Population-based Surveillance of Primary HIV-1 Infection (PHI) in Quebec (1997-2005)

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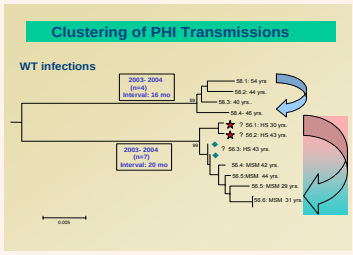
Background

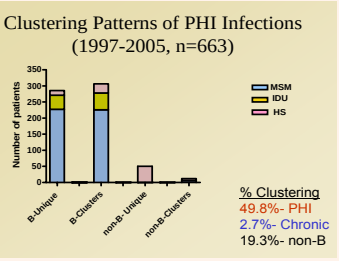
The period following primary HIV-1 infection (PHI) may account for a significant proportion of new transmission events. This study characterized the interrelationships of viral sequences from all genotyped primary and recent infections in Quebec from 1997-2005.

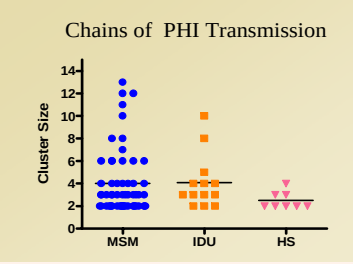
Subjects and Methods

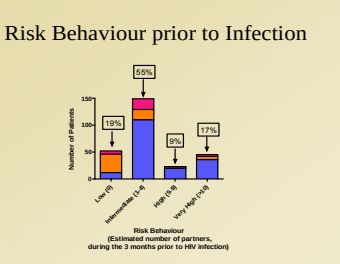
Sequence data, complied from the two provincial genotype resistance testing laboratories (2001-2005) and the Quebec PHI cohort study (1997-2005), identified a total of 719 *pol* sequenced from PHI patients, <6 months post-infection. Neighbour joining and Maximum Likelihood trees were constructed to determine sequence interrelationships of all recent infections, identifying clustered transmission events and non-B subtype infections. Clinical information on age, sex, route of transmission and time of infection was obtained from PHI cohort questionnaires and validated genotyping test requisitions.

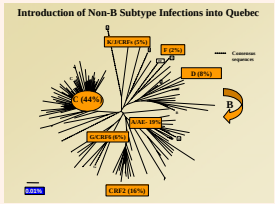
Phylogenetic Clustering of PHI Transmissions





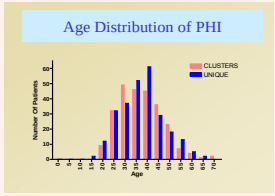






Non-B Subtype PHI Transmission Chains

Subtype	Cluster Size	Risk Factor
CRF01_AE	4	MSM
C	2	HS
C	2	HS
CRF02_AG	2	HS
CRF02_AG	2	HS

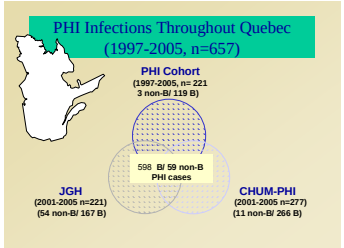


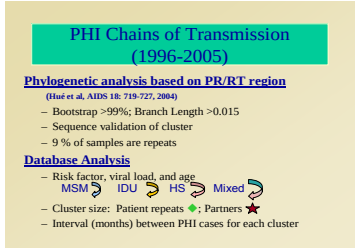
Results

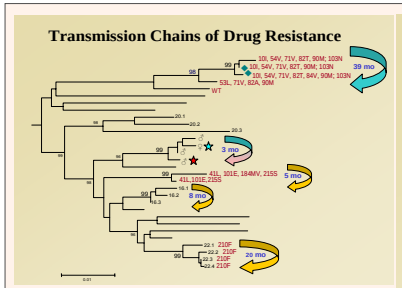
- Half of subtype B infections (298/598) are present in 72 transmission clusters having 2-14 persons/cluster.
- The median and mean time interval for the identified transmission clusters were 8 ± 4.5 months and 10.8 ± 1.1 months, respectively.
- Clustering may be related to high-risk behaviour wherein 30% of clusters included persons having >5 partners in the 3 month interval prior to their diagnosis.
- The 35-55 age-groups were the at risk population for subtype B infections.
- Non-B subtypes represented 16% of recent infections in Quebec and 9% of PHI cases (59/657). Twelve primary non-B transmissions are reported, including four CRF1 infections having MSM routes of transmission.
- The transmission of viral variants harbouring resistance mutations remains a relatively rare event. However, a major proportion (>50%) of transmitted drug resistance is present in clustered infections.

Conclusions

- Routine genotyping is important for population-based surveillance of HIV-1 transmission and the spread of non-B infections, as well as for drug resistance testing.
- The window period following acute/early infection (~10 months) may account for at least half of all reported forward transmissions.
- Non-B subtype infections are being rapidly introduced into Quebec.
- Public health policies must address evolving trends in HIV-1 transmission.







Prevalence of Resistance Mutations in PHI

Mutational Class	Phylogenetic Group	
	Single cases (n= 244)	Clusters (n=240)
Major Mutations Single Class	9.4%	10.4%
Polymorphisms	11.0%	13.5%
Dual or Triple Class MDR	2.9%	3.8%

Acknowledgements

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