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

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

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

- Fasttee 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

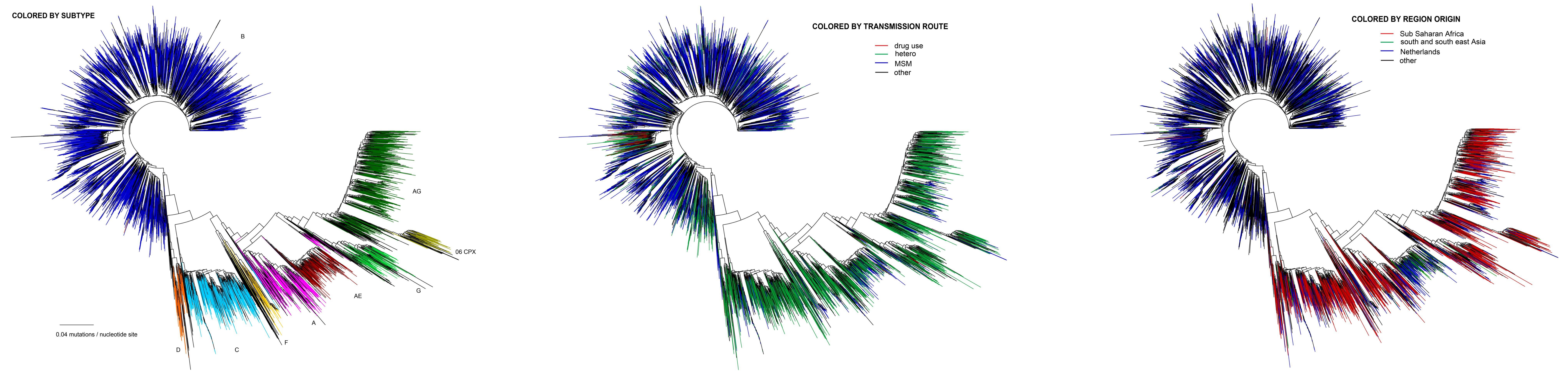

Fig.2 Phylogenetic tree of 9106 sequences colored by : subtype / route of transmission / region origin

RESULTS

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

Subtype	A	CRF01AE	CRF02AG	C	D	F	G	06cpx
Percentage (number) of sequences from MSM	13 (36)	34 (80)	14 (92)	13 (65)	6 (6)	45 (36)	5 (7)	12 (7)
Number of MSM clusters of size ≥2	3	16	7	7	1	3	2	1
Percentage (number) of sequences from MSM in clusters of size ≥2	78 (28)	79 (63)	90 (83)	74 (48)	50 (3)	86 (31)	71 (5)	57 (4)
Number of introductions counted amongst MSM	11	33	16	24	4	8	4	4
Mean outbreak size amongst MSM	3.3	2.4	5.8	2.7	1.5	4.5	1.8	1.8
Number of clusters with ≥10MSM	1	1	3	1	-	1	-	-
Percentage (number) of sequences from MSM in clusters with ≥10 MSM	42 (15)	16 (13)	76 (70)	43 (28)	-	67 (24)	-	-
Percentage of introductions amongst MSM that resulted in clusters with ≥10 MSM	9	3	19	4	-	13	-	-
Largest outbreak size amongst MSM	15	13	34	28	3	24	3	4
Median viral load in MSM at the first visit (10^3copies/ml)	49 (IQR: 13-107)	88 (IQR: 20-349)	49 (IQR: 12-166)	94 (IQR: 13-275)	46 (IQR: 38-585)	31 (IQR: 8-226)	88 (IQR: 21-349)	66 (IQR: 65-299)
Region origin MSM	64% NL	59% NL , 12%Thailand	68% NL	77% NL, 14% SSA	33% NL, 17% SSA	67% NL, 14% Lt-Am	71% NL	43% NL, 43% SSA
Region origin Heterosexual	72% SSA, 16% NL	51% NL, 32% Thailand	82% SSA, 12% NL	77% SSA, 18% NL	78% SSA, 14% NL	62% SSA, 16% Lt-Am	74% SSA, 14% NL	87% SSA
Percentage male Heterosexual	36	58	39	40	24	35	41	40

CONCLUSIONS

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

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