

HIV-1 Molecular Epidemiological profile differences among Taiwan drug abusers

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Abstract

Aims: Human immunodeficiency virus (HIV) and acquired immunodeficiency syndrome (AIDS) epidemic among drug users is a global health threat, especially the viral genotypic variation affecting the spreading of the virus. The purposes of this study were to investigate the molecular epidemiology of HIV infection among injecting drug users (IDUs).

Methods: Based on the partial env nucleotide sequence information, the phylogeny and epidemiological profile of 66 HIV strains circulating among IDUs in HIV surveillance database in Taiwan were analyzed. This HIV surveillance database was established during 2007-2009 in accordance to IRB rules. Using genotype classification of HIV as a molecular marker, the origin and the genesis of HIV epidemic were investigated.

Results: The phylogenetic analysis showed two viral strains, CRF07_BC (80.3%) and CRF01_AE (19.7%) subtypes circulating among Taiwan IDUs during 2007-2009. Three routes were identified in CRF07_BC transmission

and only one transmission chain was found in CRF01_AE spreading through the Bayesian tree analysis. The evolution rates which represent the transmission efficiency were also different between CRF07_BC and CRF01_AE viruses, 1.16×10^{-2} , 2.82×10^{-3} respectively. The transmission entry to IDUs population for both viruses could be traced back to the year 2002 by using coalescent theory approaches. But, the human genomic COMT Val158Met polymorphism frequency, which is associated with the drug abuse behavior, was not different between these two subtypes of the infection population.

Conclusions: HIV-1 CRF07_BC and CRF01_AE subtypes infection among Taiwan IDUs had different molecular epidemical profiles. CRF07_BC virus had multiple transmission routes and circulated among IDUs with greater efficiency than CRF01_AE virus. But, the human genomic COMT polymorphism showed that the genetic behavior phenomenon still were similar between these two infection groups.