Purpose of study
Antiretroviral therapy (ART) has been scaled up in resource-limited settings. This study aimed to determine the prevalence of HIV-1 drug resistance-associated mutations (DRAMs) among patients with chronic HIV-1 infection and to compare DRAMs between CRF01_AE and B subtypes.

Methods
ART-naïve Thai patients who were indicated for ART initiation between 2010 and 2011 were prospectively enrolled. Genotypic assays of reverse transcriptase and protease genes were performed within 4 weeks prior to ART. DRAMs were assessed using International AIDS Society USA 2011 list.

Summary of results
A total of 330 patients were included. HIV-1 subtypes included CRF01_AE (241, 73.0%), B (79, 23.9%), and others (10, 3.1%). Median (IQR) CD4 was 66 (23–172) cells/mm³ and median (IQR) HIV-1 RNA was 5.2 (4.6–5.8) log copies/mL. The prevalence of patients with ≥1 DRAMs to any antiretroviral agents was 17.6%; 17.0% to NNRTIs, 0.6% to NRTIs, and 0.6% to protease inhibitors (PIs). V106I (23, 7.0%), V179D (14, 4.2%), V179T (6, 1.8%), E138A (5, 1.5%), V90I (4, 1.2%), K103N (3, 0.9%), Y181C (3, 0.9%), and P225H (1, 0.3%) were DRAMs to NNRTIs. M184V (1, 0.3%) and T215S (1, 0.3%) were DRAMs to NRTIs. M46L (2, 0.6%) was the only major DRAM to PI. Minor DRAMs to PIs including I13V, M36I, H69K, and L89M were more frequently observed in CRF_01 AE but A71V/T and V77I were more common in subtype B (P < 0.05). By multivariate analysis, the factors ‘HIV-1 subtype B’ and ‘low pretreated CD4 cell count’ were associated with higher rate of DRAMs.

Conclusion
HIV-1 DRAMs, especially to NNRTIs, is emerging in a middle-income country after a widespread use of NNRTI-based ART. HIV genotypic assay prior to ART initiation in patients with chronic HIV-1 infection should be considered.

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