Abstract

The mortality and morbility has been declined dramatically since the introduction of highly active antiretroviral therapy. However, the prevalence of antiviral drug resistance has increased and becomed a public health problem. The study was focus on the prevalence, pattern and mutant variation between different subtypes of HIV-1 in drug-naïve chronic HIV infected patients in Taiwan. Viral RNA was extracted from plasma and performed the genotypic resistance test with TRUGENE HIV-1 Gonotyping Kit and OpenGene DNA Sequencing System (VGI Inc., Canada). The prevalence of resistance to any drug was 8.7% (13 in 150). The most common resistance was to non-nucleoside reverse transcriptase inhibitors (NNRTIs), accounted for 7.3% (11 in 150), and then to nucleoside reverse transcriptase inhibitors (NRTIs) 2.7% (4), protease inhibitors (PIs) 2.0% (3). There was 2 cases (1.3%) resistance to all 3 class drugs. The most common mutations conferring resistance to NRTIs were T215Y/F/S (2.7%), M41L (1.3%), D67N (1.3%), and M184I/V (1.3%). Mutations conferring resistance to NNRTIs were V179D/E (2.67%), K103N (2.0%), and V108I (1.33%). And mutations conferring resistance to PIs were L90M (1.3%), I84V (1.3%), and M46I/L (1.3%). Subtype B was the only risk factor to develop drug resistance, and no drug resistance was found in the group of all CRF01_AE patients. Totally, the prevalence of drug resistance among subtype B was 11.4% (12 in 105). L63P and M36I were the most common polymorphism in protease genes, wheres CRF01_AE predominant with M36I (97.5%), and subtype B with L63P (73.3%). Because of the prevalence of drug resistance in our population is 8.7%, and high as 11.4% among subtype B group, the genotypic resistance test should be considered to perform before drug therapy, especially for those patients initiated with NNRTIs-based regimen.

Keywords：genotypic resistance；chronic infection；HIV-1