GEOSPATIAL SPREAD OF HIV IN THE COLOGNE-BONN REGION, GERMANY FROM 2001-2016

Melanie Storch1,2, Martin Hoersch3, Anna Maria Eit-Hübinger3, Clara Lehmann1,2, Gerd Falkenheuer1,2, Jan-Christian Wasmuth2, Elena Knopf4, Jörg Janne Vehreschild5, Sanjay Mehta6, Antoine Challier7

1Department of Internal Medicine, University Hospital of Cologne, Cologne, Germany; 2German Center for Infection Research (DZIF), partner site Bonn-Cologne, Cologne, Germany; 3German Center for Infection Research (DZIF), partner site Bonn-Cologne, Bonn, Germany; 4Department of Internal Medicine I, University Hospital of Bonn, Bonn, Germany; 5Institute of Virology, University Hospital of Cologne, Cologne, Germany; 6Department of Medicine, San Diego VA Medical Center, San Diego, CA, USA

Poster no. 1280

Background

- The overall rate of new HIV infections is still increasing with a current incidence of 4.5 per 100,000, in Germany [1].
- The metropolitan region of Cologne-Bonn has one of the highest rates of new HIV infections in Western Europe (13.7 per 100k) in 2016 [2].
- Men having sex with men (MSM) bear the major burden, with 67.4% of all new HIV diagnoses in Germany occurring amongst MSM in 2017 [1].
- The high incidence among MSM in the Cologne-Bonn region may be related to several factors.
- There is a well-known MSM party scene in central Cologne [2].
- An increased prevalence of high risk behaviors associated with chemsex, which involves the use of methamphetamine, methedrone, poppers, or cocaine [3].

Objective

Providing insights into the drivers of the HIV-1 transmission of the Cologne-Bonn area

Methods

Population:

- Sociodemographic, geographic data, and pol sequence data were collected from individuals diagnosed at the University Hospital in Cologne and Bonn, between 2001 and 2016.
- 714 HIV-1 infected Antiretroviral Therapy (ART) naïve individuals, followed at the University Hospital Cologne (n=558; 78.2%) and Bonn (n=156; 21.9%) between 2001 and 2016.

Sequence Analysis and Network Inferences:

- Genetic network analyses were performed to infer putative relationships between HIV partial pol sequences.
- We used HIV-TRACE software (HIV TRansmission Cluster Engine: www.hivtrace.org) to infer transmission links between sequences with a genetic distance ≤1.5% [4].
- Sociodemographic and geographic data were used to characterize transmission clusters (Table 1).

Geospatial analyses:

- Assortativity index (AI, i.e. shared attributes) and characteristics of genetically linked individuals were analyzed.
- The geospatial diffusion of the local epidemic (i.e. viral gene flow) was evaluated using a Slatkin-Maddison approach [5] implemented in HyPhy [6].
- Geospatial dispersal of the clusters was determined by calculating the average distance between reported residence (centroids of 3-digit zip code, ArcGIS®) of genetically linked individuals using R packages maptools [7] and mapdata [8].

Results

- The HIV transmission network annotated by risk group and residence location is displayed in Figure 1A&B. 217/714 (30.4%) sequences had a putative linkage with at least one other sequence, forming 77 transmission clusters ranging in size from two to eight individuals.
- Figure 2 shows the inferred putative links and numbers of clustering individuals (blue circles) based on the centroid of zip code of residence.
- Median distance between genetically linked individuals was 23.4 kilometers (IQR 11.3-34.6), which was significantly lower than the median distance of any random sub-sampled population (median 39.68 kilometers) (IQR 23.79-62.59), p<0.001 (Figure 3A).
- Slatkin-Maddison analyses revealed increased gene flow from central Cologne towards the surrounding areas (p<0.001) (Figure 3B).
- Assortativity analysis showed, that genetically linked individuals were more likely to live in a different zip code (AI=0.0028, p=0.046) (Figure 3C).

Table 1. Population Characteristics. Baseline demographic, risk and cox characteristics in learning and non clustering individuals.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Total</th>
<th>Non-clustering</th>
<th>Clustering</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age: ≤30</td>
<td>157 (19.6)</td>
<td>58 (16.1)</td>
<td>99 (24.6)</td>
<td>0.055</td>
</tr>
<tr>
<td></td>
<td>31-40</td>
<td>265 (32.4)</td>
<td>97 (24.3)</td>
<td>0.124</td>
</tr>
<tr>
<td></td>
<td>41-50</td>
<td>211 (26.1)</td>
<td>80 (19.7)</td>
<td>0.051</td>
</tr>
<tr>
<td></td>
<td>51-60</td>
<td>59 (7.2)</td>
<td>19 (4.7)</td>
<td>0.176</td>
</tr>
<tr>
<td></td>
<td>&gt;60</td>
<td>35 (4.3)</td>
<td>16 (4.0)</td>
<td>0.720</td>
</tr>
<tr>
<td>Gender: Male</td>
<td>365 (45.1)</td>
<td>149 (42.8)</td>
<td>216 (54.5)</td>
<td>0.064</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>349 (43.2)</td>
<td>162 (40.8)</td>
<td>0.259</td>
</tr>
<tr>
<td>Residence: Bonn</td>
<td>100 (13.1)</td>
<td>41 (11.4)</td>
<td>59 (14.5)</td>
<td>0.491</td>
</tr>
<tr>
<td></td>
<td>Cologne</td>
<td>414 (51.1)</td>
<td>226 (56.2)</td>
<td>0.088</td>
</tr>
<tr>
<td>Sequence length</td>
<td>520 (69.4)</td>
<td>283 (74.5)</td>
<td>237 (59.9)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Zip code length</td>
<td>270 (31.5)</td>
<td>167 (44.3)</td>
<td>103 (25.5)</td>
<td>0.048</td>
</tr>
<tr>
<td>Total</td>
<td>217/714 (30.4)</td>
<td>121/374 (37.3)</td>
<td>96/340 (28.2)</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

Conclusion

- We inferred significant gene flow from the city center of Cologne to the surrounding areas, highlighting the role of this area in the transmission dynamics of the regional epidemic.
- We found evidence that HIV-1 transmission in Cologne-Bonn is between MSM residing closer together, but not in the same neighborhood, suggesting that geographically focused prevention efforts should encompass clusters of adjacent neighborhoods.
- Our findings highlight the importance of phylogeographic analysis to get a better understanding of local transmission clusters.
- The knowledge of these patterns can improve the efficiency of prevention and intervention efforts and can help health entities to allocate resources.
- In addition, resources can be used to ensure that strategies are optimal for priority risk groups and areas of greatest need.