

Poster presentation

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Genetic characterization of HIV-1 strains circulating in Kazakhstan

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from 2006 International Meeting of The Institute of Human Virology
Baltimore, USA. 17–21 November, 2006

Published: 21 December 2006

Retrovirology 2006, **3**(Suppl 1):P18 doi:10.1186/1742-4690-3-S1-P18

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Background

The Central Asian region is surrounded on all sides by different HIV-1 subtypes: A in Russia, C in Pakistan and India and a B/C recombinant in China. There are approximately 500,000 IDUs in the Central Asian Region. Between 1995 and 2005, 4696 HIV/AIDS cases were officially reported in Kazakhstan. The most significant route of transmission is IDU, constituting of about 84% of the total cases, following by heterosexual (12%) and bi/homosexual transmission (0.5%) (UNAIDS).

Methods

To determine the HIV-1 genetic diversity in Kazakhstan, 85 confirmed HIV seropositives samples were collected from 2001–2003. Most of the 85 strains were isolated from individuals in three sites; Uko, Ust Kamenogorsk, and Almaty. Ninety percent of those enrolled were intravenous drug users (IDUs). A region of 1.2 kb in length that included all of the protease (Pro) and the amino terminus of the reverse transcriptase (RT) protein was sequenced of all 85 samples collected. From these, 6 samples were randomly selected for nearly full genome sequencing. Both amplified product was sequenced using an ABI 3100 automated sequencer. Phylogenetic analysis was performed by first aligning the sequences obtained with reference sequences using the program MacGDE followed by a Neighbor-joining analysis performed with MEGA.

Results

Phylogenetic trees were constructed for both the ProRT fragments and the nearly full-length genomes sequenced. Based on the Neighbor-joining analysis of the 85 ProRT amplified samples 80 (94.1%) were subtype A, 4 (4.7%) were CRF02_AG, and 1 (1.2%) was subtype C. In addition, the phylogenetic analysis of the ProRT region revealed that most A subtypes clustered with those circulating in countries of the former Soviet Union (FSU). The CRF02_AG strains clustered with similar strains identified in Uzbekistan as well as the most common CRF02 reference strain. The single C strain clustered with world reference subtype C strains. Furthermore, all 6 nearly full-length sequences obtained were subtype A and showed that the Uzbekistan A is not genetically distinct from reference sequences used from Ukraine, The Republic of Georgia, or Uzbekistan.

Conclusion

The HIV epidemic in Kazakhstan is predominantly in the IDUs population. A factor that contributes to this occurrence is that Kazakhstan is located on the main route of drug trafficking. Based on both ProRT and the nearly full-length sequence analysis both the subtype A and the CRF02 strains circulating in Kazakhstan are part of the same epidemic that is threatening the rest of the FSU. The single subtype C found in the study was from a Kazakhstan citizen, seropositive since 1995, who had never traveled out of country but stated that the infection was contracted sexually from a foreigner from Iran. Continued

molecular epidemiological and virological monitoring of HIV-1 worldwide remains of great importance, since there is always the potential for other subtypes to be introduced into the Central Asian region.

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