Geographic Characteristics of HIV Genetic Clusters Among Newly Diagnosed Cases in North Carolina

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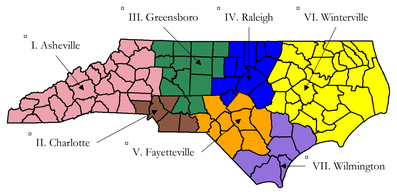
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Background

- Identifying and monitoring both geographic clusters and genetic clusters are routine parts of HIV surveillance that can help focus prevention efforts
- Incorporating geographic information in genetic clusters may help to better understand HIV transmission throughout North Carolina (NC)
- Objective: To characterize the geography of HIV genetic clusters in NC and evaluate how geography affects cluster composition and characteristics

Figure 1. North Carolina Field Services Unit Regions



Methods

- HIV-1 *pol* sequences were reported to NC HIV Surveillance Unit from clinical drug resistance testing or obtained through sequence analysis of diagnostic specimen received from the NC State Lab of Public Health (SLPH)
- Sequences from those ≥13 years old and newly diagnosed with HIV in NC from January 1, 2016 to December 31, 2018 were assessed
- Earliest sequence date included: January 2016
- Last sequence date included: December 2019
- Residential addresses at the time of HIV diagnosis were geocoded with ArcGIS Pro
- Genetic clusters were constructed with <1.5% pairwise genetic distance (TN-93) between two members and restricted to those with ≥5 persons
- Planar distances between those with genetically linked infections were calculated using address coordinates in SAS version 9.4

Results

- 2,762 persons with ≥1 *pol* sequence were included in the genetic cluster analysis
- Sequence coverage: 70.8% of those ≥13 years old and newly diagnosed with HIV in NC from January 1, 2016 to December 31, 2018

Table 1. Characteristics of those ≥13 years old and newly diagnosed with HIV in NC from January 1, 2016 to December 31, 2018 (n=3,900) and whether they were included in the cluster analysis or excluded due to missing sequence data

	Included (n=2,762) n (%)	Excluded (n=1,138) n (%)	χ^2 Test P-value
Race/Ethnicity			0.005
African American	1,797 (65)	676 (59)	
Caucasian	613 (22)	286 (25)	
Hispanic	256 (9)	136 (12)	
Other	96 (4)	40 (4)	
Age at HIV diagnosis			0.070
13-17 years old	36 (1)	14 (1)	
18-24 years old	714 (26)	266 (23)	
25-34 years old	940 (34)	360 (32)	
35-44 years old	431 (16)	208 (18)	
≥45 years old	641 (23)	290 (26)	
Gender			0.052
Female	505 (18)	246 (22)	
Male	2,233 (81)	881 (77)	
Transgender	24 (1)	11 (1)	
HIV Transmission Risk			<0.001
MSM	1,626 (59)	558 (49)	
PWID	69 (3)	30 (3)	
MSM-PWID	67 (2)	22 (2)	
Heterosexual	995 (36)	520 (45)	
Other/Unknown	5 (0)	10 (1)	
NC Field Services Unit Region			<0.001
I. Asheville	118 (4)	122 (11)	
II. Charlotte	694 (25)	279 (24)	
III. Greensboro	637 (23)	215 (19)	
IV. Raleigh	588 (21)	212 (19)	
V. Fayetteville	220 (8)	166 (14)	
VI. Winterville	346 (13)	100 (9)	
VII. Wilmington	159 (6)	44 (4)	

- 1,222 persons (44.2%) were genetically linked to at least one other person in 326 clusters with a median cluster size of 2 (Q1: 2, Q3: 4)
- Of those genetically linked to at least one other person, 606 (21.9%) persons were in clusters of ≥5 total persons

Table 2. Characteristics of those (n=606) in the 72 HIV genetic clusters with ≥ 5 members

	n (%)
Race/Ethnicity	
African American	404 (67)
Caucasian	130 (21)
Hispanic	55 (9)
Other	17 (3)
Age at HIV diagnosis	
13-17 years old	11 (2)
18-24 years old	282 (47)
25-34 years old	211 (35)
35-44 years old	51 (8)
≥45 years old	51 (8)
Gender	
Female	44 (7)
Male	557 (92)
Transgender	5 (1)
HIV Transmission Risk	
MSM	472 (78)
PWID	8 (1)
MSM-PWID	20 (3)
Heterosexual	106 (18)
NC Field Services Unit Region	
I. Asheville	22 (4)
II. Charlotte	122 (20)
III. Greensboro	157 (26)
IV. Raleigh	156 (26)
V. Fayetteville	39 (6)
VI. Winterville	75 (12)
VII. Wilmington	35 (6)

Table 3. Characteristics of the 72 HIV genetic clusters with ≥5 members

	Median (Range)
Cluster Members	6 (5-28)
	n
Unique Genetic Linkages	2,274
	Median (Q1, Q3)
Linkage Pairwise Genetic Distance (TN-93)	0.92% (0.61%, 1.23%)
Distance (Miles) Between Genetically Linked Cluster Members	26.0 (8.6, 72.8)
	n (%)
Majority of Cluster Members Living in the Same NC Field Services Unit Region	
Yes	61 (85)
No	11 (15)
Majority of Cluster Members Living in the Same NC County	
Yes	40 (56)
No	32 (44)
Cluster with a Median Distance Between Those Genetically Linked of <25 Miles	
Yes	40 (56)
No	32 (44)

Figure 2. Residential county at diagnosis of the cluster members (n=606) in the 72 HIV genetic clusters with ≥ 5 members

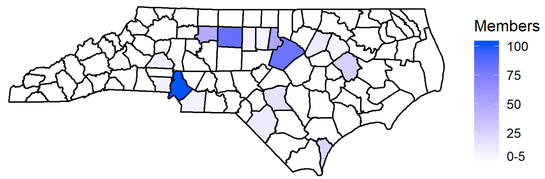


Figure 3. Cluster diagrams of the 72 HIV genetic clusters with 606 members

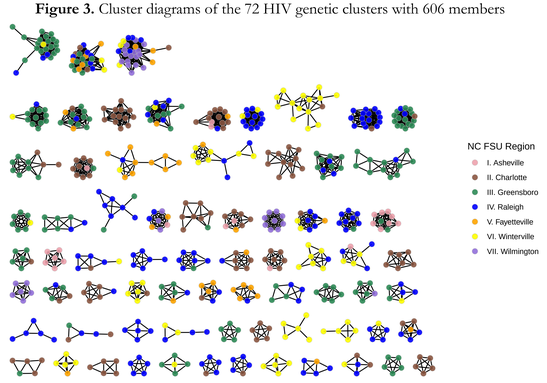
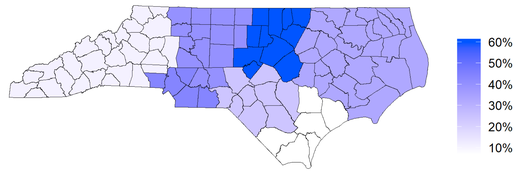


Table 4. Comparison between those in clusters with median distance between genetically linked cluster members of <25 miles and ≥25 miles

	Median Distance Between Genetically Linked Cluster Members <25 miles (n=312)	Median Distance Between Genetically Linked Cluster Members ≥25 miles (n=294)	P-value
	n (%)	n (%)	
Race/Ethnicity			0.004[a]
African American	193 (62)	211 (72)	
Caucasian	79 (25)	51 (17)	
Hispanic	35 (11)	20 (7)	
Other	5 (2)	12 (4)	
Age at HIV diagnosis			<0.001[a]
13-17 years old	9 (3)	2 (1)	
18-24 years old	140 (45)	142 (48)	
25-34 years old	111 (36)	100 (34)	
35-44 years old	32 (10	19 (6)	
≥45 years old	20 (6)	31 (11)	
Gender			
Female	27 (9)	17 (6)	---
Male	280 (90)	277 (94)	
Transgender	5 (1)	0 (0)	
HIV Transmission Risk			0.035[b]
MSM	232 (74)	240 (82)	
PWID	7 (2)	1 (0)	
MSM-PWID	14 (5)	6 (2)	
Heterosexual	59 (19)	47 (16)	
NC Field Services Unit Region			<0.001[a]
I. Asheville	8 (3)	15 (5)	
II. Charlotte	82 (26)	40 (14)	
III. Greensboro	85 (27)	72 (24)	
IV. Raleigh	91 (29)	65 (22)	
V. Fayetteville	2 (1)	37 (13)	
VI. Winterville	28 (9)	47 (16)	
VII. Wilmington	16 (5)	19 (6)	
	Median (Q1, Q3)	**Median (Q1, Q3)**	
Cluster Size	8 (6, 13)	11 (6, 23)	<0.001[c]

[a]χ^2 Test
[b]Fisher's Exact Test
[c]Wilcoxon Mann-Whiney Test

Figure 4. Percentage of the 72 HIV genetic clusters with ≥1 cluster member in the NC Field Services Unit Region



Conclusions

- Although most genetic clusters have the majority of their members residing in the same county or NC Field Services Unit Region at the time of diagnosis, most genetic clusters also have ≥1 member residing elsewhere
- Genetic clusters with median distances between genetically linked cluster members of ≥25 miles had significantly different cluster member characteristics and cluster sizes compared to genetic clusters with median distances between genetically linked cluster members of <25 miles

- Future directions:
  - Assess the mobility of the study population
  - Incorporate contact tracing data into the cluster analysis

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