C13 - Monitoring HIV incidence

CDC0365 - Phylogenetic analysis of Taiwanese HIV-1 CRF_07BC strains: tracing the origin and dissemination of this CRF in Taiwan

Y.-J. Chen¹, Y.-H. Huang¹, S.-F. Lai², Y.-M. Chen²
¹National Yang-Ming University, Institute of Public Health, Taipei, Taiwan, Republic of China, ²National Yang-Ming University, AIDS Prevention and Research Center, Taipei, Taiwan, Republic of China

Background: Previously, we reported that there was an outbreak of HIV-1 CRF_07BC among injecting drug users (IDUs) in Taiwan in 2004 and 2005. The objectives of this study were a.) to identified recent seroconverters (RS) among IDUs from prisons; and b.) to conduct a phylogenetic analysis to trace the origin and dissemination of this CRF in Taiwan.

Methods: Blood and questionnaires were collected from 351 HIV-1-seropositive inmates from 6 prisons in 2004 and 2005. RS were identified using the Calype HIV-1 BED Incidence EIA. Subtypes were determined using PCR and DNA sequencing. Phylogenetic analysis was conducted using 572-bp nucleotide (nt) sequence from V3 to V5 region of env gene.

Results: 41.6% of HIV-1-seropositive inmates were identified as RS (infection within 153 days). 100% of the IDUs from the Nantou County in the central region were RS. Among 301 patients whose subtypes were determined, 279 (93%) had CRF_07BC infection. Phylogenetic analysis using neighbor-joining demonstrated that they belonged to two clusters. All of 42 strains from the southern regions clustered with CRF_07BC strains from Yunnan province of mainland China (cluster I). The other 237 strains from the central and northern regions were in another cluster with a bootstrap value of 75. The nucleotide sequence variations between different groups were shown in the table.

<table>
<thead>
<tr>
<th>Groups</th>
<th>Cluster Ⅰ</th>
<th>Cluster Ⅱ</th>
<th>07.BC.CN.97.CN54</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cluster Ⅰ</td>
<td>0.010 (1.0%)</td>
<td>0.014 (1.4%)</td>
<td>0.052 (5.2%)</td>
</tr>
<tr>
<td>Cluster Ⅱ</td>
<td>0.014 (1.4%)</td>
<td>0.005 (0.5%)</td>
<td>0.054 (5.4%)</td>
</tr>
</tbody>
</table>

| 07.BC.CN.97.CN54 | 0.052 (5.2%) | 0.054 (5.4%) | - |

Note:

a: including 41 isolates.
b: including 204 isolates.
c: including 8 isolates in database.

Conclusions: There were two clustered of CRF_07BC infection among IDUs in Taiwan and they originated from a single source. It was first transmitted to the southern region (Tainan County) in 2002, after 1 to 2 years, the infection was further spread to the central and northern regions of Taiwan.