Reconciling Named Partner and Genetic Partner HIV-1 Transmission Networks in New York City

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Use genetic network to determine if index case and named partner are genetically linked

NETWORK CONSTRUCTION

Named-Partner Network: Connect all index cases to the named partners to form clusters
Genetic Network: Connect all nodes separated by ≤1.75% substitutions/site to form clusters

CONCLUSIONS

• Genetic data analysis can augment partner tracing by identifying previously unknown parts of the transmission network (i.e. unnamed partners)

• At least half the connections in named-partner network did not lead to transmission

• MSM and male IDUs are less likely to be genetically linked to at least one named partner than heterosexual females

• Lack of naming information does not contradict the genetic data; it merely suggests an absence of epidemiological evidence supporting transmission

• More than half of genetic links supported by epidemiological data, and much of remaining half of the genetic links may represent transmission events

• Genetic data are more informative for inferring transmission partners

COMPARING NAMED PARTNER AND GENETIC NETWORKS

• Comparing named partner and genetic networks

• At least half the connections in named-partner network did not lead to transmission

• Genetic sequences help filter out many spurious connections implied by partner naming

• Lack of naming information does not contradict the genetic data; it merely suggests an absence of epidemiological evidence supporting transmission

• More than half of genetic links supported by epidemiological data, and much of remaining half of the genetic links may represent transmission events

• Genetic data are more informative for inferring transmission partners

Figures:

Figure 1. Genetic distance (TN93) separating index cases and named partners (A) Histogram depicting TN93 genetic distance between named partners. Index cases whose named partners are phylo-linked. (B) Genetic distance separating phylo-linked named partners and time between viral genotyping. Slope is consistent with known HIV-1 substitution rate.

Figure 2. Concordance between named partner and genetic networks. (A) Genetic data mapped onto named partner network. Edges indicate partner naming. (B) Partner naming data mapped onto genetic network. Edges indicate genetic linkage (≤0.0175 substitutions/site).

Table 1. Logistic regression analysis of index case being genetically linked to at least one of their named partners. Demographic

Table 2. Index case genetically linked (TN93 distance ≤1.75%) to reciprocally named partners (mt89 partner pair). Demographic

NYC FIELD SERVICES UNIT

• New York City Department of Health and Mental Hygiene (DOH) interviews persons with newly diagnosed HIV infection (index cases) and elicits named partners, who are notified of exposure and offered HIV testing

• When resistance testing is ordered by a physician with whom the case or positive partner has initiated care, the viral nucleotide sequence is reported to surveillance

• 756 index cases named 586 unique partners that were HIV positive and had a pol sequences reported to DOH between 2006 and 2012

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<th>Demographic</th>
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<td>MSM and male IDUs are less likely to be genetically linked to at least one named partner than heterosexual females</td>
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<td>Logistic model odds ratio = 3.72 (95% CI: 2.43–5.72)</td>
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