

Oral presentation

O114 NNRTI mutations are efficiently transmitted within clusters of new HIV infections

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Purpose of the study

We have shown that almost half of all primary/recent infections (PHI) in Quebec occur within clusters (*J Infect Dis* 2007; 195: 951). Now, we have evaluated whether transmission of mutations associated with drug resistance also occurs within clusters.

Methods

HIV-1 pol subtype B sequence data from early stage infections (<6 months post-PHI) were obtained from the Quebec PHI cohort and the provincial genotyping programs (n = 859, 1998–2007). Phylogenetic analyses determined sequence interrelationships and clustering. Primary infections were classified as unique, small clusters (2–4 PHI) or larger clusters (≥5 PHI). The distributions of mutations conferring resistance to nucleoside and non-nucleoside RT inhibitors (NRTIs and NNRTIs) and protease inhibitors (PIs) were ascertained.

Summary of results

Clustering of new infections has increased from 49% to 56% from December 2005 to June 2007, and, in addition, the size of individual transmission clusters is growing over time. While the majority (95%, 403/423) of unique and small clusters identified pre-2006 represented dead end transmissions, PHI in 21 large clusters represented growing transmission cascades that increased from 6.6 ± 0.8 to 10.3 ± 1.1 PHI/cluster (n = 132 and 215, respectively). High frequencies of NNRTI mutations (e.g. K103N/R,

G190A, Y181C) were observed in large clusters (>5 PHI) compared with smaller ones (1–4 PHI) (12.1% vs. 3.3%, p < 0.0001). In contrast, viruses harbouring NRTI mutations (in particular 215 revertants) were less frequent in clusters (7.9% vs. 3.4% vs. 1.2% and 5.8% vs. 1.7% vs. 1.1% for unique, small and large clustered transmissions, respectively) and PI mutations were also less common within clusters than in non-clustered new infections.

Conclusion

A significant proportion of new HIV infections in our community arise from untreated persons, who are often unaware of their serostatus, at early stages of infection, and this further results in onward transmission of both wild-type and drug-resistant infections. NNRTI mutations are detected within transmission clusters to a far higher extent than are mutations associated with other drug classes.