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Current trends in HIV genetic diversity in Russia: increased prevalence of unique recombinant variants

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Background

During the last two decades, HIV-1 has been spreading rapidly in the Russian Federation with subtype A (sub-subtype A6) dominating in almost all territories. In 2005-2010, the genetic diversity of HIV-1 in Russia began to increase. Subtypes B, C, and recombinants CRF02_AG, CRF63_02A1 have also been identified. This phenomenon created the conditions for the new unique recombinant forms (URFs) emergence as an important component of the HIV-infection epidemic.

The objective

The objective of this study was to make the first estimates of the prevalence of HIV-1 unique recombinant forms in Russia.

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Methods

Laboratory database of nucleotide sequences obtained during 2011-2018 was used as a source of 1839 HIV-1 pol gene fragments sequences from different regions of Russia. Genotyping and recombinant analyses were carried out using the tools COMET HIV-1, REGA HIV-1 Subtyping Tool (V 3.0), RIP and jpHMM. 330 additional HIV-1 pol sequences were taken from Genbank (http://hiv-web.lanl.gov) and included into analysis.



Results

The results of genotype analysis revealed that 74.0% (1606/2169) of the sequences studied belonged to sub-subtype A6, 11.4% (247/2169) – CRF63_02A1, 5.7% (123/2169) – URFs, 5.5% (120/2169) – subtype B, the remaining subtypes accounted for 3.4%. The URFs were represented by the following variants: URF_AB, URF63_02A1, URF_02AG and mosaic patterns (URFA6_02AG, URFB_02AG, URF



The prevalence of URFs in the regions studied in 2011-2012 was 3.5%; in 2013-2014 - 5.1%; in 2016 - 5.8%; in 2017-6.9%; 2018-10.7%.



Conclusion

The study results point to the increasing genetic complexity of the HIV-1 epidemic in Russia, including due to the frequent emergence of URFs. There is a tendency to increase the prevalence and genetic diversity of URFs. The results can help to better understand and predict the future trends of the HIV epidemic in Russia.