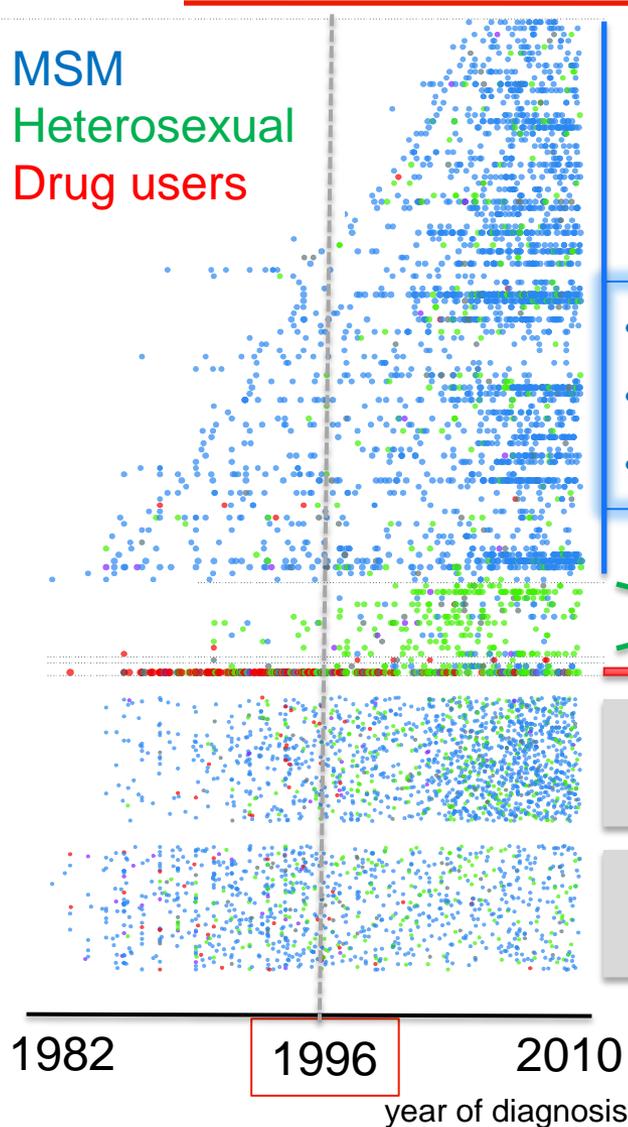


ONGOING HIV-1 SUBTYPE B TRANSMISSION NETWORKS IN THE NETHERLANDS

- MSM
- Heterosexual
- Drug users



- 5852 Subtype B polymerase sequences
- 73% (4288) MSM
- Transmission networks: ≥ 10 sequences, bootstrap $\geq 90\%$

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

Heterosexual networks

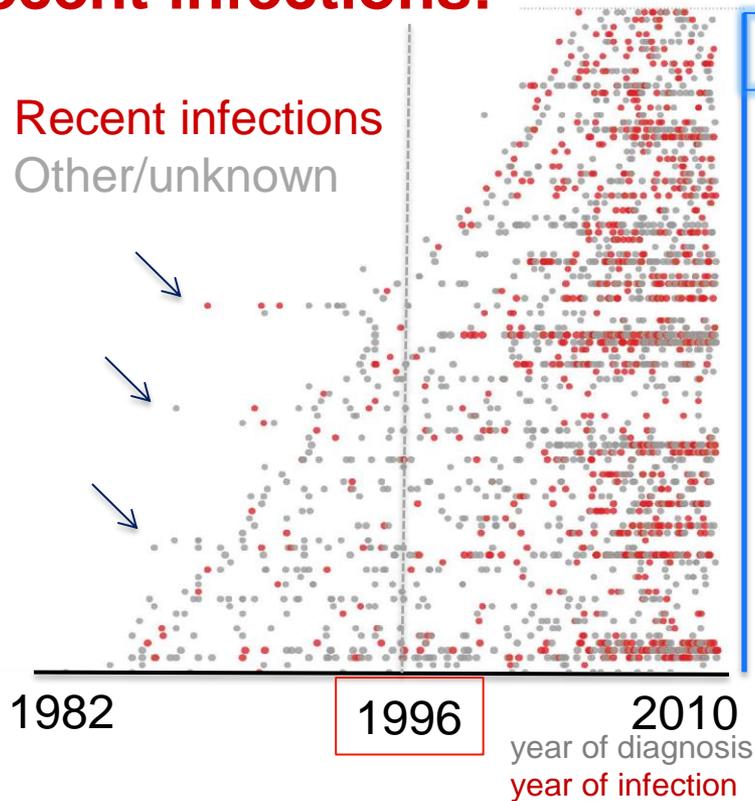
66% of all drug users in this study!

≤ 10 sequences in a cluster

Singletons (Sequences not in a cluster)

Recent infections!

- Recent infections
- Other/unknown



Networks are ongoing !

- Networks include recent infections
- Rejuvenation of pre-cART networks despite increasing median age

HIV-1 epidemic amongst MSM is sustained by well-established networks, not brought to an end by the widespread use of cART.

- Every horizontal line is a network
- Sorted by duration

Daniela Bezemer¹, Oliver Ratmann², Ard van Sighem¹, Bas E. Dutilh^{4,5}, 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, UK