

Several national HIV-1 non-B subtype sub-epidemics established in the Netherlands

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OBJECTIVE

The HIV-1 epidemic amongst men having sex with men (MSM) in the Netherlands is mainly driven by subtype B. Non-B subtypes are found mostly amongst heterosexuals immigrants from Sub-Saharan Africa. It is important to get more insight into the transmission dynamics of non-B subtypes in order to develop adequate intervention strategies.

METHODS

National ATHENA observational data base - June 1st 2015

- HIV-1 polymerase sequences were available for 38% (9106) of patients in the Netherlands



- 23861 patients in total: 57% MSM and 32% Heterosexual
- 2172 non-B sequences: 16% MSM and 69% Heterosexual

Fig.1 Sequences alignment of 1128 nucleotides length with IAS 2014 resistant sites removed using ape in R v3.2.3

- FastTree v2.1.8 gamma was used to built phylogenetic trees
- Subtypes were assigned using COMET and sub-trees were selected per subtype in FigTree v1.4.2
- All sequences per non-B subtype were selected from the Los Alamos database, and new trees built per subtype
- Large national clusters of ≥ 10 ATHENA sequences were identified

RESULTS

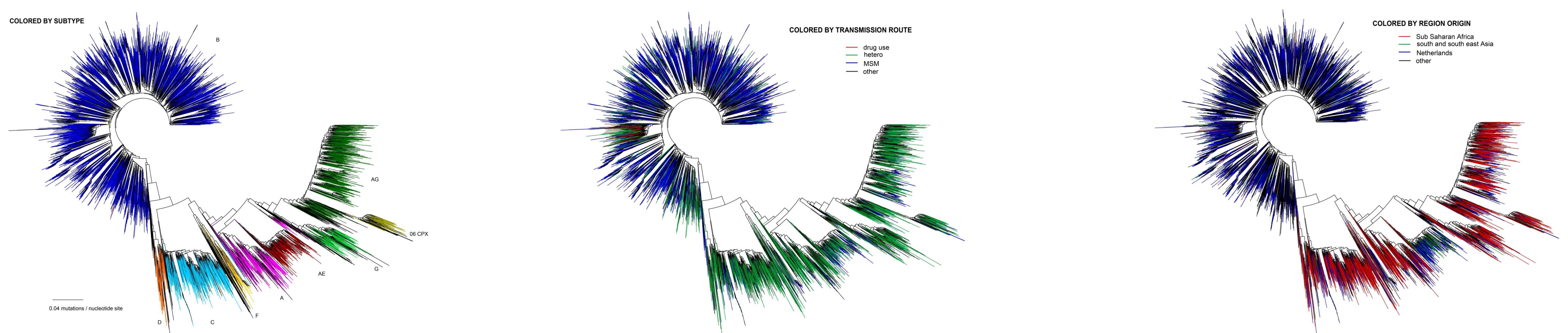


Fig.2 Phylogenetic tree of 9106 sequences colored by : subtype / route of transmission / region origin

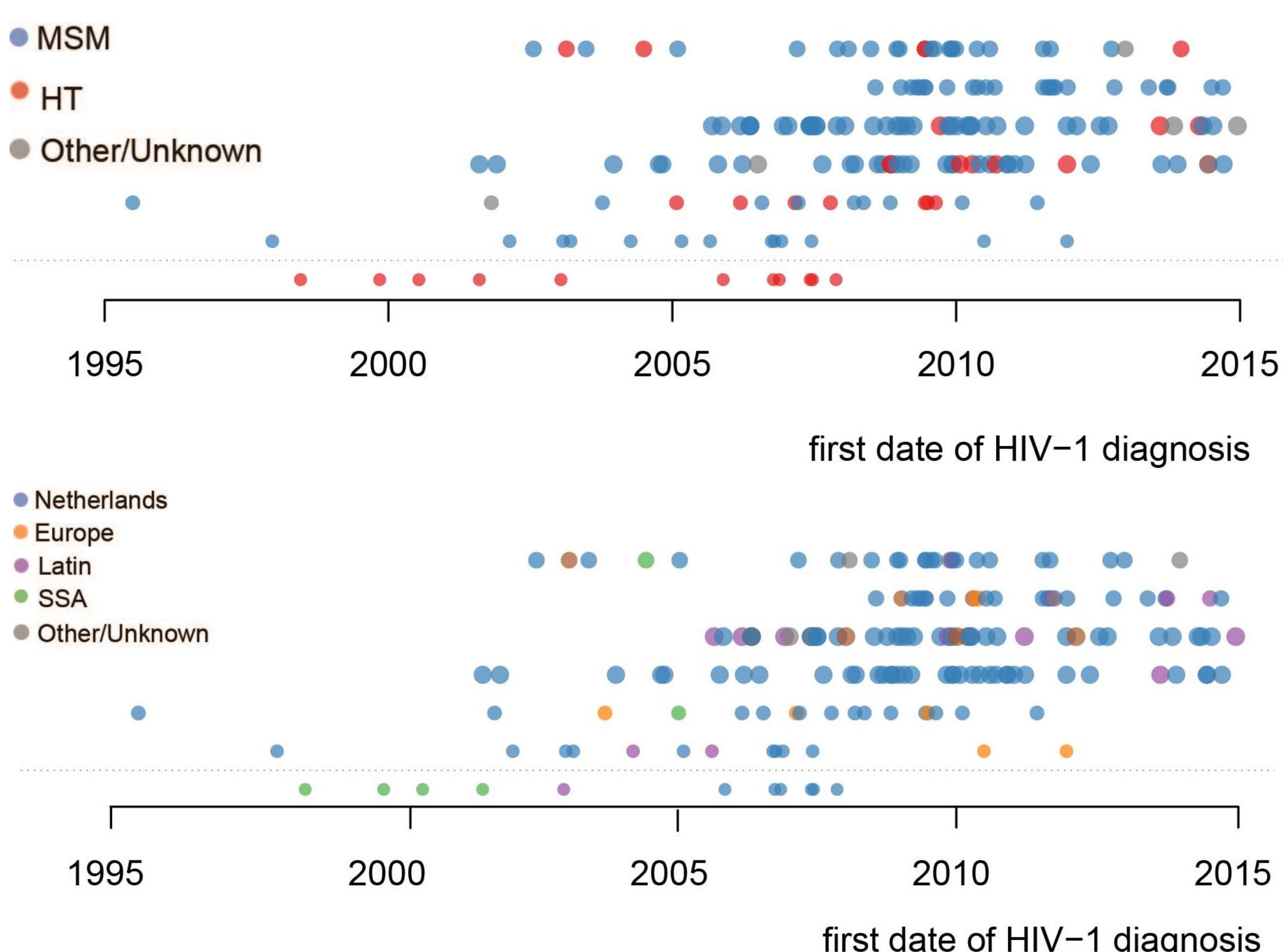


Fig.3 Seven large national non-B subtype transmission clusters with ≥ 10 ATHENA sequences

CONCLUSIONS

- Several national non-B subtype transmission clusters
- , mostly circulating amongst the minority of MSM
- Impact of small clusters needs to be investigated