Abstract

Human Immunodeficiency virus (HIV) infection is a growing public health problem in Taiwan. As of November 2003, there have been 5,550 cumulative HIV-1 infections reported to the Center for Disease Controls, Taiwan. One of the characteristics of HIV viruses is their genomic heterogeneity and genetic subtyping has been a useful tool to track the spreading patterns of HIV and to study the genesis of the epidemic in specific areas. Previous studies have shown that subtype B strains are the most prevalent and are responsible for 70% of HIV infections in Taiwan. Another HIV strain, subtype E, accounts for 25% of HIV infections. Other HIV strains, like subtypes A, C, and G, have been isolated from infected individuals in Taiwan. It is noteworthy that, besides subtype E, some intersubtype recombinants of subtypes A and G were also identified among infected individuals. Furthermore, two unique B/C recombinant viruses are spreading in China and have caused serious HIV epidemics there. With the increasing frequency of traveling and communications between Taiwan and China, it is essential for us to monitor the introduction of these B/C recombinant viruses to Taiwan. In this proposal, we would like to analyze the *gag-RT* sequences to provide the knowledge of genetic epidemiology of HIV strains and the prevalence of intersubtype recombinants in Taiwan. We have collected a total of 268 specimens from recently HIV infected individuals. Among them, 155 are from the Taipei city STD control center and 113 are from National Taiwan University Hospital. After analysis of the *gag-RT* sequences, we found that the prevalence rate of HIV subtype B virus is 89%, which is higher than the 70% reported previously in Taiwan. Therefore, HIV subtype B is still the predominant virus circulating in Taiwan and the infected population is increasing. Another HIV subtype E virus accounts for 9.3% of HIV infections in Taiwan. The proportion is decreasing 16 % as compared to previous analysis. Other HIV subtypes identified in Taiwan include 3 subtype G, 1 subtype C and 1 B/C_07 CRF virus. Overall, subtypes B and E are the dominant HIV viruses in Taiwan and the prevalence of subtype B is increasing. Since the availability of HAART(highly active antiretroviral therapy), the appearance of drug resistant viruses in treated individuals and the transmission of these drug resistant viruses have been reported by many groups. Antiviral drug resistance was observed in many primary infected individuals. As the transmission of primary drug resistant virus is increasing, the drug resistant test becomes important before patients receiving therapy. In our project, the *gag-RT* fragment amplified from patients' specimens includes both the protease and RT genes, which are the target genes of antiviral drugs. By analyzing the genetic variations observed in these specimens, we hope to estimate the prevalence of resistant HIV among primarily infected individuals in Taiwan. We analyzed three classes of drugs: NRTIs (nucleoside reverse transcriptase inhibitors,NRTIs), NNRTI (non-nucleoside reverse transcriptase inhibitors, NNRTIs), and PIs (protease inhibitors). We have collected 268 specimens from recently infected and drug naïve individuals. From analysis we know the prevalences to one class of drug resistance, which includes NRTIs, NNRTIs, and PIs, are 2.6%, 2.2%, and 0.3%, respectively. They are relatively low as compared to the reported 1-11% in US

and Europe. To be noticed, one patient developed drug resistance to two classes of drugs, NRTIs and PIs. Based on previous studies, such patients will have higher chance to fail the antiviral therapy. We will continue to follow up these patients to know the correlation between the genotypic analysis we performed and the outcomes after antiviral therapy. In Taiwan, the HAART therapy is available to HIV infected citizens covered by the national health insurance. Complete medical care and drug therapy have profoundly prolonged the life of these patients. If we can provide drug resistance test before or during antiviral therapy, it will help the clinical doctors to optimize the drug regimens and avoid any waste of medical resources.

Keywords: HIV, subtype, drug resistance