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MONITORING VECTORS OF TICK-BORNE BORRELIOSIS, HUMAN GRANULOCYTIC ANAPLASMOSIS, HUMAN MONOCYTIC EHRLICHIOSIS IN STAVROPOL REGION IN 2017

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The epidemiological situation of tick-borne borreliosis in Stavropol region continues to be a unfavourable. Infection of humans occurs not only in natural centers of the infection, but also in outlying settlements, mostly in parks, squares and cemeteries.

The main vector of borreliosis are ticks belonging to the genus *Ixodes ricinus*.

The purpose of the study is research on ticks belonging to the genus *Ixodes ricinus* which transmit *Ixodes* tick-borne borreliosis, human granulocytic anaplasmosis (HGA) and human monocytic ehrlichiosis (HME).

Monitoring of infection of ticks infect with pathogens (*Borrelia burgdorferi*, *Ehrlichia chaffeensis* and *Anaplasma phagocytophilum*) in 2017 was carried out in 7 administrative territories of Stavropol region. The ticks were collected using a cloth drag-flag method (200 pools, 1037 specimens). PCR method has been used for detection of *Borrelia burgdorferi*, *Ehrlichia chaffeensis* and *Anaplasma phagocytophilum*.

Genetic material of the human pathogens such as *Borrelia burgdorferi* sensu lato has been found in 94% of the studied pools, *Anaplasma phagocytophilum* — 22.5%, *Ehrlichia chaffeensis* — 0.5%. Because the same genres can transmit various infections, the mixed-infection method has been used. As a result of laboratory research, 20.5% of investigated pools the combination of pathogens tick-borne borreliosis and human granulocytic anaplasmosis (HGA), tick-borne borreliosis and human monocytic ehrlichiosis (HME) — 4.5%, tick-borne borreliosis, human monocytic ehrlichiosis (HME) and human granulocytic anaplasmosis (HGA) — 0.5%.

In Stavropol region the mixed-infected ticks *Ixodes ricinus* pathogens (tick-borne borreliosis, human monocytic ehrlichiosis and human granulocytic anaplasmosis) have been revealed. Considering the high level of infection caused by infected ticks, there is a probability for people to get infected in natural biotopes.

In order to prevent the emergence and spread of the infections, it's necessary to continue monitoring the infection and carry out measures for unspecified prevention.

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VARIABILITY OF THE LEVEL OF INFLUENCE OF RED VOLE POPULATIONS BY HANTAVIRUS PUUMALA IN THE REPUBLIC OF TATARSTAN IN 2015–2017

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One of the most common natural focal infectious diseases in Russia and the Republic of Tatarstan is hem-

orrhagic fever with renal syndrome (HFRS). During the period 2013–2017 in the Russian Federation, 39237 cases of HFRS were registered in 8 federal districts of the Russian Federation, in 59 regions. The Volga Federal District accounted for 82.9% of all reported cases of HFRS in the country. The average intensive incidence rate was 15.9‰ people, including 16.5‰ in the Republic of Tatarstan.

The viruses that cause HFRS belong to the genus *Hantavirus*, the family *Bunyviridae*. On the territory of Russia, serotypes of hantaviruses pathogenic for humans are recorded: *Puumala*, *Seoul*, *Amur*, *Hantaan*, *Dobrava*. In the European part of Russia the serotype *Puumala* (PUUV) prevails, the main carrier of which is the red vole *Myodes glareolus*. Infections of people occur in the habitats of the red vole, so to take measures to reduce the incidence of it is important to know which of the rodent populations are most infected with the virus PUUV.

The objectives of the study were to determine the level of infection of populations of red vole with the virus PUUV in areas of the Republic of Tatarstan with high incidence of HFRS and assess the variability in the level of infection in three years. The objective of the study was to identify the PUUV virus in individuals of the red vole from the populations of several regions of the Republic of Tatarstan in 2015–2017.

Small mouse-like rodents were caught in the spring and summer-autumn periods 2015–2017 in the areas of habitat of red vole near the settlements. In 2015–2016, five were surveyed, and in 2017 — seven districts of the Republic of Tatarstan. Isolation of total RNA from rodent lung tissue was performed using a Trizol reagent (Invitrogen, USA). For the synthesis of the viral cDNA, the reverse transcriptase Thermo Scientific RevertAid Reverse Transcriptase (Thermo Fisher Scientific, USA) was used in a standard procedure and the resulting cDNA served as the template for PCR. PCR products were sequenced using 3730 DNA Analyzer (ABI, USA). The nucleotide sequences of the PCR products were compared to sequences from the GenBank database using the BLAST program.

In total, during the period 2015–2017 years 369 specimens of the red vole were examined by the PCR method, viral RNA was detected in 59 (16.2%) samples. However, in the years mentioned, the infection of rodents varied. So, in 2015, of the 111 samples tested, a positive result was obtained in 29 (26.1%) samples, in 2016 out of 102 samples — in 6 (5.9%), and in 2017 out of 156 — in 24 (15.4%). By PCR in all positive samples, only PUUV viruses were detected, other hantavirus serotypes were not detected.

High rates contamination of rodents in 2015 were observed in Laishevsky, Nizhnekamsky, Almetyevsky, Zelenodolsky districts; in 2016 — in Nizhnekamsky and Almetyevsky; in 2017 — in Tukaevsky, Laishevsky and Mamadyshsky districts of Tatarstan.

The conducted studies evidence to the circulation of hantaviruses of serotype PUUV in populations of red vole on the territory of natural foci located in seven surveyed regions of the Republic of Tatarstan. The level of infection of the voles for three years showed a significant variability — from 5.9 to 26.1%, though overall remained high and averaged 16.2%.

Thus, with a large number of moused rodents and a high level of infection of the red vole with hantavirus *Puumala* in the regions of the Republic of Tatarstan, the unfavorable epidemiological situation of HFRS remains.