A cross-sectional study of a representative sample of boys aged 7-17 years (n=569) was carried out in Arkhangelsk. The rate of asymptomatic hyperuricemia was 27.59%. Serum level of uric acid correlated with levels of triglycerides, total cholesterol, low density lipoprotein cholesterol, fasting glycemia, systolic and diastolic blood pressure ($r = 0.49; 0.27; 0.27; 0.26; 0.34 u 0.35$, respectively; $p$
Abstract: To simultaneously analyze HIV-1 samples from all Russian regions to characterize the epidemiology of HIV infection in the country as a whole.

The most extensive study was conducted to examine nucleotide sequences of the pol gene of HIV-1 samples isolated from HIV-positive persons in different regions of Russia, with the diagnosis date being fixed during 1987-2015. The nucleotide sequences of the HIV-1 genome were analyzed using computer programs and on-line applications to identify a virus subtype and new recombinant forms.

The nucleotide sequences of the pol gene were analyzed in 1697 HIV-1 samples and the findings were that the genetic variant subtype A1 (IDU-A) was dominant throughout the entire territory of Russia (in more than 80% of all infection cases). Other virus variants circulating in Russia were analyzed; the phenomenon of the higher distribution of the recombinant form CRF63/02A in Siberia, which had been previously described in the literature, was also confirmed. Four new recombinant forms generated by the virus subtype A1 (IDU-A) and B and two AG recombinant forms were found. There was a larger genetic distance between the viruses of IDU-A variant circulating among the injecting drug users and those infected through heterosexual contact, as well as a change in the viruses of subtype G that caused the outbreak in the south of the country over time in 1988-1989.

The findings demonstrate continuous HIV-1 genetic variability and recombination over time in Russia, as well as increased genetic diversity with higher HIV infection rates in the population.

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