Do Real World Partner Services Initiated From Molecular Clusters Yield People With Viremia or New HIV?

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BACKGROUND

Molecular HIV surveillance is increasingly utilized as an approach to identify new HIV diagnoses linked to clusters.

Health departments deploy partner services to interview new HIV diagnoses – 'index clients' – and their self-reported sex/drug partners to find persons in need of HIV care services.

We examine whether the yield of viremic and newly diagnosed partners identified through partner service interviews differs by: 1) whether the index clients are in clusters or not; 2) whether the index clients are in a recent and rapid cluster (≥ 3 cases) (R3); and 3) whether the index clients are in a cluster where the number of cases added to the cluster in the past 12 months is divided by the square root of the cluster size (square root growth).

METHODS

We matched and analyzed HIV surveillance, HIV *pol* sequence, and partner services data from 2008-2018 among Chicago residents.

We constructed molecular clusters using HIV-TRACE at a pairwise genetic distance threshold 0.5%. In addition, we utilize two growth metrics: 1) CDC defined recent and rapid cluster - ≥ 3 cases in the last year; and 2) Square root growth - the number of cases added to this cluster in the past 12 months divided by the square root of cluster size, defined at distance threshold 0.5%.

We compared partners reported by index clients who were in a molecular cluster vs. those who did not cluster according to whether the partner was a new HIV diagnosis or had a previous HIV diagnosis but was recently viremic.

We examined the yield for identifying partners with new HIV diagnoses or viremia linked to indexes in molecular clusters or R3 or square root growth vs. indexes who were not in clusters or R3 or square root growth.

Routine partner services initiated from molecular clusters or growing clusters does not clearly result in higher yield of new HIV diagnoses or those with viremia.

RESULTS

Of 5,208 newly diagnosed index clients, 1,015 (19%) had HIV sequence data available and partner services initiated within 12 months of diagnosis.

Of these, 624 (62%) had HIV *pol* sequences that molecularly clustered and 182 (29%) of them named at least one partner.

The modal age range of index clients in clusters was 25-34, 51.1% were Black, 26.7% Latinx, 6.9% female and 84.4% MSM.

Of the 443 partners with HIV named, 252 (57%) were linked to indexes in a cluster and of those 16% were either new diagnoses or viremic.

There were 196 indexes with at least one HIV negative partner named and no difference in negative partners originating from index clients in a cluster versus not in a cluster.

There was a significantly significant difference in the yield of new diagnoses or viremic partners linked to index clients in a cluster versus not in a cluster (RR 1.51; p=0.049).

There was no difference in the yield of new diagnoses or viremic partners linked to index clients in recent and rapid cluster (R3) ≥ 3 cases in the last year compared to those not in a cluster (RR 1.88; p=0.10).

There was no difference in the yield of new diagnoses or viremic partners linked to index clients with the number of cases added to the cluster in the past 12 months is divided by the square root (RR 1.71; p=0.28).

Figure 1. Flow diagram of partner services, molecular cluster and HIV viremia/new diagnosis yield, Chicago IL 2008-2018.

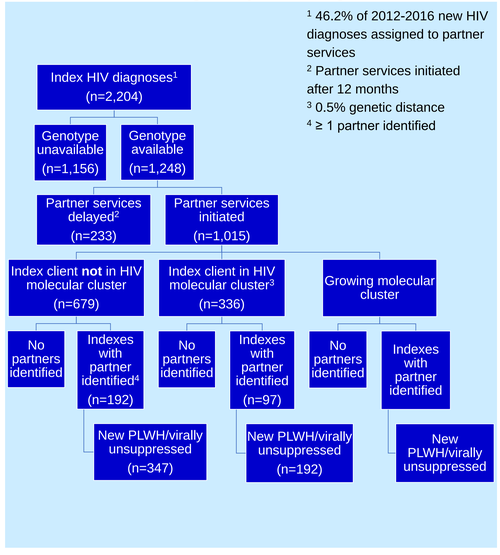
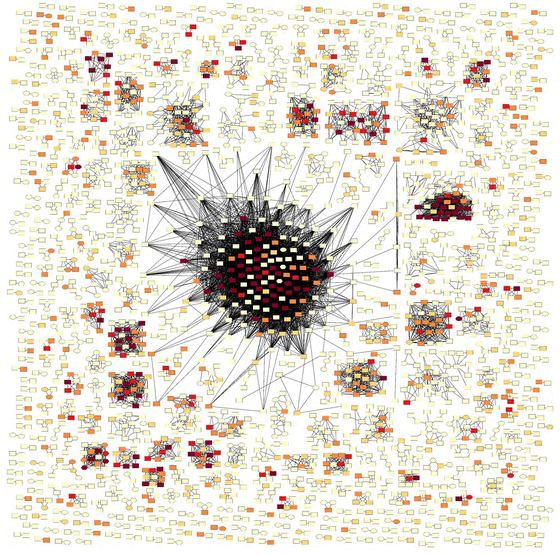


Table 1. Index and partner characteristics, Chicago IL 2008-2018.

	Index		Partners with active HIV[1]		Partners without active HIV[2]	
Variable	N	%	N	%	N	%
Age[3]						
13-24	97	37	<5	1.5	9	2.4
25-34	107	40.8	38	55.9	134	35.9
35-44	31	11.8	16	23.5	68	18.2
45-54	23	8.8	8	11.8	31	8.3
≥55	<5	1.5	<5	7.4	131	35.1
Sex at birth						
Male	244	93.1	-	-	-	-
Female	18	6.9	-	-	-	-
Current gender						
Male	244	93.1	-	-	-	-
Female	18	6.9	-	-	-	-
Race/Ethnicity						
Black	134	51.1	24	35.3	65	17.4
LatinX	70	26.7	8	11.8	34	9.1
White	43	16.4	<5	4.4	23	6.2
Other	15	5.7	33	48.5	248	67.3
MSM identified						
Yes	221	84.4	-	-	-	-
No	41	15.6	-	-	-	-
Cluster growth I[4]						
Non-clustered	169	64.5	-	-	-	-
Clustered, not rapidly growing[5]	78	29.8	-	-	-	-
Clustered and rapidly growing	15	5.7	-	-	-	-
Cluster Growth						
Not clustered	169	64.5	-	-	-	-
Clustered, <1	49	18.7	-	-	-	-
Clustered, ≥1	44	16.8	-	-	-	-

[1] Newly diagnosed and/or unsuppressed virus
[2] Virally suppressed or HIV negative
[3] At diagnosis
[4] CDC definition
[5] ≥3 cases in the last year
[6] Number of cases added to this cluster in the past 12 months divided by the square root of cluster size, defined at distance threshold 0.5% (continuous outcome dichotomized at 1)

Figure 2. Network Visualization of molecular clusters and growth parameters, Chicago IL 2008-2018.



CONCLUSIONS

Partner services deployed based upon molecular cluster data may not increase new HIV case finding or identification of those with viremia.

Utility of molecular cluster data in identifying at risk HIV negative persons who could benefit from intervention is unknown.

Determining optimal partner services strategies, such as two-steps from cluster or three-steps as well as the frequency of revisiting clusters is critically needed.

Mathematical modeling and computational simulation may provide guidance into optimization of partner services efforts that follow molecular cluster identification.

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