

The increase of HIV -1 genetic diversity in Hong Kong China

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Background

HIV-1 group M viruses are characterized into 9 pure subtypes and 43 circulating recombinant forms (CRFs). They account for major part of the global HIV epidemic. Recent studies identified the presence of unique recombinant forms (URFs) in Hong Kong and their complexities continue to increase. This study aims to characterize the HIV-1 genetic diversity in Hong Kong.

Methods

This study included plasma samples of 1045 HIV-1 patients in Hong Kong who were recruited from 2003 to 2008. The 1126bp pol sequences including protease and partial reverse transcriptase (PR-RT) were generated by an in-house genotyping system. A pol phylogenetic tree was then plotted with neighbor-joining algorithm plus bootstrap replicates. For unassigned-genotype pol sequences, evidence of recombination was then determined by using sliding-window based bootscan plots and their epidemiological patient background information was also collected.

Results

This study highlighted the extent of HIV-1 genetic diversity in Hong Kong. Subtype B (450/1045; 43.1%) and CRF01_AE (469/1045; 44.9%) variants remain predominant. Among the non-B/non-CRF01 samples (126/1045; 12.1%), 3 subtypes, 10 CRFs, 1 unassigned subtype and another 33 recombinants with 11 mosaic combinations were observed (Table 1). Interestingly, variants with CRF02_AG and subtype G recombination were found circulating among the non-Chinese Asians in Hong Kong through heterosexual transmission starting from 2007 while the subtype B and CRF01_AE recombinants were found among the local Chinese population mainly through sexual transmission route starting from 2004.

Conclusions

This study demonstrated the complex recombination of HIV-1 in Hong Kong. The high number of mosaic patterns in the pol gene suggests that the actual diversity of recombination in the HIV-1 genome in our region should be much higher. Thus, a surveillance system is necessary for tracking the distribution of new HIV-1 genetic variants in Hong Kong.