Phylogenetics of a Recent HIV Outbreak among People who Inject Drugs in Scotland

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background

- People who inject drugs (PWID) are at high risk for HIV if they share equipment
- Harm reduction in the UK and the rest of Europe dramatically decreased incidence in this group in the 1980s
- Recently a number of PWID outbreaks have been reported in Greece[1], Romania[2] and Ireland[3], linked to the economic recession, funding cuts, homelessness and the injection of new psychoactive substances
- In 2014 a rise of subtype C HIV diagnoses with two drug resistant mutations among PWID was noted in Scotland
- ➢ We used phylogenetic analysis to investigate whether cases were related and whether the strain had spread elsewhere in the UK

methods

- Phylogenetic analysis of viral sequences provides an alternative and independent route to reconstructing transmission networks
- The West of Scotland specialist virology centre sequences *pol* for all new HIV diagnoses
- The National Health Service portal collects clinical notes, including
  - hepatitis C status, date of last negative, sex, risk group, age, nationality, history of drug use, incarceration and homelessness
- All Scottish subtype C sequences were analysed (n=228)
- Closely related sequences from the UK HIV Drug Resistance Database (n=762) and from public databases(n=1144) were used as background

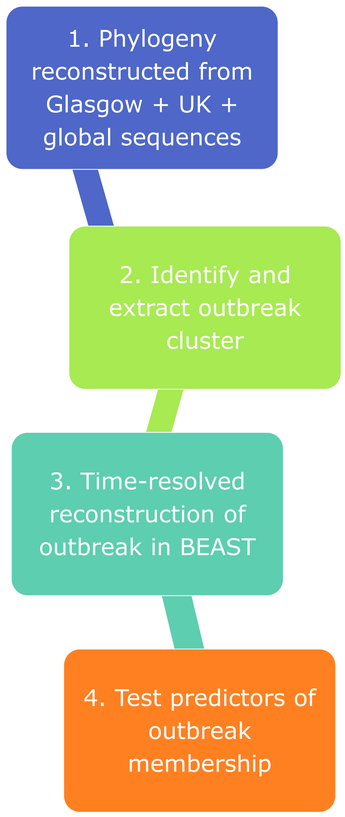


Figure 1: Phylogenetic and epidemiological analysis workflow

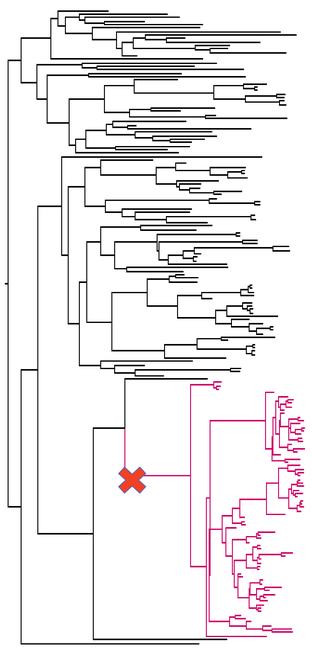
conclusions

- ➢ Over 100 linked HIV cases among PWID in Scotland, the biggest outbreak since the 1980s
- ➢ The strain hasn't been detected outside Scotland. Single network
- ➢ PWID with a history of homelessness were over-represented
- ➢ High rates of hepatitis C suggested needle sharing
- ➢ Rapid growth was seen after 2008, indicating a possible role for the economic recession
- ➢ Harm reduction services were not reduced in Scotland; however these are not being accessed.
- ➢ No association was seen between the outbreak and cocaine injection (and no patients reported injecting new psychoactive substances)
- ➢ Recent PWID outbreaks highlight a need for real-time phylogenetic analysis

results

1. Identification of outbreak cluster

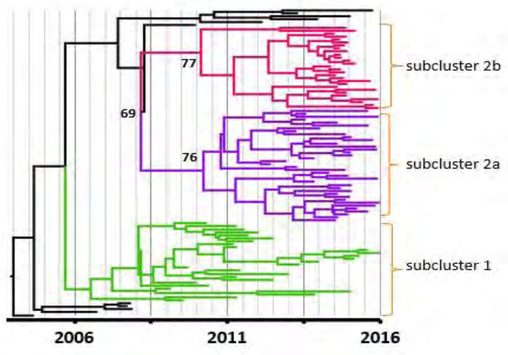
Figure 2: Maximum likelihood phylogeny of 2134 subtype C sequences



- Within phylogeny, tight cluster of 104 sequences with both mutations, all from Scotland
- Mean genetic distance <1% with 7 patients with *pol* sequences exactly identical to another, 2 pairs and 1 triad

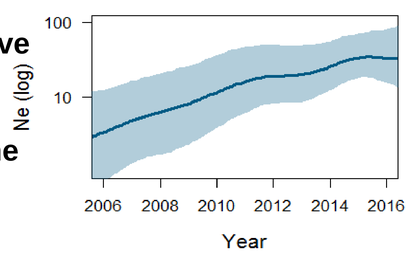
2. Spread among PWID has been rapid and recent

Figure 3: Time-resolved phylogeny of outbreak



- Common ancestor mid-2004
- Oldest outbreak sequence female PWID from 2005
- 2 active subclusters, 1 inactive
- Growth rate accelerated in 2008

Figure 4: Viral effective population size (Ne) through time



3. The role of needle sharing and homelessness

- Individuals in the outbreak were mostly male (61%), white British (99%), HCV positive (99%).
- 40% had a recorded history of incarceration and 45% reported having been homeless.
- We ran two binary logistic regression models

Comparing outbreak members and other subtype C diagnoses in Scotland

- PWID is a strong predictor: OR 124 (p<0.0001)

Comparing outbreak members to other Scottish HIV+ PWID

- Homelessness is a significant predictor: adjusted OR 3.91 (p=0.02)
- No role for cocaine injection (which increases injection frequency)

references

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2. Botescu A, Abagiu A et al. HIV/AIDS among injecting drug users in Romania: Report of a recent outbreak and initial response policies. In: European Monitoring Centre for Drugs and Drug Addiction; 2016.
3. Giese C, Igoe D et al. Injection of new psychoactive substance snow blow associated with recently acquired HIV infections among homeless people who inject drugs in Dublin, Ireland, 2015. Euro Surveill 2015; 20(40).

acknowledgements

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