

Molecular epidemiology of HIV-1, HCV, and HBV infections among convicts in Taiwan jails

Abstract:

Background: The AIDS virus molecular lab continually surveillance the HIV virus strains circulating among prisons and jails in Taiwan during 2004-2006. By using molecular epidemiology methods, we access the distribution of subtypes of HIV-1, HCV and HBV in the injection drug users for supporting the information for disease control.

Methods: We collected the newly HIV positive patients from several jails or prisons in Taiwan. Blood samples and questionnaires were collected from 132 HIV-1-infected outpatients and inmates in prisons in 2006. PCR, DNA sequencing and phylogenetic analysis were used to determine the subtypes of HIV-1, HCV and HBV.

Results: The major subtype of HIV-1 circulating among prisons and jails were CRF07_BC. The prevalence rate were 17.2% (102/593) and 99.5% (590/593) for HBV and HCV respectively. The results of HCV subtypes showed that 2a was major subtype among different location, coinfectd with HBV, and 01_AE subtype. In addition, there were several subtype such as 3a, 3b, 4, 5a, 6a and 6r that were newly been found in Taiwan.

Key words: HIV, HBV, HCV, Co-infection.