

The Novel CRFs Reveals Higher Prevalence of Superinfection of HIV in China

Hongxiong Guo

Jiangsu Provincial Center for Disease Control and Prevention, Nanjing, China

Received: March 10, 2016; **Accepted:** March 16, 2016; **Published:** March 22, 2016

Corresponding author: Hongxiong Guo

Recombination is one of the most important forces driving HIV evolution with a way of large genetic fragment replacement. It is estimated that recombination occurs at more than 2.8 crossovers per genome per cycle [1]. The novel recombinant having the distinct structure with its parent's sequences is the product of at least two kinds of subtypes or CRFs. Therefore, the frequently prevalence or appearance of a novel Circulating Recombinant Form (CRF) implies the prevalence of super-infection of various HIV in a local area. Since the first CRF of HIV CRF01_AE was identified in 1996, 72 CRFs and hundreds URF was identified [2]. During recent years, a lot of CRFs or URFs was reported, especially in Southeast Asia.

✉ guohongxiong@jscdc.cn

Jiangsu Provincial Center for Disease Control and Prevention, Nanjing, China.

Tel: 861058900240

In China, CRF01_AE was the first CRF which was introduced from Thailand about early 1990s [3]. CRF07_BC and CRF08_BC were identified among Intravenous Drug Users (IDUs) in 2000 in Yunnan Province in China [4]. Among fragments of CRF07/08_BC circulating in China, B subtype is B' introduced from Thailand and C subtype from India through IDUs. These two CRFs have been the major HIV which accounts for more than 83.2% in China and prevail among various HIV-positive populations [5]. In 2009, Guo et al. for the first time reported the recombinants formed between CRF01_AE/CRF07_BC among a cohort of IDUs with an epidemiological link [6]. As we knew, intravenous injection of drugs had been the predominant route among transmission ways of HIV in China, especially this route play a major role on CRF07_BC and CRF08_BC spread.

Citation: Guo H. The Novel CRFs Reveals Higher Prevalence of Superinfection of HIV in China. *J HIV Retrovirus*. 2016, 2:1.

From 2014 to present, more and more CRFs were identified in China [7-18]. These CRFs include the recombinant between CRF01_AE and CRF07_BC, between CRF01_AE and subtype B, between subtype B and subtype C, among CRF01_AE, subtype B', and subtype C. The recombinant from two or three same subtypes and CRF in various area often has the distinctly genome structure and break point of recombination occurring. For example, the genome structure and break point of recombinant of CRF01_AE/07_BC identified in Jiangsu province by Guo et al. is significantly different with that in Guangxi province by Dong.

The recombinants formed from same subtypes also were found among various populations with higher risk behavior. However, more recombinants were identified for the first time among men who sex with men. These reveal multiple infection of various subtype is common in China, especially among men who have sex with men.

More effort is made on controlling and preventing HIV spread in China and the speed of HIV spread has been reducing during recent years. However to control HIV prevalence still faces to a great challenge. Currently, men who sex with men are predominant among the newly diagnosed HIV-positive population, and the HIV prevalence among young people has been rapidly increasing [19]. In these populations, the usage of condom is very low. It accelerates HIV transmission and multiple infections, followed by recombination between various subtypes.

Recently, the novel recombinant of HIV frequently emerged in China. It implies that higher superinfection of HIV exist and the importance of the management for HIV positive population and early diagnose of HIV infection on stopping HIV spread in China.

References

- 1 Neher RA, Leitner T (2010) Recombination rate and selection strength in HIV intra-patient evolution. *PLoS Comput Biol* 6: e1000660.
- 2 Carr JK, Salminen MO, Koch C, Gotte D, Artenstein AW, et al. (1996) Full-length sequence and mosaic structure of a human immunodeficiency virus type 1 isolate from Thailand. *Journal of Virology* 70:5935-5943.
- 3 Feng Y, He X, Hsi JH, Li F, Li X, et al. (2013) The rapidly expanding CRF01_AE epidemic in China is driven by multiple lineages of HIV-1 viruses introduced in the 1990s. *AIDS* 27: 1793-1802.
- 4 Su L, Graf M, Zhang Y, Briesen HV, Xing H, et al. (2000) Characterization of a Virtually Full-Length Human Immunodeficiency Virus Type 1 Genome of a Prevalent Intersubtype (C/B9) Recombinant Strain in China. *Journal of Virology* 74: 11367-11376.
- 5 He X, Xing H, Ruan Y, Hong K, Cheng C, et al. (2012) Group for HIV Molecular Epidemiologic Survey. A comprehensive mapping of HIV-1 genotypes in various risk groups and regions across China based on a nationwide molecular epidemiologic survey. *PLoS One* 7:e47289.
- 6 Guo H, Guo D, Wei JF, Yang H, Huan X, et al. (2009) First detection of a novel HIV Type 1 CRF01_AE/07_BC recombinant among an epidemiologically linked cohort of IDUs in Jiangsu, China. *AIDS Res Hum Retroviruses* 25: 463-467.
- 7 Ning C, Li X, Tang W, Zhou B, Cai W, et al. (2015) Identification of a novel HIV-1 intra-circulating recombinant form 01_AE in China: a descendant of the previously identified CRF01_AE transmission clusters 1 and 6. *Sci China Life Sci* 58:724-726.
- 8 Li Z, Li J, Feng Y, Kalish ML, Lu H, et al. (2015) Genomic characterization of two novel HIV-1 unique (CRF01_AE/B) recombinant forms among men who have sex with men in Beijing, China. *AIDS Res Hum Retroviruses* 31: 921-925.
- 9 Yan J, Xin R, Li Z, Feng Y, Lu H, et al. (2015) CRF01_AE/B/C, a Novel Drug-Resistant HIV-1 Recombinant in Men Who Have Sex with Men in Beijing, China. *AIDS Res Hum Retroviruses* 31:745-748.
- 10 Li Z, Wei H, Feng Y, Li J, Kalish ML, et al. (2015) Genomic characterization of two novel HIV-1 second-generation recombinant forms among men who have sex with men in Beijing, China. *AIDS Res Hum Retroviruses* 31: 342-346.
- 11 Guo H, Hu H, Zhou Y, Huan X, Qiu T, et al. (2014) The identification of a novel HIV-1 CRF01_AE/B recombinant using the near full length genome in Jiangsu Province, China. *AIDS Res Hum Retroviruses* 30:1239-1242.
- 12 Zhao K, Du J, Zheng W, Yu XF (2014) HIV-1 transmission among injection drug users leads to novel recombinants circulating in southern China. *AIDS Res Hum Retroviruses* 30: 1006-1009.
- 13 Feng Y, Li X, Zang X, Guo Q, Sun L, et al. (2014) Identification of a novel HIV-1 second-generation recombinant form (CRF01_AE/CRF07_BC) in Jilin, China. *AIDS Res Hum Retroviruses* 30: 819-822.
- 14 Guo H, Hu H, Zhou Y, Yang H, Huan X, et al. (2014) A Novel HIV-1 CRF01_AE/B recombinant among men who have sex with men in Jiangsu Province, China. *AIDS Res Hum Retroviruses* 30:706-710.
- 15 Li X, Feng Y, Yang Y, Chen Y, Guo Q, et al. (2014) Near full-length genome sequence of a novel HIV-1 recombinant form (CRF01_AE/B) detected among men who have sex with men in Jilin Province, China. *AIDS Res Hum Retroviruses* 30: 701-705.
- 16 Li X, Ning C, Chen Y, Feng Y, Wei M, et al. (2014) Near full-length genome identification of a novel HIV-1 recombinant form (CRF01_AE/B'/C) among heterosexuals in Jilin, China. *AIDS Res Hum Retroviruses* 30: 695-700.
- 17 Feng Y, Wei H, Hsi J, Xing H, He X, et al. (2014) Identification of a novel HIV Type 1 circulating recombinant form (CRF65_cpx) composed of CRF01_AE and subtypes B and C in Western Yunnan, China. *AIDS Res Hum Retroviruses* 30: 598-602.
- 18 Hsi J, Wei H, Xing H, Feng Y, He X, et al. (2014) Genome sequence of a novel HIV-1 circulating recombinant form (CRF64_BC) identified from Yunnan, China. *AIDS Res Hum Retroviruses* 30:389-393.
- 19 Geng GZ, Gao G, Ruan YH, Yu MR, Zhou YH (2016) Behavioral Risk Profile of Men Who Have Sex with Men in Beijing, China: Results from a Cross-sectional Survey with Randomized Response Techniques. *Chin Med J (Engl)* 129: 523-529.