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OUTBREAK OF A WEST AFRICAN HIV-1 RECOMBINANT, CRF02_AG, IN CENTRAL ASIA

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OBJECTIVES: Molecular epidemiology was used to track the HIV epidemic as it spread throughout Central Asia. The epidemic in the former Soviet Union is characterized by the high relative prevalence of a specific variant of subtype A, (A(FSU)). While limited information about genetic subtypes is available for Uzbekistan and Kazakhstan, this is the first report describing genetic subtypes in Kyrgystan and Tajikistan.

METHODS: HIV-infected subjects were identified from surveillance in high-risk populations in Uzbekistan, Kazakhstan, Kyrgystan and Tajikistan (i.e., FSW, IDU). Genetic sequence analysis of a partial pol amplicon from PBMC DNA was completed and phylogenetically compared to HIV strains from the larger epidemic.

RESULTS: Two hundred and forty-five HIV strains from 4 countries were analyzed. Most (78%) were subtype A (FSU) but 22% were CRF02_AG, a circulating recombinant form common in West Africa. The highest relative prevalence of CRF02_AG was in Tajikistan (50%), followed by Uzbekistan (26%), Kyrgystan (5%) and Kazakhstan (4%). All of the CRF02_AG strains were monophyletic. In Tajikistan and Uzbekistan there were 4 strains that were unique recombinants formed from CRF02_AG and subtype A (FSU). Each of the 4 strains was genetically different in subtype structure from the others but all were monophyletic with A (FSU) and CRF02_AG in the relevant segments of the genome.

CONCLUSIONS: In these 4 countries in Central Asia, where dynamic HIV epidemics are occurring, subtype A (FSU) was the predominant genetic form of HIV-1, but CRF02_AG was also present to varying degrees, depending on the country. The highest concentration was in IDU in Tajikistan, where half of the strains either were entirely CRF02_AG, or recombinant between CRF02_AG and subtype A (FSU). This genetic information demonstrates that all of these strains were descended from one founder, but the location of the origin and the direction of spread was not apparent from the genetic relationships and requires further study.

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