

EXAMINING HIV TRANSMISSION CLUSTERS AMONG NEWLY-DIAGNOSED ASYLUM SEEKERS IN MONTREAL, QUEBEC

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Background

- Migrants represent an increasing proportion of people living with HIV in Canada.¹
- In recent years, Montreal has witnessed a change in its local HIV epidemiology. In 2015-2016, people from HIV-endemic countries represented 15-20% of all newly declared HIV infections, compared to 51% in 2017.²
- Asylum seekers (AS) who are newly diagnosed with HIV through the Immigration Medical Exam (performed within 30 days from arrival) represent a key population for whom there is a paucity of data regarding HIV transmission dynamics following arrival in Canada.

Objectives

- We aimed to identify and characterize HIV transmission clusters among newly-diagnosed AS (ndAS) and between ndAS and people living with HIV in Quebec.
- We aim to track linkage of viral variants with the overall goal of improved understanding of an evolving HIV epidemic among this key sub-population.

Table 1. Baseline participant characteristics

		MUHC Cohort (n=83)	JGH Cohort (n=22)
Sex	Male	37 (44.6%)	17 (77.3%)
	Female	46 (55.4%)	5 (22.7%)
Country of Origin	Haiti	36 (43.4%)	12 (54.5%)
	Nigeria	18 (21.7%)	0 (0%)
	Central Africa		
	DRC	5 (6.0%)	1 (4.5%)
	Angola	3 (3.6%)	0 (0%)
	Cameroon	3 (3.6%)	1 (4.5%)
	Tchad	2 (2.4%)	0 (0%)
	East Africa		
	Burundi	2 (2.4%)	2 (9.1%)
	Rwanda	1 (1.2%)	0 (0%)
	Eritrea	2 (2.4%)	0 (0%)
	Kenya	1 (1.2%)	0 (0%)
	Malawi	1 (1.2%)	0 (0%)
	North Africa		
	Algeria	1 (1.2%)	0 (0%)
	South Africa		
	South Africa	1 (1.2%)	0 (0%)
	Zimbabwe	1 (1.2%)	0 (0%)
	West Africa		
	Cote d'Ivoire	2 (2.4%)	1 (4.5%)
	Guinea	1 (1.2%)	1 (4.5%)
	Togo	1 (1.2%)	0 (0%)
	Americas		
	Colombia	1 (1.2%)	0 (0%)
	Guatemala	1 (1.2%)	0 (0%)
	Dominican Republic	0 (0%)	1 (4.5%)
	Mexico	0 (0%)	1 (4.5%)
	Saint Vincent	0 (0%)	1 (4.5%)
	Brazil	0 (0%)	1 (4.5%)
HIV Subtype	B	37 (44.6%)	15 (68.2%)
	C	12 (14.5%)	2 (9.1%)
	AG	17 (20.5%)	2 (9.1%)
	G	6 (7.2%)	0 (0%)
	A1	2 (2.4%)	1 (4.5%)
	AE	1 (1.2%)	0 (0%)
	D	1 (1.2%)	1 (4.5%)
	F1	1 (1.2%)	0 (0%)
	CRF	6 (7.2%)	1 (4.5%)

Methods

- Retrospective chart reviews of ndAS linked to HIV care between June 1, 2017 and December 31, 2018 at the McGill University Health Centre (MUHC) and the Jewish General Hospital (JGH) were performed to obtain baseline genotypes.
- Phylogenetic trees were reconstructed using Neighbor-joining and Maximum Likelihood analysis. Clustering of linked viral sequences was based on strong bootstrap support (>98%) and short genetic distances (0.01–0.05 substitutions/site) or posterior probabilities.
- Cohort sequences were combined with sequences from the Quebec HIV Genotyping Program to create population-level phylogenetic trees.
- Clusters were characterized by sex, country of origin, HIV risk population and subtype, and estimated recency.

Figure 1. HIV-1 subtype B – Haitian origin subtree

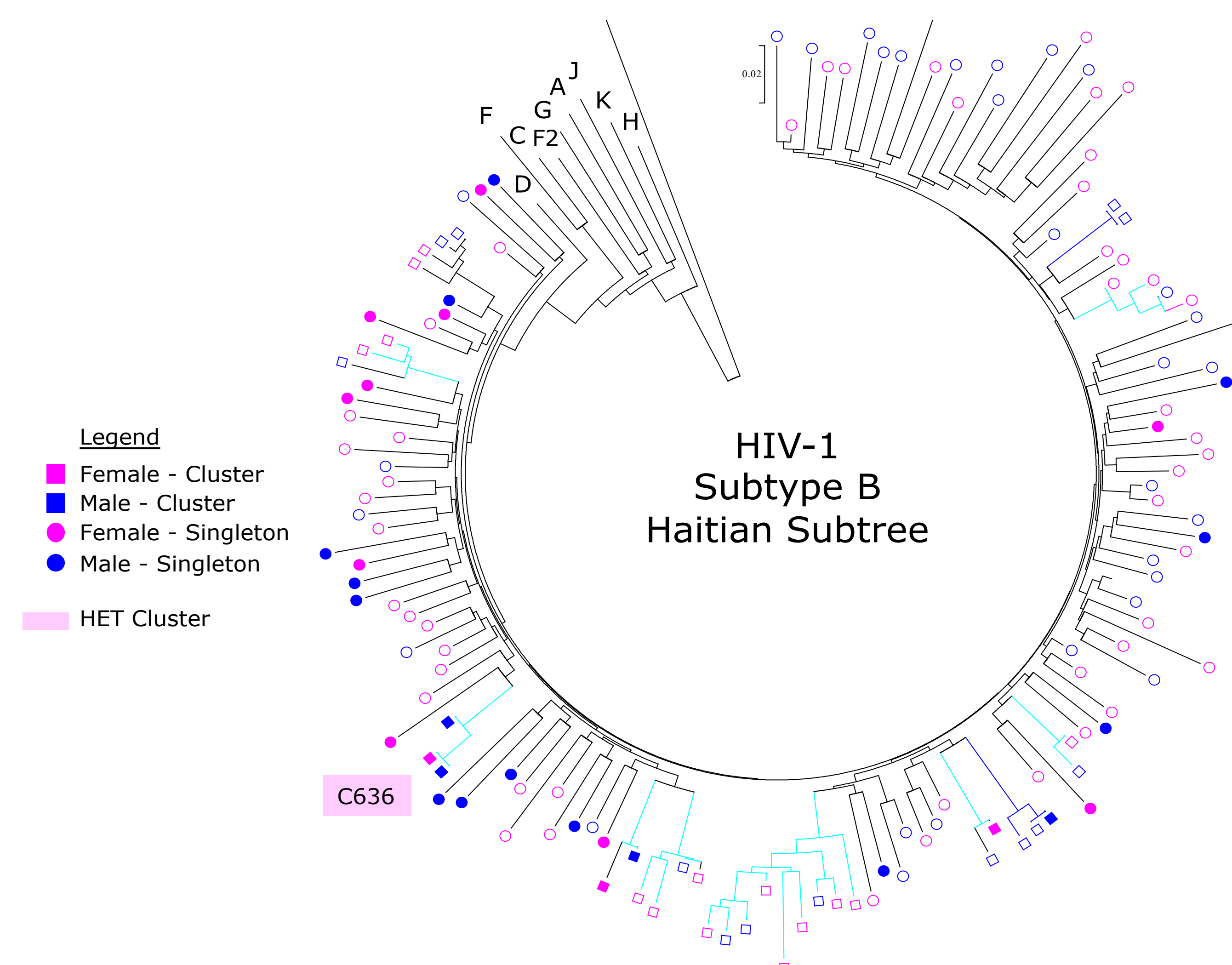


Table 2. Cluster characteristics

Cluster Number	Cluster Size	HIV Subtype	Country of Origin	Sex	Age	Date of Arrival into Canada	CD4 at Genotype [cells/ul]	VL at Genotype [copies/ml]
C636.01	3	B	Haiti	M	48	9-Aug-2017	167	32908
C636.02	3	B	Haiti	M	43	17-Oct-2017	347	99274
C636.03	3	B	Haiti	F	34	16-Sep-2017	687	19896
CT270.01	2	B	Haiti	M	40	15-Sep-2017	209	2549
CT270.02	2	B	Haiti	F	33	13-Sep-2017	191	68743
CAG41.01	2	AG	Nigeria	M	44	3-Dec-2017	333	181853
CAG41.02	2	AG	Nigeria	F	35	3-Dec-2017	316	11524
G5.01	2	G	Nigeria	M	40	18-Dec-2017	11	112947
G5.02	2	G	Nigeria	F	36	18-Dec-2017	531	40988

Results

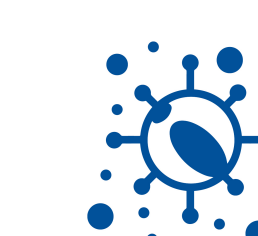
- Sequences were obtained from 105 ndSA; 13/105 (12%) were clustered. Haitian specific phylogenetic tree was created for HIV subtype B (Figure 1).
- Nine (9/105; 9%) individuals belonged to four clusters having no overlap with Quebec sequences (Table 2). Three were male-female clusters (each with one male and female): one Haitian subtype-B and two Nigerian clusters (subtype-G and subtype-CRF02_AG). All were known heterosexual couples. The fourth represented a Haitian subtype-B cluster with two males and one female (none of whom were known partners).
- The remaining four (4/105; 4%) individuals clustered with sequences from Quebec: two male-female clusters (one Saint Vincent subtype-B, one Haitian subtype-B) and two male-male clusters (one Haitian subtype-B, one Algerian subtype-B).
- Regardless of CD4 counts, viral loads and dates of arrival, it was not possible to determine when HIV transmission occurred.

Conclusions

- Our pilot study identified one recent HET M-M-F cluster that occurred within a specific ethno-cultural group.
- Phylogenetics cannot determine directionality of transmission.
- Our study shows that HIV clustering is occurring among ndAS and at a population level, highlighting the potential role of phylogenetic monitoring as part of routine HIV surveillance.

References

- ¹ Li A. Immigrants, refugees and non-status people with HIV. *Canadian AIDS Treatment Information Exchange (CATIE)* 2009.
- ² Mercure, Sarah-Amelie. Personal communication. November 28, 2018.



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