Phylogenetic insights on HIV epidemic control among MSM and Heterosexual groups in Quebec from 2014-2020

02342 Session R04

Bluma G. Brenner[1,2], Ruxandra-Ilinca Ibanescu[1], Maureen Oliveira[1], Réjean Thomas[3], Isabelle Hardy, Amy Tang, Jean-Pierre Routy, Michel Roger and the Montreal Primary HIV Infection cohort

[1]Lady Davis Institute for Medical Research, [2]McGill University, Montreal, QC, Canada; [3]Clinique médicale l'Actuel, [4]Université de Montréal, and McGill University Health Centre, Montréal, Québec, Canada

Background

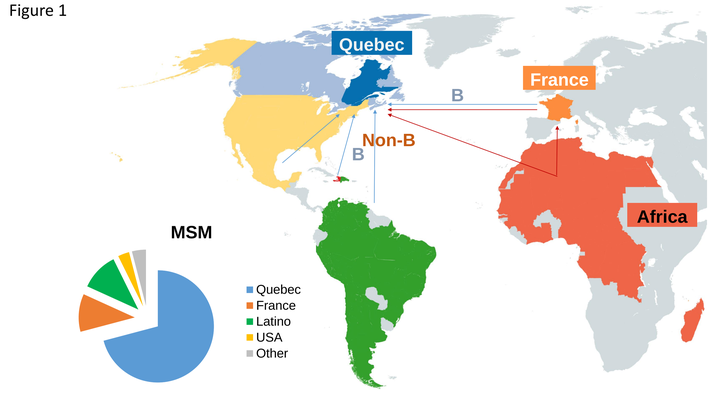
The Ending the HIV Epidemic by 2030 initiative includes phylogenetics as a molecular framework to track patterns of HIV spread towards timely identification and responses to large cluster outbreaks, In this study, phylogenetic and available epidemiological data were combined to elucidate shifting trends in HIV-1 spread among Men having Sex with Men (MSM) and Heterosexual (HET) populations in Quebec

Methods

Phylogenetic Ilinkage of sequences datasets obtained from the provincial genotyping program (2002-2020) were updated annually using MEGA-10 methodologies. Newly infected individuals were assigned a unique phylogenetic identifier based on sex, viral subtype, and cluster group association (generally high bootstrap >95% and low genetic distance <1%). Phylogenetic clustering profiles in 2014-2020 were compared to 2007-2013 in three principal risk populations.

- The MSM core group included first subtype B male singleton transmissions and male-male clusters (n=2236 in 2007-2013 and 1331 in 2014-2020). Clinical data from the Montreal PHI cohort, SPOT rapid testing site and l'Actuel revealed that persons born outside Quebec contribute to ~25% of subtype B MSM infections.
- The subtype B Heterosexual (HET) group included female singleton transmission, female only and mixed gender clusters (n= 591 in 2007-2013 and 313 in 2013-2020). The subtype B epidemic included largely historic (pre-2007) large cluster outbreaks amongst People Who Inject Drugs (PWID). This group also includes subtype B HET variants introduced among migrants from the Caribbean and Americas.
- The non-B subtype HET group was comprised of mixed gender epidemics originating from Africa and Europe (n=710, and 746 in 2007-2013 and 2014, respectively). Non- B subtype domestic crossover into MSM included 124 and 96 infections in 2007-2013 and 2014-2020, respectively.

Figure 1

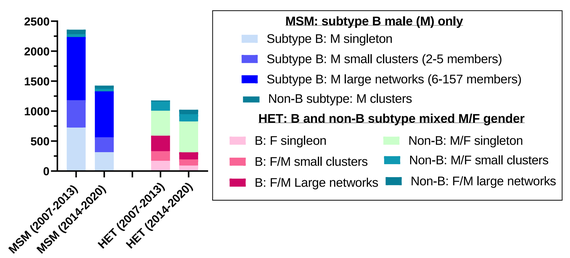


Results

Epidemic control in different risk groups over the 2014–2020 periods

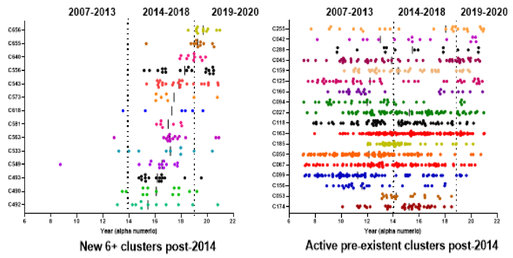
	Type	Epidemic decline in 2014–2020
MSM (40%)	Singleton	56.4% ↓
	Small networks	42.8% ↓
	Large networks	27.2% ↓
HET Subtype B (47%)	Singleton	46% ↓
	Small networks	37% ↓
	Large networks	54% ↓
HET non-B subtype	Singleton	24% ↑
	Small networks	21% ↓

Distribution of new infections amongst MSM and HET groups genotyped over the 2007-2013 and 2014-2020 periods

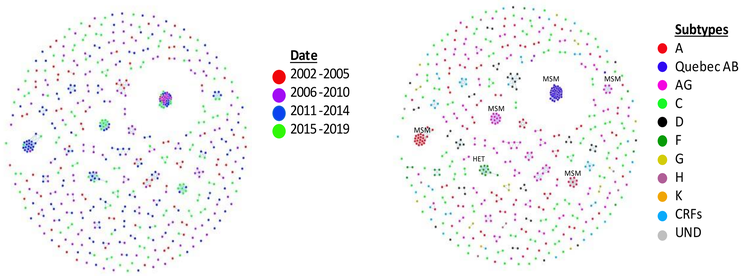


Select super-transmissible variants sustain the growth of the epidemic amongst MSM between 2014 -2020

Type of cluster			Added infections post-2014		
	n	Median cluster size (range)	Added infections	Median gain/cluster (range)	% 2014-2020 Large clusters
New Subtype B MSM 6+ clusters post -2014	14	11 (6-30)	148	7 [5-24)	19%
Active expansion of pre-existent MSM clusters	20	40 (15-157)	487	13 (4-92)	63%



Introduction and spread of non–B subtype HET and MSM epidemics



Results and Conclusion

Among MSM, there was 50% decline in new infections associated with singleton or small networks from 2014-2020 compared to 2007-2013. Epidemic expansion since 2014 was fueled by the active expansion and secondary waves of 20 super-spreader variants, adding 8—-96 members/cluster. In addition, 14 new 6+ cluster outbreaks after 2014 and COVID-19 (Figure 3A, n=14, median cluster size 11). Data from Clinique médicale l'Actuel showed 24% of newly diagnosed MSM (2016-2020) were born outside Canada, 40% of whom acquired circulating super-spreader variants in the province.

The subtype B heterosexual epidemic showed a 50% decline over the 2014-2020 period. Phylogenetics revealed that 62% of new infections after 2014 were singletons (30%) or associated with small cluster networks (32%). Large cluster growth post-2014 included expansion of 3 pre-existent large PWID clusters (10/54, 5/53, 13/43). Several new large clusters arose post-2014 reflecting recent outbreaks in Quebec city (n=14), Abitibi Val d'Or (n=14) and St Jean sur Richilieu (n=8 of 16 members).

Overall, non-B subtype infections remained steady (median 100 annually) over the 2014 to 2020 period. Several non-B subtype clusters reflect the domestic crossover and spread of subtype A and CRF02_AG variants among MSM populations.

Conclusions: Phylogenetics provided a more nuanced understanding of transmission dynamics in key core groups. Annual numbers of new HIV-1 infections have declined by half among MSM and HET groups with subtype B infections, concomitant to improved "90-90-90" and PreP prevention paradigms. Epidemic control must address the episodic genesis and expansion of super-transmissible variants (<5% of strains). Recent arrivals to the province accounted for a growing number of subtype B and non-B subtype infections. HIV prevention efforts must continue in the post-COVID era, tailored to avert potential; transmission cascades in younger persons, PWID and new arrivals to the province.

Acknowledgements

The authors thank the participants, coordinators, and recruiting physicians participating in the Montreal Primary HIV cohort at clinical sites: Hugues Charest, coordinator of the Quebec genotyping program and Mario Legault, administrative coordinator for the Montreal PHI cohort, Réseau sida et maladies infectieuses; Drs J. Szabo, C. Milne, S. Lavoie, J. Friedman, M. Duchastel, F. Villielm, F. Asselin, M. Boissonnault, P. J. Maziade, S. Lavoie, M. Milne, N. Z. Miaki, and M. E. Thériault (Clinique médicale l'Actuel); Drs B. Trottier, P. Côté, B. Lessard, M. A. Charron, S. Dufresne, M. E. Turgeon, S. Vézina, E. Huchet, J. P. Kerba, M. Poliquin, S. Poulin, P. Rochette, P. Junod, D. Longpré, R. Pilarski, E. Sasseville, L. Charest, A. Hamel, A. Cloutier-Blais, S. Massoud, and F. Chano (Clinique médicale urbaine du Quartier Latin); Drs D. Rouleau, L. Labrecque, C. Fortin, V. Hal-Gagne, M. Munoz, B. Deligne, V. Martel-Laferrière, B. Trottier, M.E. Goyer (Centre hospitalier de l'Université de Montréal); Drs M Teltscher, J. Szabo, B. Lebouché, A. de Pokomandy, C. T. Costiniuk, J. Cox, E. Beauchamp, L. P. Haraoui (McGill University Heatlh Centre Chronic Viral Illness Service).

Bluma G. Brenner
Lady Davis Institute
3755 Cote Ste. Catherine Rd.
Montreal, Quebec, CANADA H3T 1E2
bluma.brenner@mcgill.ca (514-340-8260)