


Evidence of Local HIV Transmission in the African Community of King County, Washington

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Abstract Little is known about the frequency of ongoing HIV transmission within U.S. African immigrant communities. We used HIV surveillance and partner services data to describe African-born persons newly reported with HIV infection in King County (KC), WA from 1/1/2010 to 12/31/2013. We performed phylogenetic clustering analysis of HIV-1 pol to identify putative transmission events within this population. From 2010 to 2013, 1148 KC adults were reported with HIV, including 102 (9 %) born in Africa. Forty-one African-born cases were interviewed and reported diagnosis after arrival in the U.S. Fourteen (34 %) reported ≥ 1 negative test prior to diagnosis, and 9 (26 %) reported ≥ 1 negative test after U.S. arrival. Pol genotypes were available for seven of these nine. For two of these seven, a KC case was the nearest phylogenetic neighbor; two others were infected with subtype B virus. We found substantial evidence of ongoing HIV transmission in the African community of KC.

Keywords Migrants · HIV · African · Subtypes · Immigrants

Introduction

There is increasing recognition of the disproportionately large impact of HIV on African-born residents of the U.S. [1–4] Previous studies and surveillance data suggest that the HIV epidemic among African-born people in the U.S. reflects the epidemic in Africa: primarily heterosexual transmission, with a much larger proportion of HIV-infected women than has been observed in other populations in the U.S. [1–6] While many HIV-infected African people diagnosed in the U.S. were likely exposed to HIV before arriving in this country, data from Western Europe suggest that there is some level of local transmission within African migrant destination countries, including the U.S. [7–10] Molecular epidemiology can complement clinical and surveillance data to provide additional insight into the region of HIV exposure. [11, 12] We undertook the current study both to estimate the degree of local HIV transmission in newly diagnosed African-born people reported with HIV, and to describe HIV testing patterns in this population, in King County (KC), WA.

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Methods

In WA, providers, medical facilities and laboratories are required to report HIV diagnoses to the local health jurisdiction. In KC, Public Health–Seattle and KC (PHSKC) collects genotypic sequences from WA laboratories conducting genotypic sequencing for the Molecular HIV Surveillance component of the National HIV Surveillance

Table 1 Participant characteristics: Total reported, not previously diagnosed, and interviewed for partner services, African-born PLWHA in King County, WA, 2010–2013

Patient characteristic	Total N = 97		Total not previously diagnosed N = 61		Interviewed N = 48	
	N or mean (median)	% (or range)	N or mean (median)	% (or range)	N or mean (median)	% (or range)
Gender						
Men	35	36.1	24	39.3	20	41.6
Women	62	63.9	37	60.7	28	58.3
Age, years	41.8	22.3–62.4	42.3	23.1–62.2	42.2	23.1–62.2
Years from arrival in the U.S. to HIV case report	4.6 (0.6)	8 days– 26.7 years	6.9 (5.1)	8 days– 26.7 years	7.3 (5.7)	8 days– 26.7 years
Region of birth^a						
East Africa	83	85.6	50	82.0	39	81.3
West Africa	8	8.3	6	9.8	5	10.4
Middle Africa	4	4.1	3	4.9	3	6.3
Southern or North Africa	2	2.0	2	3.2	1	2.1
HIV transmission category						
Heterosexual sexual contact	11	11.3	8	13.1	6	12.5
No risk reported or no risk identified	84	86.6	51	83.6	40	83.3
Male to male sexual contact	3	3.1	2	3.3	2	4.2
HIV subtypes^b						
A1	14	23.3	13	28.9	10	28.6
B	3	5.0	3	6.7	3	8.6
C	34	56.7	21	46.7	15	42.9
D or G	4	6.7	4	8.9	4	11.5
CRF02AG	5	8.3	4	8.9	3	8.6

Includes cases ≥ 18 years of age diagnosed on or after Nov 1 2009

^a Categorization of region based on United Nations Statistics Division classification of continental regions [16]

^b N for subtypes: Total = 60, Total not previously diagnosed = 45, Interviewed cases = 35

Table 2 Morbidity and mortality outcomes for African-born PLWHA in King County, WA, 2010–2013

Outcome	Total N = 97		Interviewed N = 48	
	N or mean	% or range	N or mean	%
Diagnosed with AIDS within 3 months of HIV diagnosis	38	39.2	25	52.1
Death during study period	1	1.0	0	0
First CD4 count $< 200^a$	31	33.3	21	44.7
Mean CD4 count at diagnosis (median) ^a	305 (289)	7-991	279 (234)	7-991

^a Four patients overall and 1 interviewed were missing CD4 count at diagnosis

System. The HIV/AIDS case report includes country of birth, time since arrival in U.S., and self-reported HIV testing history.

PHSKC routinely offers persons newly reported with HIV assistance with partner notification. Foreign-born persons are asked questions about HIV testing history after

arrival in the U.S., and sexual behavior related to travel abroad. Non-English speaking patients are interviewed with a telephone interpretation service.

We analyzed surveillance and partner services interview data for adults (18 years or older newly reported with HIV in KC from 2010 to 2013). We used CDC HIV surveillance

Table 3 Reason for HIV testing and previous HIV testing history among interviewed, newly diagnosed PLWHA, King County, WA, 2010–2013

	Women N = 25		Men N = 16		Total N = 41	
	N	%	N	%	N	%
Reason for HIV testing at time of diagnosis ^a						
Symptoms/illness	8	36.4	8	53.3	16	43.2
Routine testing or provider recommended testing	6	27.3	2	13.3	8	21.6
Exposed to HIV	5	22.7	1	6.7	6	16.2
Prenatal screening	1	4.6	0	N/A	1	2.7
Other	2	9.1	4	26.7	6	16.2
Any negative HIV test prior to diagnosis	10	40.0	4	25.0	14	34.2
Any negative test before arriving in US ^b	8	36.4	3	23.0	11	28.6
Previous negative HIV test in U.S. ^c	7	31.8	2	16.7	9	26.4

N/A Not applicable

^a Four patients (three women and one man) were missing reason for testing and are excluded

^b Six patients (three women and three men) were missing information on testing before arrival in the U.S. and are excluded

^c Seven patients (three women and four men) were missing date of U.S. arrival and are excluded

definitions for HIV transmission categories. We present descriptive statistics.

HIV Gene Sequence Analysis

Phylogenetic analyses are now a common approach to studying HIV transmission, as viruses with closely related gene sequences can be inferred to represent transmission clusters. We used phylogenetic analysis of HIV gene sequences to identify potential transmission clusters that may represent local transmission among African-born residents. We used a longer timeframe for this analysis than for our analyses with HIV surveillance and partner services data (2010–2013), including HIV *pol* sequences collected between January 1, 2008 and February 28, 2014. See digital supplemental content for more detailed information about our analysis.

We identified phylogenetic clusters as ≥ 2 sequences with a shared ancestral node, and assessed the robustness of each cluster with FastTree likelihood-based support values [13] and maximum pairwise genetic distances using Cluster Picker. [14] The University of Washington Institutional Review Board approved the use of PHSKC records for this study.

Results

From 2010 to 2013, 1127 cases were reported as newly diagnosed on or after Nov 1, 2009, including 97 (9 %) cases among African-born persons. These 97 patients accounted for 49 % of 197 black persons newly reported with HIV during the study period.

Case investigations determined that 36 (37 %) of these 97 cases had been previously diagnosed elsewhere, and 33 of these reported previous diagnosis before arrival in the U.S. Of the remaining 61 cases who were presumably newly diagnosed in KC, 48 (79 %) were interviewed. Across these three groups (newly reported, presumably newly diagnosed, and interviewed patients), approximately 60 % were women, and mean age was 41–43 years (Table 1). Among total cases, patients had spent a mean of 4.7 years in the U.S. prior to diagnosis. Most patients were from East African countries (86 % of total newly reported cases), primarily from Ethiopia and Kenya (45 and 19 % of all cases, respectively). Over 80 % of patients had no HIV transmission risk identified or reported; presumably most of these acquired HIV through heterosexual contact. Among interviewed cases, 15 (31.3 %) were non-English speakers.

Thirty-nine percent of total cases, and 52 % of interviewed cases, were diagnosed with AIDS within 3 months of HIV diagnosis (Table 2). Among interviewed cases, 45 % had a CD4 count less than 200 at the time of diagnosis.

Among the 48 interviewed PLWHA, seven reported HIV diagnosis before arrival in the U.S. and were excluded from further analysis. Of the remaining 41, the most frequently reported reason for testing was because of symptoms or illness (N = 16, 43 %, Table 3). Among this group of interviewed cases, only 14 (34 %) reported ever having tested for HIV prior to their diagnosis. Eleven (29 %) of 35 PLWHA who were asked if they had ever been HIV tested before arriving in the U.S. reported they had. Of the 34 PLWHA who provided complete date of U.S. arrival, 9 (26 %) reported testing HIV negative since their arrival in the U.S.

Table 4 Putative transmission pairs or clusters, based on phylogenetic analysis of HIV-1 *pol* sequences

N linked individuals	Pairwise distance ^a	Node support ^a	Putative transmission cluster	HIV-1 Subtype	Region(s) of origin	Previous negative test in U.S. for one partner?	Epidemiologic link in putative transmission clusters? ^b
2 (one pair)	<i>0.0011</i>	<i>1</i>	yes	C	Africa, North America	no	no
2	<i>0.0030</i>	<i>1</i>	yes	G	Africa	no	yes
2	<i>0.0040</i>	<i>0.998</i>	yes	C	Africa	no	no
2	<i>0.0050</i>	<i>1</i>	yes	A1	Africa	yes	no
2	<i>0.0060</i>	<i>1</i>	yes	C	Africa, North America	no	yes
3 (cluster)	<i>0.0081</i>	<i>1</i>	yes	C	Africa	no	yes
2	<i>0.0200</i>	<i>1</i>	yes	CRF02AG	Africa, North America	no	no
2	<i>0.0259</i>	0.893	yes	C	Africa	no	^c
2	<i>0.0296</i>	0.880	yes	CRF02AG	Africa	yes	no
2	0.0334	0.720	no	A1	Africa	no	
3	0.0359	0.516	no	A1	Africa, Asia, North America	no	
2	0.0369	0.881	no	C	Africa	no	
2	0.0381	0.827	no	C	Africa	no	
2	0.0391	0.718	no	CRF02AG	Africa	no	
2	0.0422	<i>0.997</i>	yes	H	Africa	no	^c
3	0.0423	0.012	no	C	Africa	no	
2	0.0472	0.483	no	CRF02AG	Africa	no	
3	0.0487	<i>0.998</i>	yes	C	Africa, North America	no	^c
2	0.0530	0.375	no	G	Africa, Europe	no	
4	0.0530	<i>0.972</i>	yes	CRF02AG	Africa, North America	no	no
2	0.0539	0.208	no	A1	Africa	no	
2	0.0551	0.118	no	A1	Africa	no	

^a Values which meet genetic distance or node support thresholds are shown in bold and are italicized

^b Epidemiologic link defined as two individuals who acknowledged sexual contact with other individuals in the transmission pair/cluster

^c Partner services data were not available for at least one patient; epidemiologic links cannot be determined for these clusters

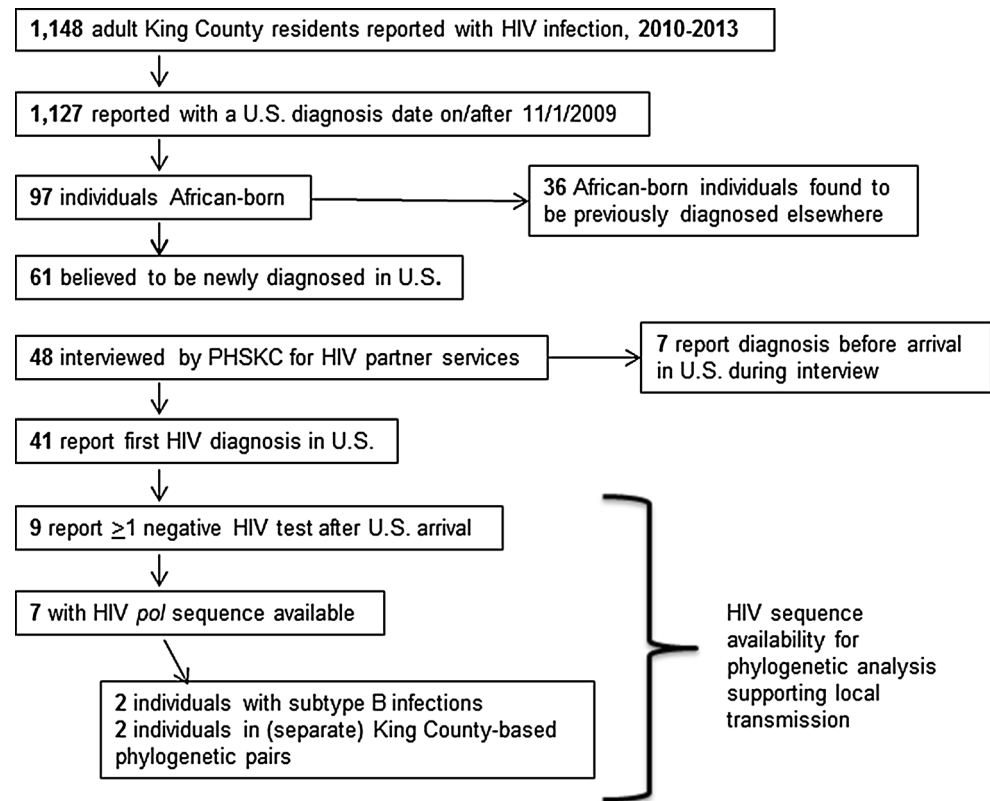
The 41 interviewed patients not previously diagnosed identified 45 sex partners, 6 (13.3 %) of whom had been diagnosed with HIV infection prior to the partner services investigation. Of these six, three had been interviewed and all were African-born. Nine (23.1 %) partners not known to be previously HIV-infected were newly HIV tested as a result of the investigations, four (44 %) of whom tested HIV positive. Of these four, 3 (75 %) were African-born.

Our phylogenetic analysis was based on 112 African-born KC residents with an available HIV-1 *pol* sequence. Of these, 42 (30 %) shared a most recent common ancestor with an individual from KC, while the remaining 70 individuals were related most closely to *pol* sequences obtained

from individuals in Africa. The 42 African-born KC residents linked to other KC residents made up 22 putative transmission pairs/clusters (Table 4; 1 cluster of 4, 4 clusters of 3, 17 pairs).

Assessing the validity of these 22 putative transmission pairs/clusters depends on defining *ad-hoc* thresholds for genetic distance and/or node support. Only 7 putative pairs/clusters (of the 22) would pass both conservative distance and support thresholds (<3.0 % distance and >0.90 node support). The 12 clusters which met either of the *ad-hoc* thresholds included 23 (21 %) of the 112 African-born PLWHA with sequences available. We assessed epidemiologic links between individuals in 9 putative transmission pairs/clusters which passed genetic

Fig. 1 Study flow diagram



distance and/or support thresholds and for whom interview data were available; 3 (33 %) clusters included an individual who identified at least one other cluster member as a sexual partner. Of 7 individuals with a *pol* sequence available and a previous negative test in the U.S., 2 were in putative Seattle-based transmission clusters (Fig. 1). Two other African-born individuals with a previous negative test in the U.S. were infected with subtype B, offering additional sequence-based evidence for local HIV transmission.

Discussion

We found that almost half of all cases of newly reported HIV among blacks in KC, WA 2010-13 occurred in African-born persons, and among those who were not known to be HIV-infected before arrival in the U.S. 26 % reported having tested HIV negative in the U.S. This finding was corroborated by phylogenetic analyses, which linked 21 % of African-born cases to a non-subtype B case reported in KC. Thirty-nine percent of African-born cases were diagnosed with AIDS within 3 months of their HIV diagnosis, a measure commonly used to indicate late HIV diagnosis, and less than half had ever been HIV tested before diagnosis. These findings demonstrate significant levels of

ongoing HIV transmission among local African-born persons, as well as the inadequacy of existing efforts to test persons born in Africa.

Studies from the UK using different approaches have estimated that approximately one-third of UK African-born PLWHA acquired HIV in the UK. [7, 9] Wiewel et al. [15] recently estimated that among African-born persons interviewed for partner services from 2006 to 2012 in NYC, 34 % likely acquired HIV in the U.S. We believe that the remarkable consistency of these results with our findings strengthens the evidence that a significant proportion of HIV-positive members of the African community are likely acquiring HIV after arrival in the U.S.

Our study had several limitations. First, among interviewed patients, we excluded patients who reported diagnosis with HIV before arriving in the U.S. If we were to include these seven patients in our denominator of interviewed patients, it would slightly decrease the proportion of patients who we believe acquired HIV in the U.S. Secondly, although we think that most people who had previously tested HIV-negative in the U.S. acquired HIV in the U.S., HIV acquisition may have occurred during travel outside the U.S. While we asked many patients about sex in the context of travel, for some this information was missing. Some other persons may have misreported their HIV testing history, but the fact that our findings are consistent

with prior work and our phylogenetic analyses suggests that our findings are valid. Additionally, interviewed PLWHA were somewhat more likely to have been diagnosed with AIDS within 3 months of HIV diagnosis than other PLWHA. This may be because hospitalized individuals are easier to locate. As such, interviewed cases may reflect a group of patients who were more likely to be hospitalized. Finally, our estimate of the proportion of cases likely infected in the U.S. is based on a small number of interviewed patients, and as such, may somewhat over- or underestimate the proportion who acquired HIV in the U.S.

In summary, we found that African-born persons in KC, WA are at high risk for late HIV diagnoses, and that 26 % of HIV cases in African-born persons likely occur as a result of transmission within the U.S. These findings highlight the need to consistently collect country of origin of persons with HIV, to identify African-born persons as a priority population for HIV prevention, and to develop culturally appropriate interventions to increase HIV testing among persons from Sub-Saharan Africa.

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Compliance with Ethical Standards

Conflict of interest The authors declare that they have no conflict of interest.

Research Involving Human Participants and/or Animals This article does not contain any studies with animals performed by any of the authors.

Informed Consent The University of Washington Institutional Review Board approved the use of Public Health—Seattle and King County records for this study, including a waiver of consent.

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