# Phylogenetic insights on HIV transmission dynamics among MSM and recent Migrants to Quebec

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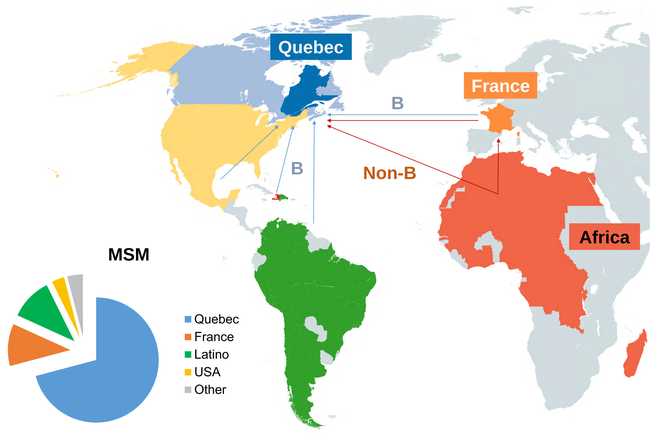
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## Background

Phylogenetic analyses of the interrelationships of viral sequences, using novel statistical tools, provide molecular epidemiological frameworks to reconstruct HIV transmission networks. We applied these methods to gain novel insights on HIV transmission patterns in Quebec, uncover cryptic at-risk populations, and elucidate epidemic drivers that cannot be identified by traditional epidemiological approaches.

## Methods

Genetic analyses were performed on subtype B pol sequences derived from newly-infected Men having Sex (MSM, n=4800) and Heterosexuals subgroups, including People who Inject Drugs (PWID) and migrants from Haiti and the Americas (n=1836). Phylogenetic analyses were also conducted on non-B viral subtypes originating from migrants from Africa, Asia and Europe (n=1578). Growth trajectories of transmission networks (6+ members/cluster) were analyzed using Maximum-Likelihood MEGA10 and/or HIV-TRACE (Transmission Cluster Engine) platforms.

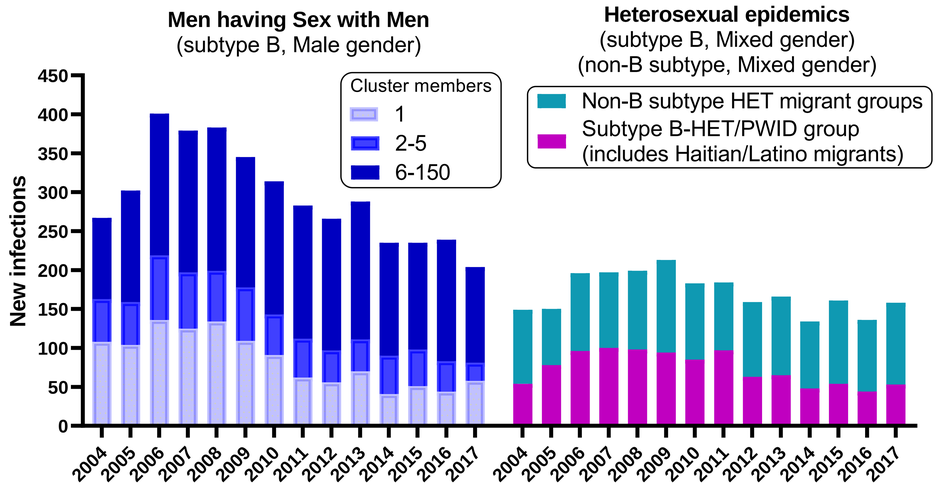



**Transmission clustering dynamics of provincial epidemic in MSM and HET risk groups**

| Risk group | Transmission cluster group | | | | |
|---|---|---|---|---|---|
| | Singleton | Small cluster 2-5 members | | Large clusters 6+ members | |
| | % cases | % cases | Median Size [IQ] | % cases | Median size [IQ] |
| MSM | 26.1 | 20.2 | 3[2-4] | 52.9 (42) | 31 [13-71] |
| Subtype B HET & PWID | 77.3 | 16.6 | 3[2-4] | 6.6 | 16 [9-43] |
| Non-Subtype B HET | 75.0 | 21.4 | 2 [2-3] | 3.5 | 21 [11-45] |

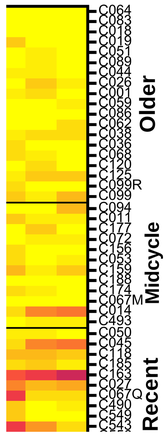
## Results

**New infections in the province (2004-2017)**

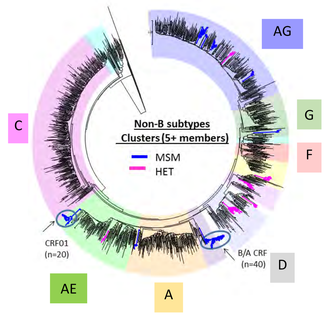



**The epidemic among MSM shows steady declines post-2008 associated with declines in community viral load, single tablet regimens (eg. TDF/FTC/EFV), and PreP.**

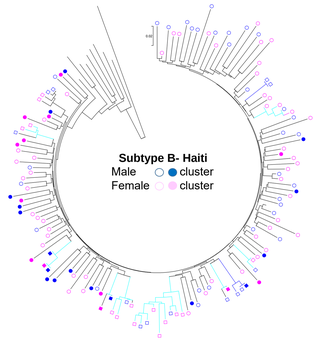
**Growth of the HIV epidemic amongst MSM is sustained by persistent large cluster sub-epidemics**




**Non-B subtype Heterosexual epidemics**



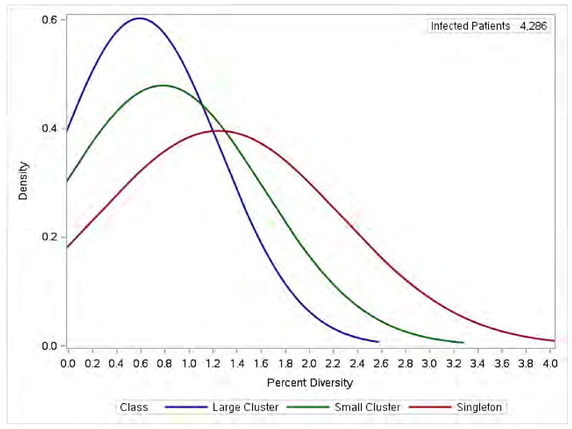

**Non-B subtype Heterosexual epidemics**




## Conclusion and Discussion

Half of new infections (n=2328) among MSM segregated as solitary "dead-end" transmissions (n= 1478) or small transmission networks having 2-5 members/cluster (n=850). The remaining half of new infections (n=2371) were in large transmission networks (6-150 members, mean 42 members/cluster). Phylodynamics showed a marked decline in singleton transmissions and small cluster outbreaks post-2008, concomitant to advances in Treatment-as-Prevention paradigms. This was offset by an increase in large cluster transmissions rising from 37% of infections in 2004 to 65% of new infections among MSM in 2017. HIV-TRACE maps showed differential features of forty large cluster sub-epidemics (members' age, sex, sequence diversity). Heat maps of individual clusters distinguished "actively-growing" clusters and "newly emerging" clusters from older low-risk clusters. Phylogenetics uncovered the cryptic introduction and spread of subtype B and non-B subtype sub-epidemics among migrants to the province.

**Large cluster outbreaks are fueled by early stage infections showing low genetic diversity**




## Aknowledgements

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