GEOGRAPHIC PATTERNS IN HIV TRANSMISSION CLUSTERS IN LOS ANGELES COUNTY

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BACKGROUND

- Clusters of HIV transmission can serve as alerts for prioritizing public health action[1]
- These clusters can comprise:
  - Geographic clusters of diagnosis in time and space or
  - Clusters of genetically linked cases
- Los Angeles County (LAC) is divided into
  - 507 ZIP codes
  - 26 Health Districts
  - 8 Service Planning Areas
- We assessed whether the relationship between geography and genetic transmission clusters in the LAC is strong enough to influence HIV prevention and care resource allocation.

What is the geographical component of HIV transmission clusters in LAC?

METHODS

Study Population: 8,152 persons diagnosed with an HIV infection in 2010-2016 and reported to the LAC Department of Public Health with ≥ 1 HIV *pol* sequences

Variables: Race/ethnicity, gender, country of birth, age at diagnosis, first CD4+ count, diagnosis date, transmission risk, and geography

Genetic Network: Used HIV-TRACE[2] to construct molecular transmission clusters using partial *pol* sequences (genetic distance ≤0.015 substitutions/site)[3]

Inclusion Criteria:

- Age at diagnosis ≥13
- Residence at diagnosis in LAC
- Genetically linked (4,125 people)

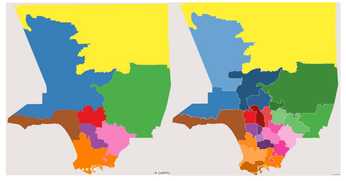


Figure 1. Service Planning Area (left) and Health District (right)

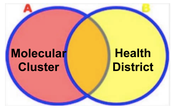
Outcome Measures:

1) **Assortativity,** tendency for people to be genetically linked to others with the same characteristic

2) **Concordant time-space pairs**, the proportion of genetically linked pairs from the same geographic region and diagnosis year

3) **Jaccard coefficient,**[4] the intersection divided by the union of sets of geography (Health District) and genetic cluster

$$Jaccard(A,B) = \frac{A \cap B}{A \cup B}$$



We found low magnitude associations between HIV transmission clusters and geographic residence at diagnosis

Genetic clustering may be a better indicator of HIV transmission patterns than time-space clusters of diagnosis in urban HIV endemic areas

RESULTS

ASSORTATIVITY

Geographic assortativity is present across the network, but magnitude is low.

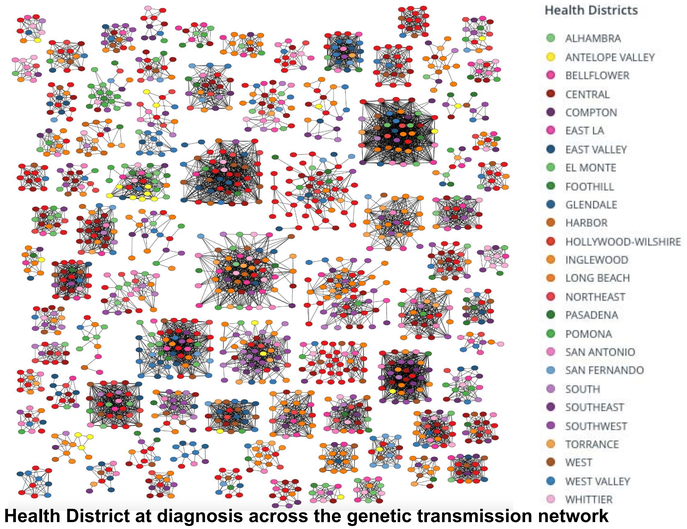


Figure 2. Health District at diagnosis across the genetic transmission network

Table 1. Assortativity across Transmission Network.		
Attribute	Assortativity Coefficient	*p*-value
ZIP Code	0.02	**<0.001**
Age	0.07	**<0.001**
Health District	0.09	**<0.001**
Transmission Risk	0.13	**<0.001**
Service Planning Area	0.15	**<0.001**
Race/Ethnicity	0.27	**<0.001**

ZIP code was the least assortative trait & race/ethnicity was the most assortative

Linked cases are infrequently diagnosed in the same geographic region and year

CONCORDANT TIME-SPACE PAIRS

TIME

- 2,328 were linked in the same year (56%)

SPACE

- 696 were linked in the same ZIP code (17%)
- 1,802 were linked in the same Health District (44%)
- 2,644 were linked in the same Service Planning Area (64%)

TIME-SPACE

- 175 were linked in the same year and ZIP code (4%)
- 773 were linked in the same year and Health District (19%)
- 1,255 were linked in the same year and Service Planning Area (30%)

Greater geographic similarity associated with younger age and cis-men

Less geographic similarity associated with transgender women, African-Americans, and foreign born

JACCARD COEFFICIENT

Table 2. Multivariate Generalized Linear Model Relating Individual Characteristics to Jaccard Coefficient (Health District)			
Characteristic	Adjusted Odds Ratio	95% Confidence Interval	*p*-value
Age at Diagnosis			
13-19	1.20	1.04, 1.39	**0.011**
20-29	Ref.	-	-
30-39	0.89	0.18, 0.96	**0.004**
40-49	0.90	0.80, 1.00	0.056
50+	0.94	0.80, 1.08	0.394
Transmission Risk/Gender			
Cis-men	1.22	1.11-1.34	**<0.001**
Cis-women	1.04	0.86, 1.27	0.633
Transgender-women	0.60	0.47, 0.57	**<0.001**
Cis-MSM	Ref.	-	-
People who inject drugs (all genders)	0.97	0.81, 1.16	0.760
Race/Ethnicity			
White	0.96	0.87, 1.06	0.466
African American	0.83	0.76, 0.91	**<0.001**
Hispanic/Latino	Ref.	-	-
Other	0.87	0.78, 0.96	**0.010**
Country of Birth			
U.S. Born/Territory	Ref.	-	-
Foreign-born	0.89	0.82, 0.98	**0.020**
Unknown	0.95	0.87, 1.04	0.324
CD4⁺ count at Diagnosis			
<200	1.16	1.03, 1.30	**0.010**
200-499	1.08	0.99, 1.17	**0.061**
≥500	Ref.	-	-
Unknown	1.10	1.00, 1.21	**<0.001**

CONCLUSIONS

- Our conclusions are limited by incomplete genotype test results (~60% of new diagnoses have a reported genotype. However:
- We found statistically significant, but weak associations between HIV transmission clusters and geographic residence at diagnosis
- Within an urban setting with endemic HIV, genetic clustering serves as better indicator of HIV transmission patterns than time-space clustering

References

1. Centers for Disease Control and Prevention. Detecting and Responding to HIV Transmission Clusters: A Guide for Health Departments (2018)
2. Kosakovsky Pond et al. (2018) *MBE* Vol 35:1812–1819.
3. Ragonnet-Cronin et al. (2019) *Lancet HIV*; 6: e164–72.
4. Jaccard (1912) *New Phytologist*; 11:37-50

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