4036030 RACP/M : MAJOR : CLINICAL PATHOLOGY ; M.Sc. (CLINICAL PATHOLOGY)
KEY WORD : AIDS / HIV-1 / GENOTYPING / DRUG RESISTANCE / MUTATION

EKACHAI JENWITHEESUK : DRUG RESISTANCE GENOTYPING IN HIV-1 ISOLATED FROM THAI PATIENTS. THESIS ADVISOR : WASUN CHANTRATITA Ph.D., MALAI VORACHIT D.Sc., BUDSABA RERKAMNUAYCHOKE D.M.Sc., ASDA VIBHAGOOL M.D. 80 p. ISBN 974-664-536-6

The purpose of this study was to determine the prevalence of drug resistant-conferring mutations in HIV-1 infected Thai patients whom were naïve and experienced in antiretroviral drug administration.

Fifteen naïve patients and eighty-three HIV-1 infected Thai patients who had been treated with any antiretroviral drug for at least 8 weeks were studied. HIV-1 RNA was reverse transcribed and amplified by RT-PCR. Direct sequencing of the HIV-1 reverse transcriptase and protease was then performed. Changes in nucleotide and amino acid sequences were determined by comparing these sequences with the pNL4-3 reference sequence. Data on mutations associated with resistance to antiretroviral drugs were obtained from literature.

Of the fifteen isolates from the naïve group, no transmission cases of variants associated with significant resistance to protease inhibitors (PIs) or nucleotides (NRTIs) and non-nucleoside reverse transcriptase inhibitors (NNRTIs) were detected. Adversely, in the group with drug experience (n=83), three individuals (3.6%) had genotypes associated with resistance to antiretroviral agents. A virus with known resistant-conferring mutations to any NRTIs, NNRTIs and PIs was found in 48 (57.8%), 8 (9.6%), and 29 (34.9%) individuals, respectively. Multinucleoside (Q151M) and multinonnucleoside (K103N) resistant viruses were identified in 3 (3.6%) and 1 (1.2%) individuals, respectively.

The HIV-1 strain from the naïve group had very few pre-existing mutations to NRTIs, NNRTIs and PIs, which suggested that the transmission of resistant strains is still uncommon in HIV-1 infected naïve Thai patients. However, about two-thirds and one half of the patients in the drug experienced group had one or more mutations associated with resistance to reverse transcriptase and protease inhibitors respectively. In addition, all patients in both groups carried variations that claimed to contribute to PI resistance. Most of these mutations are likely to reflect the natural polymorphism of the protease. Their impact on long-term therapy should be evaluated in future studies.