Carnival meets Oktoberfest: Molecular Epidemiology of the HIV Epidemic in Three German Metropolitan Regions

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Background

- By inferring potential transmission links between risk groups, demographic subpopulations, and geography, one may better understand the drivers of HIV spread locally, and the links between epidemics outside the region.
- High rates of new HIV diagnoses are observed in Cologne/Bonn, Hannover, and Munich; regions which host some of the largest annual festivals in Europe (i.e. Oktoberfest, Carnival, Schuetzenfest, Christopher Street Day with 1 to 6 million visitors each).

Objective

To use molecular epidemiology to characterize the transmission dynamics of the HIV epidemic in three German metropolitan regions.

Methods

- **Participants:** 2,774 unique HIV positive individuals, receiving care at the University Hospital of Cologne/Bonn (n=1,766), Munich (n=641) and Hannover (n=334) in Germany.
- **HIV partial pol sequences, clinical and socio-demographic data were obtained between 1999 – 2016.**
- **Measures:**
  - Phylogenetic and network analyses were performed to infer putative relationships between all HIV partial pol sequences.
  - After quality filtering, putative transmission linkages were inferred when two sequences were ≤1.5% genetically different (TN93 distance measure).
  - Multiple inferred linkages were resolved into transmission clusters.
- We further applied a computationally efficient network based approach to analyze relationships between all publicly available HIV sequences (n=150,396) found in the Los Alamos National Laboratory HIV Sequence database [https://www.hiv.lanl.gov/content/index](https://www.hiv.lanl.gov/content/index).

Results

- **Characteristics of the sampled population:**
  - A German map of the sampled population using the first 3 numbers of the zip code of residence is displayed in **FIGURE 1.**
  - 595/2,774 (21.4%) sequences linked with at least one other sequence, forming 184 transmission clusters, ranging in size from 2 to 18 sequences; **FIGURE 2.**
  - Clustering individuals were significantly more likely to be younger, reporting MSM contact as main risk factor and infected with subtype B.
  - Among those reporting heterosexual sex as main risk factor, men were more likely to cluster than women (p<0.01). Of the 78 clustering men reporting heterosexual sex as main risk factor, 34 (43.6%) had links only with men reporting MSM contact.
  - 32/184 transmission clusters contained sequences from more than one region.
  - Clustering men were significantly more likely to be found in a position bridging regional HIV epidemics than clustering women (p=0.03).
- **By combining our sample with publicly available HIV sequences, we found a total of 236 clusters that linked sequences from our sample (total n=547) and LANL database (n=1,407, of which 31% were from other German centres).**

**Table. Population characteristics**

<table>
<thead>
<tr>
<th>Age [median (IQR)]</th>
<th>Not clustering, N=2,179 (78.6%)</th>
<th>Clustering, N=595 (21.4%)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male Sex</td>
<td>1,681 (77.1)</td>
<td>540 (90.7)</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>Subtype B</td>
<td>1,510 (69.2)</td>
<td>532 (89.4)</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>Risk</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MSM</td>
<td>1,053 (48.3)</td>
<td>395 (66.3)</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>HTS</td>
<td>509 (23.3)</td>
<td>113 (18.9)</td>
<td></td>
</tr>
<tr>
<td>IDU</td>
<td>111 (5)</td>
<td>26 (4.3)</td>
<td></td>
</tr>
<tr>
<td>ENDEMIC*</td>
<td>285 (13)</td>
<td>7 (1.1)</td>
<td></td>
</tr>
</tbody>
</table>

**Figure 1: Map of sampled population**

**Figure 2: HIV Transmission Network by region, sex and risk behavior**

Conclusions

- **Transmission clusters were mostly comprised of younger MSM.**
- **Links between HIV risk groups were frequent and mostly observed between men reporting heterosexual sex as main risk and MSM.**
- Regional epidemics were interlinked (primarily men to men links) and also linked to other epidemics across Germany and the world.
- Men were more likely to be found in a position bridging regional HIV epidemics than women.
- Results highlight the pitfalls of focusing prevention efforts on specific risk groups or specific locales.