IDENTIFYING AND INVESTIGATING A RAPIDLY GROWING HIV TRANSMISSION CLUSTER IN TEXAS

Background

Analysis of HIV nucleotide sequence data collected through the National HIV Surveillance System can identify rapidly growing transmission clusters. The Centers for Disease Control and Prevention (CDC) identified a molecular cluster in Texas that grew substantially during July 2015–June 2016. The Texas Department of State Health Services and CDC staff performed this investigation to define the extent of the cluster and underlying risk network, characterize the epidemiology and factors facilitating transmission, characterize timing of transmission, and prioritize intervention opportunities. Although HIV genotype testing is considered standard of care and recommended for all new diagnoses, it is only performed and reported to the health department for approximately 50% of new diagnoses each year. This cluster was selected for investigation due to the rapid growth, tight geographic distribution, and young demographic that is a known high risk population.

Objective 1: Define the extent of the underlying risk network

Methods:

-Abstracted information from previously performed partner services interview to elicit partners and other persons at risk for disease -Partners identified from partner services database, notes from interviews and online social networks -If partners of molecular cluster case had a genotype sequence available, analysis was conducted to determine if it was demonstrably different from this cluster. Partners with dissimilar sequences were excluded.

<u>Results:</u>

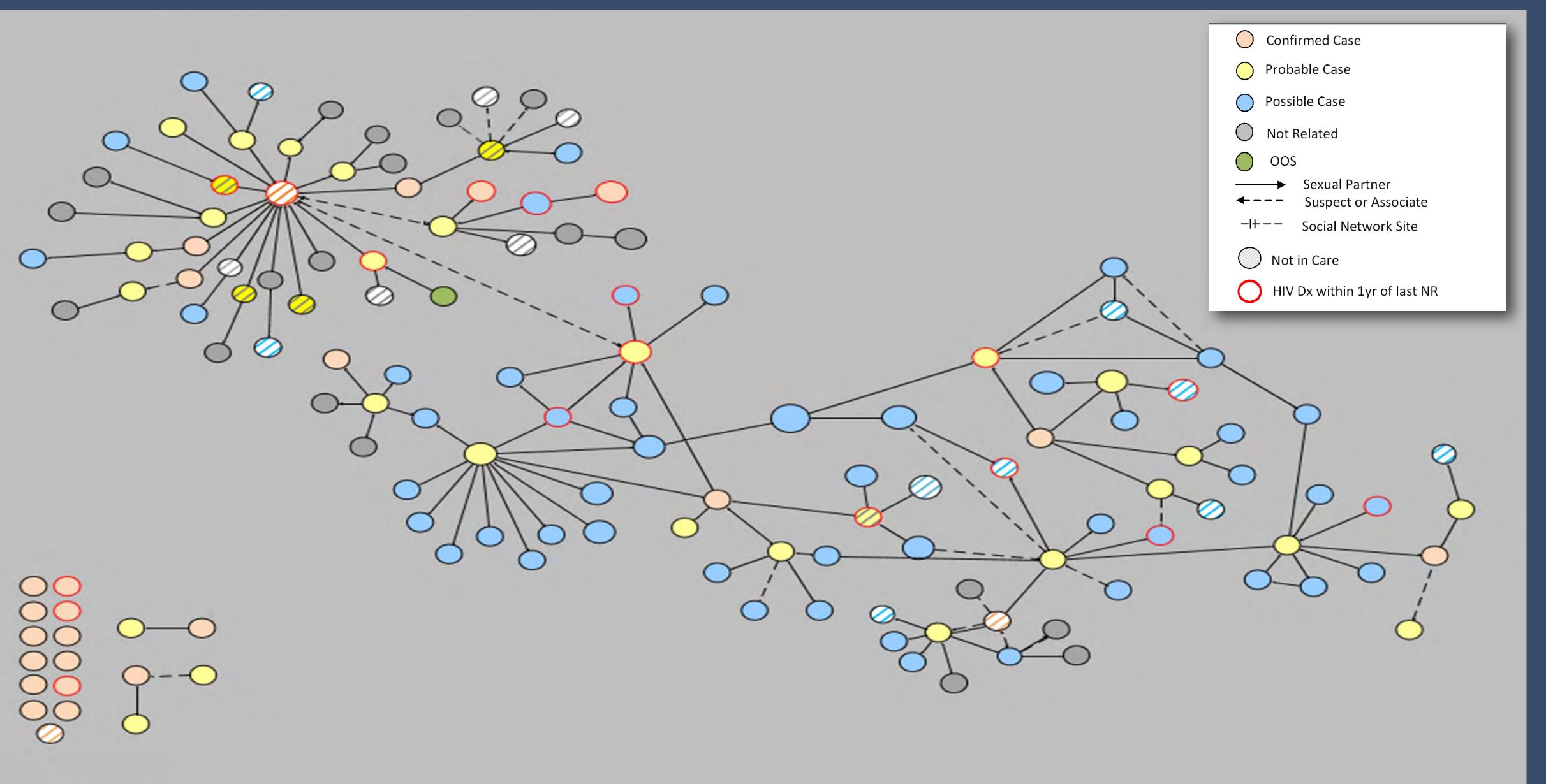
Case Definitions:

-Confirmed Cluster Case (n=27)— HIV positive person who is linked to the cluster through their HIV genotype, a genetically similar strain

-Probable Cluster Case (n=34)— HIV positive person who is a sexual or needle sharing partner of a confirmed cluster case -Possible Cluster Case (n=54)— HIV positive person who is a social network contact of a confirmed cluster case or a sexual or needle sharing partner of a probable cluster case

-Sequence Available and Not Related (n=24)- persons who would have been in the probable or possible groups, but have a genetically dissimilar HIV strain

Figure 1: This map shows the linkages between the confirmed, probable, possible and not related cases. There is high connectivity in one area of the map with a single individual, however evidence shows that they were infected after many other cases in this cluster and likely not a major node of transmission. The right half of the map shows a larger network with much crossover of partners. Additionally, it is concerning that there are still so many confirmed cases which were not linked to the cluster through partner services data, highlighting the high number of anonymous partners in this cluster.



<u>Discussion:</u>

Partner services data indicate that the transmission network is much larger than the molecular cluster identified. Molecular cluster analysis identified links that partner services data may have missed. Intervention on the persons in the genotype cluster alone is not enough, as the cluster is likely larger than we know due to many cluster cases which were not interviewed or did not name partners.

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Objective 2: Understand epidemiology of the transmission cluster and characterize timing of transmission

<u>Methods:</u>

-Reviewed and systematically abstracted medical records from providers across Texas and partner services data from August to October 2016 -Assessed likely exposure and infectious windows

-Assessed length of time to achieve viral suppression

-Descriptive analysis of key cluster variables

-Assessed early infection indicators

Results:

Figure 2: This diagram shows the curve of possible time of HIV acquisition (green), diagnosis month or year (red), and time the person was infectious before achieving viral suppression (orange). The yellow sections indicate that the patient presented with symptoms consistent with acute infection but were not tested for HIV. Note that the left side of the chart is measured in years while the right side was in months, due to the rapid growth in the cluster observed from 2013-2016. This diagram highlights that there were a good number of cases with

before diagnosis with HIV, as well as several persons who had long periods after diagnosis before achieving viral suppression.

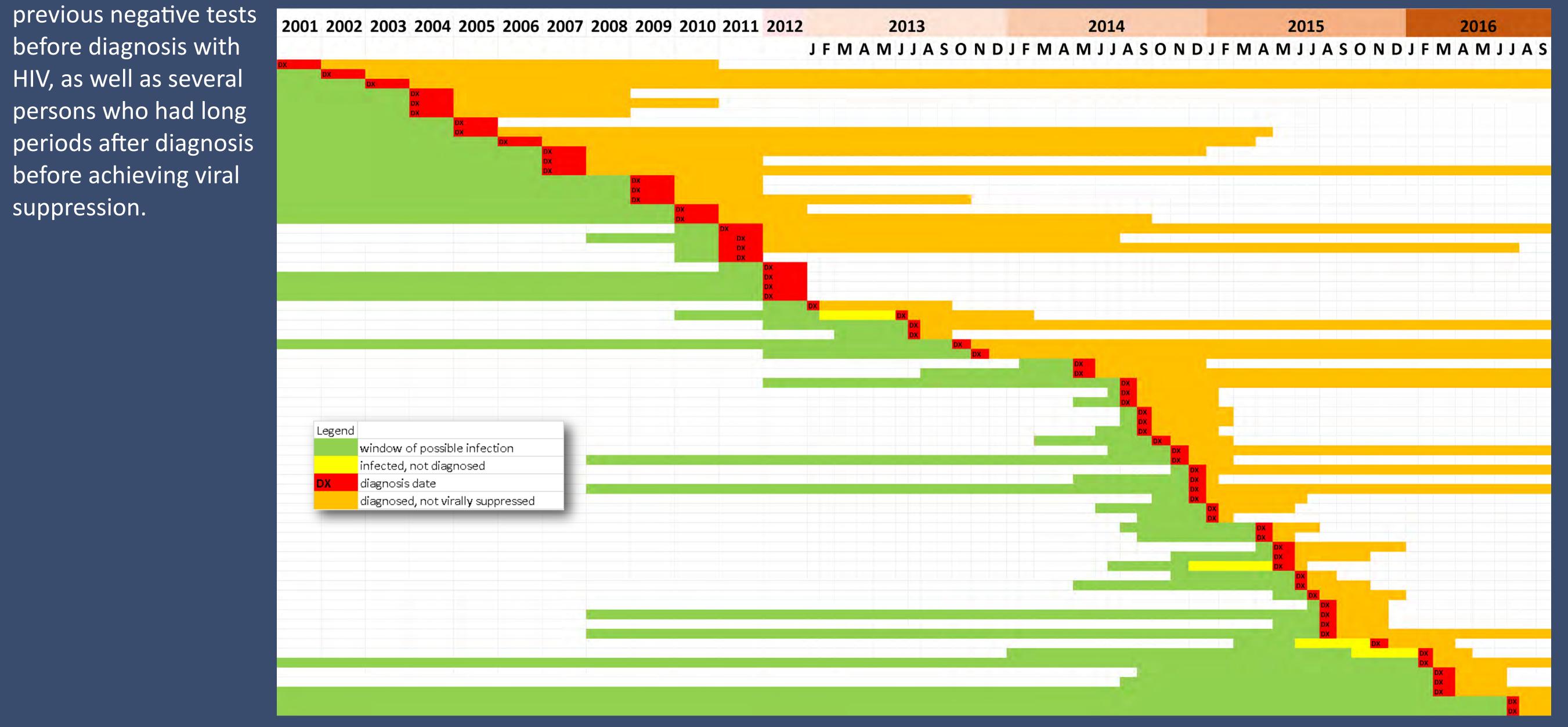


Table 1: Characteristics and Demographics of Cluster.

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		n	%
Sex at Birth	Male	76/76	100%
Residence at Diagnosis	Bexar County (San Antonio)	59/76	78%
	Other County in Texas	15/76	20%
	Other State	2/76	2%
Current Residence (Oct 2016)	Bexar County (San Antonio)	53/76	70%
	Other County in Texas	16/76	21%
	Other State	7/76	9%
Current Age (Oct 2016)	17-19	5/76	7%
	20-29	54/76	72%
	30-39	13/76	17%
	40+	3/76	4%
Race/Ethnicity	Hispanic	66/76	87%
	Black	5/76	6%
	White	2/76	3%
	Other Race	3/76	4%
Behavioral Risk Factors	MSM	68/76	90%
	MSM/IDU	7/76	9%
	No Identified Risk	1/76	1%
	Ever had previous negative test	42/69	60%
Early Infection Indicators (data availal	ble Stage 0 at diagnosis	21/69	30%
for n=69)	Reported symptoms consistent with acute infection	15/69	21%
	Self reported or documented negative test within 3 months	14/69	20%
Insurance at Diagnosis	Private health insurance (self or parents)	24/76	32%
	Uninsured	25/76	33%
	Other or Unknown	26/76	34%

Discussion:

There is strong evidence that this cluster resulted from recent active transmission and not from an increase in testing. Many cases in this cluster had indications of early HIV infection, either through testing or symptoms around diagnosis. Several cases were not virally suppressed at the time of analysis.

Objective 3: Characterize community factors that may have facilitated transmission and identify potential intervention opportunities

Methods:

-Review of partner services interview electronic records -Review of partner services interview paper charts -Review of risk factors noted in medical records

<u>Results:</u>

Venues for Partner Se

Use of Condoms

Lifetime number of sexual p

Drug Use Behavio

Other Sexually Transmitte

HIV Care informat

A large percentage of cases in this cluster (72%) indicated that they had anonymous sex partners, which along with large numbers of lifetime sexual partners, little condom use likely contributed to the growth of this cluster. Additionally the intricate nature of this cluster and underlying social sexual network indicates that there are still persons at risk. Many of the cases in this cluster had encounters with medical care for other STD diagnoses. Despite these factors, none of the persons involved in this cluster were on PrEP (Pre-Exposure Prophylaxis) prior to diagnosis. While many cases are currently in care, many others have unsuppressed viral loads for prolonged periods or no evidence of suppres-

Our investigation identified an actively growing transmission cluster of primarily young Hispanic MSM that was substantially larger than the molecular cluster; the underlying risk network (involving undiagnosed and HIV negative partners) is likely even larger, given the large number with anonymous partners and confirmed cases without identified links through partner services to the cluster. High risk sexual behavior, limited PrEP access, inconsistent use of the HIV diagnostic algorithm, and delays in achieving viral suppression among some cluster cases likely contributed to rapid growth. These findings reveal opportunities for prioritization of persons associated with this cluster for linkage to care and PrEP referral for negative partners. Twenty-five partner service follow up investigations (field records) were initiated for re-initiation in care of HIV positive individuals. Additionally, 28 negative partners who were linked to this cluster and at high risk for HIV infection have been re-tested, one new positive case has been identified. Several actions were also taken to address the community factors that contributed to this cluster. DSHS staff have drafted a Dear Colleague letter which outlines rapid growth clusters and stresses the importance of using the full APHL recommended diagnostic testing algorithm, as well as a health alert to recommend ways to identify acute HIV cases, and stress the importance of genotype testing. Steps have been made to revise training of Disease Intervention Specialists to better collect information on anonymous partners as well as get access to the dating apps that were frequented by persons in this cluster for future intervention opportunities. DSHS has also increased funding for HIV prevention activities in this region of Texas including additional PrEP services, targeted testing, and prevention outreach.

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Table 2: Factors contributing	to the growth of cluster.

		n [°]	%
Selection	GRINDR	15/22	68%
	Bars	10/21	48%
	Bathhouse	7/21	33%
	JACK'D	6/19	32%
	Facebook	6/20	30%
	Craigslist	4/18	22%
ms	Sometimes	34/46	74%
	Never	8/46	17%
	Always	3/46	7%
partners (n=30)	Median =45	Range 2-300	
viors	Alcohol	52/56	93%
	Marijuana	26/38	68%
	Crack/Cocaine	14/33	42%
	Methamphetamine	10/29	34%
	Injection Drug Use	7/36	19%
ted Diseases	Any documented STD history*	88/139	63%
	30 days or more after HIV diagnosis*	51/139	37%
	Concurrent with HIV diagnosis*	31/139	22%
	Within 12 months prior to HIV diagnosis*	18/139	13%
ation	Evidence of care in past 12 months	47/52	90%
	Evidence of linkage to care	59/69	86%
	Evidence of current viral suppression	47/76	76%
	Evidence of ARV initiation	51/69	74%
	Evidence of treatment interruption/poor adherence	22/44	50%
or all 139 Confirm	ed. Probable. and Possible patients using data from STD*MIS.		

*STD History was determined for all 139 Confirmed, Probable, and Possible patients using data from STD*N

[§]n is where data available for each patient in medical record or partner services notes.

Conclusions and Public Health Interventions

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Disclaimer: The findings and conclusions in this presentation are those of the author(s) and do not necessarily represent the official position of the Centers for Disease Control and Prevention.