

HIV Transmission Patterns Among Immigrant Latinos Illuminated by the Integration of Phylogenetic and Migration Data

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Abstract

Latinos represent a growing proportion of HIV cases in North Carolina (NC). Understanding how immigrants are involved in local HIV transmission is important to guide interventions. We used phylogenetics to characterize Latino involvement in local HIV transmission chains. Transmission clusters were identified from maximum-likelihood phylogenies constructed with HIV *pol* sequences from 177 Latinos and 1,496 non-Latinos receiving care in NC. Highly supported clusters involving one or more Latinos were characterized. Migration data were obtained from interviews and chart review. Factors associated with cluster membership were identified using log-binomial regression. Most Latinos were male (76%), immigrants (83%), and had HIV-1B (99%). Immigrants were more likely to report heterosexual risk (67% vs. 23%) than U.S.-born Latinos ($p < 0.01$). We identified 32 clusters that included one or more Latinos; these involved 53 Latinos (30%) and 41 non-Latinos. Immigrant and U.S.-born Latinos were equally likely to be in clusters, but immigrants were more likely to be in clusters with another Latino (78% vs. 29%; $p = 0.02$). Cluster composition by ethnicity and risk behavior varied by cluster size; larger clusters contained fewer immigrants and more men who have sex with men (MSM). Factors associated with immigrant membership in local transmission clusters included age < 30 years [RR 2.34 (95% CI 1.47–3.73)], Mexican origin [RR 2.55 (95% CI 1.29–6.88)], and residing in the United States longer before diagnosis [RR 1.53 (95% CI 1.09–2.15), per 10 years]. While some Latinos immigrate with HIV infection, many immigrants are involved in transmission networks after arrival, particularly MSM. HIV testing and prevention interventions must consider this heterogeneity and may be better targeted by integrating phylogenetic analyses.

Introduction

LATINOS ARE THE LARGEST and one of the fastest growing ethnic minority groups in the United States¹ and are disproportionately affected by HIV.² In North Carolina (NC), as in other areas of the southeastern United States, the Latino population has increased dramatically. The state experienced a nearly 400% increase in the Latino population from 1990 to 2000, one of the highest increases among all U.S. states.³ The group more than doubled in size between 2000 and 2010; an estimated 800,120 persons identifying as Latino resided in NC in 2010 (8.4% of the total NC population, which increased

from 4.7% in 2000).⁴ In tandem with increased Latino population growth in NC, Latinos represent an increasing proportion of the local HIV epidemic. From 1995 to 2009, new HIV cases among Latinos rose from 1% to 8% of cases reported to the state.^{5,6}

The extent that Latinos are involved in local HIV transmission networks, through local HIV acquisition, or immigration with infection acquired abroad followed by onward transmission in the region remains unclear. In our previous analysis of HIV-infected Latinos receiving care in NC, most Latino immigrants were diagnosed with HIV within 10 years of U.S. arrival.⁷ Latinos were also significantly more likely to

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present to care with advanced HIV disease compared to non-Latinos,⁸ implying a long period between HIV acquisition and clinical presentation. While these findings suggest that many infections may be acquired abroad, only phylogenetic analyses can provide a better estimation of the degree immigrants may be involved in local transmission. The process of migration has been hypothesized to increase the risk of HIV acquisition through the loss of previously stable social and sexual networks and engagement in riskier behaviors in the United States.^{9,10} In our prior HIV phylogenetic studies in NC, Latinos were less likely to be identified in larger local transmission networks ($n \geq 3$ individuals) compared to non-Latinos,¹¹ suggesting either importation of infections, incomplete sampling among this group, or differing network characteristics (i.e., fewer concurrent partnerships).

In this study, we integrated behavioral, migration, and HIV sequence data to elucidate HIV transmission patterns among HIV-infected Latinos in NC. Our overall objective was to characterize HIV transmission patterns to assess Latino involvement in local HIV transmission chains and determine if transmission occurs predominately within the ethnic group or is integrated with non-Latinos. Elucidating HIV transmission networks involving Latinos will inform targeted HIV testing and prevention efforts among this vulnerable group.

Materials and Methods

Study design and population

We conducted a cross-sectional analysis of 177 Latinos and 1,496 non-Latinos who received care at University of North Carolina (UNC) clinics between 1999 and 2011 and who had an HIV *pol* sequence available for analysis. Latino/Hispanic ethnicity was self-identified (defined as a person of Mexican, Puerto Rican, Cuban, South or Central American, or other Spanish culture or origin, regardless of race). Of the Latino patients, 102 participated in face-to-face interviews conducted from 2010 to 2011 to collect behavioral and migration history. Most of these Latino patients (70%) were also enrolled in the UNC Center for AIDS Research HIV Clinical Cohort (UCHCC). The remaining 75 Latinos were included from the UCHCC database but not interviewed. The interview data collection has been described previously.⁷ In brief, interviews were conducted in Spanish or English by a native culturally competent interviewer with extensive experience working with the local Latino population. Questions spanned HIV testing, partnerships, risk behaviors, and migration history, including birth location, immigration year, return visits, and location of HIV testing. Latinos who were not interviewed were similar to the interviewees by immigrant status, sex, and initial CD4 counts but were more likely to have an earlier year of diagnosis [median 2001 (IQR 1998–2004) vs. 2007 (IQR 2002–2008)].

Clinical and demographic data were abstracted from institutional databases and medical charts using standardized methods. Patients with reported transmission risk behaviors were categorized as heterosexual, men who have sex with men (MSM) [without regard to number of experiences disclosed or sexual orientation], injection drug use (IDU), or other/unknown. Participants reporting IDU in addition to heterosexual or MSM risk were categorized as IDU. Non-Latinos were selected as references from the UCHCC; all had received care at UNC from 1999 to 2011 and had an HIV *pol* sequence available for analysis.

HIV-1 sequences and phylogenetic inference

Full length protease (PR) and partial reverse transcriptase (RT) sequences were extracted from genotypes obtained during clinical care. Most assays were HIV GenoSure or GenoSure Plus (Laboratory Corporation of America, Research Triangle Park, NC) or the TRUGENE HIV-1 assay (Siemens Healthcare Diagnostics, Tarrytown, NY). Sequences were sampled from 1997 to 2011. In the event that a patient had multiple genotypes, only the oldest sequence was included in the analysis. Subtypes were identified with the Subtype Classification and Evolutionary Algorithms.¹² Mutations associated with transmitted drug resistance (TDR) were identified using the 2009 standardized surveillance list from the World Health Organization.¹³ Sequences were aligned with the MUSCLE algorithm,¹⁴ and edited manually¹⁵ with stripping of gapped positions. Maximum-likelihood (ML) phylogenies were initially reconstructed using FastTree¹⁶ with the general time reversible model of nucleotide substitution. Statistical support of clades was initially assessed with local support values [Shimodaira–Hasegawa (SH) test] in FastTree.

Transmission clusters were defined as clades that included at least one sequence from a Latino patient, with short genetic distances ($\leq 1.5\%$ mean intracluster genetic distance difference), and supported by SH test $\geq 90\%$ and by confirmatory analyses. We reconstructed the initial ML tree using references available in the Los Alamos National Laboratory (LANL) HIV database (www.hiv.lanl.gov) using Viroblast¹⁷ to identify the top 10 related sequences for each study sequence ($n=244$ unique LANL sequences; sequences believed to be from the same study population were excluded). Any cluster formed by study sequences that was then disrupted by inclusion of the references was not considered robust. The clusters were further confirmed using the more computationally intensive RAXML v.7.0.4¹⁸ to construct an ML tree under the same model conditions. Trees were reconstructed first using the complete sequences and then evaluating the third-base codon position only (to assess false clustering due to convergent evolution if sequences share similar drug resistance mutations). Bootstrapping of 1,000 replicates was also performed on the complete sequence tree. Clusters with topology similar to the initially reconstructed clusters and involved in at least one sequences from a Latino patient were analyzed.

Statistical analyses

Our primary outcome was whether a Latino patient was a member of any transmission cluster. We assessed cluster composition by race/ethnicity, immigrant status, transmission risk group, and sex for both small clusters “pairs” ($n=2$ members) and larger clusters ($n \geq 3$ members). For immigrant Latinos, factors associated with membership in “local” clusters were evaluated. Local clusters were considered larger clusters (≥ 3 members) or pairs that involved U.S.-born Latinos, non-Latinos, or immigrants whose partnerships were reported to have formed after immigration (therefore probable transmission in NC) and remained with high branch support after inclusion of the LANL references. Differences in categorical variables were tested with the Pearson’s χ^2 test and continuous variables with the Kruskal–Wallis test. An exploratory predictive log binomial model was fit to the data, using variables found to be associated ($p < 0.20$) with the

outcome in bivariable analyses. Data were analyzed using Stata v.11.0 (StataCorp Corp., College Station, TX).

Results

Study population characteristics

Latinos were predominantly immigrant men with reported heterosexual risk. Overall, 147 (83%) Latinos were immigrants and 30 (17%) were U.S. born; 76% were men (Table 1). Most Latinos (73%) were antiretroviral (ART) naive at the time of sequence sampling [median sample year 2006 (IQR 2002–2009)] and 62% were sampled within a year following diagnosis [median year of diagnosis 2004 (IQR 2000–2007)]. The median age at diagnosis was 30 years (IQR 25–39). Immigrants were more likely to have lower CD4 counts at entry (median 190 vs. 301 cells/mm³; *p*=0.01) and report heterosexual risk (67% vs. 23%; *p*<0.001) than U.S.-born Latinos.

The reference group of non-Latinos (*n*=1496) was predominantly male (71%); 64% were black and 33% white. Less than half (46%) were ART naive at sampling and these patients included a larger proportion of patients diagnosed before 2000 [median year 1999 (IQR 1994–2004)]. TDR prevalence was similar across groups (9%).

Among the 147 Latino immigrants, 65% originated in Mexico and 32% in Central America (Table 1). The country of origin was unavailable in the medical records for three immigrants who were not interviewed. The median age at immigration was 25 years (IQR 19–31) and the median year

of first immigration was 1998 (IQR 1991–2002). Most (87%) were diagnosed in NC and a median of 6 years (IQR 2–10) elapsed from immigration to diagnosis. Only five patients were diagnosed outside the United States. Among the subset of the immigrants interviewed (*n*=87), 74% had not returned to their country of origin since first immigration and most (69%) perceived becoming HIV infected in the United States.

Composition of transmission clusters involving Latinos

Sequences from 53 (30%; 46 immigrant and 7 U.S. born) Latinos and 41 non-Latinos were identified in 32 discrete clusters containing at least one Latino sequence on the phylogenetic trees identified by FastTree and confirmed with RAxML (Fig. 1). A similar topology was noted when analyzing the third codon position (data not shown) indicating no false clustering due to similar drug resistance mutations. One additional cluster (*n*=2 sequences; bootstrap 92% RAxML) was noted in initial analyses but excluded because of disruption by the addition of LANL references. While most clusters were small (22 were pairs; labeled P1–P22 in Fig. 1), there were 10 larger clusters (C1–C10 in Fig. 1; five were triplets, three had *n*=4, one had *n*=5, and one had *n*=18 members). Nearly all sequences from Latinos and those involved in clusters (99%) were subtype B; two were subtype C (P12). There was no significant difference in cluster membership by immigrant status (31% immigrants vs. 23% U.S. born were in clusters; *p*=0.67). However, immigrants in clusters were more

TABLE 1. CHARACTERISTICS OF STUDY POPULATION OF 177 LATINOS AND THE REFERENCE GROUP OF 1,496 NON-LATINOS ENROLLED IN THE UNC CENTER FOR AIDS RESEARCH HIV CLINICAL COHORT

Variable	Latino group		Non-Latino reference group
	Immigrant n (%)	U.S. born n (%)	n (%)
Total	147	30	1496
Age <30 years at diagnosis	69 (47)	14 (47)	555 (37)
Male sex	109 (74)	26 (87)	1,056 (71)
Risk group			
MSM	39 (27)	17 (57)	604 (40)
Heterosexual	98 (67)	7 (23)	627 (42)
IDU	2 (1)	6 (20)	178 (12)
Other/unknown	8 (5)	0 (0)	87 (6)
Race/ethnicity			
Latino	147	29	—
White	—	—	501 (33)
Black	—	—	956 (64)
Other	—	—	39 (3)
HIV diagnosis year ≥2000	116 (79)	19 (63)	714 (48)
HIV sequence sampling year ≥2005	88 (60)	21 (70)	700 (47)
ART-naive sequence ^a	104 (73)	17 (59)	691 (46)
Transmitted drug resistance ^b	9 (9)	1 (6)	61 (9)
CD4 count <200 cells/mm ³ at clinic entry	77 (53)	8 (27)	582 (39)
Region of origin ^c			
Mexico	93 (65)	—	—
Central America ^d	45 (32)	—	—
South America/Caribbean ^e	6 (4)	—	—

^aAt time of sequence sampling.

^bAmong ART-naive sequences.

^cRegion of origin unavailable for three patients.

^dIncludes Costa Rica (2), El Salvador (13), Guatemala (9), Honduras (18), and Panama (3).

^eIncludes Columbia (2), Peru (2), and Dominican Republic (2).

MSM, men who have sex with men; IDU, injection drug use; ART, antiretroviral therapy.

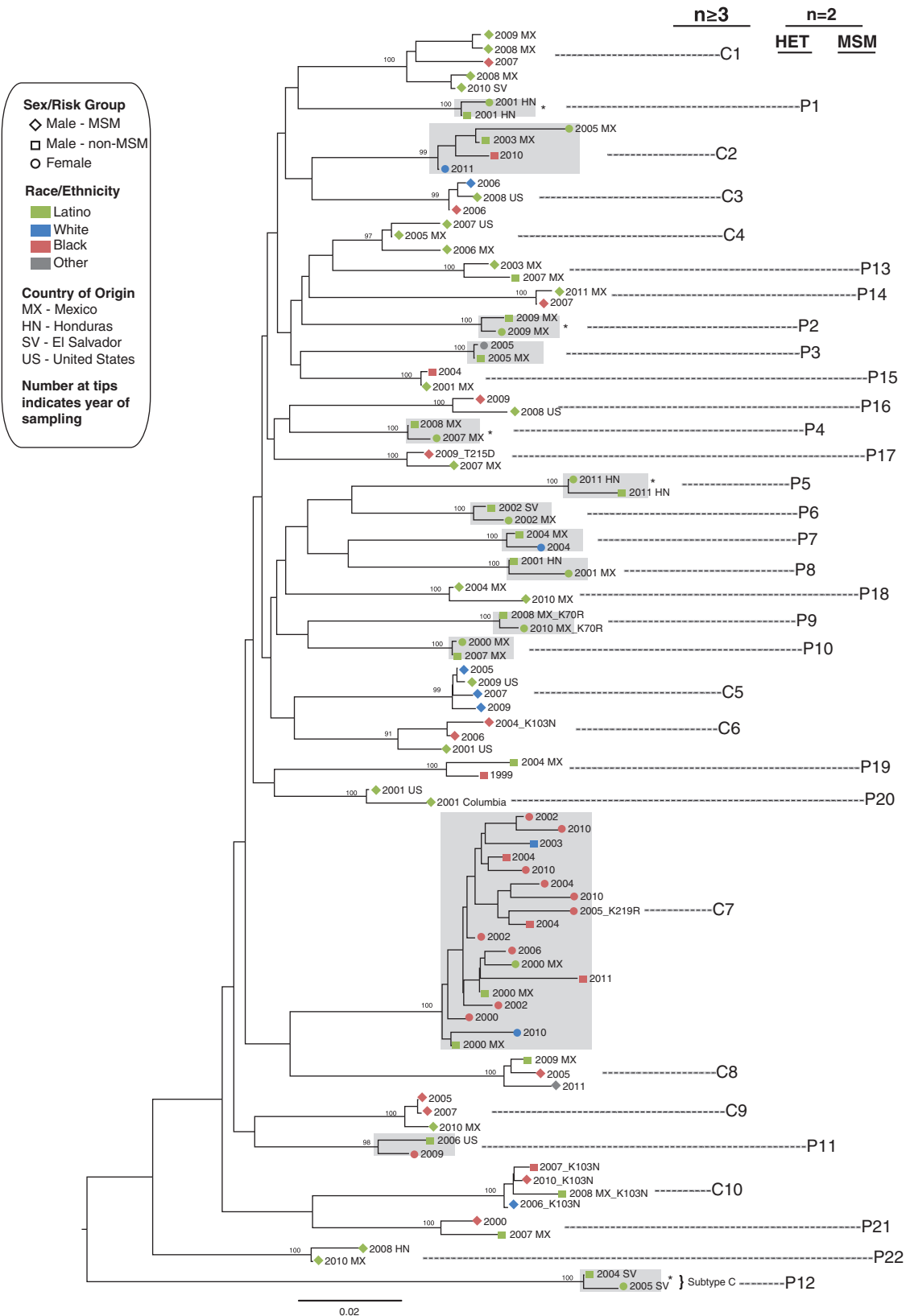


FIG. 1. Maximum-likelihood phylogenetic tree showing the HIV transmission clusters ($n=32$) involving ≥ 1 Latino sequences from initial tree built with sequences from 177 Latinos and 1496 non-Latinos (only clusters involving Latino sequences with bootstrap support $>90\%$ and supported by confirmatory analyses are shown here). Nodes defining clusters are labeled with bootstrap support generated by RAxML. Larger clusters ($n \geq 3$ members) are labeled C1–C10. Small cluster “pairs” ($n=2$ members) that are heterosexual (HET) are labeled P1–P12 and men who have sex with men (MSM) are labeled P13–P22. Sequences with transmitted drug resistance (TDR) are labeled with identified mutations. *Cluster pairs ($n=5$) involving partners immigrating from the same country and where partnerships began prior to immigration. Clusters involving women ($n=14$) are highlighted in *gray*.

likely to group with another Latino (78% vs. 29%; $p=0.02$) including 13 of 22 sequences in small clusters (pairs), 69% (9/13) of which were heterosexual pairing.

Among immigrants, all Latinas were in a cluster ($n=11$) and a similar proportion of MSM and heterosexual men (75% and 68%, respectively) were in clusters with other Latinos; overall, 76% (35/46) were in a cluster with another immigrant. Cluster composition by race/ethnicity and risk group varied by cluster size (Table 2). Small clusters (“pairs”; $n=2$ members) had a lower proportion of MSM and a higher proportion of immigrants compared to large clusters ($n \geq 3$). Of the 44 patients involved in the 22 pairs, 35 (80%) were Latinos, 91% of these were immigrants, and 73% were men. The nine non-Latinos members in these pairs included six men (all black) and three women (one black, one white, and one Native American).

Most pairs (12/22; 54%) were male–female pairs reporting heterosexual risk (P1–P12 in Fig. 1). These heterosexual pairs were predominantly composed of immigrants (9/12; 75%) and most were known partners; in seven of these the partners shared the same country of origin and in five the partnerships began prior to immigration and HIV diagnosis. These five pairs (P1, P2, P4, P5, and P12) were considered potential “nonlocal” clusters because HIV transmission may have occurred outside the United States prior to immigration. In the remaining 10 pairs (P13–P22) both individuals were men (including 14 Latinos and six black men), in six pairs both members endorsed MSM risk, in three clusters one man reported MSM risk and the other heterosexual risk (two were Latino), and in one both men reported heterosexual risk (one was Latino). In total, 71% (10/14) of Latino men in these male-only clusters reported MSM risk.

Ten larger clusters (≥ 3 members; C1–C10) were identified, which included sequences from 18 Latinos and 32 non-Latinos (23 black, 8 white, and 1 other). Immigrants who were in large clusters were more likely to have lived in the United States longer prior to diagnosis compared to immigrants who were not members of clusters or pairs [median 10 years (IQR 5–13) vs. 6 years (IQR 2–10); $p=0.03$]. These larger clusters also included a higher proportion of Latino MSM compared to Latinos who were not found in any cluster (mean % MSM 72% in large clusters vs. 27% not in any cluster; $p=0.02$). Only two larger clusters (C2 and C7) were

composed exclusively of heterosexuals. One of these clusters had 18 members (C7), 13 of whom were women. Two clusters composed only of men included a Latino man reporting heterosexual risk (C8 and C10). In total, 12% (5/42) of Latino men in any pair or cluster reported heterosexual risk but clustered with MSM or other men (behavioral data from three of these Latino men were obtained from an interview). One larger cluster of ART-naive MSM involved TDR (K103N mutation) among all four members (C10).

Latino immigrants in local HIV transmission clusters

Most of the Latino transmission clusters (85%) were considered local clusters and were further evaluated to explore factors associated with immigrant membership in local transmission chains (either through onward HIV transmission or acquisition). In the bivariable analysis, immigrants in local clusters were more likely to be diagnosed in NC (97% vs. 83%; $p=0.04$), report MSM risk (44% vs. 21%; $p=0.005$), reside in the United States longer before diagnosis (median 9 vs. 6 years; $p=0.01$), and be of Mexican origin (86% vs. 57%; $p=0.002$) (Table 3). CD4 count, RNA viral load, diagnosis year, or TDR was not associated with local cluster inclusion. In the multivariable model, younger age [risk ratio (RR) 2.34 (95% CI 1.47–3.73)], longer U.S. residence before diagnosis [RR 1.53 (95% CI 1.09–2.15) per 10 years], and originating in Mexico [RR 2.55 (95% CI 1.29–6.88)] remained independently associated with cluster membership among immigrants (Table 3).

Discussion

Our primary objective was to better understand HIV transmission patterns among Latinos residing in NC by combining HIV sequence and migration data. We found evidence for ongoing local HIV transmission after arrival for many Latino immigrants. Among the 147 immigrants in our study, 24% were identified in local transmission clusters after excluding those immigrants whose partnerships were reported prior to U.S. arrival. Immigrants in clusters were significantly more likely to be in clusters with other Latinos (76% with another immigrant Latino), indicating within-ethnicity transmission; however, sequences from immigrant and U.S.-born Latinos were equally likely to be in transmission clusters. Based on our

TABLE 2. COMPOSITION OF SMALL ($n=2$ MEMBERS) AND LARGE CLUSTERS ($n \geq 3$ MEMBERS CLUSTERS) INVOLVING LATINOS COMPARED TO LATINOS NOT FOUND IN CLUSTERS

Variable	No cluster	Clusters with ≥ 1 Latino		P ^a
		Small (pairs; $n=2$)	Large ($n \geq 3$)	
Total clusters, n	—	22	10	
Age ≤ 30 years at diagnosis, mean %	43%	59%	60%	0.81
Female, mean %	25%	27%	12%	0.19
MSM, mean %	27%	34%	72%	0.05
Race/ethnicity, mean %				
Latino	100%	80%	43%	0.001
Black	—	16%	37%	0.04
White	—	2%	17%	0.05
Latino Immigrant, mean %	81%	73%	31%	0.003

^a p -value represents comparisons between small and large clusters calculated with Kruskal–Wallis rank test. MSM, men who have sex with men.

TABLE 3. FACTORS ASSOCIATED WITH MEMBERSHIP IN LOCAL TRANSMISSION CLUSTERS INVOLVING LATINOS AMONG 147 LATINO IMMIGRANTS

Variable	In cluster	Not in cluster	P ^a	Adjusted ^b		
				RR	95% CI	p
Number of patients	36	111				
Age <30 years at diagnosis	21 (58%)	48 (48%)	0.12	2.34	1.47, 3.73	<0.001
Sex and transmission risk						
Female	6 (17%)	32 (29%)	0.02	Ref	Ref	Ref
MSM	16 (44%)	23 (21%)		1.58	0.73, 3.40	0.24
Male, non-MSM	14 (39%)	56 (50%)		1.01	0.45, 2.22	0.99
Mexican origin ^c	31 (86%)	62 (57%)	0.002	2.55	1.29, 6.88	0.01
Year of HIV diagnosis, median (IQR)	2005 (2001–2008)	2004 (1999–2007)	0.21	—	—	—
Years from migration to HIV diagnosis, ^d median (IQR)	9 (4–12)	6 (2–9)	0.01	1.53 ^e	1.09, 2.15	0.01
Diagnosed in North Carolina ^f	35 (97)	89 (83)	0.04	3.76	0.52, 27.27	0.52
CD4 count (cells/mm ³), ^g median (IQR)	219 (76–384)	182 (46–356)	0.23	—	—	—
Viral load (log ₁₀ copies/ml), ^g median (IQR)	4.9 (4.3–5.2)	4.7 (4.1–5.3)	0.31	—	—	—

^aUnadjusted *p*-value based on Pearson's χ^2 test for categorical variables and the Kruskal–Wallis test for continuous variables.

^bAdjusted log-binomial model includes age at diagnosis, sex and transmission risk, Mexican origin, years from migration to HIV diagnosis, and diagnosed in NC.

^cCountry of origin unavailable for three patients.

^dYear of immigration missing for 12 patients.

^ePer 10 year increments elapsed from first migration to diagnosis.

^fLocation of diagnosis missing for four patients.

^gFirst available at clinic entry.

RR, risk ratio; MSM, men who have sex with men; ART, antiretroviral therapy.

multivariable analysis, young Latino immigrants, those of Mexican origin, and those with longer periods of U.S. residence prior to diagnosis were more likely to be involved ongoing HIV transmission locally and thus may benefit from intensified prevention measures. Endorsing sex with men was not a significant predictor in the multivariable analysis.

Although most immigrants reported heterosexual risk, a higher proportion of MSM was identified in transmission clusters. Larger clusters (≥ 3 members) were also almost entirely composed of MSM; only two Latinas were identified among all the larger clusters. Higher HIV prevalence among established immigrant Latino MSM has been reported compared to U.S.-born and recently arrived immigrant Latino MSM, suggesting HIV acquisition after arrival.¹⁹ The phylogenetic analysis in our study not only shows such local transmission, but reveals characteristics of these cluster members. Although transmission directionality cannot be discerned, we identified within ethnicity transmission and clustering with non-Latinos. Larger clusters frequently included black MSM, a group of particular concern in the region as surveillance data reveal increasing HIV incidence rates in this group.²

Phylogenetic cluster analysis can also reveal probable HIV transmission routes that may be unidentified or misclassified by patient history. Therefore, these methods can help assess the degree of nondisclosure of MSM activity, a particular concern among immigrants as homosexuality and HIV remain stigmatized within Latino communities.^{20,21} In our study, a higher proportion of Latino men, most of whom were Mexican immigrants, reported heterosexual risk than expected compared to U.S. surveillance data in which MSM risk predominates among Mexican-born men.²² We found that 12% of Latino men who were cluster members reported heterosexual risk but were identified in clusters with only men or MSM

suggesting such evidence of nondisclosure, although this appears to be minimal. Thus, culturally appropriate prevention programs for immigrants who endorse sex with men and those who endorse sex with women are needed.

Most of the Latino clusters identified in this study likely represent an HIV transmission event that occurred locally and signify groups of ongoing HIV transmission. Five of the 32 clusters (16%) were pairs consisting of known heterosexual partners from the same originating country, and most of these persons reported the partnership predated immigration. All the Latinas in clusters, except for two, were identified in heterosexual pairs. The degree of local HIV transmission could be underestimated by excluding these pairs as "local clusters," as it is possible that transmission could have occurred prior to, during, or following immigration. The study is also limited by recall or reporting bias, as not all Latinos were interviewed for behavioral data. Our findings are also limited to NC where immigrants largely originate in Mexico.

Transmission patterns may vary by geographic location within the United States and by country/region of origin. Additionally, the limitations inherent to phylogenetic analyses can lead to a limited view of the actual/complete transmission network. Incomplete sampling of persons involved in transmission can result if these people are undiagnosed, receive care at another clinic, or never had a genotype. Unsampled third parties may also be involved in transmission, thereby preventing any inferences that can be made on a direct linkage between two individuals or the directionality of transmission. Our study is strengthened by the stringent criteria used to define clusters, including short branch lengths and high bootstrap values, and by the incorporation of a large number of sequences from non-Latinos from the region.

To date, few epidemiological studies have incorporated phylogenetic analyses to understand HIV transmission

patterns among immigrants or migrants^{23–25} and none has been specifically conducted among immigrant Latinos in the United States. Most prior studies have focused on regions with high HIV diversity, assessing clusters of HIV subtypes to evaluate linkages across borders due to migration²⁵ and importation of non-B subtypes through immigration in Europe.^{26–28} As subtype B predominates in the Americas, not surprisingly, only two sequences from Latinos in our study were non-B subtypes. Nevertheless, by incorporating migration data, such as originating country and migration dates, inferences can be made as to the degree that HIV transmission may have occurred locally or within ethnic groups in regions dominated by one subtype. Among heterosexual migrants in the Netherlands and former Dutch colonies, the majority with subtype B, phylogenetic analysis revealed that HIV transmission was found to occur primarily within ethnic groups.²³

In conclusion, our study reveals a previously undescribed view of HIV transmission among immigrant Latinos in a region characteristic of the southeastern United States. As in many areas of the southeast, new HIV diagnoses continue to be reported among Latinos and other racial/ethnic groups. Ongoing monitoring of phylogenetic and migration data may help better target prevention interventions. Interventions with a continued focus on early testing and linkage to care, particularly among young, Mexican immigrants, that consider the heterogeneity (i.e., diversity in originating countries and risk behaviors) among Latinos are needed. Molecular epidemiology studies conducted in the U.S. southeast and migrant sending communities in Mexico and Central America will also further inform the degree of HIV connection or relatedness between the two regions. Studies with broader geographic sampling in the United States could also be used to help better define population-level HIV transmission patterns among established immigrant and U.S.-born Latinos.

Sequence Data

A subset of sequences analyzed in this study is available in GenBank under accession numbers JX160108–JX161480.

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Author Disclosure Statement

No competing financial interests exist.

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