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## Epidemiology and Genetic Background of HIV-1 Strains Circulating in Shandong, China

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from 2005 International Meeting of The Institute of Human Virology  
Baltimore, USA, 29 August – 2 September 2005

Published: 8 December 2005

*Retrovirology* 2005, **2**(Suppl 1):S99 doi:10.1186/1742-4690-2-S1-S99

Shandong is a relatively developed coastal province in China with 17 cities, a population of 91.23 million, and increasing numbers of HIV/AIDS cases. We investigated the epidemiology of circulating HIV-1 strains from 97 HIV-1 infected cases from 1992 to 2004 in Shandong. Fragments of HIV-1 *env* C2-V3, *gag* P17/P24, 1st exon of *tat* and adjacent region were PCR amplified and sequenced, followed by phylogenetic, homology and recombination analysis. We found 7 circulating HIV-1 subtypes/CRFs, which are B' (75.3%), CRF01\_AE (10.3%), CRF07\_BC, CRF08\_BC (i.e. B'/C, 4.1% respectively), B, C and CRF02\_AG (2.1% respectively). Subtype B' was found mostly in paid blood donors, while B'/C recombinants were primarily in injecting drug users. The remaining subtypes distributed mainly in sexually transmitted subjects. Genetic divergence and amino acid sequence analysis showed that B' strains are closely related to B.CN.RL42; B'/C strains to 97CN54A and 97CNGX6F; CRF01\_AE strains to 01\_ae.th.90.cm2; CRF02\_AG, C and B strains were related to standard strains from Cameroon, Ethiopia and America, respectively. Genetic divergence of *env* of B' strain showed that it started circulating in Shandong 7–10 years ago. The large strain variation and occurrence of CRFs signify the rapidly increasing HIV-1 epidemic in Shandong, and have implications for vaccine design.