Differences in outbreak size for HIV-1 non-B subtypes amongst MSM 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. Therefore a phylogenetic tree of non-B polymerase sequences allows identifying the introductions into the MSM population in the Netherlands. This can be used to estimate the proportion of introductions that actually resulted in onward transmission and assess whether this differs between subtypes.

National ATHENA observational data base - June 1st 2015

- HIV-1 polymerase sequences were available for 38% (9106) of patients in the Netherlands
  - Of 23861 patients in total: 57% MSM and 32% Heterosexual
  - Of 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
  - Fastee v2.1.8 gamma was used to built a phylogenetic tree
  - Subtypes were assigned using COMET
  - Sub trees were selected per subtype in FigTree v1.4.2
  - Clusters pertaining MSM were defined by visual inspection of the sub trees

RESULTS

Table 1. Clustering of MSM within the non-B subtypes

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- Several non-B subtypes sub-epidemics established amongst MSM in the Netherlands
- Differences in outbreak frequency amongst subtypes, 3 - 19 percent

CONCLUSIONS

- Differences in outbreak size amongst subtypes
- Subtype AE showed most introductions into the MSM population, with links to Thailand
- Subtype F showed links to Latin-America
- Other non-B subtypes mostly showed links to Sub Saharan Africa