MOLECULAR EPIDEMIOLOGY AND PHYLOGENETIC ANALYSIS OF MINOR HIV-1 SUBTYPES IN HONG KONG: EMERGENCE AND SPREAD OF CRF07_BC AND SUBTYPE C

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INTRODUCTION
Over 6,400 HIV-1 infections have been recorded in Hong Kong since 1984, with about 500 new cases annually. Due to the geographical locations, about 45% of local patients are infected by CRF01 AE variants, whereas subtype B variants account for another 40% of the cases. Possibly owing to the frequent international business and leisure traveling activities, a noticeable increase in non-B and non-AE infections has been observed in recent years.

AIMS
1. Conduct a molecular epidemiological and phylogenetic analysis on CRF07_BC and subtype C to illustrate their transmission and spread in our locality
2. Summarise the prevalence of various HIV-1 subtypes in Hong Kong during the year of 1994 to 2013

METHODS
HIV-1 partial pol sequences were available from a routine antiretroviral surveillance program during 2000 – 2013. Reference sequences from different geographical locations were downloaded from the Los Alamos HIV database (http://www.hiv.lanl.gov). Each group of pol sequences were multiple aligned by ClustalW. Neighbor-joining trees were constructed by PhyML and confirmed with 1000 bootstrap replicates.

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RESULTS – SUBTYPE C
The neighbor-joining tree for subtype C revealed seven lineages and the sizes were relatively small (Figure 2) Clusters 1, 3 to 7 consisted of mostly heterosexual non-Chinese Asians and had likely been imported from South-East Asia. Cluster 2 was purely Chinese heterosexual males infected via commercial sex workers or casual sex partners in Hong Kong or China.

RESULTS – SUBTYPE DISTRIBUTION
A total of 2,315 HIV-1 patients were enrolled in the surveillance program, in which 42.1% and 39.7% of them were infected by subtype B and CRF01 AE, respectively. CRF07_BC (4.9%, 114/2315) and subtype C (4.2%, 96/2315) accounted for the third and fourth highest number of newly diagnosed infections in our locality (Figure 3 & 4).

CONCLUSIONS
The large cluster observed in CRF07_BC suggested a potential outbreak among MSMs social group, especially because the sequences were mainly collected within 2010 to 2013. The spread of subtype C largely remained within non-Chinese Asians population though its spread to local heterosexual Chinese population was noticeable. These findings may have impact on clinical management and public health intervention and should therefore alert public health workers to prevent further outbreak.