

SUSTAINED APPEARANCE OF DRUG RESISTANCE-ASSOCIATED MUTATIONS IN HIV-1 CRF01_AE PROTEASE AND REVERSE TRANSCRIPTASE DERIVED FROM PROTEASE INHIBITOR-NAIVE THAI PATIENTS

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Abstract. Previous studies revealed that HIV-1 CRF01_AE viruses derived from antiretroviral drug-naïve Thai patients contained several protease (PR) inhibitor (PI) resistance-associated mutations. In this report, we examined the sustained appearance of drug resistance-associated mutations in CRF01_AE PR and reverse transcriptase (RT). Peripheral blood samples were collected every 3 months from April 2008 to April 2009 from 39 HIV-1-infected Thai patients, including 17 drug-naïve and 22 RT inhibitors (RTIs)-treated individuals, and polymerase chain reaction-mediated amplification and sequencing analysis of the viral genome encoding PR and RT were performed. We successfully analyzed the deduced amino acid sequence of CRF01_AE PR and RT derived from samples continuously collected from 15 drug-naïve and 20 RTIs-treated patients. Drug resistance-associated mutations were continuously detected in CRF01_AE PR derived from most patients. The continuous appearance of such PR mutations was observed not only in the proviral DNA genome derived from peripheral blood mononuclear cells, but also in the viral RNA genome of plasma virus. In contrast, RTI resistance-associated mutations were only sporadically detected in samples derived from drug-naïve and RTIs-treated patients, except for the continuous appearance of two mutations in samples derived from two drug-naïve patients. Our results demonstrate that many PI resistance-associated mutations and only a few RTI resistance-associated mutations continuously appear in CRF01_AE viruses derived from PI-naïve patients residing in northern Thailand.

Key words: HIV-1 CRF01_AE virus, drug resistance-associated mutations, reverse transcriptase, protease

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