

O3. HIV-1 Transmission from MSM to heterosexuals and increasing proportions of circulating recombinant forms in the Nordic countries

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Background

Increased knowledge about HIV-1 transmission dynamics in different transmission groups and geographical regions is fundamental for assessing and designing prevention efforts against HIV-1 spread.

Methods

HIV-1 pol sequences and clinical data of 51% of all newly diagnosed HIV-1 infections in Sweden, Denmark and Finland 2000-2012 (N=3802) were analysed together with a large reference sequence dataset (N=4537) by trend analysis and phylogenetics.

Results

Analysis of the 8 dominating subtypes and CRFs in the Nordic countries (A, B, C, D, G, CRF01_AE, CRF02_AG, and CRF06_cpx) showed that the subtype B proportion decreased while the CRF proportion increased over the study period. A majority (57%) of the Nordic sequences formed transmission clusters, with evidence of mixing both geographically and between transmission groups. Detailed analyses showed multiple occasions of transmissions from MSM to heterosexuals and that active transmission clusters more often involved single than multiple Nordic countries. Finally, Denmark had a larger proportion of domestic subtype B spread compared with Sweden and Finland.

Conclusion

We found different HIV-1 transmission patterns between countries and transmission groups in a large geographical region of Europe by combining epidemiological and surveillance data with phylogenetic analyses. Our results may have implications for public health interventions.