The purpose of the work is to develop universal recommendations for clinicians for the management of patients with tick-borne borreliosis.

Tasks of the study was to compare the distinctive features of epidemiological anamnesis, clinical manifestations, indicators of laboratory and instrumental diagnostics and criteria of dispensary registration of patients with tick-borne borreliosis of erythema and non-erythema form.

We have analyzed about 34 patients from the maps of municipal institutions in Ulyanovsk. Forms of borreliosis were divided evenly into erythemic and non-erythemic forms in 17 patients (50%)

In the first 7 days 9 (26%) patients addressed, on 8–14 days — 5 (15%), on 15–30 days — 4 (12%) and 16 (47%) arrived at a later date. The complaint in 100% was the presence of itching and in 50% of erythema, which was accompanied by subjective sensations (burning sensation or compaction — 17 (50%), increase — 9 (26%) patients. In 3 (8%) patients complications with the defeat of the musculoskeletal system (rheumatoid arthritis) were revealed. Serological diagnosis (ELISA) was performed in 17 (50%) patients. Antibodies were found in 14 (41%), IgM levels ranged from 0.470 to 0.633. Terms of appearance were different (15–43 days). In 3 (9%) people the level was below normal. The remaining half of the patients were not examined for various reasons. Clinical and electrocardiographic manifestations of dysfunction of the circulatory system were noted in non-erythematous form (50%).

Serological diagnosis of tick-borne borreliosis by ELISA, due to the late appearance of antibodies in the early stages of little informative, which necessitates the introduction of modern rapid methods. Patients with non-erythematous form of tick-borne borreliosis require more attention and detailed laboratory and instrumental diagnosis, as there is a risk of complications from vital organs and systems.

4.4 doi: 10.15789/2220-7619-2018-4-4.4

DETECTION OF GENETIC MARKERS OF TICK-BORNE RICKETTSIOSIS WITH THE PCR

E.I. Bondarenko[1], M.T. Gafarova[2], L.D. Shchuchinova[3], L.V. Shchuchinov[3], A.N. Shvalov[4], V.A. Lubova[5], G.N. Leonova[5]

[1]"Vector-Best", Novosibirsk, Russia; [2]Vernadsky Crimean Federal University, Simferopol, Republic of Crimea, Russia; [3]Federal Service for Surveillance on Consumer Rights Protection and Human Wellbeing in the Altai Republic, Gorno-Altaisk, Russia; [4]State Research Center of Virology and Biotechnology "Vector", Koltsovo, Novosibirsk Region, Russia; [5]Somov Institute of Epidemiology and Microbiology, Vladivostok, Russia

There are seven species of pathogenic rickettsia belong to the spotted fever group were reported to be circulating in Russian: *R. conorii, R. sibirica, R. heilongjiangensis, R. slovaca, R. aeschlimannii, R. helvetica* and *R. raoultii*. But only first three of them were reported to cause the confirmed diseases in our country. The regions that are endemic for *R. sibirica* and *R. heilongjiangensis* are: coast of Primorsky Krai, the Amur River, coast of lake Baikal, the Reserve Krasnoyarsk Stolby, Altai, Khakassia. Crimean peninsula was reported to be endemic by *R. conorii*. All of these regions are the popular places for tourism. Real-time PCR test system "RealBest DNA Rickettsia species" (AO "Vector-Best", Novosibirsk) was developed to detect the DNA markers of the pathogenic rickettsia in clinical specimens. It also can be used for detection of rickettsia in ticks without defining the species. Using the developed test system, more than 7000 tick from 10 regions of Russia were tested. The percentage of rickettsia-infected ticks varied from 7 to 92% in dependence of region and tick's species. After the sequencing of DNA of positive samples in regions of genes *gltA, ompA, ompB* and *sca4* it was determined that there are 11 rickettsia species are circulating with 7 of them that are pathogenic: *R. sibirica, R. heilongjiangensis, R. conorii, R. slovaca, R. aeschlimannii, R. massilae* and *R. mongolotimonae*.

Also using the developed test system the DNA-markers of *R. sibirica* and *R. heilongjiangensis* were determined in the clinical samples (blood samples, urine, swabs of skin eschar, eschar biopsy) derived from patients that were hospitalized in the Far East, Western and Eastern Siberia with the diagnosis "tick-borne rickettsiosis". With the goal of the ability of determination of these two pathogens, the PCR test system "RealBest DNA Rickettsia sibirica/Rickettsia heilongjiangensis" was developed additionally. Using this test system it was found, that the frequency of presence of *R. heilongjiangensis* in tick varies from 0.7 for *I. persulcatus* to 29% for *H. oncinna*. The occurrence of the *R. sibirica* varies from 0.6 for *D. silvarum* up to 17% в *D. nuttalli*. It was proven that both of the developed PCR test systems can be successfully used for determination of circulating pathogenic rickettsia in natural foci, detection of their DNA markers in ticks for the diagnosis of the tick bitten people, as well as for analysis of clinical samples in the laboratory diagnostics tick-borne rickettsiosis.

4.5 doi: 10.15789/2220-7619-2018-4-4.5

DATABASE OF LEPTOSPIRA PROTEIN SPECTRA FOR MASS-SPECTROMETRY IDENTIFICATION

N.V. Breneva[1], A.P. Samsonova[2], E.M. Petrov[2], Zh.A. Konovalova[1], A.S. Ostyak[1], S.V. Balakhonov[1]

[1]Irkutsk Antiplague Research Institute of Rospotrebnadzor, Irkutsk, Russia; [2]Gamaleya State Research Centre for Epidemiology and Microbiology, Moscow, Russia

Leptospirosis is found all over the world both in humans and in many species of agricultural, domestic and wild animals. The disease caused by individual serovars of the pathogen is characterized by a severe clinic and high mortality. *Leptospira* grow very slowly and only on special nutrient media. Together with the difficult pathogen isolation there is also the problem of its identification. According to the modern genosystematics several molecular biology methods were proposed to determine the *Leptospira* species. Mass-spectrometry direct profiling of proteins is easy to set up and widely used to diagnose most bacterial infections, while the available databases of *Leptospira* spectra are absent.

The aim of this study was the development of a protein spectra database for identification of the *Leptospira* species.

Our database contains information about 28 *Leptospira* reference strains of 28 serovars including eight most common species *L. interrogans*, *L. borgpetersenii, L. kirschneri, L. santarosai, L. noguchii, L. inadai, L. weilii, L. biflexa*, as well as the protein spectra of these strains in the format for the software "MALDI Biotyper 3.0". According to the serological classification the presented strains belong to 21 serogroups: *Icterohaemorrhagiae, Grippotyphosa, Canicola, Pomona, Tarassovi, Australis, Sejroe, Autumnalis, Bataviae, Ballum, Pyrogenes, Javanica, Hebdomadis, Louisiana, Panama, Lyme, Sarmin, Djasiman, Mini, Manhao, Sema-*