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Molecular genetics of hiv-1 strains spreading in russia

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Introduction: HIV-1 epidemic in Russia is dominated by a monophyletic subtype A1 variant, derived from a strain originating in Central Africa, which began to spread among IDUs in 1995. The generalized epidemic observed in Russia affects populations at risk (IDUs, CSWs, and MSM), with rates of HIV-1 incidence being among the highest in the world. The number of HIV-1 cases recorded in Russia has exceeded 800 000, but experts estimate that the total amount of the infected individuals is about 2 000 000 (> 1% of the population of Russia).

Objectives: To analyze phylogenetic clustering and predicted coreceptor usage in Russian HIV-1 sequences.

Methods: Plasma samples were collected in the Moscow area (13 samples, 2010) and the Perm area (10 samples, 2011). RNA was extracted from paper spots and directly amplified by RT-PCR. Sequences of PR-RT and V3 were obtained for 14 and 17 samples, respectively; full-length genome sequencing was performed for two samples. Phylogenetic sequence analysis was done via maximum likelihood with RAxML. Genotypic prediction of coreceptor usage was done by V3 net charge and the online programs Geno2Pheno and PSSM.

Results: Five samples from the Perm area, sequenced in PR-RT, were A1. Among the nine samples from the Moscow area, sequenced in this segment, six were A1, two – CRF02_AG, and one belonged to subtype B. Full-length genome sequencing of the two samples from the Moscow area demonstrated that one of them was A1 and the other – CRF02_AG. CCR5 coreceptor usage was predicted by all methods in all the 17 V3 sequences (nine samples were isolated in the Perm area and eight – in the Moscow area).

Conclusions: Molecular-epidemiological studies demonstrated that the nascent HIV-1 epidemic was associated with the introduction of diverse viruses in distinct risk groups. The rapid spread of the homogenous IDU-A strain resulted in this virus' becoming predominant across Russia and most Eastern European and Central Asian countries of the former Soviet Union. It is obvious that the social and economic deterioration and the massive rise in drug abuse did play a role in this explosive epidemic. The new stage (generalized epidemic) is characterized by active propagation of HIV-1 subtype A1 and multiple outbreaks of CRF02_AG infection. The latter strain is similar in sequence to isolates from Uzbekistan and Kyrgyzstan, rather than African or Western European, which is likely related to labor migration. This is the first report of the circulation of CRF02_AG in the Moscow area. Of interest, double recombinants A/AG have already been detected in Russia and Kyrgyzstan. It is also intriguing that none of the sequences of this study contained major drug resistance mutations.

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