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Project Title: Establishment of HIV/HBV/HCV genomic database among different risk group in Taiwan
Project Number: DOH97-DC-2011
Executing Institute: CDC
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Abstract:

Human immunodeficiency virus type1 (HIV-1) is the pathogen known for causing acquired immunodeficiency syndrome (AIDS). Since the first isolation of HIV in 1983, the numbers of HIV-infection has been rapidly increasing. In 1996, Dr. David Ho advocated the HAART (Highly active antiretroviral therapy), so called combination therapy to lengthen the duration of HIV infection and improve the life quality of HIV-infected individuals. Recently a great advance has been made against HIV-1 by combination antiretroviral therapy worldwide; however, the failure of the treatments with certain reasons had appeared. One important reason is the occurrence of drug-resistant quasispecies during the therapy, especially that resistant to protease inhibitors (PIs) and reverse transcriptase inhibitors (RTIs) are the major obstacles. Recently some researchers found that there were drug resistant mutations occurred in drug-naïve HIV-1(+) patients, it's also called natural polymorphism that will make light to heavy drug resistance to HAART.

In order to understand the prevalence of HIV-1 subtypes and drug resistant associated natural polymorphism, this study analyzed the correlation between subtypes and drug associated natural polymorphism on HIV-1 protease and reverse transcriptase. The specific primers were designed for RT-PCR method to amplify HIV-1 envelope, protease and reverse transcriptase gene fragments , according to HIV-1 C2V3、gag、pol regions. The result of subtypes showed that there were 162 (62.6%) B subtype, 6 (2.3%)A/E subtype and 91 (35.1%)CRF_07 BC subtype. The frequencies of primary mutation occurred in protease and reverse transcriptase genes were low, except for 1 cases at T69 position and 3 cases at K103 position of reverse transcriptase genes ; others were secondary mutations.

Keyword: HIV, HBV, HCV, IDU, Drug resistance