Poster Session # P-B2
Abstract 240

Conference on Retroviruses and Opportunistic Infections
February 23-26, 2015
Seattle, Washington

Comparing Confirmed Epidemiologic Partners to Unconfirmed Epidemiology Partners in a San Diego HIV Transmission Network

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Background

- HIV molecular epidemiology is being evaluated as a tool to more efficiently target prevention efforts.
- Although simulations have demonstrated that interventions targeting network "hubs" may be most efficient, data to guide real time implementation strategies are limited.

Objective

To compare the demographic and HIV risk behaviors of epidemiologically and phylogenetically linked transmission partners with epidemiologically unconfirmed and phylogenetically linked transmission pairs inferred by molecular epidemiology alone

Hypothesis

Demographic and behavioral risk characteristics will be different between genetically linked and epidemiologically confirmed and unconfirmed transmission pairs inferred by genetic analysis.

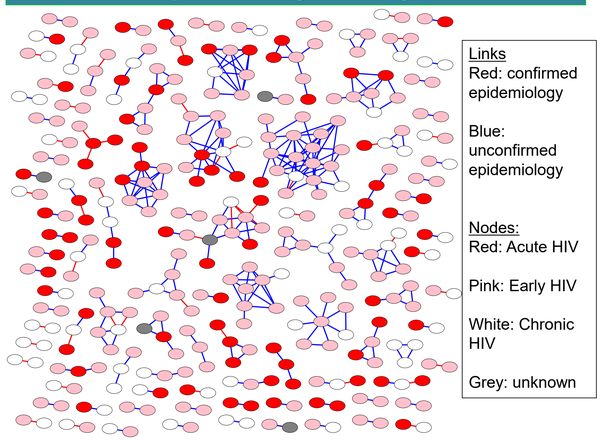
Methods

- Screening for acute HIV-1 infection was offered between 1996 and 2014 at multiple San Diego sites and persons with acute and early infection, and their social/sexual partners, were enrolled.
- A partial transmission network was inferred based on the nucleotide phylogenetic distances between HIV-1 *pol* sequences.
- Two individuals in the network were linked whenever their pol sequences were ≤1.5% distant (TN93 model).
- A subset of phylogenetically linked paiirs were supported by bi-directionally confirmed epidemiological linkage.
- An edge filtering algorithm based on phylogenetic conditional independence was applied to each triangle in the network, and a subset of triangles were converted to chains
- Differences in demographic and HIV risk behaviors were investigated using a mixed effects logistic regression model.
  - To control for clustering of partnerships, each cluster was treated as a random effect

Table 1: Demographics & Risk Behaviors

Study Participants (N = 334)	
Male (N, %)	321 (97.0%)
MSM (N, %)	307 (97.2%)
Mean Age (IQR)	33 yrs, (26 – 39)
Race (N, %) – White	244 (76.0%)
Ethnicity (N,%) – Hispanic	89 (27.1%)
HIV stage (N, %) – Acute	77 (23.4%)
Early	177 (53.8%)
Chronic	75 (22.8%)
Median CD4 cells/mm^3 (IQR)	498 (334 – 638)
Mean logVL (IQR)	4.99 (4.35 – 5.61)
Median sex partners prior 1 mo (IQR)	2 (1-3)

Figure 1: Epidemiologically Unconfirmed Partnerships Belong to Larger Clusters



Partnerships	Median cluster size, IQR	p-value
Confirmed epidemiology	2, (1 – 7.5)	<0.0001
Unconfirmed epidemiology	9, (3 – 18)	

Results

1008 HIV sequences were screened for phylogenetic linkages. A total of 334 unique individuals were represented in 336 genetically linked partnerships.
•48 (14%) supported by confirmed epidemiologic links while 288 (86%) were not supported

Confirmed epidemiologically linked pairs:
•Had fewer sex partners in the past month and were associated with smaller inferred transmission clusters [Table 2, Figure 1]
•Were associated with a higher mean degree of 1.85 compared to a mean degree of 0.95 for unconfirmed epidemiologically linked pairs
•Were more likely to include a female partner (N=12 female and M to F transgender persons), a chronically infected partner, and closer dates of presentation

Table 2: Significant Differences For Confirmed Epidemiologic Partners

Partner-pair characteristics	N	OR	95%CI	p-value
Differences in:				
Sex	332	6.99	(1.61 - 30.4)	0.01
Age within 5 years	336	0.5	(0.25 - 0.99)	0.04
Race/ethnicity	328	0.93	(0.46 - 1.9)	0.85
MSM	327	0.52	(0.05 - 5.17)	0.58
Stage of HIV infection at enrollment	327	3.7	(1.79 - 7.62)	< 0.001°
Diagnosis date	336	0.997	(0.996 - 0.999)	< 0.001°
Number of sexual partners*	302	0.76	(0.6 - 0.96)	0.02
Unprotected anal or vaginal intercourse*	274	0.77	(0.31 - 1.88)	0.56
Unprotected anal intercourse*	265	0.54	(0.2 - 1.47)	0.23
Methamphetamine use*	43	1.03	(0.09 - 12.4)	0.98
Any drug use*	43	1.06	(0.17 - 6.71)	0.95

*Within past month; °significance likely secondary to study design

Conclusions

• Linked partnerships that are identified using genetic sequence data alone may represent a higher risk population with regard to targeted interventions.
• Epidemiologically-confirmed transmission pairs identified by contact tracing may not identify the highest yield targets for network-based interventions
• The higher node to edge ratio associated with epidemiologically-unconfirmed nodes suggests that targeted prevention interventions in this group may results in greater network disruption.
• Methods should be evaluated to define the most effective prospective method to characterize these clusters (i.e. demographics, venue, geography) in order to deliver targeted interventions in real time.

Acknowledgements

CFAR T32 Training Grant: NIH Grant 93062a
Primary Infection Resource Consortium: NIH Grant AI106039
CROI 2015 Young Investigator Scholarship