

GENOTYPIC AND PHENOTYPIC CHARACTERIZATION OF NOVEL HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1) CIRCULATING RECOMBINANT FORM (CRF33_01B) IN MALAYSIA

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ABSTRACT

The human immunodeficiency virus type 1 (HIV-1) exhibits tremendous genetic diversity that is driven by high rates of mutation and recombination, coupled with high viral turnovers and the persistent nature of infection. By these mechanisms, HIV-1 group M, that is largely responsible for the global pandemic, diversified into 11 subtypes and subsubtypes (A1, A2, B, C, D, F1, F2, G, H, J and K) and various types of recombinants. HIV-1 recombinants with epidemic spread are known as circulating recombinant forms (CRFs). Five strains of CRFs have been reported so far in Asia: CRF01_AE, CRF15_01B and CRF34_01B in Thailand; CRF07_BC and CRF08_BC in China.

The central objective of the study was to investigate the evolutionary histories and behaviours of major HIV-1 CRF in Malaysia and also in East Asia. By analysing contemporarily collected virus specimens using a suite of established molecular biology and phylogenetic methods, we identified and defined a novel CRF circulating in Kuala Lumpur, Malaysia. We estimated the prevalence for this recombinant and constructed and characterised an infectious DNA clone that may be valuable for use in vaccine clinical trials in the future.

Finally, we tested the hypothesis if presently available genetic sequencing technology and computational biology tools are adequate to unravel evolutionary processes that occurred in the past by studying the date of origin of a HIV-1 CRF, divergence times and migration patterns of select major HIV-1 strains in epidemic regions where archival information are not readily available to reconstruct past epidemiological events.