ONGOING HIV-1 SUBTYPE B TRANSMISSION NETWORKS IN THE NETHERLANDS

Daniela Bezemer1, Oliver Ratmann2, Ard van Sighem1, Bas E. Dutilh4,6, Nuno R. Faria6, Rob van den Hengel1, Luuk Gras1, Peter Reiss1, Frank de Wolf2, Christophe Fraser2, and the ATHENA observational cohort

1 HIV Monitoring Foundation, Amsterdam, the Netherlands; 2 Imperial College, London, United Kingdom; 4 CMBI, Nijmegen, the Netherlands; 5 Federal University of Rio de Janeiro, Brazil; 6 University of Oxford, United Kingdom

dnladnla@gmail.com

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

RESULTS

• Every horizontal line is a network
• Sorted by duration
• Recent infections!
• Other/unknown

MSM
• 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
cART introduced year of diagnosis

• 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

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 ≥90%
• Median pairwise patristic distance of the sub-tree is below the 5-10 percentile threshold of the whole-tree patristic distance distribution