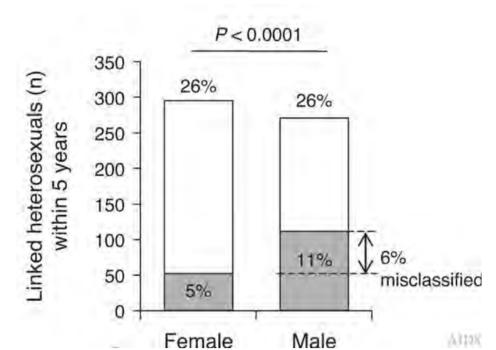


Nondisclosed MSM Link Together in HIV Transmission Networks



Manon Ragonnet-Cronin^{1,2}, Stéphane Hué³, Emma B. Hodcroft², Anna Tostevin⁴, David Dunn⁴, Anton Pozniak⁵, Tracy Fawcett⁶, Alison E. Brown⁷, Valerie Delpech⁷ and Andrew J. Leigh Brown² on behalf of the UK HIV Drug Resistance Database

background



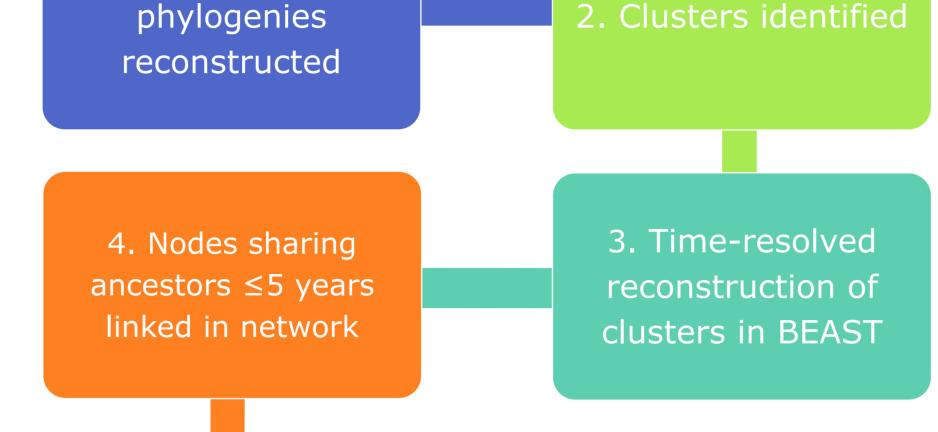
- are the group at highest risk of HIV in the UK and globally
- Among them, those who do not disclose their same-sex behaviour are more likely to exhibit risky behaviour and to have sex with women
- Phylogenetic analysis has revealed that 29% of selfreported male HET cluster with MSM¹
- We investigated transmission network structure among risk groups based on the relatedness of their HIV sequences.

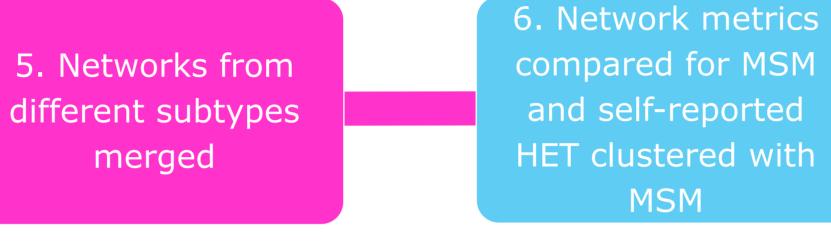
men who have sex with men

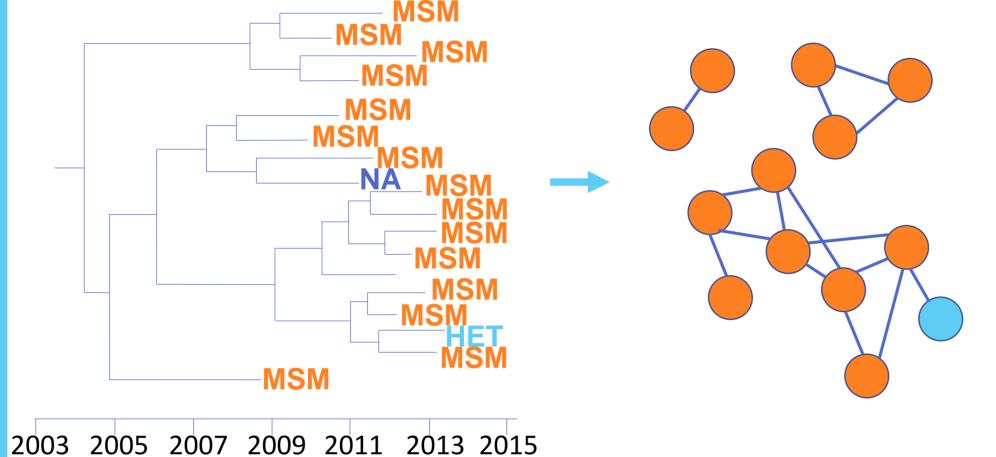
female heterosexuals

HETm male heterosexuals

methods 1. HIV pol







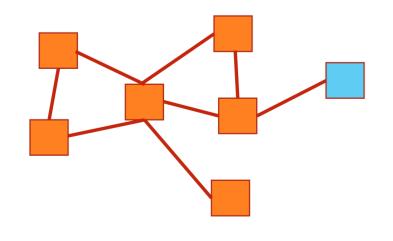
- Sequences and epidemiological data (sex, risk group, ethnicity) come from the UK HIV Drug Resistance Database: 60,000 patients representing ~60% of UK cases
- 50,025 UK HIV sequences were analysed along with 130,000 public sequences as background
- Phylogenies were reconstructed from subtype A1, B 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

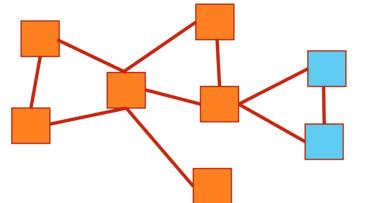
results

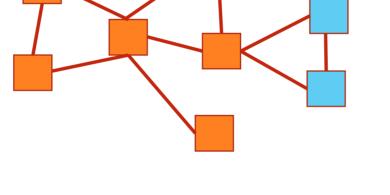
- 1. Demographics of pnMSM
- 223 clusters comprised 955 MSM and 249 pnMSM (18% of all clustered HETm)
- pnMSM were:
 - more likely to be Black-African (Fisher's test, p<0.0001),
 - less likely to have a recent infection (12.5% vs 74.9% of MSM, p < 0.0001)
- 2. PnMSM are in peripheral positions in MSM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



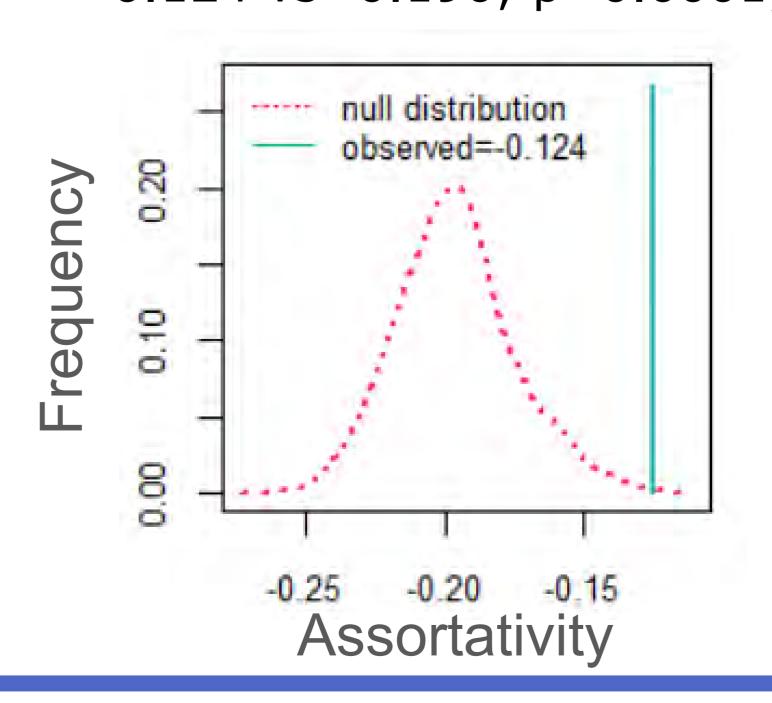
- Betweenness measures how central to a node a cluster is (how many of the shortest paths go through it).
- We calculated betweenness for each pnMSM and compared it to the MSM they clustered with
- Betweenness was significantly lower for pnMSM than for other MSM (2.37 vs 4.11, p<0.005)

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 selfreported 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)

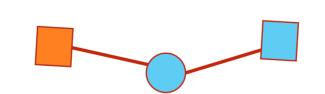


3. Nondisclosed MSM may provide a bridge between the MSM and HET epidemics



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

- 1. Hue et al., "Phylogenetic analyses reveal HIV-1 infections between men misclassified as heterosexual transmissions," AIDS 28(13), 1967 (2014).
- 2. 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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1 Department of Medicine, University of California, San Diego, USA; 2 Institute of Evolutionary Biology, University of Edinburgh, UK; 3 London School of Hygiene and Tropical Medicine, UK; 4 Research Department of Infection and Population Health, UCL, UK; 5 Chelsea and Westminster Hospital, London, UK; 6 Leeds Teaching Hospitals NHS Trust, UK; 7 Public Health England, London,

www.hivrdb.org

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