

## POSTER 72

### UNUSUAL EVOLUTIONARY CHARACTERISTICS OF CRF15\_01B: EVIDENCE FOR PREFERRED CONFIGURATION OF HIV-1 RECOMBINATION

Yutaka Takebe, Yue Li, Huanan Liao, Saiki Hase, and Rie Uenishi

AIDS Research Center, National Institute of Infectious Diseases, Tokyo 162-8640, Japan

Reconstruction of both evolutionary history and spatial process from viral genome information provides fundamental understanding of the evolutionary dynamics underlying epidemics. We applied newly developed phylogenetic inference tools (Bayesian molecular clock and phylogeography methods) to elucidate the spatial and temporal dynamics of global dissemination of HIV-1 CRF01\_AE and its related circulating recombinant forms (CRFs) in Asia (CRF15\_01B and CRF34\_01B in Thailand; CRF33\_01B and CRF46\_01B in Malaysia).

The Bayesian molecular clock approach revealed the possible timeline of global dispersal processes of CRF01\_AE as follows: Ancestral CRF01\_AE that is dated back to ~1968 was moved out of Africa to Thailand decade later (in ~1980) and swiftly disseminated into heterosexuals in South Vietnam in ~1981. CRF01\_AE was then spread into injecting drug user (IDU) populations in southern and northern Vietnam/Guangxi, China in ~1989 and ~1994, respectively. By a similar approach, the timing of the emergence of CRF34\_01B (Thailand) and CRF33\_01B and CRF46\_01B (Malaysia) was dated to ~1994, ~1993 and ~2001, respectively.

In contrast, we did unexpected observations on CRF15\_01B. While CRF15\_01B strains indeed exhibit identical recombinant structure, they do not form a cluster in phylogenetic trees, strangely behaving as if they were independent strains. This indicates that CRF15\_01B-like recombinants were not in a single lineage and were most likely generated by independent recombination events, despite of their extraordinary relatedness of recombinant structure. This strong convergence implies the presence of extremely strong selection pressure in favor of selecting CRF15\_01B-like recombinants. CRF15\_01B possesses "pseudotyped" structure where the external portion of envelope is replaced with subtype B' in a backbone of CRF01\_AE. Our observation suggests that this "pseudotype" configuration may have a selective advantage for escaping from host immune pressure, most likely reflecting antibody-mediated purifying selection.