ticks with *Borrelia burgdorferi* sensu lato *(B. burgdorferi* s.l.*)* and *Borrelia miyamotoi* in the Khabarovsk region during 2017–2018.

A total number of 1238 ixodic ticks were tested on the presence of the *B. burgdorferi* s.l. and 710 ticks were tested on the presence of *B. miyamotoi* DNA via Real-time PCR. Identification of the nucleic acids of the pathogens was performed using PCR kits "RealBest DNA B. miyamotoi", "RealBest DNA B. burgdorferi s.l." ("Vector-Best", Novosibirsk) according to the manufacturer's instructions.

The infestation rate of *Ixodes persulcatus* ticks (31.4±1.74%) with *B. burgdorferi* s.l. was statistically higher compared to *Dermacentor silvarum* (12.8±4.87%, $p < 0.05$) and *Haemaphysalis* spp. (16.6±2.86%, $p < 0.05$). No significant difference between infestation rates of different species of ticks with *B. miyamotoi* was found. During the start of the epidemic season was registered an elevation of vectors infestation rate with *B. burgdorferi* s.l. with a peak in July (33.1±4.33%, $p < 0.05$) followed by a consequent decline down to 11.8±5.53% ($p < 0.05$) in September. A decline in infestation rate of *B. miyamotoi* vectors from 10.4±2.63 to 5.8±1.46% ($p < 0.05$) was registered. From July to September the DNA of *B. miyamotoi* was not found. It is of importance that 14 ticks had a coinfection with *B. burgdorferi* and *B. miyamotoi* in 2017–2018. The Ct DNA value of *B. burgdorferi* s.l. was higher in most of the cases compared with Ct DNA value of *B. miyamotoi*.

The infestation rate of Ixodic ticks with *B. miyamotoi* was significantly lower compared to *B. burgdorferi* s.l. in Khabarovsk Region. The obtained results imply that during the start of the epidemic season (April-May) the risk of exposure of the population to *B. miyamotoi* is higher compared to summer-autumn period. Thus, it is important to study the competition between the pathogens in ticks and its value on the manifestation of the diseases in humans.

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PATHOGENS, PESTICIDE RESISTANCE AND GENETIC DIVERSITY OF HUMAN HEAD LICE

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Pediculosis capitis or head louse infestation is the most prevalent parasitic infestation of humans. It is commonly perceived as an age-dependent rite of passage, and as an embarrassing social nuisance; however, head louse outbreaks do not raise any substantial public health concerns due to their assumed low capacity for transmitting the louse-borne pathogens associated with *Pediculus humanus humanus*, the human body louse. The purpose of this study was to screen head lice, *Pediculus humanus capitis* from Georgia, USA and Madagascar for *Bartonella quintana* and *Acinetobacter* sp. to determine the risk of exposure of rural populations with different levels of economic development to these pathogens. Other aims were to examine these lice for the occurrence of genetic markers for permethrin resistance using restriction fragment length polymorphism (RFLP/PCR) analysis and to evaluate the genetic structure of these head louse populations using microsatellite typing. The *kdr* permethrin resistance biomarker for the T917I mutation was detected by RFLP/PCR in 99.9 and 70% of lice from Georgia and Madagascar, respectively. *Bartonella* DNA was detected at similar levels in both set of samples (10.3 and 12.6%), while *Acinetobacter* sp. DNA was detected more frequently in Georgia lice (80.8%) than in Malagasy lice (42.1%). Microsatellite typing based on 3 sites revealed significant genetic heterogeneity among the lice tested, although head lice from Georgia were separated in 2 closely related clusters, while Malagasy lice exhibited more genetic diversity using Principal Component Analysis and Bayesian clustering. The results provide the first information regarding these combined characteristics of head louse infestations at these locations and can be used as a baseline for temporal surveillance of changes in circulating head louse populations, for monitoring louse susceptibility to permethrin-based pediculicides, and to track potential exposures and outbreaks due to louse-borne pathogens.

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WHOLE GENOME-BASED CHARACTERIZATION OF *COXIELLA BURNETII* STRAINS ISOLATED IN RUSSIAN FEDERATION

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Information on the whole genome structure of the *Coxiella burnetii* strains circulating in Russian Federation (RF) is currently unavailable. The identification and study of differential-significant genetic markers of *C. burnetii* that are important from the epidemiological point of view remains a priority, including determining the hostal specificity.

The aim was whole genome-based characterization of *C. burnetii* strains isolated from different hosts.

We performed whole genome sequencing of four *C. burnetii* strains isolated from two host types (the human and the arthropods) in RF using the MiSeq technology (Illumina, USA). Genome assembling and alignement using Dugway 5J108-111 as the reference was performed with SPADes 3.9.0 genome assembler. Comparative analysis of the whole genomes of Russian strains was carried out between the investigated genomes and the whole genomes sequences of *C. burnetii* available in the NCBI database.

It was confirmed the conception of closed pangenome of species *C. burnetii* characterized by a low intraspecies genetic diversity, including the population circulating in the territory of RF. However, in Russian strains of *C. burnetii* unlike foreign strains the analysis of the variable part of the genome and the composition of unique genes revealed deletions of a part of them, which allows us to speak about their unique genomotype. Analysis showed pronounced clustering within a group of Russian strains by host type, the differences between genomes within clusters were minor. Comparing the number of deleted genome fragments it was found that surprisingly strains from arthropods had a significantly greater genome reduction compared with strains from human. These data are in contrast with the conclusions of a number of authors that the genomic reduction of *C. burnetii* strains isolated from arthropods is limited.

Thus, this corpus of data allow us to characterize the genomes of *C. burnetii* strains isolated in the territory of RF and to make assumptions about the hostal specificity of this pathogen, prompting further studies of its mechanisms.