- Calculate Tamura-Nei 93 genetic distance between each sequence pair
- Connect all nodes separated by ≤ 2% genetic distance to form clusters
- Inferred 2,399 clusters, comprising 8,801 nodes (individuals) and 19,637 edges (connecting potential transmission partners)

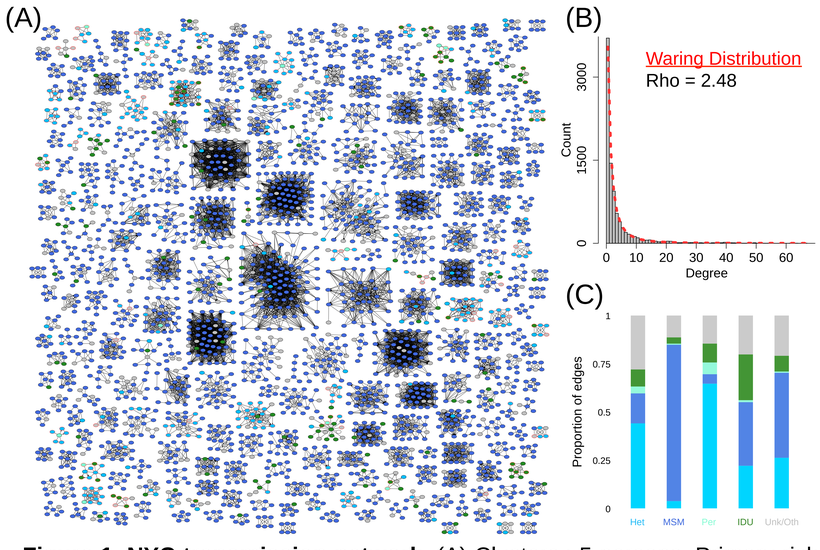


Figure 1. NYC transmission network. (A) Clusters ≥5 persons. Primary risk factor: heterosexual, men who have sex with men (MSM), perinatal, injection drug users (IDU), & unknown/other. Females outlined in red. Inferred transmission direction (arrows) based on acute/early infection status. (B) Degree distribution. Red line is Waring distribution. (C) Partners by risk factor.

Table 1. NYC transmission network clustering patterns and logistic regression analysis

Attribute	Clustered *n* (%)	Not Clustered *n* (%)	Adjusted Odds Ratio[1]	*p*-value
Total	8801 (22.5%)	30,334 (77.5%)		
Sex				
Male	7389 (27.13%)	19,839 (72.9%)	–	–
Female	1412 (11.9%)	10,495 (88.1%)	0.67	<0.001
Status				
Acute	94 (79.0%)	25 (21.0%)	1.64	0.036
Early	904 (63.5%)	519 (36.5%)	–	–
Prevalent	7803 (20.8%)	29,790 (79.2%)	0.21	<0.001
Primary Risk Factor				
MSM	5453 (38.7%)	8632 (61.3%)	2.43	<0.001
Heterosexual	1360 (15.5%)	7410 (84.5%)	–	–
IDU	532 (9.1%)	5317 (90.9%)	0.52	<0.001

[1]Regression model includes unknown and 'other' risk factors and NYC borough (not shown)

MSM are more likely to cluster than heterosexuals, who are more likely to cluster than IDU

Acute/early infections are more likely to cluster than prevalent cases

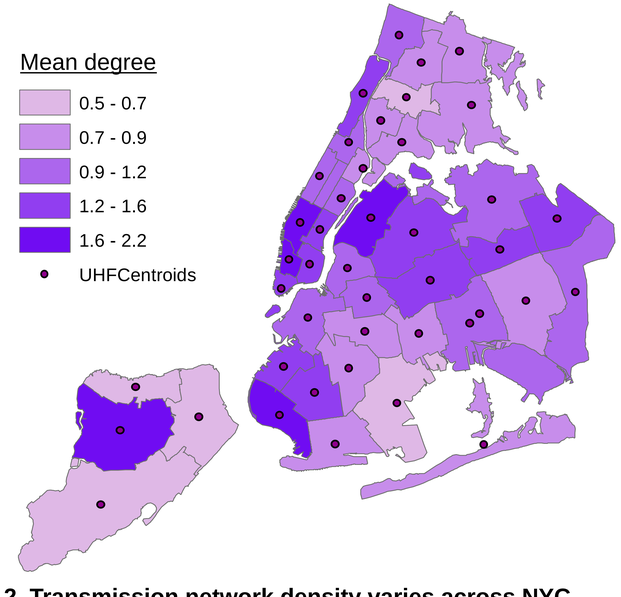


Figure 2. Transmission network density varies across NYC.

Table 2. Geographic size of NYC transmission clusters

Attribute	Median distance between nodes (mi)	*p*-value
Sex		
Male	6.2	–
Female	4.9	0.006
Status		
Acute	6.9	0.208
Early	6.1	–
Prevalent	6.0	0.110
Primary Risk Factor		
MSM	6.4	<0.001
Heterosexual	4.8	–
IDU	5.6	0.009

[1]Logistic regression model includes unknown and 'other' risk factors and NYC borough (not shown)

MSM and IDU have potential transmission partners spread over a greater median distance than heterosexuals

LANL Sequence Database Comparison

- Among individuals connected in NYC network, MSM were more likely to cluster with individuals residing outside of NYC than heterosexuals (36.6% vs 8.2%; p <0.001), but not with individuals from other countries in the LANL database (86,216 non-US sequences)
- IDU were more likely than heterosexuals to have an international connection in the LANL database (18.5% vs 6.2%; p < 0.001)

Conclusions

- **Risk factor plays a role in predicting the geographic spread of HIV transmission clusters**
- **MSM have the most geographically expansive clusters**
- **IDU clusters are not geographically constrained (locally or internationally) compared with heterosexual clusters**

Acknowledgments

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