

Analysis of Human Immunodeficiency Virus Type 1 (HIV-1) CRF07_BC in China Using BEAST

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It has been reported that HIV-1 subtypes B' and C from Thailand and India, respectively, were introduced into Yunnan province of China in the late 1980s, via drug-trafficking routes and resulted in the initial outbreak of CRF07_BC virus among injection drug users in this region. Since then, this recombinant virus spread to many other regions and became one of main HIV-1 subtypes in mainland China nowadays. However, the contradictory results have been reported on the origin and transmission route of this virus. We conducted a comprehensive analysis to clarify this issue.

We retrieved the viral samples from more than one public databases and created five datasets: 1) *env* gene, 2) *gag* gene of subtype C origin, 3) *gag* gene of subtype B origin, 4) *pol* gene of subtype C origin and 5) *pol* gene of subtype B origin. These datasets included more locations (15 provinces), more sampling time points (1996-2011) and the longer genome regions of viral genes. Moreover, the most recent version of a Bayesian inference method for phylogeographic analysis was employed in the study.

The results showed that the origin of the CRF07_BC virus was Yunnan, but the transmission routes in China are quite complicated. The virus spread to other regions not only from Xinjiang but also from Yunnan, Sichuan etc. Our results suggest that it is not proper to simply conclude that the virus spread only from Xinjiang or Yunnan.

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