

HIV-1 subtype B transmission networks in the Netherlands

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Background

We performed a study using polymerase HIV-1 subtype B sequences obtained from patients as part of resistance testing to get insight in **epidemiological and demographic characteristics of HIV-1 transmission** in the Netherlands in order to understand the heterogeneity and connectedness of the epidemic.

Methods

In recent literature, a pair-wise sequence difference $\leq 1.5\%$ is considered a **maximum distance for possible transmission pairs**. Applying this threshold criterion on all possible subtype B sequence pairs from which resistant-associated amino acid positions were deleted, we identified for each sequence the most likely transmission partner as the partner with the smallest pair-wise distance.

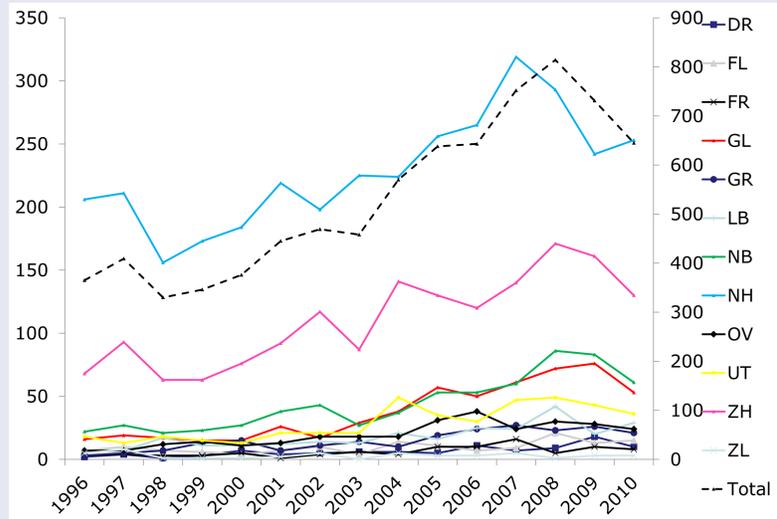
Results

As of January 2011, 29% (5537) of 18,872 patients included in the ATHENA nationwide observational cohort had an HIV-1 subtype B sequence. 45% (2482) of patients sequences resembled at least one other sequence, with a median of 3 (IQR = 1-8; Range 1-64). **73% (4039) of all sequences were obtained from MSM; 49% (1995) of these MSM sequences were part of a possible transmission pair.** Of these 1995 transmission pairs, **92% (1837) bore most resemblance to sequence obtained from other MSM**, whilst 4% (84) resembled a sequence from someone recorded to be heterosexually infected. **The age at diagnosis for MSM was 37.5 years (IQR 30.4-44.1).** The age difference between pairs was median 6.9 years (IQR 3.1-12.1). 48% of all patients were living in the province of North-Holland compared to 37% of the total population. 876 (of 2087) sequences from patients living in Amsterdam at HIV diagnosis are in pairs. Of these 67% (590) form a pair with an individual also from Amsterdam, in total 74% (635) form a pair with an individual from North-Holland and; 6% with an individual from Utrecht; and 9% with an individual from South-Holland. While for instance in total 55% of sequences samples taken from individuals living in Groningen and 37% of individuals living in Utrecht at diagnosis formed a pair with an individual living in the same province, and respectively 12% and 31% formed a pair with an individual from North-Holland.

Conclusions

The study indicates that HIV transmission takes mainly place on a local scale but it also shows **substantial geographic and generation connectedness**. However the study is limited by the fact that not all patients have their HIV sequence taken, and availability varies by region. The preliminary results presented in this abstract form part of an on-going phylogenetic study that aims to illustrate to what extent different sub-epidemics are present geographically over time, and will also consider non-B subtypes and sequences available online from the rest of the world.

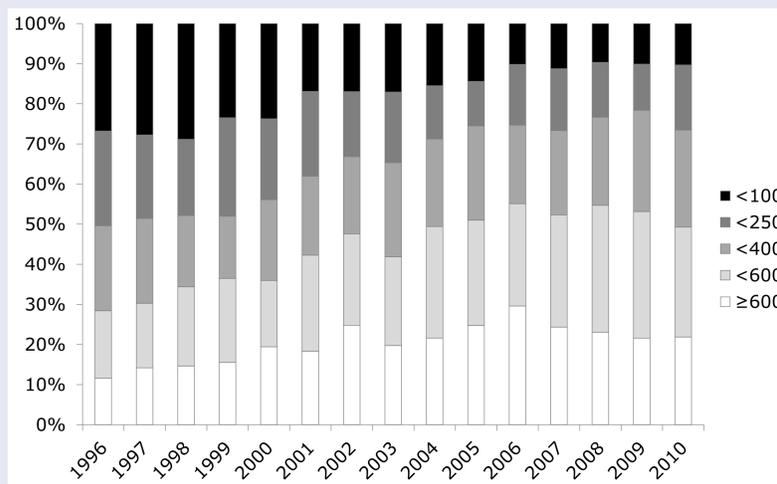
Annual number of HIV-1 diagnoses for MSM by province



Who & Where is the HIV-1 epidemic amongst MSM?

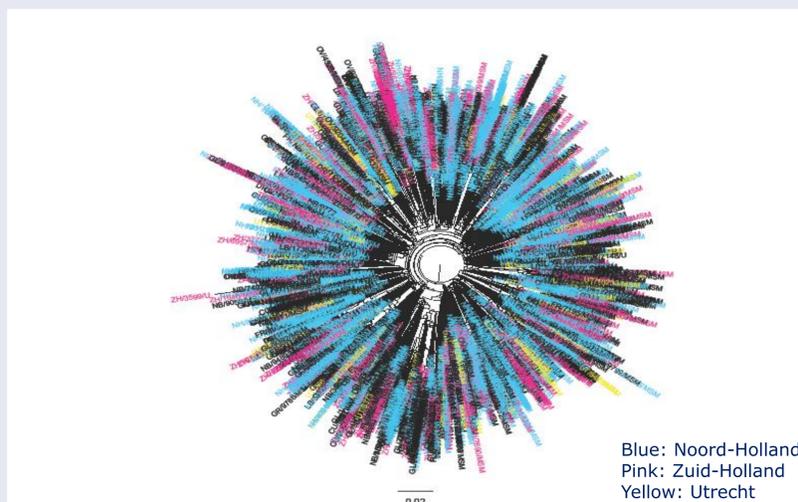
- **60% of diagnoses in Noord-Holland and Zuid-Holland**
- **Until 2008 an overall increase in annual diagnoses**
- **Opting-out testing policies since 2007 at several STI clinics might have caused a peak in diagnoses followed by a decrease in diagnoses**

CD4 count at diagnosis for MSM



- **Over time, HIV diagnosis at an earlier stage of infection**

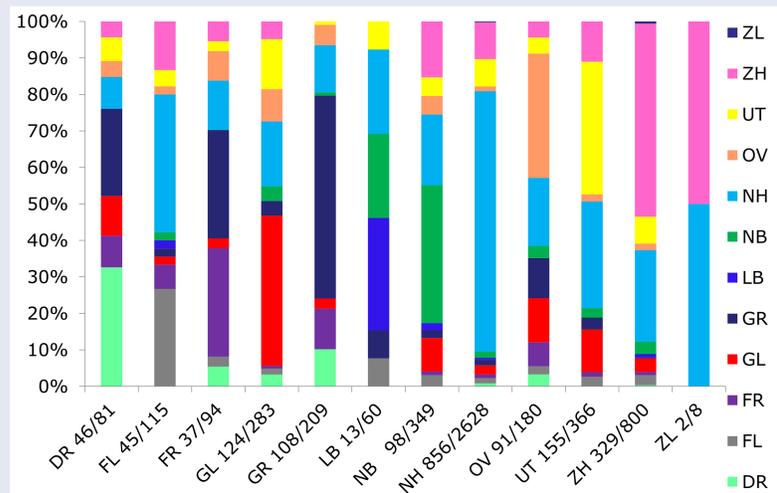
Phylogenetic tree of subtype B polymerase sequences



- **Provinces are mixed in the phylogenetic tree of pol sequences**
- **48% of sequences from Noord-Holland**

almost identical sequences
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most likely transmission pairs

Closest sequence pairs by province



- **Most transmission pairs within same province, neighbouring provinces or Noord-Holland**