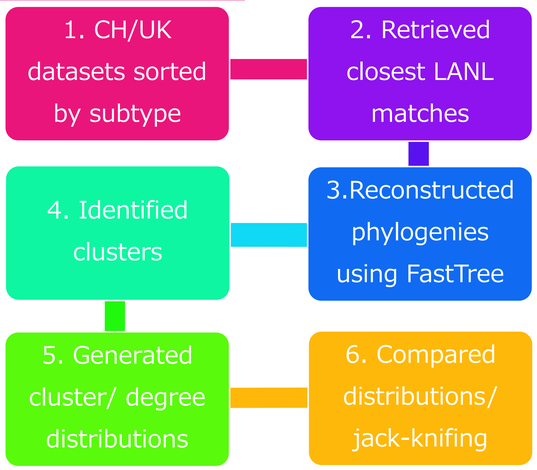
A Direct Comparison of two Densely Sampled Western European HIV Epidemics: the United Kingdom and Switzerland

Manon Ragonnet*[1], Mohaned Shilaih*[2], Huldrych Günthard[2], Jürg Böni[3], Sabine Yerly[4], David Dunn[5], Valerie Delpech[6], Roger Kouyos*[2] and Andrew Leigh-Brown*[1], on behalf of the Swiss HIV Cohort Study and the UK HIV Drug Resistance Database

background

- Switzerland (CH) and the UK have the most densely sampled HIV epidemics (60% coverage).
- The epidemics are historically similar.
- Published studies suggest different patterns of clustering, but this could be due to different cluster definitions and methods rather than to different epidemic dynamics.
- ➢ We applied the same **bioinformatics pipeline** to both datasets to **compare clustering patterns**.

methods



- Data from the UKdb and SHCS.
- No sensitive data shared.
- Degree distributions extrapolated from cluster distributions: cluster of 3 -> 3 individuals with degree 2.
- UK degree distribution down-sampled to investigate the effect of epidemic size.

MSM men who have sex with men
HET heterosexuals
IDU injection drug users

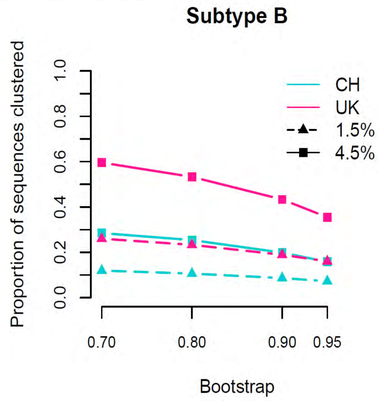
results

Figure 1: Epidemiological characteristics and subtype composition of the CH and UK epidemics

	CH	UK
	A1: 435 B: 8390 C: 419	A1: 2507 B: 31450 C: 15815
Sex	Female 24%	Female 26%
Risk	MSM 44%, HET 36%, IDU 17%	MSM 48%, HET 47%, IDU 2.6%
Ethnicity	White 88%	White 53%

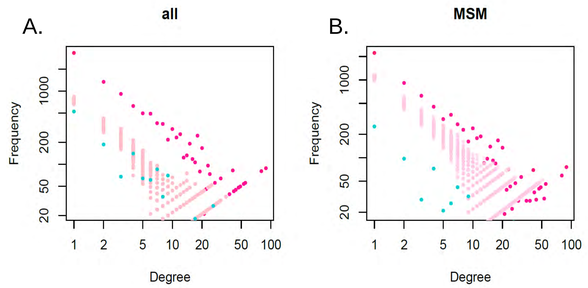
- UK has a larger non-B, non-White epidemic (Figure 1). UK subtype C has crossed over into non-HET risk groups.
- ➢ Analysis focused on subtype B.

Figure 2: Proportion of sequences clustering at different genetic distance (1.5% and 4.5%) and bootstrap (70%-95%) thresholds



- CH less clustered than UK at all thresholds: 16% vs 34% on average (Figure 2). Same pattern observed for subtypes A and C.
- UK has more larger clusters ($p<0.01$ for clusters larger than 11).
- ➢ Ukdb is more likely to capture partners.

Figure 3: Degree distribution for all risk groups (A.) and MSM only (B.)

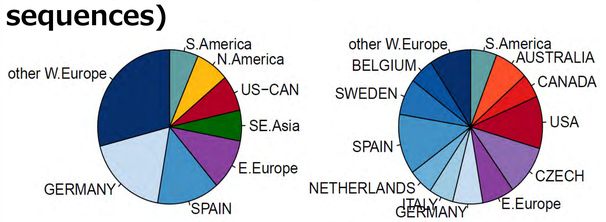


Note: CH is shown in blue , the UK in pink and the down sampled UK epidemic in pale pink (100 jack-knife replicates). Bootstrap=95%, GD=4.5%.

- UK subtype B 3.75 x CH dataset.
- UK dataset jack-knife sampled to same size.
- Degree distribution re-estimated.
- Jack-knifed UK samples more similar to CH (Fig 3A) → role of epidemic size.
- Among MSM, down sampled UK epidemic remained more clustered (Fig 3B) → epidemic size alone does not explain the difference between CH & UK.

- 17% of CH & 7% of UK clusters contain ≥1 foreign sequence (1.5% GD).
- Most linked sequences (>50%) came from other Western European countries.
- For the UK another 25% were from other Anglophone countries (Figure 4).

Figure 4: Origin of close foreign linkages for CH (93 sequences) & the UK (248 sequences)



conclusions

- We set out to compare clustering patterns between CH and the UK.
- Spread of non-B in CH is limited as compared to the UK and has not extended to MSM.
- CH is less clustered than the UK.
- Role of epidemic size: down sampled UK degree distributions much more similar to CH.
- Reduced clustering maintained among MSM → CH MSM more likely to be part of international clusters not captured by SHCS.
- Epidemic size, insularity and sampling time all play a part in explaining the differences observed.
- It remains difficult to disentangle the differences in contact processes, transmission processes and sampling procedures.

acknowledgements

1. University of Edinburgh, UK; 2. University Hospital Zurich, Switzerland; 3. University of Zurich; 4. University Hospital Geneva; 5. MRC Clinical Trials Unit, London; 6. Public Health England, London.

www.hivrdb.org
www.shcs.ch

This work was supported through the PANGEA-HIV Consortium with support provided by the Bill & Melinda Gates Foundation and by NIH GM110749.