

rate of *Coxiella burnetii* in ticks and rodents from different landscapes in four regions of Ukraine (North, South, East and West) in order to identify enzootic areas, and also to assess the risk of infection for humans in these regions.

Methods & Materials: During 2014–2016, we tested specimens of ticks and rodents collected by regional public health facilities in four regions of Ukraine: North (Zhytomyr and Cherkasy Oblasts), South (Odessa Oblast), East (Donetsk Oblast) and West (Ivano-Frankivsk Oblast). Ticks were collected from cattle, dogs and from environment using active method (flagging). Indirect immunofluorescence assay (IFA) was used to identify *C. burnetii*

Results: During the study period, 9,792 specimens of ticks were tested. As a result, *C. burnetii* corpuscles were found in ticks pool from all four region of Ukraine: Donetsk Oblast – 21.05 ± 6.6% of pools; Odesa Oblast – 11.84 ± 2.06%; Ivano-Frankivsk Oblast – 3.86 ± 1.34%, and Zhytomyr Oblast – 14.29 ± 9.3%; samples from Cherkasy Oblast were negative.

During testing of 357 rodents from 19 rayons of Odesa Oblast, *C. burnetii* was detected in 6.3 ± 2.16% of the pools, including: Danube-Dniester area – 7.41 ± 5.04%; Transnistrian area – 5.71 ± 2.77%; the city of Odesa and neighboring areas – 6.67 ± 4.56%. Q fever pathogen was found in 3 rodent species: *Mus musculus*, *Apodemus arvalis*, and *Microtus arvalis*.

Conclusion: Our study has identified new enzootic territories for Q fever in all four regions of Ukraine and confirmed that existing natural foci of the diseases remain active. Study results have become the basis for determining the landscape and geographic areas with high and low risk of infection for human. Further studies of the pathogen circulation and risk factors are needed to prevent spread of Q fever and outbreaks in population living in enzootic areas.

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Molecular survey of tick-borne pathogens (TBP) in dogs in Italy



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Purpose: Dogs are common feeding hosts of *Ixodes ricinus* and infected animals may act as reservoir for human tick-transmitted infectious agents and as carriers of ticks into human settings.

The aim of this work was to evaluate the presence of tick-borne zoonotic bacteria by molecular methods in dogs from North Eastern Italy.

Methods & Materials: A total of 150 blood samples were collected from dogs entering a municipal kennel. After DNA extraction, the presence of *B. burgdorferi* s.l., Spotter Fever Group (SFG) *Rickettsia* spp., *Anaplasma* spp. and *Ehrlichia* spp. was screened by real-time or conventional PCR. PCR-based assays were carried out for genes 23S rRNA (*B. burgdorferi* s.l.), *gltA* (SFG *Rickettsia* spp.) and 16S rRNA (*Anaplasma* spp. and *Ehrlichia* spp.). Species identification of *Anaplasma* spp. and *Ehrlichia* spp. positive samples was obtained by comparison of nucleotide sequences of conventional PCR products amplifying a portion of 16S rRNA and/or *groEL* genes to nr/nt database by BLAST.

Results: Thirteen dogs (8.7%) were positive to *Anaplasma* spp. (9 animals, 6.0%) or *Ehrlichia* spp. (4 animals, 2.7%); 5 showed sequence similarity ranging from 99% to 100% with *A.*

phagocytophilum, 2 with *A. platys*, 2 with *Anaplasma* spp., 3 with *Ehrlichia canis* and 1 to *Ehrlichia* spp. Neither *B. burgdorferi* s.l. nor SFG *Rickettsia* spp. were found.

Conclusion: The results demonstrate the presence of zoonotic TBPs in dogs from North Eastern Italy. Infected dogs, other than representing a reservoir, provide a picture of the circulation of pathogens in the territory and give an idea of the risk for humans of entering into contact with these infectious agents. The findings confirm that, in spite of the climate changes, in North Eastern Italy the prevalence of SFG *Rickettsia* spp. is still lower than in Central and Southern Italy where *Rickettsia conorii* is largely diffuse.

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Molecular survey of zoonotic agents in rodents from an urban environment, Hungary



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Purpose: Along with several effects, urbanization causes significant changes in the distribution of animal populations and procures a closer coexistence between animals and humans, therefore potentially induces changes in zoonotic disease transmissions as well. Rodents are reservoirs for several zoonotic pathogens. Among others, leptospirosis and hantaviral infections are the most widespread zoonotic diseases worldwide. Hepatitis E virus is a significant causative agent of acute hepatitis with various host groups, some of them may have zoonotic potential. In this study, we performed a molecular survey of pathogens among wild rodents living in urban environment, thus occur in close proximity to humans.

Methods & Materials: Small rodents were collected in the city of Pécs (Southwest Hungary) using live traps, and screened for pathogens by different types of PCR methods (TaqMan-based real-time PCR, RT-PCR, PCR), using specific primer sets, followed by DNA sequencing and molecular sequence analyses.

Results: Altogether 338 rodents, belonging to 5 species (*Apodemus agrarius*, *A. flavicollis*, *A. sylvaticus*, *Microtus arvalis* and *Myodes glareolus*) were tested. A total of 18% of the rodents were infected with *Leptospira* species (all the rodent species), 9% of them were infected with Tula hantavirus and Dobrava-Belgrade orthohantavirus (*M. arvalis*, *M. glareolus*, *A. agrarius*), and 3% of them (*M. arvalis*) were infected with Hepatitis E virus (*Orthohepevirus C*, presumably a novel *Microtus*-specific genotype). Dual infections were detected also: *Leptospira* with hantaviruses in 9 (2.6%) rodents, *Leptospira* with HEV in 4 (1%) rodents, Tula hantavirus with HEV in 2 (0.5%) animals. Multiple co-infections with all three pathogens were not found. However, dual infections suggest that the same rodent host can be infected with several pathogens at the same time.

Conclusion: In this study, rodent-borne pathogens (*Leptospira* spp., DOBV) with significant importance for further clinical considerations were identified. Although these pathogens were already known in Hungary, we provide important surveillance data on them from rodents within urban territories for the first time in the country, pointed out serious threat to public health. Along with these results, a new genotype of Hepatitis E virus was detected also,