Abstract

Human immunodeficiency Virus type1 (HIV-1) is the major pathogen known for causing acquired immunodeficiency syndrome (AIDS).Since the first isolation of HIV in 1983，AIDS has been rapidly increasing . In 1996 , Dr. David Ho advocated the HAART (Highly active antiretroviral therapy)，so called combination therapy. Recently a great advance has been made against HIV-1 by combination antiretroviral therapy worldwide , however , there appears failure of the treatment with certain reasons. 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 obstacle. 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 sexuality and 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 376 (85.6%) B subtype、39(8.9%)A/E subtype、16(3.6%) B/C subtype、2 (0.4%) A/G and 7(1.5%) C subtype. In drug resistant natural polymorphism analysis showed that in protease gene , there were 304 (73%) PR mutations at L63 、173 (42%) at V77 and 134 (32%) at M36 position. In reverse transcripatse gene , there were 45 (67.1%) RT mutations at K70 and 12 (17.9%) at S68 position. The frequencies of primary mutation occurred in protease and reverse transcriptase genes were low , most of them were secondary mutations.

Keywords：HIV-1；PROTEASE；RT