PHYLOGENETICS OF THE DANISH HIV EPIDEMIC:
-THE ROLE OF VERY LATE PRESENTERS
BACKGROUND

- Very late presenters (VLP)
  - CD4 cell count < 200 cells/mm³
AIM

To describe the HIV epidemic in Denmark based on sequences from newly diagnosed individuals, with special emphasis on very late presenters (VLP)
DATA COLLECTIONS

Danish HIV Sequence Database

National Surveillance of HIV and AIDS

Anne M. Audelin: aud@ssi.dk
THE DANISH HIV EPIDEMIC

- MSM: 46%
- HTX: 37%
- IDU: 6%
- OTH: 11%
PHYLOGENY, – CLUSTER DEFINITION

- Evolutionary relationship between species
  - Illustration of sequence similarities
  - Assume epidemic link

Cluster definition:

- Number of sequences
  - > 3

- Bootstrap (1000 replicas)
  - > 90%

- Average intra-clustal branch length
  - < 0.015 nucleotide sub. / site

- Cluster diameter
  - < 0.025 nucleotide sub. / site

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Presented at the 10th Eu Meeting on HIV & Hepatitis, 28-30 March 2012, Barcelona
RESULTS - HIV PHYLOGENY

1515 sequences from 1515 individuals

46 clusters

1/3 of all patients

Neighbor Joining tree, of Pr and RT ~1200 bp
### RESULTS - PHI CLUSTER

<table>
<thead>
<tr>
<th></th>
<th>Count</th>
<th>Cluster Count (%)</th>
<th>Non-Cluster Count (%)</th>
<th>Univariate p-value¹</th>
</tr>
</thead>
<tbody>
<tr>
<td>PHI</td>
<td>260</td>
<td>133 (51%)</td>
<td>127 (49%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>VLP</td>
<td>460</td>
<td>100 (22%)</td>
<td>360 (88%)</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

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## RESULTS - RISK GROUPS CLUSTER

### MSM Cluster
- **No. clusters**: 37
- **Cluster Count (%)**: 337 (67%)
- **Non-Cluster Count (%)**: 359 (35%)
- **Univariate p-value**: <0.001

### HTX Cluster
- **No. clusters**: 4
- **Cluster Count (%)**: 82 (16%)
- **Non-Cluster Count (%)**: 474 (47%)
- **Univariate p-value**: <0.001

### IDU Cluster
- **No. clusters**: 5
- **Cluster Count (%)**: 54 (12%)
- **Non-Cluster Count (%)**: 40 (4%)
- **Univariate p-value**: <0.001
RESULTS - HIV PHYLOGENY

82 Patients
1/3 PHI
1/8 VLP

2001-2010
## MULTIPLE LOGISTIC REGRESSION

<table>
<thead>
<tr>
<th></th>
<th>Cluster Count (%)</th>
<th>Non-Cluster Count (%)</th>
<th>OR</th>
<th>95% CI</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subtype B</td>
<td>478 (89%)</td>
<td>538 (53%)</td>
<td>8.9</td>
<td>5.5-14.5</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>IDU</td>
<td>54 (12%)</td>
<td>40 (4%)</td>
<td>3.1</td>
<td>1.6-6.0</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Danish infection</td>
<td>373 (74%)</td>
<td>391 (39%)</td>
<td>2.5</td>
<td>1.9-3.3</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>MSM</td>
<td>337 (67%)</td>
<td>359 (35%)</td>
<td>2.2</td>
<td>1.3-3.7</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Danish origin</td>
<td>379 (76%)</td>
<td>507 (50%)</td>
<td>1.4</td>
<td>1.0-1.9</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>
## RESULTS – CHARACTERISTICS OF CLUSTER SIZE

<table>
<thead>
<tr>
<th></th>
<th>Clustering</th>
<th>Non Clustering</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Large (&gt;10)</td>
<td>Medium (7-10)</td>
</tr>
<tr>
<td>Number patients</td>
<td>294</td>
<td>130</td>
</tr>
<tr>
<td>Age, years Median (IQR)</td>
<td>34 [29-41]</td>
<td>38 [31-47]</td>
</tr>
<tr>
<td>PHI (%)</td>
<td>101 (34%)</td>
<td>19 (15%)</td>
</tr>
<tr>
<td>VLP</td>
<td>32 (12%)</td>
<td>39 (28%)</td>
</tr>
<tr>
<td>MSM</td>
<td>215 (73%)</td>
<td>68 (52%)</td>
</tr>
<tr>
<td>HTX</td>
<td>32 (11%)</td>
<td>35 (27%)</td>
</tr>
<tr>
<td>IDU</td>
<td>33 (11%)</td>
<td>19 (15%)</td>
</tr>
<tr>
<td>Log$_{10}$VL (mean, SD)</td>
<td>4.7 (0.75)</td>
<td>4.8 (0.8)</td>
</tr>
</tbody>
</table>
CONCLUSIONS

- Primary source of HIV epidemic
  - Younger
  - MSM

- Very late presenters
  - mainly outside clusters
  - if in cluster, small clusters
  - diagnosis for better prognosis
ACKNOWLEDGEMENT

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