

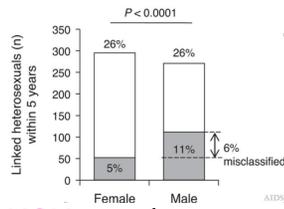


Nondisclosed MSM Link Together in HIV Transmission Networks



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on behalf of the UK HIV Drug Resistance Database

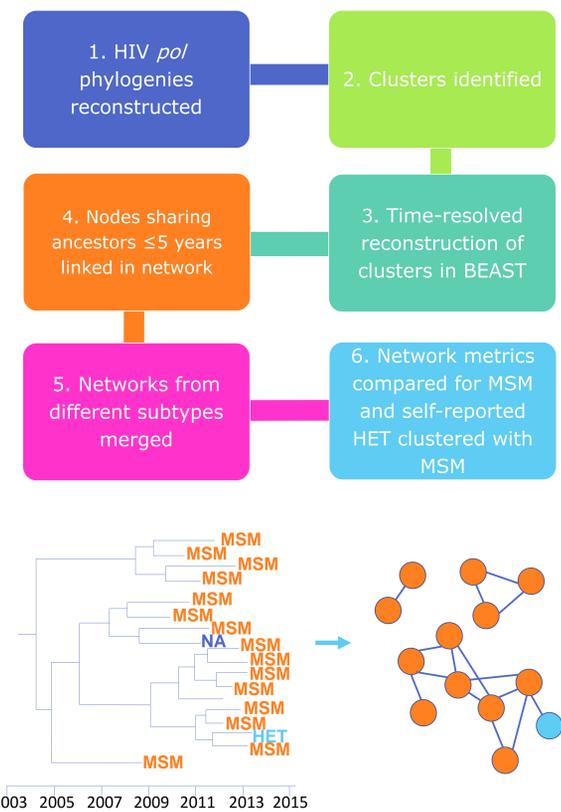
background



- MSM are the group at highest risk of HIV in the UK and globally
- Among them, those who **do not disclose** their same-sex behaviour are more likely to exhibit risky behaviour and to have sex with women
- Phylogenetic analysis has revealed that **29%** of self-reported **male HET cluster with MSM**¹
- We investigated **transmission network structure** among **risk groups** based on the relatedness of their **HIV sequences**.

MSM men who have sex with men
HETf female heterosexuals
HETm male heterosexuals

methods



- Sequences and epidemiological data (sex, risk group, ethnicity) come from the **UK HIV Drug Resistance Database**: 60,000 patients representing **~60% of UK cases**
- 50,025 UK HIV sequences were analysed along with 130,000 public sequences as background
- Phylogenies were reconstructed from subtype A1, B and C sequences
- Individuals were linked in the network (clustered) if their sequences shared an ancestor in the previous 5 years²
- Self-reported HET who clustered only with MSM were identified as **potential nondisclosed MSM (pnMSM)**
- The position (betweenness, assortativity and brokerage) and demographics of pnMSM in clusters was compared to that of MSM.

conclusions

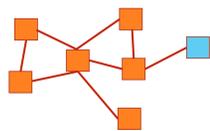
- Phylogenetic analysis can be used to classify HIV transmission route and provide insights on difficult to study populations
- A proportion of self-reported male heterosexuals are likely to have been infected through sex with men¹
- HETm in MSM clusters:
 - Are being **diagnosed later** than MSM
 - Are in **peripheral positions** indicating that they have fewer partners and transmit less between groups
 - Link to **each other**
 - May be putting **female partners** at risk.
 - May underestimate their own risk
 - May not **access services**/ feel targeted by prevention messages directed towards MSM

results

1. Demographics of pnMSM

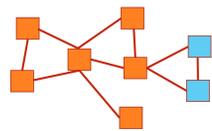
- 223 clusters comprised 955 MSM and 249 pnMSM (18% of all clustered HETm)
- pnMSM were:
 - more likely to be Black-African (Fisher's test, $p < 0.0001$),
 - less likely to have a recent infection (12.5% vs 74.9% of MSM, $p < 0.0001$)

2. PnMSM are in peripheral positions in MSM clusters

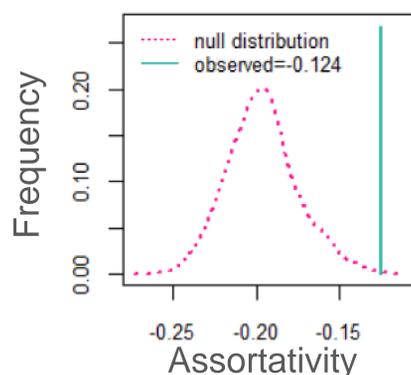


- Betweenness** measures how central to a node a cluster is (how many of the shortest paths go through it).
- We calculated betweenness for each pnMSM and compared it to the MSM they clustered with
- Betweenness was significantly lower for pnMSM than for other MSM (2.37 vs 4.11, $p < 0.005$)

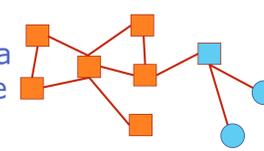
2. Nondisclosed MSM link to each other in MSM networks



- Assortativity** is the tendency for nodes that share attributes to link to each other
- We measured assortativity by self-reported risk group in clusters
- We analysed only clusters with at least 2 MSM and 2 pnMSM
- Observed assortativity was significantly higher than that estimated when labels were randomised within clusters (t.test, -0.124 vs -0.196 ; $p < 0.0001$)



3. Nondisclosed MSM may provide a bridge between the MSM and HET epidemics



- We used a **Gould-Fernandez brokerage analysis** to count the number of occurrences in the full network of two configurations:
 - HETf linking MSM and HETm
 - HETm linking MSM and HETf
- Self-reported **HETm were more likely to broker relationships between MSM and HETf** (Fisher's exact test $p < 0.0005$; OR 2.24).
- Of 1341 self-reported male heterosexuals in the network, 54 (4.02%) linked an MSM and a HETf, compared to only 32/1711 (1.87%) of HETf linking MSM and HETm.

references

- Hue *et al.*, "Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions," *AIDS* 28(13), 1967 (2014).
- Leigh Brown *et al.*, "Transmission network parameters estimated from HIV sequences for a nationwide epidemic," *J. Infect. Dis.* 204(9), 1463 (2011).

acknowledgements

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