HIGH RATES OF EXTERNAL (NON-DOMESTIC) INFECTION SOURCES FOR NEWLY HIV-1 DIAGNOSED HETEROSEXUAL MEN AND WOMEN IN SEATTLE AND KING COUNTY, USA.

Grollemund PM[1], Buskin SE[2], Lechtenberg R[2], Herbeck JT[3], and Ratmann O[1].

[1] Statistics Section, Department of Mathematics, London SW72AZ, United Kingdom; [2]HIV/STD Program, Public Health-Seattle & King County, Seattle, United States; [3]Department of Global Health, University of Washington, Seattle, United States.

PURPOSE OF STUDY

The UNAIDS Cities initiative aims to fast-track HIV-1 prevention interventions within metropolitan areas. However, little is known what proportion of infections have a local source case, which we denote by λ. Here we report estimates of λ among self-reporting heterosexual men and women in Seattle and King County (SKC), Washington State, USA, through viral phylogenetic analysis.

DATA

We used a viral sequence database maintained by Public Health Seattle & King County [1]; this database contains 12606 sequences of 9491 individuals from 15932 HIV-1 infected individuals that live, were diagnosed, or started ART in King County since 1982.

Table 1. Characteristics of the infected individuals.

	Heterosexual/ pot. bisexual	Origin US-born	Ethnicity white	Partial pol sequence
Yes	3273	12846	10319	6441
No	12658	3086	5613	9491

METHODS

HIV-1 phylogenies were generated for all non-B partial pol sequences from SKC and international background sequences from the LANL online database using FastTree 2.1.8. Viral subtrees were attributed to SKC and other world regions with ancestral state reconstruction using the Sankoff algorithm in phyloscanner 1.6.6 [2]. Subtrees attributable to SKC were extracted, and their sizes recorded. Each SKC subtree corresponds to a partially observed local transmission chain.
Some transmission chains, in particular small ones, may not have been sampled at all. To estimate λ, we used a Bayesian data augmentation approach. Incomplete transmission chains were sampled from unobserved complete transmission chains via a Binomial model according to an overall sampling fraction ρ, to yield the likelihood of observing the number and sizes of SKC subtrees. Unobserved complete transmission chains were modelled with the Chinese Restaurant process [3].

RESULTS

A sequence is found for 2273 (49.9%) of 4948 heterosexual/ potentially bisexual individuals, and 1437 (63.2%) of 2273 were infected with a non-B subtype. Phylogenetic analysis revealed 372 distinct transmission chains, of which 65 (17.5%) emerged in the last five years and 359 (96.5%) contained at most 3 sequenced individuals.

The maximum likelihood phylogenetic tree for subtype 01_AE is shown in **Figure 1**, suggesting many small transmission chains among heterosexuals in Seattle. **Table 2** gives estimates of the proportion of infections with a local source case with and without adjustments for incomplete sequence sampling, and further characteristics of transmission chains among heterosexuals. **Figure 2** illustrates the origin of HIV introductions by world region, and lists the most represented world region origins of introductions.

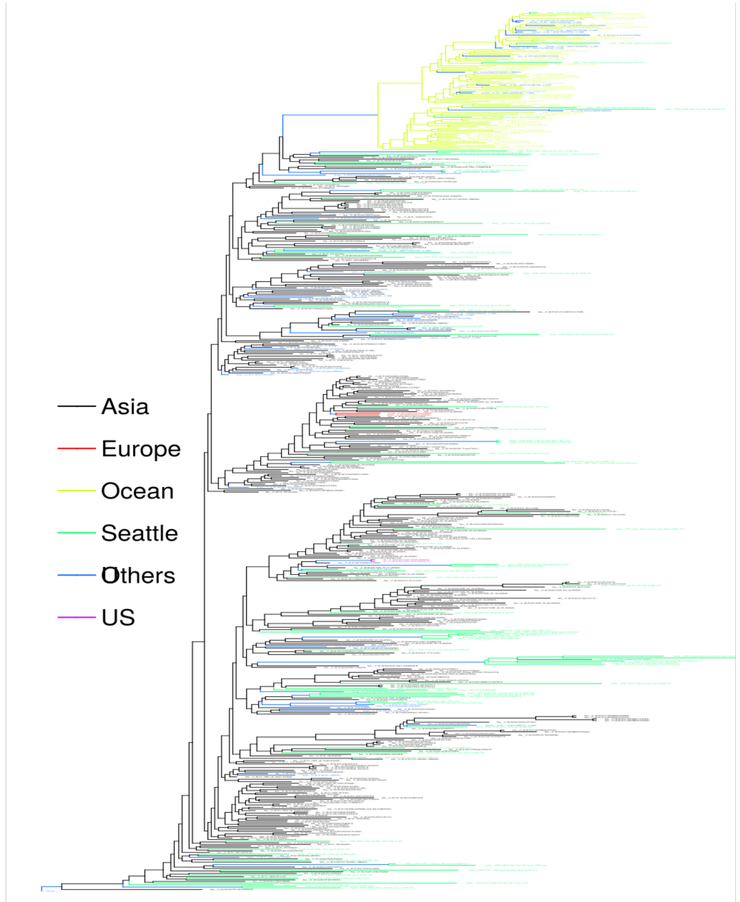

Figure 1. Maximum likelihood tree for subtype 01_AE colored according to the world region of birth.

Table 2. Importation rate estimates and characteristics of the individuals of the transmission chains.

	Non-local source case		Origin US-born	Ethnicity white
Crude	69% [50%−76%]	**Yes**	9.9%	6.7%
Adjusted	55% [54%−58%]	**No**	90.1%	93.3%

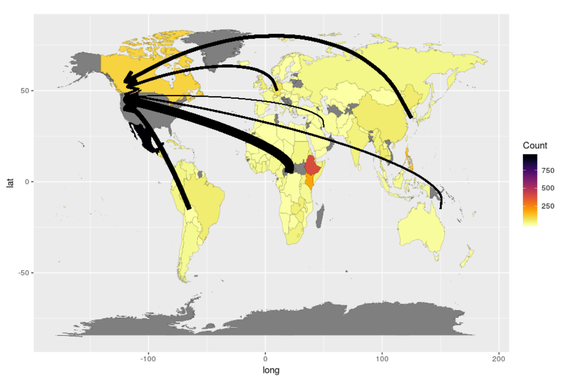

Figure 2. Origins of foreign-born heterosexual men & women. The most represented source locations of the partially observed transmission chains are Sub-Saharan Africa (74.2%), Asia (17.5%), Europe (4.6%) and Ocean (1.9%).

DISCUSSION

This study indicates that control efforts to the epidemic in Seattle among heterosexuals need to be tailored to individuals who are at risk of introducing HIV to local communities.

Limitations of this study include: some infected individuals may be undiagnosed to date, which we did not account for in the population denominator; non-B sequences were studied as a proxy of heterosexual men & women, though analysis is being extended to individuals with subtype B infection; model adequacy is under investigation.

ACKNOWLEDGEMENTS

This work is supported by a grant from the US National Institutes of Health (R01AI127232).

[1]Public Health - Seattle & King County HIV/AIDS Epidemiology Unit and Washington State Department of Health the Infectious Disease Assessment Unit. *HIV/AIDS Epidemiology Report 2017*. Volume 86. 2017.

[2]Chris Wymant et al. “PHYLOSCANNER: inferring transmission from within-and between-host pathogen genetic diversity”. In: *Molecular biology and evolution* 35.3 (2017), pp. 719–733.

[3]David J Aldous. “Exchangeability and related topics”. In: *École d’Été de Probabilités de Saint-Flour XIII—1983*. Springer, 1985, pp. 1–198.