Welcome to the second issue of the EDENext Public Health Telegram, the newsletter from the EDENext project focusing on our vector-borne disease research results with direct or indirect impacts on Public Health issues.

EDENext is investigating the biological, ecological and epidemiological components of vector-borne disease introduction, emergence and spread, and creating new tools to control them.

EDENext comprises five specialised vector groups. In this issue we concentrate on the work of the tick-borne diseases (TBD) group. Future issues will examine mosquito-borne diseases (Diptera, Culicicæ), culicoides-borne diseases (Diptera, Ceratopogonidae) and sand fly or phlebotome-borne diseases (Diptera, Psychodidae).

EDENext is seeking to make research more visible, comprehensible and applicable to the public and policy makers, embedding the research results from each vector group in the context of Public Health and vector-borne disease control in Europe. The EDENext Public Health Telegram was established to inform interested individuals and institutions about research results on vector-borne diseases with direct or indirect impact on public health issues.

For more details about the project, visit www.edenext.eu

In this issue, research results from the EDENext Tick-borne disease (TBD) group (01/2012 – 05/2013) include:

1. Tick-borne viruses-an overview
2. Effect of deer density on tick infestation of rodents and TBE hazard, Part I and II
3. The impact of Crimean-Congo haemorrhagic fever (CCHF) on Public Health
4. Discovery of CCHF tick vector in Hungary
5. High TBEV infection rate in Austrian horses
6. Tick-borne diseases in Romania
7. Driving forces for tick range expansion
8. Woodland fragmentation increases Lyme disease risk

Tick warning sign in a forest in Germany
Rainbo research results & Public Health

1. Tick-borne viruses—an overview

Ticks are recognised as vectors for several pathogens of Public Health relevance. Hubálek and Rudolf (2012) offer an extensive overview of the currently known European tick-borne viruses with a special focus on their taxonomy, host and tick vector range, pathogenicity for vertebrates including humans, and their significance for Public Health. Besides the known highly pathogenic Crimean-Congo haemorrhagic fever virus (CCHFV) and tick-borne encephalitis virus (TBEV), the authors also report other tick-borne virus pathogens such as louping-ill and African swine fever virus.

2. Effect of deer density on tick infestation of rodents and TBE hazard, Part I and II

The occurrence and population dynamics of wild ungulates, in particular deer, represent some of the most important risk factors for the risk assessment of diseases transmitted by the pan-European tick species *Ixodes ricinus*. The spatial and temporal variation in the abundance of deer does not only affect the number of ticks in the environment, but also the rate of ticks infected with various pathogens. In the case of tick borne encephalitis, the probability of TBEV circulation is enhanced above a certain threshold deer density as shown in a joint study carried out in Italy and Slovakia and published within two EDENext publications (Cagnacci et al., 2012; Bolzoni et al., 2012). The effect of variable deer population density also has consequences on the pattern of tick infestation of the yellow-necked mouse (*Apodemus flavicollis*), one of the most important small mammal hosts supporting high TBEV circulation through co-feeding ticks in the natural habitat. By comparing sites in Italy and Slovakia with moderate and low deer population density to the presence and/or absence of TBEV occurrence in these areas, researchers from the Fondazione Edmund Mach and the Slovak Academy of Sciences have obtained quantitative estimates of the variation of the number of co-feeding ticks on rodents (Cagnacci et al., 2012) and included these estimates within a mathematical model (Bolzoni et al., 2012) that allows for the computation of the basic reproductive number of the infection and various host densities.


3. The impact of Crimean-Congo haemorrhagic fever (CCHF) on Public Health

Crimean-Congo haemorrhagic fever (CCHF) is a haemorrhagic fever in humans, caused by infection with the Crimean-Congo haemorrhagic fever virus (CCHFV). It is the only biosafety level 4 agent currently present in Europe. Every year, more than 1,000 human clinical cases and up to 50 fatalities are reported from more than 30 countries in Asia, the Middle East, south-eastern Europe and Africa. CCHF can be considered a major emerging disease threat to the European Union due to its high infectiousness, potential of human-to-human transmission and present lack of suitable prophylaxis and therapeutic interventions. Additionally, the ongoing range expansion of its tick vectors within Europe (see 4) underlines the imminent threat this disease poses to Public Health in Europe. The EDENext study by Mertens et al. (2013) summarises the current state of knowledge about CCHF and provides guidance for Public Health analysts and managers. Special emphasis is given to the importance of vector and virus distribution, the impact of climate and the different modes of virus transmission, as well as to the current limitations in diagnostics, treatment and vaccination. Based on this knowledge, recommendations for protection measures for individuals and the population at large, including case management options, and Public Health management and communication strategies are proposed. CCHFV is primarily transmitted by ticks of the genus *Hyalomma*, which can be found in many regions of southern and south-eastern Europe (see 4). Up to 20% of these ticks have been found positive for CCHFV in endemic areas of Turkey. Mammals such as hedgehogs, hares, sheep and cattle are infested by these ticks and thereby may become infected and amplify the virus, yet without suffering from any clinical disease. The virus circulates in a tick-vertebrate-tick cycle, but can also be transmitted horizontally and vertically within the tick population. Most human infections occur by tick bites and by crushing infected ticks, but infections are also possible through contact with blood and other body fluids of viraemic animals. Moreover, there are several reports about person-to-person transmissions following unprotected handling of infected blood samples from patients, by accidental needle stick injuries, and by accidents during surgery. Currently, there is no CCHFV vaccine available and the therapy is restricted to symptomatic treatment.

4. Discovery of CCHF tick vector in Hungary

Crimean-Congo haemorrhagic fever (CCHF) is a zoonotic viral disease transmitted primarily by tick species of the genus *Hyalomma* (see 3). These ticks are endemic to regions with (sub)tropical or Mediterranean climates, such as Albania, Turkey and Uzbekistan. Migratory birds may occasionally carry *Hyalomma* larvae and nymphs from their original habitat to European countries north of the Mediterranean basin. However, it was previously assumed that the cool climate in these areas of Europe would prevent the ticks from completing their life cycle successfully and therefore both prohibit the development of adult ticks possible of transmitting CCHF and the establishment of *Hyalomma* populations. In the EDENext study by Hornok and Horváth (2012) ticks were collected from cattle and wild ruminants in a region of southern Hungary, where, according to prediction models, *Hyalomma* ticks are most likely to occur and establish themselves in the future. Adult *Hyalomma marginatum rufipes* males were found on two occasions. This tick species was therefore detected for the first time in Hungary, marking the (so far) northern-most occurrence of this CCHF vector in Central Europe. A human case of CCHF as well as CCHF virus seropositive animals have already been reported in Hungary. The northern spread of *Hyalomma* ticks and thus potentially of the CCHF virus is of uttermost importance to European Public Health. To monitor and possibly prevent the further expansion of this zoonotic disease beyond its original range, further investigations of the current distribution of CCHF tick vectors in Europe have to be undertaken.

5. High TBEV infection rate in Austrian horses

To evaluate the status of West Nile virus (WNV) within the domestic horse population in Austria, the sera of 257 horses of the same breed, distributed among three federal states, were screened via a commercial ELISA for flaviviruses antibodies. ELISA-positive sera were further tested by virus-specific neutralisation assays for the three flaviviruses circulating in Austria: WNV, Usutu virus (USUV) and tick-borne encephalitis virus (TBEV). While no specific WNV antibodies could be determined, a comparatively high seropositivity rate of 40.4% for TBEV-specific antibodies was detected, with a significantly higher antibody prevalence in younger horses and in stallions. This result is remarkable as comparable studies in Austria and Germany show significantly lower TBEV prevalences in horses and other domestic animals. The age and gender aspect is equally surprising, and is contradictory to results from comparable studies. TBEV is a virus associated with tick-borne encephalitis, a viral infectious disease causing inflammations of the central nervous system in various vertebrate species, including humans, but very little is known about the disease in horses. Overall, the results of the study by Rushton et al. (2013) indicate the necessity of further investigations of TBE prevalence in equines and other domestic animals in Central Europe for the sake of evaluating the Public Health risk posed by TBEV.

6. Tick-borne diseases in Romania

The geopolitical position of Romania as a bridge connecting southern and central Europe has to be respected in regard to its implication for the Public Health system of the European Union, of which Romania has been a member since 2007. In this country, cases of Lyme disease and tick-borne encephalitis have been identified. However, little is known about the Public Health impact of these diseases, and none of the other tick-borne pathogens present in Europe have been reported as causes of infection in Romania. Therefore, the EDENext study by Paduraru et al. (2012) in which various zoonotic tick-borne pathogens (including Rickettsia monacensis, R. helvetica, Anaplasma phagocytophilum, Ehrlichia muris, Francisella tularensis, and Babesia sp. EU1) are described for the first time in Romania can be considered an important step towards future evaluations of the prevalence of these diseases in the country and the implications of these results for national and international (European Union) Public Health surveillance.

7. Driving forces for tick range expansion

The distribution of the tick *Ixodes ricinus*, which serves as a vector of a large variety of pathogens of medical and veterinary importance (among others, babesiosis, Lyme borreliosis and tularemia), has increased significantly all over Europe over the past decades. *I. ricinus* specimens are now detected in more northern areas and habitats at higher altitudes than their prior range. Medlock et al. (2013) assume ongoing climatic change to be a driving factor of the tick range expansion among several other anthropogenic factors. Milder climatic conditions may allow one of the tick’s major host species, the European roe deer (*Capreolus capreolus*), whose abundance has increased in several regions as a consequence of current wildlife management, to spread to and inhabit previously inhospitable areas at higher altitude, thereby serving as a means of transport for the ticks. Furthermore, increasing temperatures reduce the length of snow cover, impacting positively the survival and spread of the ticks. Among other driving factors, land use changes due to agriculture and forestry management in various European countries over the past decades, and thereby suitable habitat expansion for *I. ricinus*, including urbanized areas, are discussed in regard to their effects on the tick range expansion. In conclusion, the authors note that multiple factors drive the range expansion of *I. ricinus* in Europe and that enhanced tick surveillance with harmonised approaches for international data comparison would allow better follow-up of tick population trends at the European Union level, thereby improving the prediction of health risks related to tick-borne diseases.

8. Woodland fragmentation increases Lyme disease risk

Over the past decades, the increase in the number of reported cases of Lyme disease throughout Europe has led to growing Public Health concern regarding the pathogenicity of this disease. Lyme disease, or Lyme borreliosis, is the most frequent vector-borne disease of humans in the Northern Hemisphere. The causative agent is the spirochaete *Borrelia burgdorferi* sensu lato, which is transmitted in Europe mainly by the tick species *Ixodes ricinus*. Lyme disease is strongly connected to various environmental factors, particularly in forest and agricultural landscapes, where the activity ranges of ticks and their hosts (including humans) overlap. However, these factors are not homogeneously distributed among the different landscapes. An understanding of the underlying processes in the transmission system is crucially needed to explain the spatial distribution risk of Lyme disease.

In this EDENext study, Li et al. (2012) demonstrate a cellular automata model for Lyme disease. The study includes a heterogeneous landscape model with three interactive components (hosts, tick population and a disease transmission function). Scenarios of various landscape configurations are simulated and compared. Based on the simulation results, the authors conclude that Lyme disease risk correlates to the density, shape and aggregation level of woodland areas, among others due to the latter’s impact on the local host population and thus spread of the disease-carrying ticks. This
correlation is useful for understanding and predicting the occurrence of tick-borne diseases in dynamic forest landscapes.

Contributions

Contributions to this issue came from Dr. Nils Kley, Dr. Yvonne Gall and Prof. Dr- Martin H. Groschup (all Friedrich-Loeffler-Institut, Greifswald-Isle of Riems, Germany). We are grateful for critical proofreading by Dr. Annapaola Rizzoli (Edmund Mach Foundation, Italy) and other members of the tick-borne disease work package, who have co-authored the scientific publications cited in this telegram. Finally, we’d like to thank Andrew Lewer (Argoat Communications) for editorial assistance.