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HIV Transmission Dynamics among Foreign-born Persons in the United States

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Abstract

Background—In the United States (U.S.), foreign-born persons are disproportionately affected by HIV and differ epidemiologically from U.S.-born persons with diagnosed HIV infection. Understanding HIV transmission dynamics among foreign-born persons is important to guide HIV prevention efforts for these populations. We conducted molecular transmission network analysis to describe HIV transmission dynamics among foreign-born persons with diagnosed HIV.

Methods—Using HIV-1 polymerase nucleotide sequences reported to the U.S. National HIV Surveillance System for persons with diagnosed HIV infection during 2001–2013, we constructed a genetic distance based transmission network using HIV-TRACE and examined the birth region of potential transmission partners in this network.

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The findings and conclusion presented in this article are those of the authors and do not necessarily represent the views of the Centers for Disease Control and Prevention.

Results—Of 77,686 people, 12,064 (16%) were foreign-born. Overall, 28% of foreign-born persons linked to at least one other person in the transmission network. Of potential transmission partners, 62% were born in the United States, 31% were born in the same region as the foreign-born person, and 7% were born in another region of the world. The majority of transmission partners of male foreign-born persons (63%) were born in the United States, whereas the majority of transmission partners of female foreign-born (57%) were born in their same world region.

Discussion—These finding suggests that a majority of HIV infections among foreign-born persons in our network occurred after immigrating to the United States. Efforts to prevent HIV infection among foreign-born persons in the U.S. should include information of the transmission networks in which these individuals acquire or transmit HIV in order to develop more targeted HIV prevention interventions.

Keywords

Molecular; HIV; Transmission; Foreign-born

Background

In the United States, the foreign-born population is disproportionately affected by HIV. In 2010, foreign-born persons accounted for 16% of diagnosed HIV cases in the United States¹ while representing 13% of the population in the United States.² Data from the Centers for Disease Control and Prevention (CDC) show that among certain racial/ethnic groups, foreign-born persons account for a large proportion of individuals with a diagnosis of HIV infection.

Risk of HIV transmission differ among foreign-born and U.S.-born persons with a diagnosis of HIV infection, which may pose challenges to HIV prevention and care efforts for these persons. During 2007–2010, there was a larger proportion of women among foreign-born persons with diagnosed HIV, than among US-born persons. Among foreign-born men, almost 21% of HIV diagnoses was attributed to heterosexual contact, compared with 12% among US-born men.¹ These types of differences in HIV transmission patterns can have an impact in terms of accessing HIV prevention services if funding for HIV prevention activities in areas with a large foreign-born population is based on HIV transmission patterns among US-born individuals. These differences in HIV transmission patterns, coupled with data that indicate that a large proportion of foreign-born persons are likely being infected with HIV after migrating to the United States,^{3–5} also suggest that we need to better understand the context in which HIV transmissions are occurring among foreign-born populations.

Analyses of HIV-1 nucleotide sequence data allows us to understand how HIV spreads within and among groups, providing public health officials and health care professionals with opportunities to intervene.^{6–11} By building transmission networks based on HIV nucleotide sequence data, we can identify persons who have closely related sequences, indicating that they have a direct or indirect epidemiologic connection and represent potential transmission partners.¹¹ Exploring who are the potential transmission partners of foreign-born persons with a diagnosis of HIV infection in the United States may allow us to

determine whether transmissions involving this group occur primarily with other foreign-born persons or with U.S.-born persons. This information can help inform the design of HIV prevention interventions targeting foreign-born populations. For example, given that 40% of Hispanic/Latino foreign-born persons have difficulties communicating in English,¹² establishing through network analysis that a significant proportion of infections among this group occurs primarily with other Hispanic/Latino foreign-born persons, can justify the need to further develop culturally appropriate HIV prevention interventions in Spanish for this population.

Few studies have explored HIV transmission networks among foreign-born populations in the United States. A previous CDC analysis identified potential transmission links between HIV-diagnosed individuals in the United States and persons in other countries, but did not explore the extent and characteristics of those relationships.¹³ Another study focusing on HIV transmission patterns among Hispanics/Latinos in North Carolina showed that foreign-born Hispanics/Latinos were more likely to be in clusters with other Hispanics/Latinos compared to U.S.-born Hispanics/Latinos.¹⁴

Since 2001, the CDC's U.S. National HIV Surveillance System (NHSS) has funded the collection of HIV-1 nucleotide sequence data from persons with diagnosed HIV infection. In addition, NHSS also collects demographic, clinical, laboratory and HIV risk information from these persons. Using NHSS data, we describe HIV transmission networks among foreign-born persons with diagnosed HIV infection in the United States; explore factors associated with belonging to a transmission network, and potential transmission links to other foreign-born and U.S. born persons.

Methods

We analyzed HIV-1 pol nucleotide sequences and case surveillance data reported through NHSS for persons aged 13 years or older with HIV infection diagnosed during 2001–2013. Using a local installation of HIV-TRACE (www.hivtrace.org) we followed a previously described protocol^{11,16} to construct an HIV transmission network including the earliest available sequence per person; 80% of these sequences were obtained within 1 year since diagnosis. We also limited the analysis to sequences of at least 500 nucleotides. We aligned each HIV sequence to the HIV reference sequence HXB2 (positions 2253–2869), then conducted pairwise comparison of sequences to calculate Tamura-Nei 93 genetic distance,¹⁷ which is a measure of the differences between two sequences, and identified pairs that fell below 0.015 substitutions/site genetic distance. Pairs whose distance was below the threshold were considered potential transmission partners. After we identified the pairs meeting this criterion, we conducted analysis to understand characteristics of the network, sub-setting the dataset to focus on foreign-born persons overall and by region/sub region of birth.

Data on world region/sub region of birth was based on U.S. Census categorization² (Africa, Asia, Caribbean, Europe, Latin America, Other) with the “Other” region including countries in Oceania and North America (excluding the United States.), which had very few cases each. Data on sex assigned at birth (male/female), age (<13 y, 13–19 y, 20–29 y, 30–39 y,

40–49 y, 50–59 y, 60+ y), transmission category (male-to-male sexual contact [MSM], male-to-male sexual contact and injection drug use [MSM-IDU], injection drug use [IDU], heterosexual contact, other), population of area of residence at diagnosis (nonmetropolitan areas <50,000 population, metropolitan areas 50,000–499,999 population, metropolitan statistical areas [MSAs] 500,000 population, unknown), and U.S. regions (Northeast, Midwest, South and West) were collected through the NHSS using standard CDC classification schemes.¹⁸

Analysis

Descriptive analysis was conducted to characterize foreign-born persons with diagnosed HIV infection by demographic characteristics (including region of birth) and HIV transmission risk. Additional analysis was conducted to describe characteristics associated with membership in a transmission network. Foreign-born persons who linked to 1 other person were compared with foreign-born persons who did not link with anyone. A multivariate logistic regression model assessed factors associated with membership in a transmission cluster among foreign-born persons. The model included sex, age at HIV diagnosis, transmission category, population of area of residence at diagnosis, U.S. census region, and world region/sub region of birth. Finally, analysis was conducted to describe the number and proportion of potential transmission partners of foreign-born persons by world region of birth, gender, age, transmission category, area of residence, and U.S. census region. Three separate multivariate models assessed factors associated with a foreign-born person having a potential transmission partner born in the United States (versus not being born in the United States), born in their own world region (versus not born in their own world region), and born in another region of the world (versus born in the United States or in their own world region). For these last analyses, each potential transmission partner for a person was weighted based on the number of links associated with the person (k). The weight is simply $1/k$ for each of the k links. This procedure accounts for bias arising from persons with multiple links.¹¹

Results

We identified 77,686 HIV-1 nucleotide sequences that met our inclusion criteria, 12,064 (16%) of which belonged to foreign-born persons. (Table 1) Of the foreign-born persons with sequences included in this analysis, 6696 (56%) were born in Latin America, 1839 (15%) were born in Africa, 1746 (14%) were born in the Caribbean, 1164 (10%) were born in Asia, 503 (4%) were born in Europe, and 116 (1%) were born in other regions. Seventy-five percent of foreign-born persons with sequences were male, 62% were 20–39 years of age, 46% were MSM, 93% resided in a population of area of residence at diagnosis <500,000, and were divided almost equally among the Northeast (34%), South (33%), and West (29%) regions of the United States.

Membership in a transmission cluster

Overall, 28% of foreign-born persons included in our analysis linked to 1 other person/s. (Table 2) Foreign-born persons from Europe (44%) and Asia (39%) had the highest proportion of persons with 1 or more links (besides persons born in other regions). A higher

proportion of foreign-born males (34%) than foreign-born females (11%) were in transmission clusters. By age at HIV diagnosis, foreign-born persons 20–29 years of age (37%) had the highest proportion of members in transmission clusters, whereas by transmission risk, foreign-born MSM had the highest proportion of members in transmission clusters (43%). Finally, foreign-born persons that resided in a population of area of residence at diagnosis < 500,000 (39%), and persons residing in the western region of the United States (37%) had the highest proportion of members in transmission clusters.

Factors associated with membership in a transmission cluster

Controlling for other variables in the multivariate model, factors associated with a significantly higher likelihood of membership in a transmission cluster included being born in Latin America, the Caribbean, Asia, Europe, and in other regions compared with being born in Africa; being younger than 60 years old; being male; being an MSM or MSM IDU compared with being heterosexual; and residing in the Northeast or West regions of the country compared with residing in the South. (Table 2)

Place of birth of potential transmission partners

When examining place of birth of potential transmission partners of foreign-born individuals with HIV diagnosed in the United States, our data indicated that 62% of potential transmission partners were born in the United States, 31% were born in the same region as the foreign-born persons, and 7% were born in another region of the world. Differences existed in terms of place of birth of potential transmission partners among foreign-born populations. Our results indicate that place of birth of potential transmission partners for individuals born in Africa were almost equally split between born in the United States (48%) and born in Africa (43%). For persons born in Latin America, the Caribbean, Asia, Europe, and Other regions the majority of potential transmission partners were born in the United States (60%, 65%, 68%, 79%, and 79% respectively). (Table 3)

The majority of transmission partners of male foreign-born persons (63%) were born in the United States, whereas the majority of transmission partners of female foreign-born (57%) were born in their same world region. By age at HIV diagnosis of foreign-born individuals, our results show that for all age groups the majority of transmission partners were born in the United States; however, when examining place of birth of potential transmission partners by transmission category, our data shows that the majority of transmission partners of heterosexual foreign-born individuals (52%) were born in their same world region, whereas the majority of transmission partners of IDU, MSM, MSM-IDU, and Other foreign-born individuals were born in the United States (67%, 66%, 81%, and 51% respectively). Finally, when examining population of area of residence at diagnosis and U.S. census region of residence of foreign-born individuals, our data shows that the majority of transmission partners for all categories in these two variables that describe residence status, were born in the United States. (Table 3)

Factors associated with place of birth of potential transmission partner

The model assessing factors associated with foreign-born individuals having a potential transmission partner born in the United States showed that foreign-born individuals from

Europe were more likely to have a transmission partner born in the United States compared with African-born individuals, as were foreign-born MSM and MSM-IDU compared with heterosexuals. While foreign-born individuals residing in the Northeast were less likely to have a partner born in the United States compared with individuals residing in the South. (Table 4)

The analysis of factors associated with foreign-born individuals having a potential transmission partner from their same world region showed that foreign-born individuals from Asia, the Caribbean, and Latin America were less likely to have a partner from their same world region compared with African-born individuals. Foreign-born males (compared with females), and foreign-born MSM and MSM-IDU (compared with heterosexuals) were also less likely to have a partner from their same world region. (Table 4)

Finally, the analysis of factors associated with foreign-born individuals having a potential transmission partner from another region of the world showed that foreign-born individuals from Latin America were less likely to have a partner from another region of the world compared with African-born individuals, whereas foreign-born MSM and foreign-born residing in the Northeast and Western regions of the United States were more likely to have a transmission partner from another region compared with foreign-born heterosexuals and foreign-born residing in the Southern region of the United States, respectively. (Table 4)

Discussion

We found that most foreign-born persons with diagnosed HIV infection who had a potential transmission partner in our network were partners with US-born persons, suggesting that HIV transmission among foreign-born persons in the United States occurs primarily with US-born persons. This finding suggests that a majority of HIV infections among foreign-born persons in our network occurred after immigrating to the United States. Previous studies in the United States indicating that immigrant populations are more than likely infected with HIV after immigration have focused on specific populations, have been limited in their geographic scope, and have used methods other than transmission network analysis.^{3,14,19,20,21} Our findings using national data corroborate and expand on findings from these smaller studies.

Although the majority of HIV transmissions among foreign-born persons in the United States occur with US-born persons, persons born in Africa and Latin America shared the same birth region with a large proportion of their potential transmission partners. This may partially be explained by immigration patterns among these groups, which according to U.S. Census data have been very active in the last 25 years, with more than 50% of immigrants from Africa and Latin America immigrating to the United States after 1990.² It is possible that individuals from these areas arrived to the United States infected with HIV (knowingly or unknowingly) with transmission partners also infected with HIV, or that the availability of larger numbers of potential sexual partners from their own regions, with whom these individuals shared culture and language, was a facilitator for new immigrants to get infected or infect others in their newly established sexual networks. HIV transmission links among foreign-born sharing the same language have been reported previously,¹³ indicating that

shared culture and language is a possible path that facilitates HIV transmission among foreign-born individuals.

Our analysis also indicated that foreign-born women and heterosexuals were more likely to have potential transmission partners from their own regions. Because HIV in the United States is concentrated among MSM, the risk of acquiring HIV in the United States is lower for heterosexuals than it is for MSM. Whether HIV infections among foreign-born women are occurring before or after immigration is unclear, although research on HIV prevention among African-born foreign-born persons indicates high levels of knowledge regarding HIV transmission routes,²² potentially indicating exposure to HIV-related issues prior to arriving in the United States. If infections among foreign-born females are occurring in the United States within sexual networks with partners from their same world region, it might be an indication of a lack of awareness of personal risk regarding HIV, which has been documented in research focusing on HIV prevention among foreign-born persons.²³ Immigration status may also play a role in placing women at risk. Wariness of initiating HIV care due to fears related to immigration status has already been reported among African foreign-born persons;²⁴ these same fears may be preventing foreign-born women from accessing basic HIV prevention services, such as HIV counseling and testing. More research needs to be conducted in order to better ascertain where and how foreign-born women are getting infected with HIV, but public health officials in communities with large female foreign-born populations should consider developing HIV prevention messages that are culturally and linguistically appropriate, and delivering them through venues where foreign-born populations have reported feeling secure, such as schools, churches, and community centers.²⁵

Although the updated National HIV/AIDS Strategy: Updated to 2020 (NHAS 2020)²⁶ does not specifically mention foreign-born MSM as a priority population, foreign-born MSM were almost 15% of all MSM receiving an HIV diagnosis between 2007–2010.¹ Research indicates that some foreign-born MSM may be, as of recently, engaging in high-risk sexual behaviors such as oral and anal sex without condoms, using illegal substances before or during sex, and exposing themselves to body fluids during sex.²⁷ Our finding that more than two thirds of all foreign-born MSM and MSM-IDU in transmission clusters had US-born transmission partners has important implications for the development of HIV prevention campaigns targeting these men, as it implies that the majority of HIV infections among foreign-born MSM might be occurring in the United States. Public health professionals developing HIV prevention campaigns or interventions targeting MSM in the United States need to strategize how to include foreign-born MSM as potential targets of these campaigns given their active participation in MSM transmission clusters in this country. Research indicates that prevalence of HIV among some foreign-born MSM increases as years after immigration increase,^{28, 29, 30} suggesting that infections occur soon after they have immigrated to the United States. It has been suggested that this increased risk of HIV infection early after their arrival to the United States might be occurring because of the lack of effective HIV prevention campaigns targeting foreign-born MSM in their countries of origin, and because many foreign-born MSM migrate to the United States so that they can experience sexual and lifestyle freedoms.²⁷ These factors make the timing in which HIV prevention interventions reach these men a crucial factor to consider. HIV prevention staff

working in communities with high prevalence of HIV among MSM that also have a large foreign-born population may want to first focus their HIV prevention activities targeting foreign-born MSM on social networks or venues that include both foreign-born and US-born MSM as opposed to social networks or venues that are predominately attended by foreign-born persons. HIV prevention activities targeting these men should be targeted at places where they feel comfortable and accepted by other MSM (both foreign-born and non-foreign born), such as gay bars, adult bookstores, bathhouses, high-traffic streets in gay neighborhoods, parks, beaches, gay pride festivals, and dance parties for gay men. Interventions for these men should focus on delivering culturally appropriate messages²³ that discuss their risk for HIV infection, their need for testing frequently for HIV, and ways in which they can protect themselves, including nonoccupational postexposure prophylaxis (nPEP)³¹ and pre-exposure prophylaxis (PrEP).³² Referrals to health care providers should also be part of these interventions, not only because health care providers can prescribe the medication required for nPEP or PrEP, but also because of research associating recent HIV testing among foreign-born MSM with having seen a health care provider and disclosing male to male attraction/sexual behavior to a health care provider.²⁹

Limitations

This analysis is subject to several limitations. First, given that only certain states/cities in the United States have been funded to collect nucleotide sequence data, our analysis may be affected by selection bias. Foreign-born individuals from other state/cities not included in our analysis may differ in terms of their participation in HIV transmission networks and potential transmission links to other foreign-born and U.S. born persons, compared to participants in our analysis. Nonetheless, some of the states/cities funded have the largest proportions of foreign-born persons in the United States as well as the highest burden of HIV (e.g., New York, California, Texas, and Florida).^{*} Second, although others have used different thresholds to calculate the Tamura-Nei 93 genetic distance between two sequences,³³ the decision to use the 0.015 threshold was based on previous molecular transmission analyses of NHSS data, which reported robust results using this threshold even when comparing results using different thresholds (0.010 & 0.020).^{11,13} Third, some foreign-born persons travel home seasonally and may have partners there. If these persons also had a link to someone in the US and were therefore included in the analyses of where foreign-born persons' partners were from, this would result in an overestimate of the proportion of foreign-born persons with a US contact. Fourth, transmission category is based on self-reported data, and failure to report certain HIV risk behaviors could affect inferences about routes of transmission. This might be particularly relevant for some foreign-born marginalized populations who might not report accurately their HIV risk behaviors. When missing, transmission category was imputed, which could affect our estimates. Fifth, even

Note: States/cities contributing data include Alabama, Alaska, Arizona, Arkansas, California, Chicago, Colorado, Connecticut, Delaware, District of Columbia, Federation of Micronesia, Florida, Georgia, Guam, Hawaii, Houston, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Los Angeles, Louisiana, Maine, Marshall Islands, Maryland, Massachusetts, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New Mexico, New York, New York City, North Carolina, North Dakota, Northern Mariana Islands, Ohio, Oklahoma, Oregon, Palau, Pennsylvania, Philadelphia, Puerto Rico, Rhode Island, Samoa, San Francisco, Seattle-King County, South Carolina, South Dakota, Tennessee, Texas, Utah, Vermont, Virgin Islands, Virginia, Washington, West Virginia, Wisconsin, Wyoming

though 80% of sequences were obtained within 1 year since diagnosis, HIV testing targeting MSM in the United States has intensified as a result of NHAS, which may lead to the detection of more recent infections among foreign-born MSM, thus, the greater likelihood of identifying them in clusters. It is possible that other foreign-born populations such as African foreign-born persons might have been either infected earlier, infected prior to arrival, or in more sparsely sampled networks, and that is why they cluster less frequently. Finally, although we have identified potential transmission links between persons, we cannot establish direct transmission links between any two persons or assess directionality of transmission. However, it is still possible to draw conclusions from a large number of potentially indirect links.

Conclusion

Our study describes potential HIV transmission links among diverse foreign-born populations in the United States. Continued monitoring of transmission network data coupled with collection of migration data should help public health officials seeking to address NHAS objectives to develop HIV prevention interventions targeting foreign-born populations that are disproportionately affected by HIV.

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Table 1
CHARACTERISTICS OF PERSONS DIAGNOSED WITH HIV WITH SEQUENCES AVAILABLE, BY LOCATION OF BIRTH, UNITED STATES, 2001–2013

Characteristics	Africa N= 1839		Asia N=1164		Caribbean N= 1746		Europe N= 503		Latin America N= 6696		Other N= 116		Total Foreign-born N= 12,064		US-born N=65,622		Total N= 77,686		
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	
Sex																			
Female	1051	57%	160	14%	749	43%	66	13%	1022	15%	11	9%	3059	25%	15332	23%	18391	24%	
Male	788	43%	1004	86%	997	57%	437	87%	5674	85%	105	91%	9005	75%	50290	77%	59295	76%	
By age at diagnosis																			
13–19y	49	3%	21	2%	53	3%	7	1%	161	2%	4	3%	295	2%	4427	7%	4722	6%	
20–29y	432	23%	318	27%	344	20%	145	29%	2065	31%	22	31%	3326	28%	22962	35%	26288	34%	
30–39y	709	39%	463	40%	454	26%	174	35%	2361	35%	37	35%	4198	35%	17364	27%	21562	28%	
40–49y	436	24%	261	22%	467	27%	129	26%	1425	21%	40	21%	2758	23%	13705	21%	16463	21%	
50–59y	171	9%	84	7%	302	17%	29	6%	523	8%	7	8%	1116	9%	5672	9%	6788	9%	
60+y	42	2%	17	1%	126	7%	19	4%	161	2%	6	2%	371	3%	1492	2%	1863	2%	
By transmission category																			
Heterosexual females	552	30%	99	9%	492	28%	32	6%	567	8%	3	3%	1745	14%	8509	13%	10254	13%	
Heterosexual males	243	13%	79	7%	379	22%	29	6%	496	7%	5	4%	1231	10%	4430	7%	5661	7%	
IDU-females	11	1%	6	1%	12	1%	3	0%	26	0%	1	1%	59	1%	2405	4%	2464	3%	
IDU-males	11	1%	24	2%	19	2%	11	2%	103	2%	1	1%	169	1%	3159	5%	3328	4%	
MSM	166	9%	706	61%	355	20%	307	61%	3974	59%	90	78%	5598	46%	33946	52%	39544	51%	
MSM IDU	6	0%	29	2%	10	1%	30	6%	153	2%	6	5%	234	2%	3139	5%	3373	4%	
Other	850	46%	221	19%	479	27%	91	18%	1377	21%	10	9%	3028	25%	10034	15%	13062	17%	
Population of area of residence at diagnosis																			
Metropolitan Areas (50,000–499,999)	81	4%	63	5%	66	4%	23	5%	302	5%	2	2%	537	5%	8427	13%	8964	12%	
Metropolitan Statistical Area (< 500,000)	1712	93%	1069	92%	1648	94%	468	93%	6261	94%	109	94%	11267	93%	55068	84%	66335	85%	
Non-Metropolitan Areas (<50,000)	10	1%	4	0%	10	1%	3	0%	87	1%	1	1%	115	1%	1922	3%	2037	3%	
Unknown	36	2%	28	2%	22	1%	9	2%	46	0%	4	3%	145	1%	205	0%	350	0%	
U.S. Census region																			

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Characteristics	Africa N= 1839		Asia N=1164		Caribbean N= 1746		Europe N= 503		Latin America N= 6696		Other N= 116		Total Foreign-born N= 12,064		US-born N=65,622		Total N= 77,686	
	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%	N	%
Midwest	154	8%	68	6%	18	1%	18	4%	188	3%	2	2%	448	4%	5726	9%	6174	8%
Northeast	592	32%	400	34%	850	49%	233	46%	1952	29%	33	28%	4060	34%	14484	22%	18544	24%
South	638	35%	200	17%	826	47%	88	17%	2141	32%	26	22%	3919	32%	33951	52%	37870	49%
West	426	23%	472	41%	33	2%	155	31%	2381	36%	52	45%	3519	29%	11282	17%	14801	19%

TABLE 2
CHARACTERISTICS ASSOCIATED WITH MEMBERSHIP IN A TRANSMISSION CLUSTER AMONG FOREIGN-BORN PERSONS, UNITED STATES, 2001–2013

Characteristics	0 Links		1 + Links		Prev. Ratio (adjusted)	95% CI
	N	Row %	N	Row %		
Total	8,679	72%	3,385	28%		
World region/sub region						
Africa	1683	91%	156	8%	ref	ref
Asia	711	61%	453	39%	2.5*	2.0 2.9
Caribbean	1502	86%	244	14%	1.5*	1.2 1.7
Europe	284	56%	219	43%	2.7*	2.2 3.2
Latin America	4436	66%	2260	34%	2.2*	1.8 2.5
Other	63	54%	53	46%	2.6*	2.1 3.4
Sex						
Female	2736	89%	323	11%	ref	ref
Male	5943	66%	3062	34%	1.4*	1.2 1.6
Age at diagnoses						
13–19y	208	70%	87	29%	2.0*	1.4 2.7
20–29y	2086	63%	1240	37%	2.0*	1.5 2.7
30–39	3030	72%	1168	28%	1.6*	1.2 2.1
40–49	2139	78%	619	22%	1.4*	1.1 1.9
50–59	889	80%	227	20%	1.5*	1.1 2.1
60+	327	88%	44	12%	ref	ref
Transmission category						
Heterosexual	2622	88%	354	12%	ref	ref
IDU	190	83%	38	17%	1.0	0.7 1.3
MSM	3170	57%	2428	43%	2.0*	1.8 2.3

Characteristics	0 Links		1 + Links		Prev. Ratio (adjusted)	95% CI	
	N	Row %	N	Row %		1.5	2.2
MSM+IDU	141	60%	93	40%	1.8*	0.9	1.2
Other	2556	84%	472	16%	1.1	0.9	1.2
Population of area of residence at diagnosis							
Metropolitan Areas (50,000–499,999)	405	75%	132	25%	1.3	0.9	2.1
Metropolitan Statistical Area (500,000)	8052	71%	3215	29%	1.4	0.9	2.1
Non-Metropolitan Areas (<50,000)	96	83%	19	16%	ref	ref	ref
Unknown	126	87%	19	13%	0.8	0.5	1.5
U.S. census region							
Midwest	351	78%	97	22%	1.0	0.9	1.2
Northeast	2929	72%	1131	28%	1.2*	1.1	1.3
South	3088	80%	831	21%	ref	ref	ref
West	2208	63%	1311	37%	1.2*	1.1	1.3

* Significant at p 0.05

TABLE 3

CHARACTERISTICS ASSOCIATED WITH LOCATION OF BIRTH OF POTENTIAL TRANSMISSION PARTNER OF HIV-INFECTED FOREIGN-BORN PERSONS, UNITED STATES, 2001–2013.

	Partner from the United States	Partner from the same region	Partner from another region
Characteristics	N (%)	N (%)	N (%)
Total	2104 (62)	1042 (31)	239 (7)
World region/sub region			
Africa	76 (48)	67 (43)	13 (9)
Asia	306 (68)	74 (16)	74 (16)
Caribbean	158 (65)	71 (29)	15 (6)
Europe	173 (79)	13 (6)	34 (15)
Latin America	1351 (60)	814 (36)	95 (4)
Other	42 (79)	3 (6)	8 (15)
Sex			
Female	123 (38)	185 (57)	16 (5)
Male	1982 (63)	858 (28)	223 (7)
Age at diagnosis			
13–19y	55 (64)	28 (33)	3 (3)
20–29y	819 (66)	343 (28)	78 (6)
30–39	707 (60)	370 (32)	91 (8)
40–49	380 (62)	192 (31)	46 (7)
50–59	119 (52)	92 (41)	16 (7)
60+	23 (52)	17 (39)	4 (9)
Transmission category			
Heterosexual	156 (44)	185 (52)	12 (4)
IDU	25 (67)	12 (30)	1 (3)
MSM	1609 (66)	632 (26)	187 (8)
MSM+IDU	75 (81)	11 (12)	7 (8)
Other	239 (51)	203 (43)	31 (6)
Population of area of residence at diagnosis			
Metropolitan Areas (50,000–499,999)	90 (68)	37 (28)	6 (4)
Metropolitan Statistical Area (< 500,000)	1990 (62)	993 (31)	232 (7)
Non-Metropolitan Areas (<50,000)	15 (78)	4 (22)	0 (0)
Unknown	10 (52)	9 (45)	1 (3)
U.S. census region			
Midwest	74 (76)	21 (22)	2 (2)
Northeast	680 (60)	245 (31)	105 (9)
South	540 (65)	263 (32)	28 (3)
West	804 (61)	405 (31)	102 (8)

TABLE 4
FACTORS ASSOCIATED WITH LOCATION OF BIRTH OF POTENTIAL TRANSMISSION PARTNER OF HIV-INFECTED FOREIGN-BORN PERSONS, UNITED STATES, 2001–2013.

Characteristics	Partner from the United States		Partner from the same region		Partner from another region	
	Prevalence Ratio (adjusted)	95% CI	Prevalence Ratio (adjusted)	95% CI	Prevalence Ratio (adjusted)	95% CI
World region/sub region						
Africa	REF	REF	REF	REF	REF	REF
Asia	0.58	0.95–1.16	0.49*	0.37–0.64	1.47	0.82–2.67
Caribbean	1.05	0.97–1.21	0.75*	0.58–0.97	0.64	0.31–1.33
Europe	1.08*	1.01–1.24	0.18*	0.10–0.32	1.38	0.74–2.58
Latin America	1.12	0.90–1.09	1.08	0.90–1.29	0.41*	0.23–0.73
Other	0.99	0.97–1.30	0.19*	0.06–0.57	1.31	0.57–3.03
Sex						
Female	REF	REF	REF	REF	REF	REF
Male	1.13*	1.04–1.23	0.72*	0.62–0.82	0.99	0.53–1.84
Age at diagnosis						
13–19y	1.09	0.91–1.30	0.89	0.58–1.37	0.49	0.11–2.06
20–29y	1.07	0.92–1.25	0.89	0.64–1.24	0.65	0.23–1.77
30–39	1.04	0.89–1.21	1.02	0.73–1.41	0.76	0.28–2.07
40–49	1.05	0.90–1.23	0.96	0.69–1.34	0.72	0.26–1.98
50–59	1.02	0.86–1.20	1.09	0.77–1.53	0.74	0.25–2.17
60+	REF	REF	REF	REF	REF	REF
Transmission category						
Heterosexual	REF	REF	REF	REF	REF	REF
IDU	1.14	0.97–1.33	0.65	0.40–1.05	0.81	0.11–5.66
MSM	1.11*	1.03–1.19	0.61*	0.52–0.71	2.05*	1.06–3.95
MSM+IDU	1.17*	1.06–1.31	0.32*	0.18–0.56	1.80	0.70–4.65
Other	1.04	0.96–1.13	0.87	0.76–1.01	1.66	0.86–3.21

Characteristics	Partner from the United States		Partner from the same region		Partner from another region	
	Prevalence Ratio (adjusted)	95% CI	Prevalence Ratio (adjusted)	95% CI	Prevalence Ratio (adjusted)	95% CI
Population of area of residence at diagnosis						
Metropolitan Areas (50,000–499,999)	REF	REF	REF	REF	REF	REF
Metropolitan Statistical Area (500,000)	0.99	0.91–1.07	1.02	0.77–1.34	1.24	0.54–2.83
Non-Metropolitan Areas (<50,000)	1.06	0.86–1.29	0.89	0.39–2.01	0.00	0
Unknown	1.25	0.82–1.90	0.78	0.14–4.29	0.00	0
U.S. census region						
Midwest	1.03	0.95–1.12	0.74	0.51–1.09	0.55	0.14–2.15
Northeast	0.95*	0.91–0.99	1.03	0.91–1.16	2.14*	1.42–3.24
South	REF	REF	REF		REF	REF
West	0.96	0.92–1.01	1.11	0.99–1.26	1.80	1.19_2.73

* Significant at p 0.05