

ONGOING HIV-1 SUBTYPE B TRANSMISSION NETWORKS IN THE NETHERLANDS

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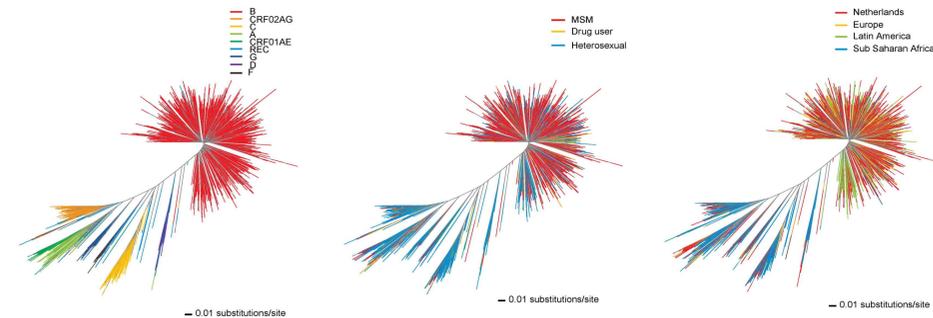
OBJECTIVE

Identify the transmission networks that constitute the HIV-1 epidemic amongst MSM in the Netherlands since the introduction of cART in 1996

DATA selection

As of November 2011 in the ATHENA database:

- 19,095 HIV-1-infected patients registered
- 7,589 (40%) have pol sequence available



5852 Subtype B polymerase sequences

- 73% (4288) MSM

International context of subtype B transmission networks:

- 10 most similar sequences available in Los Alamos database from other countries
- 2468 unique sequences added to the phylogenetic tree

TRANSMISSION NETWORK SELECTION FROM PHYLOGENETIC TREE

- In total 8,320 subtype B sequences in FastTree

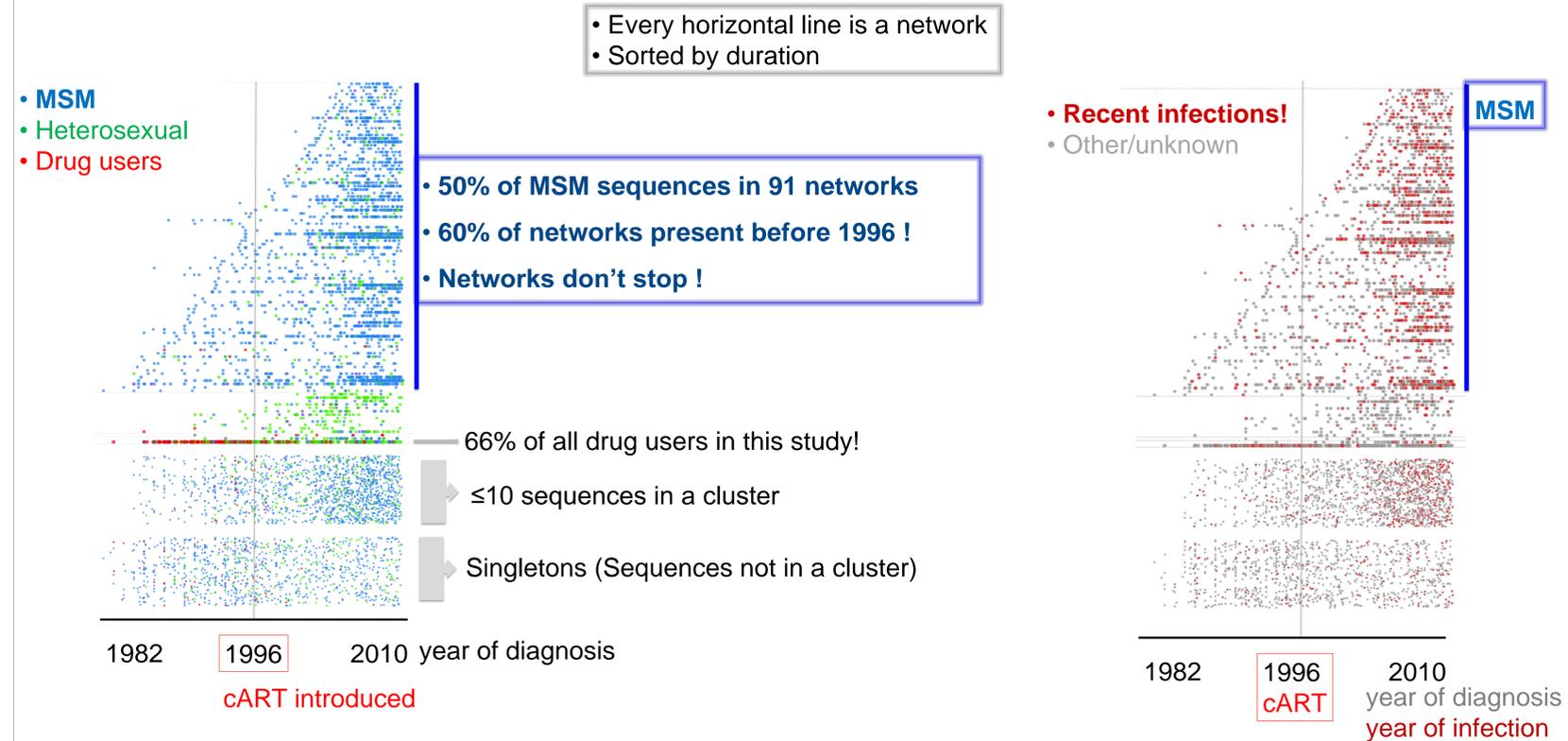
Definition of established national transmission networks:

- ≥ 10 ATHENA sequences in a phylogenetic cluster
- Bootstrap $\geq 90\%$
- Median pairwise patristic distance of the sub-tree is below the 5-10 percentile threshold of the whole-tree patristic distance distribution



RESULTS

ONGOING TRANSMISSION NETWORKS !



- MSM
- Heterosexual
- Drug users

- 50% of MSM sequences in 91 networks
- 60% of networks present before 1996 !
- Networks don't stop !

66% of all drug users in this study!

≤ 10 sequences in a cluster

Singletons (Sequences not in a cluster)

1982 1996 2010 year of diagnosis
cART introduced

1982 1996 2010 year of diagnosis
cART year of infection

- Age at diagnosis in the MSM pre-cART networks increased linearly by 0.38 years of age per calendar year between 1996-2010 ($p < 0.0001$)
- 'Los Alamos' sequences included in the MSM networks mainly form separate clusters

CONCLUSIONS

- The subtype B HIV-1 epidemic amongst MSM is sustained by multiple pre-cART transmission networks
- Networks are not brought to an end by the widespread use of cART
- Networks persist through transmission to next generations of MSM