Networks, phylogenetics:intervention transmission
## Disclosure

<table>
<thead>
<tr>
<th>Category</th>
<th>Companies/funders</th>
</tr>
</thead>
<tbody>
<tr>
<td>Research grants</td>
<td>Merck, Gilead</td>
</tr>
<tr>
<td>Speakers fee</td>
<td>Viiv, Abvie, Gilead</td>
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<tr>
<td>Other</td>
<td>Co-owner/scientific director Virology Education</td>
</tr>
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</table>
How can we use (real time) phylogenetics/sexual networks insights to optimise transmission interventions

How can we use (real time) phylogenetics/sexual networks insights to evaluate these interventions
End HIV transmission

- Great enthusiasm for decreasing the number of new HIV infections:
  - Global goal UNAIDS: no new HIV infections by 2030.
Transmission prevention

- **Source:** find (early) and treat/counsel, keep them suppressed

- **Recipient:** behaviour, biomedical prevention
Challenges phylogenetics & networks

1. Dense sampling
2. Timing of samples (ideally all recent infections)
3. Detailed epidemiological information regarding risk (group, behaviour)
Sources of HIV infection among men having sex with men and implications for prevention

Oliver Ratmann,¹* Ard van Sighem,² Daniela Bezemer,² Alexandra Gavryushkina,³ Suzanne Jurriaans,⁴ Annemarie Wensing,⁵ Frank de Wolf,¹ Peter Reiss,²,⁶ Christophe Fraser,¹ ATHENA observational cohort
1. Sources of HIV infection among MSM and implications for prevention
2. Dutch cohort 11863 MSM,
3. Identified the source for 617 recent infections (1996-2010) by phylogenetic analysis of chronic infections
Sources 1996-2010

1. 71% from undiagnosed men
2. 43% from men in their first year of infection
3. 6% from men who started therapy
Conclusions

1. Lack of substantial reductions is due to frequent early transmission and continued low testing rate of men at risk of transmission

2. Increased annual testing and uptake of PREP in high risk MSM key role.
Near real-time monitoring of HIV transmission hotspots from routine HIV genotyping: an implementation case study

Art F Y Poon, Réka Gustafson, Patricia Daly, Laura Zerr, S Ellen Demlow, Jason Wong, Conan K Woods, Robert S Hogg, Mel Krajden, David Moore, Perry Kendall, Julio S G Montaner, P Richard Harrigan
• Routine resistance genotyping for all new infections in British Columbia
• Analysed and followed clusters, if >5 individuals the characteristics of clusters were shared with public health officials
• Anonymous
# Ten most active clusters

<table>
<thead>
<tr>
<th>New cases</th>
<th>Current size</th>
<th>MSM</th>
<th>IDU (%)</th>
<th>On therapy</th>
<th>TDR*</th>
<th>PCS=0†</th>
<th>Age ≤30 years‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>11</td>
<td>414</td>
<td>10/280 (4%)</td>
<td>245/294 (8%)</td>
<td>214/325 (66%)</td>
<td>11/204 (4%)</td>
<td>30/313 (10%)</td>
</tr>
<tr>
<td>1</td>
<td>7</td>
<td>84</td>
<td>48/52 (92%)</td>
<td>10/59 (17%)</td>
<td>64/78 (82%)</td>
<td>1/78 (1%)</td>
<td>22/78 (28%)</td>
</tr>
<tr>
<td>3</td>
<td>9</td>
<td>86</td>
<td>45/51 (88%)</td>
<td>9/57 (16%)</td>
<td>65/79 (82%)</td>
<td>1/76 (1%)</td>
<td>25/78 (32%)</td>
</tr>
<tr>
<td>7</td>
<td>23</td>
<td>99</td>
<td>45/48 (94%)</td>
<td>7/56 (12%)</td>
<td>68/88 (77%)</td>
<td>0/81</td>
<td>42/87 (48%)</td>
</tr>
<tr>
<td>17</td>
<td>4</td>
<td>48</td>
<td>24/30 (80%)</td>
<td>6/34 (18%)</td>
<td>31/46 (67%)</td>
<td>0/43</td>
<td>7/44 (16%)</td>
</tr>
<tr>
<td>49</td>
<td>5</td>
<td>26</td>
<td>11/12 (92%)</td>
<td>3/12 (25%)</td>
<td>21/24 (88%)</td>
<td>0/23</td>
<td>15/24 (62%)</td>
</tr>
<tr>
<td>55</td>
<td>12</td>
<td>49</td>
<td>28/29 (97%)</td>
<td>3/31 (10%)</td>
<td>38/49 (78%)</td>
<td>17/48 (35%)</td>
<td>22/49 (45%)</td>
</tr>
<tr>
<td>200</td>
<td>4</td>
<td>18</td>
<td>8/10 (80%)</td>
<td>1/13 (8%)</td>
<td>10/15 (67%)</td>
<td>0/13</td>
<td>1/14 (7%)</td>
</tr>
<tr>
<td>203</td>
<td>7</td>
<td>9</td>
<td>9/9 (100%)</td>
<td>0/9</td>
<td>8/9 (89%)</td>
<td>8/8 (100%)</td>
<td>3/8 (38%)</td>
</tr>
<tr>
<td>217</td>
<td>5</td>
<td>8</td>
<td>4/5 (80%)</td>
<td>1/7 (14%)</td>
<td>8/8 (100%)</td>
<td>0/8</td>
<td>0/8</td>
</tr>
</tbody>
</table>

Data are n/N (%). MSM—men who have sex with men. IDU—injecting drug users. TDR—transmitted HIV drug resistance. PCS—programmatic compliance score. *Before treatment. †A PCS of 0 indicates complete adherence to the International Antiviral Society-USA treatment guidelines. ‡At first sample collection date.

**Table:** Summary statistics of the ten most active phylogenetic clusters from October, 2014, to October, 2015
Search and Destroy: Source

- Initiate treatment in index case and keep him/her in care (clinical guidelines, treatment as prevention)
- Trace contacts (counsel partners),
- Test
- Treat
- Keep them in care
Limitations and Challenges

- Ethical and legal and cultural (stigma) considerations which differ per setting
- Density: The more and the earlier infections are diagnosed the easier it become to perform cluster analysis (screening strategies)
Discussion

- How can we use (real time) phylogenetics/sexual networks insights to optimise transmission interventions
- How can we use real time phylogenetics/sexual networks insights to evaluate these interventions
Way forward

- We propose to install (real time) phylogenetical and epidemiological based surveillance networks for all new HIV infections.
- Use the insights generated by these systems to develop mathematical models to design cost effective intervention strategies.
- To implement search and destroy strategies.