

The Public Health Applications of Molecular Epidemiology: *Use of HIV-1 Pol Sequences to Identify HIV Transmission Networks in Los Angeles County*

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Molecular Epi: A Public Health Tool

- Molecular epidemiology plays a critical role in public health activities
 - Outbreak Investigations: commonly used to Identify transmission in bacterial foodborne outbreaks
 - Used to identify and contain other communicable disease networks (e.g. cluster of TB cases for strain PCR 08263 in homeless in LAC)
- New roles for molecular epidemiology in other fields are emerging



Molecular Epi: HIV

- Recent studies show how molecular epidemiology can also be applied to study HIV transmission networks and may inform screening activities

Transmission networks of drug resistance acquired in primary/early stage HIV infection

AIDS 2008

Bluma G. Brenner^a, Michel Roger^b, Daniela D. Moisi^a,
Maureen Oliveira^a, Isabelle Hardy^b, Reuven Turgel^a, Hugues Charest^c,
Jean-Pierre Routy^d, Mark A. Wainberg^a, and the Montreal PHI
Cohort and HIV Prevention Study Groups

OPEN ACCESS Freely available online

PLOS Medicine 2008

Episodic Sexual Transmission of HIV Revealed by Molecular Phylodynamics

Fraser Lewis^{1,2,3}, Gareth J. Hughes^{1,4}, Andrew Rambaut¹, Anton Pozniak², Andrew J. Leigh Brown^{1*}

A public health model for the molecular surveillance of HIV transmission in San Diego, California

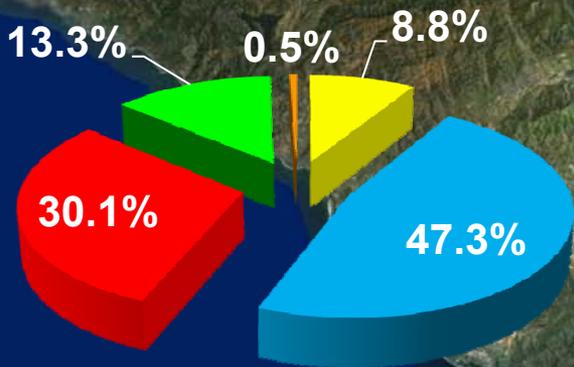
AIDS 2009

Davey M. Smith^{a,b}, Susanne J. May^c, Samantha Tweeten^d,
Lydia Drumright^a, Mary E. Pacold^a, Sergei L. Kosakovsky Pond^a,
Rick L. Pesano^e, Yolanda S. Lie^e, Douglas D. Richman^{a,b},
Simon D.W. Frost^a, Christopher H. Woelk^a and Susan J. Little^a



Population	Estimated HIV/AIDS Cases
9,848,011	61,700

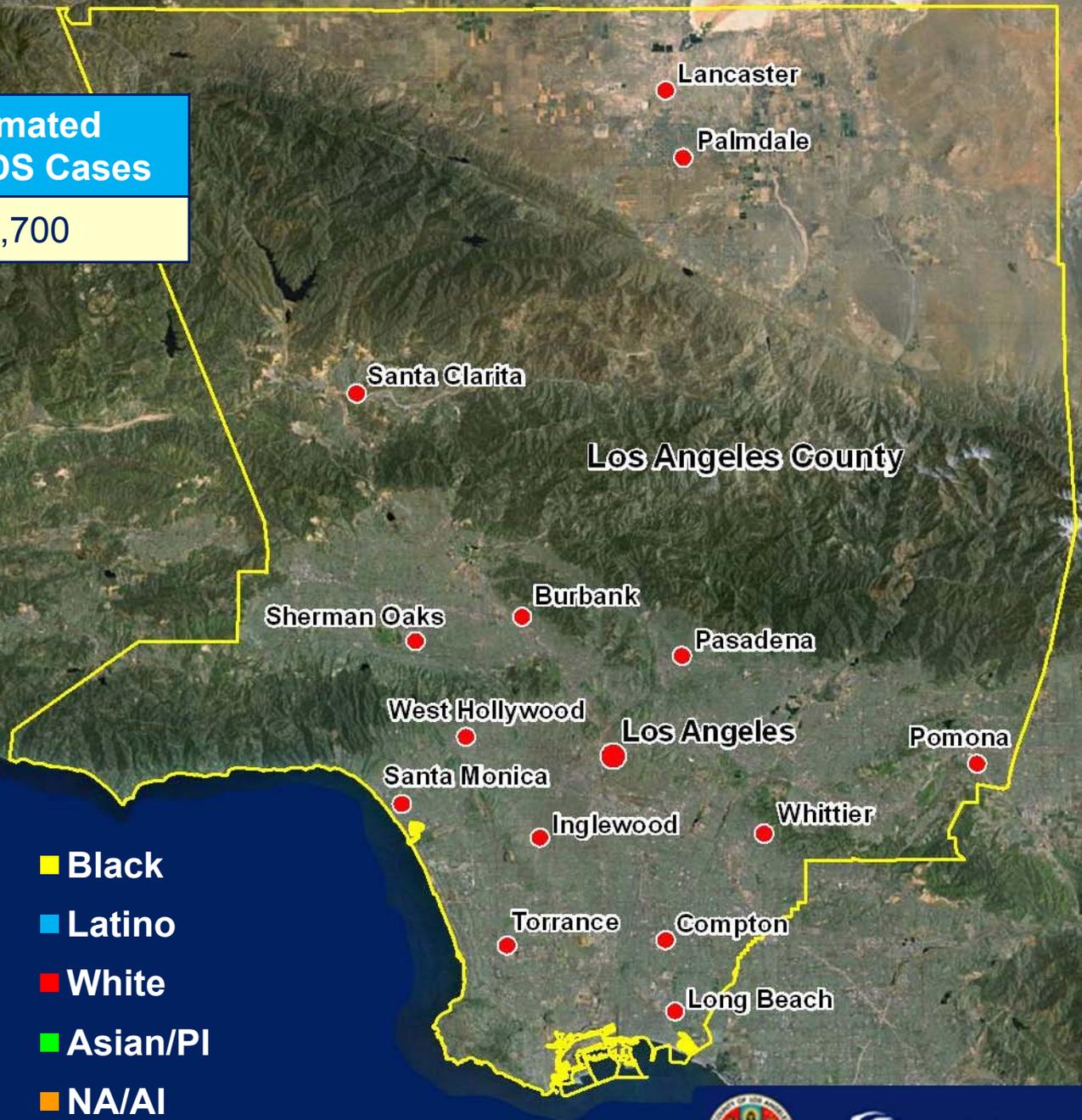
Overall, Race/Ethnicity



HIV/AIDS Cases



- Black
- Latino
- White
- Asian/PI
- NA/AI



Study Objective

- Examine demographic, geographic, and clinical factors associated with transmission networks or “clusters” among patients in the Los Angeles County (LAC) Ryan White system of care between 2001 – 2008



Methods

- Sample: 3,201 HIV+ patients in the LAC Ryan White system who received a genotype test between 2001 – 2008
 - Cohort represented patients with detectable viral load and a genotype test
 - Includes individuals failing therapy and newly diagnosed patients entering care
- Using unique HIV pol sequences, analysis of genetic relatedness was used to define clusters (ref: Pond 2005)



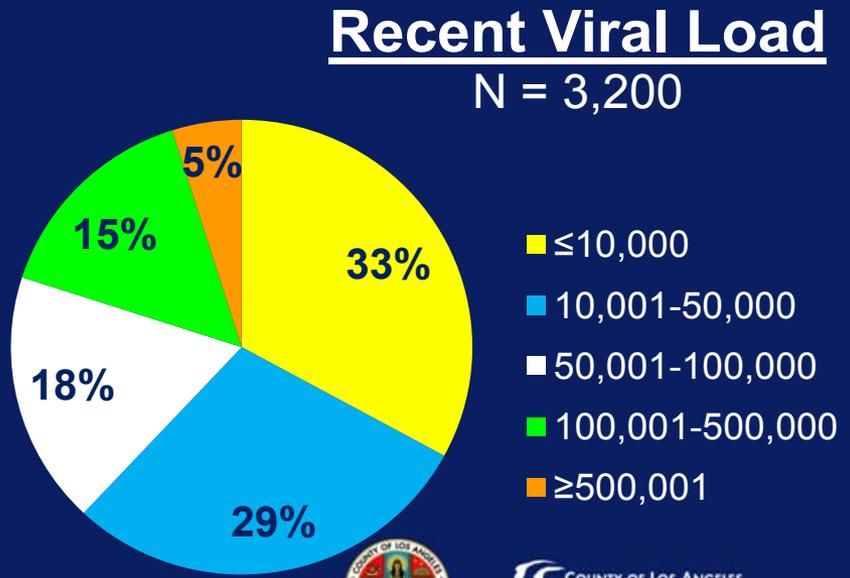
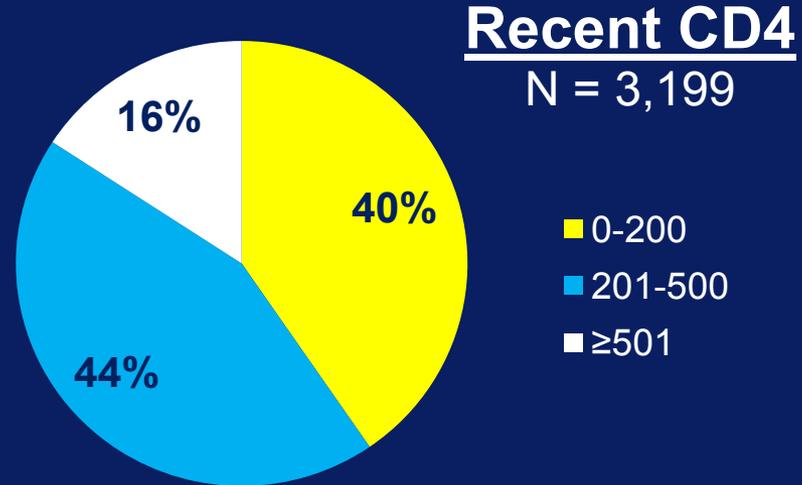
Methods Cont'd

- Clustering was conservatively defined at a genetic distance of $<1\%$ (ref: D. Smith 2009, AIDS)
- Identified clusters were then examined by:
 - Gender, race/ethnicity, age at time of specimen collection, most recent CD4 count, most recent viral load, and one of 8 service planning areas (SPAs) within LAC
- Clusters were then mapped using reported SPA of residence (ArcGIS)



Demographic Characteristics of Sample

Characteristic	N	%
All Clients	3,201	
Male	2,732	85%
Female	429	13 %
Transgender	38	1%
Unknown	2	0.1%
White	602	19%
African American	660	21%
Latino	1,807	56%
Asian Pacific		
Islander	77	2%
Other/Unknown	55	2%
≤18*	39	1 %
19-24*	179	6%
25-29*	350	11%
30-39*	1,220	38%
40-49*	1,052	33%
50+*	361	11%
Mean Age (Range)*	38.3 years (0-77)	
Median Age*	38 years	



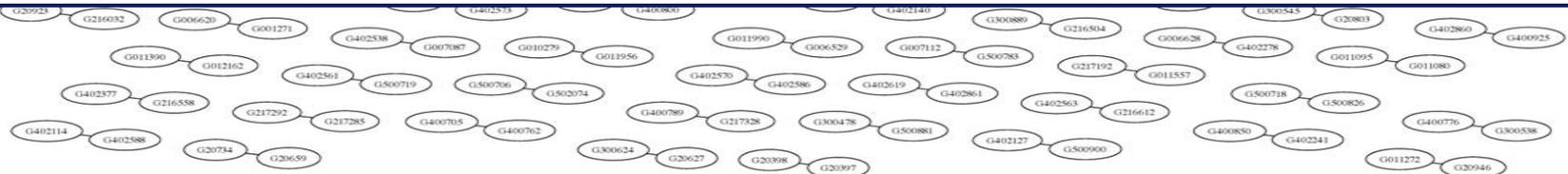
*Age at time of specimen collection



Clusters Identified

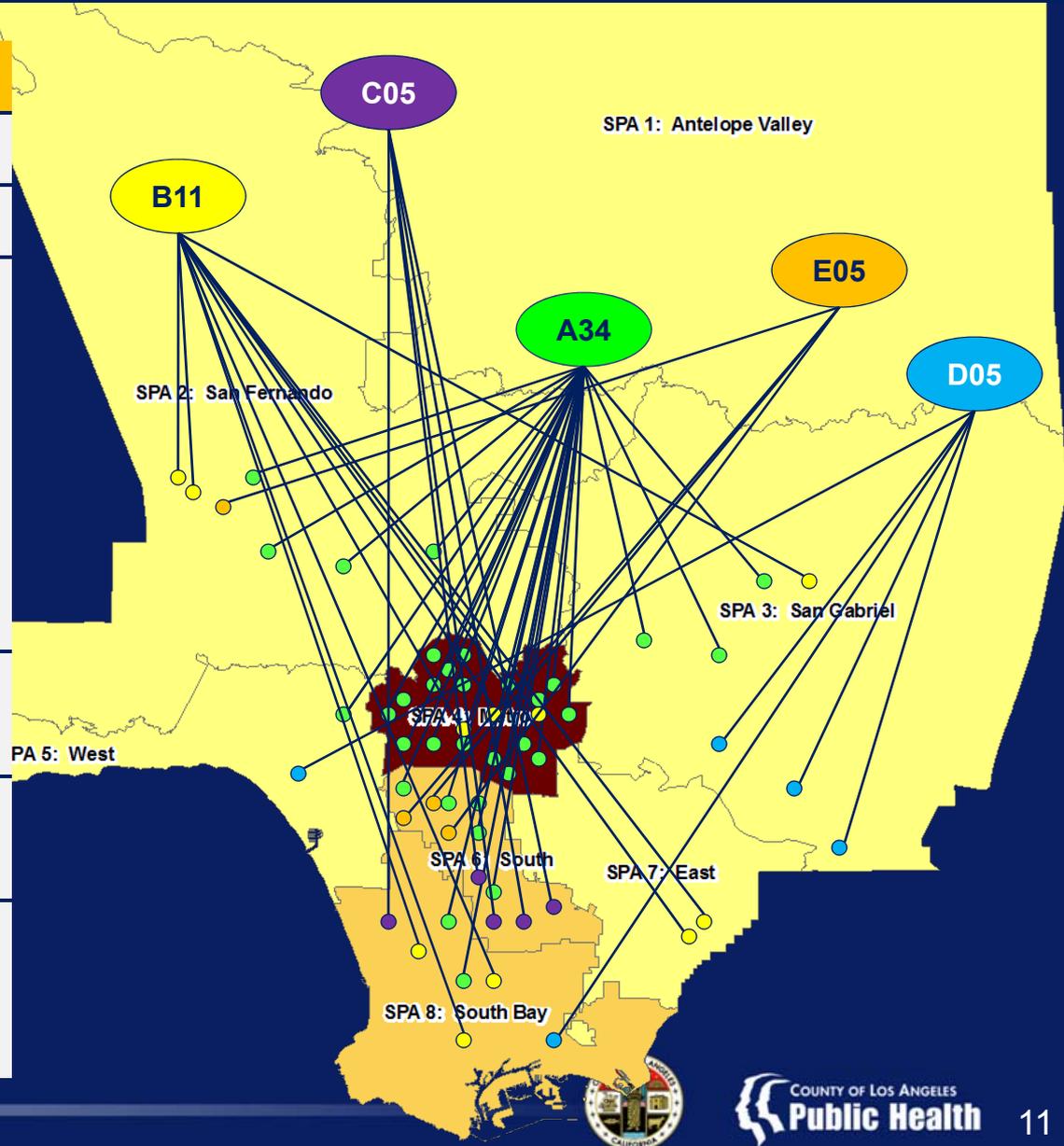
- 3,201 sequences were analyzed
- 165 unique clusters were identified
- Represents 13% (N=413) that clustered into highly related HIV sub-populations

<u>Cluster Size</u> (# of sequences in a cluster)	<u># of Clusters at 1%</u> N(%)
2	137 (4.6%)
3	13 (0.44%)
4	10 (0.34%)
5	3 (0.1%)
11	1 (0.03%)
34	1 (0.03%)
Total # of Clusters Identified	165



Cluster Characteristics and Distribution by SPA

Characteristic	Cluster E
N	5
Male	100%
White	80%
African American	
Latino	20%
Asian Pacific Islander	
Other/Unknown	
Mean Age (Range)*	31.2 yrs (25-37)
Mean CD4 (Range)	328.4 (142-578)
Mean Viral Load (Range)	231,483.2 (77,205-750,000)



*Age at time of specimen collection

Source: Annual HIV Surveillance Report; Reported cases through 12/31/10

Cluster Characteristics and Distribution by SPA

Characteristic	Cluster A	Cluster B	Cluster C	Cluster D	Cluster E
N	34	11	5	5	5
Male	97%	100%	100%	100%	100%
White	41%	9%		20%	80%
African American	12%		100%		
Latino	41%	91%		60%	20%
Asian Pacific Islander	3%				
Other/Unknown	3%			20%	
Mean Age (Range)*	40.6 yrs (26-57)	37.2 yrs (25-49)	25.6 yrs (16-47)	44.4 yrs (35-60)	31.2 yrs (25-37)
Mean CD4 (Range)	269.5 (2-775)	290.5 (53-782)	237.6 (67-498)	480.8 (287-780)	328.4 (142-578)
Mean Viral Load (Range)	84,276.5 (1,085-750,000)	74,668.2 (2,445-240,000)	264,061.8 (51,731-750,000)	101,042.6 (10,420-201,921)	231,483.2 (77,205-750,000)

Summary of Results

- Molecular epidemiology can be used to study transmission networks in LAC
- Larger clusters were overwhelmingly comprised of men, and each cluster contained a unique combination of dominant race/ethnicity, age range, and geographic location



Limitations

- Available sequences were from a small subset of Ryan White medical clients (3,200 out of 13,000 patients/yr)
- The sample is limited to Ryan White patient sequences. Other individuals who may be in cluster but not in the Ryan White system would not be represented in this analysis



Public Health Implications

- Transmission networks and their characteristics can inform prevention strategies that target high risk networks
 - Partner Services, ART expansion, targeted condom distribution, social marketing
- Knowledge about transmission networks can improve social and sexual network tracing to identify HIV+ persons unaware of status



Los Angeles County Next Steps

- Examine transmission clusters using Los Angeles County surveillance data
- Analysis of resistance patterns within networks





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For More Information

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