

# SURVEILLANCE OF SUBTYPE AND GENETIC VARIATION OF THE CIRCULATING STRAINS OF HIV-1 IN THAILAND

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**Abstract.** Two HIV-1 strains, CRF01\_AE and subtype B', were reported in Thailand during the early years of the epidemic. Recently, an intersubtype recombination of HIV-1 strain was found in Thailand. Eight-hundred and twenty-eight samples collected during years 1995-2004 from high-risk groups in Bangkok, northern, northeastern, and southern region of Thailand were studied. HIV-1 *env* nucleotide sequences were used for phylogenetic analysis of the circulating HIV-1 strain. By single HIV-1 region (*env*) genotyping, CRF01\_AE was found in 97.3% and HIV-1 subtype B was found in 2.7%. A predominance of CRF01\_AE was found in all geographic regions. Parallel analysis of the HIV-1 *gag* and *env* genes demonstrated that 2.1% and 4.0% of recombinant HIV-1 strains were found using p17 and p24 region sequences, respectively. The recombinant *gag* gene was also found in one southern isolate. Phylogenetic analysis of HIV-1 isolated from 20 provinces in 2002 suggested the northern and northeastern isolates were more related than the southern isolates which had the lowest genetic diversity of 0.13. The GPGQ V3 loop tip was also present in isolates from all regions. The molecular epidemiological data from this study may be useful for surveillance design as well as targeting prevention efforts. It also provides information regarding new antigenic regions of circulating strains responsible for the HIV-1 epidemic in Thailand.

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