

### 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. Chen<sup>1</sup>, Y.-H. Huang<sup>1</sup>, S.-F. Lai<sup>2</sup>, Y.-M. Chen<sup>2</sup>

<sup>1</sup>National Yang-Ming University, Institute of Public Health, Taipei, Taiwan, Republic of China, <sup>2</sup>National 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 identify 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 Calypte 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.

Groups	Cluster	Cluster	07_BC.CN.97.CN54
Cluster	0.010 ( 1.0 % )	0.014 ( 1.4 % )	0.052 ( 5.2 % )
Cluster	0.014 ( 1.4 % )	0.005 ( 0.5 % )	0.054 ( 5.4 % )
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.

(07BC.CN.97.97CN001 - 07BC.CN.97.C54A - 07BC.CN.97.C54D - 07BC.CN.97.C54D - 07BC.CN.97.CN54 - 07BC.CN.97.C54 - 07BC.CN.98.98CN009 - 07BC.CN.-.CNGL179)

**Conclusions:** There were two clusters 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.