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HIV/AIDS

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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Objectives

HIV-1 subtype B and CRF01_AE are the pre-dominant strains in Hong Kong. A noticeable increase in non-B and non-AE infections has been observed in recent years. This study aimed to conduct a molecular epidemiological and phylogenetic analysis on CRF07_BC and subtype C to illustrate their transmission and spread in our locality.

Methods

HIV-1 partial *pol* sequences were available from a routine antiretroviral surveillance program during 2000 - 2013. The HIV-1 subtypes were initially determined by the REGA automated subtyping tool and further confirmed by phylogenetic analysis. Reference sequences from different geographical locations were downloaded from the Los Alamos HIV database.

Results

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.

Within these two minor subtypes, most of the men-who-have-sex-with-men (MSMs, 93.8%, 61/65) and suggest use injecting drug users (IDUs, 74.1%, 20/27) were infected with CRF07_BC whereas 72.0% (85/118) heterosexual patients were infected with subtype C.

By plotting the neighbor-joining tree of all CRF07_BC sequences, we identified one distinct large cluster, consisting of 72 local and 18 reference sequences. Chinese MSMs (75%, 54/72), together with a few Caucasian or Asian MSMs dominated this cluster. The majority of these MSMs were infected via casual sex partner (85.2%, 46/54) within Hong Kong or China (68.5%, 37/54). Based on the patients' first serology positive dates, this cluster was likely to have been imported from China in around 2006 - 2007 by two MSMs. Two small clusters were also identified within CRF07_BC, which consisted of a few IDUs or heterosexual males infected via commercial sex worker in South-East Asian countries.

The neighbor-joining tree for subtype C revealed seven lineages and the sizes were relatively small. All but one clusters included heterosexual non-Chinese Asians and had likely been imported from South-East Asia. The last cluster was purely Chinese heterosexual males infected via commercial sex workers or casual sex partners.

Conclusions

In Hong Kong, the prevalence of non-B and non-AE variants was thought to be very low and the transmission was sporadic. 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.