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Presence of Rickettsia species DNA in Ixodes ticks and in the blood of patients with fever in Belarus in years 2014-2015

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Background: Ticks are the main vectors of infectious diseases of humans and animals in natural conditions of Belarus. They are capable of transmitting more pathogens than any other arthropods. Four main tick borne pathogens (*Borrelia burgdorferi sensu lato* tick-borne encephalitis virus, *Rickettsia spp*, *Anaplasma phagocytophilum*) were detected in seasons in years 2010-2015 in ticks in Belarus, with prevalence of *Borrelia burgdorferi sensu lato* and *Rickettsia spp*. Rickettsioses are caused by obligate intracellular bacteria within the genus *Rickettsia*. Until recently, Mediterranean spotted fever (MSF) caused by *Rickettsia conorii* was considered the only tick-borne rickettsiosis in Europe. However, 'new' TBR have been described in Europe during last years. For instance, other subspecies such as *R. conorii caspia* and *R. conorii israelensis* have been involved in MSF. Dermacentor-borne necrosis erythema and lymphadenopathy/tick-borne lymphadenopathy (DEBONEL/TIBOLA) cases caused by *Rickettsia slovaca*, *Rickettsia raoultii*, and *Rickettsia rioja* been described in several countries where *Dermacentor marginatus* ticks (the mainly implicated vector) are present. *Rickettsia helvetica* has also been involved as a human pathogen in cases of fever with and without rash and in patients with meningitis and carditis.

Material/methods: 1 223 ticks of the genus *Ixodes* were collected on the territory of the Republic of Belarus during the period of their activity from May to September in years 2014-2015. 30 samples of the blood of patients were collected from patients that were treated at the Hospitals of Infectious Diseases in Belarus. Isolation of genetic material (DNA) was performed using the RiboPrep® reagents kits (InterLabService Ltd.). All ticks and samples of blood were analyzed by PCR amplification for the presence *Rickettsia spp*. and Big Die terminator v. 3.1 Cycle Sequencing Kit (Applied Biosystem, UK) for sequencing analysis.

Results: Out of 1 223 surveyed ticks in 409 (33,44%) the presence of DNA of *Rickettsia spp.* were estimated. Selective sequencing analysis revealed DNA *Rickettsia raoultii* in 46 ticks out of 54 (85,2%) and DNA *Rickettsia helvetica* 8 samples out of 54 (14,8%). In blood of four out of 30 patients with fever and tick bites, DNA of *Rickettsia spp.* were detected. DNA of *Rickettsia raoultii* were identified by sequencing analysis in all *Rickettsia* positive blood samples.

Conclusions: Thus, in ticks, collected in a seasons of activity in years 2014-2015 revealed a high content of *Rickettsia spp.* (33,44.% of the samples). DNA of two pathogenic species (*Rickettsia raoultii* (85,2%) and *Rickettsia helvetica* (14,8%)) were found in *Ixodes* ticks. The presence of DNA of *R. raoultii sp. nov.* (the causative agent of tick-borne spotted fever) in serum of patients in Belarus were detected for the first time. How often these infections agents cause disease symptoms in patients with fever in Belarus needs further investigations.