

VBORNET Newsletter 3, February 2010

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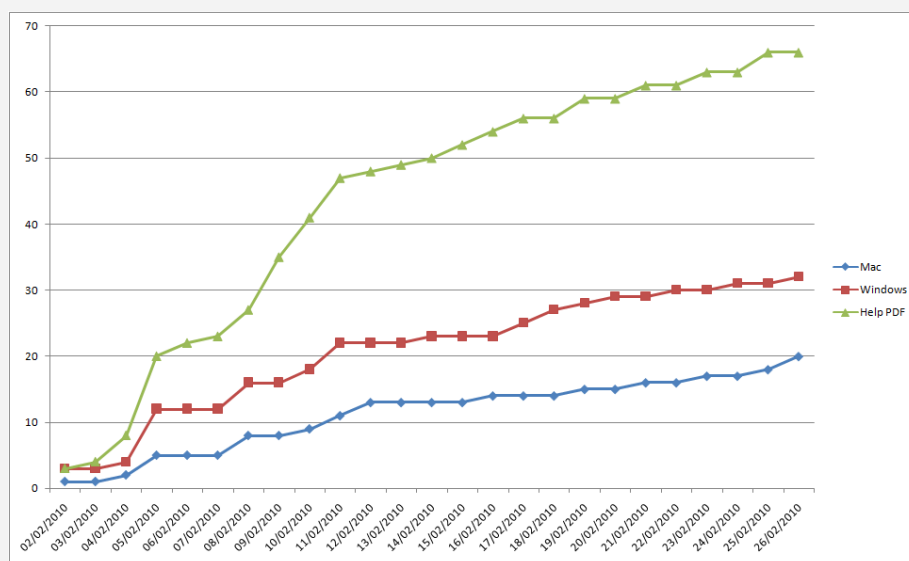
1. VBORNET STATUS

Dear VBD Expert,

This is the third VBORNET Newsletter, and the First which includes in addition to news items related to mosquitoes also items related to ticks and phlebotomines. All have been reviewed and commented by consortium members. This year VBORNET mainly focuses on vector distribution, and spread issues.

Whilst most selected news items are identified through focused internet searches, mainly using News-Digger, a search tool developed at the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Teramo (Italy), we are also interested in 'breaking news' you may have to report as VBD experts. Kindly send any contributions directly to our Paolo Calistri, our news letter editor (see below).

In our previous Newsletter, which was a special issue on invasive mosquito species in Europe and its overseas territories, we also launched the VBORNET vector distribution tool. We are glad to report here that already more than 60 experts have replied positively. The graph below shows the downloads today of Mac and Windows versions of the vector distribution tool and of the instructions for use pdf file. We now are looking forward to data being uploaded!



In the coming weeks we will contact all experts which showed interest to contribute personally. This will enable a first assessment of which data and expertise may be available for the first VBORNET annual meeting which is planned from the first till the third of June at the Institute for Tropical Medicine in Antwerp (Belgium).

We also will look at geographical and vector related data gaps and start a search for additional expertise.

In the mean time, we look forward to your contributions to VBORNET and the Newsletter!

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2. SCIENTIFIC ADVANCES: MOSQUITOES

Usutu virus infection in a patient who underwent orthotopic liver transplantation, Italy, August-September 2009

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Euro Surveill. 2009;14(50):pii=19448.

We report a case of Usutu virus (USUV)-related illness in a patient that underwent an orthotopic liver transplant (OLT). Post transplant, the patient developed clinical signs of a possible neuroinvasive disease with a significant loss of cerebral functions. USUV was isolated in Vero E6 cells from a plasma sample obtained immediately before the surgery, and USUV RNA was demonstrated by RT-PCR and sequencing. This report enlarges the panel of emerging mosquito-borne flavivirus-related disease in humans.

Link to the article: <http://www.eurosurveillance.org:80/ViewArticle.aspx?ArticleId=19448>

Key words: Usutu virus, Mosquito-borne diseases

First human case of Usutu virus neuroinvasive infection, Italy, August-September 2009

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Euro Surveill. 2009;14(50):pii=19446.

We report the first worldwide case of Usutu virus (USUV) neuroinvasive infection in a patient with diffuse large B cell lymphoma who presented with fever and neurological symptoms and was diagnosed with meningoencephalitis. The cerebrospinal fluid was positive for USUV, and USUV was also demonstrated in serum and plasma samples by RT-PCR and sequencing. Partial sequences of the premembrane and NS5 regions of the viral genome were similar to the USUV Vienna and Budapest isolates.

Link to the article:

<http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19446>

Key words: Usutu virus, Mosquito-borne diseases

VBORNET comment: 2010-02-25

Usutu virus (USUV) a mosquito-borne flavivirus (*Flaviviridae*) of the Japanese encephalitis serogroup and related to West Nile virus appeared in the summer of 2001 in Austria which was the first time that it emerged outside Africa (Weissenböck et al. 2007). In the past years the Usutu virus showed a tendency to spread further in Central Europe as a variety of bird species were found infected with the virus in Hungary, Switzerland and Northern Italy. USUV, showing a differential vulnerability in birds, is highly pathogenic for blackbirds and certain owls whereas many other bird species seem resistant. The study

in Austria showed that USUV infections in humans occur, though USUV only shows a low pathogenicity for human beings (Weissenböck et al. 2007). The two publications above demonstrate however that USUV can cause severe disease in immuno-compromised individuals and point to the fact that this mosquito born disease deserves attention.

Developing Global Maps of the Dominant *Anopheles* Vectors of Human Malaria

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Reference: PLoS Med 7(2): e1000209

Despite advances in mapping the geographical distribution and intensity of malaria transmission, the ability to provide strategic, evidence-based advice for malaria control programmes remains constrained by the lack of range maps of the dominant *Anopheles* vectors of human malaria. This is because appropriate vector control depends on knowing both the distribution and epidemiological significance of *Anopheles* vectors. Recent attempts to delineate *Anopheles* distributions have been conducted with mapping techniques ranging from those based on expert opinion and simple interpolations to those employing more sophisticated statistical methods. Consequently, these studies are difficult to compare and impossible to synthesize globally. In addition, whereas in some regions *Anopheles* species distributions and their contribution to human malaria transmission are well known, uncertainty arises when suites of vectors contribute to local transmission, when the margins of the species ranges are poorly defined, and/or when there is simply a lack of any, or reliably identified, distribution records. Furthermore, contemporary maps of anophelines that are competent vectors for malaria are important in assessing local receptivity to reintroduction. To help address these needs, the Malaria Atlas Project (MAP, <http://www.map.ox.ac.uk>) has extended its activities to collate anopheline occurrence data to map the contemporary geographic distributions of the dominant mosquito vectors of human malaria. The plans for, and progress of, this initiative are described here.

Link to the article: <http://www.plosmedicine.org/article/info:doi/10.1371/journal.pmed.1000209>

Key words: *Anopheles* vector, Distribution map, Malaria

VBORNET comment: 2010-02-23

Among the 462 formally named *Anopheles* species (with a further 50 provisionally designated and awaiting description), approximately 70 have been shown to be competent vectors of human malaria and from this set, 52 candidate dominant vector species (DVS) were chosen for inclusion in the MAP vector distribution mapping project. These species have been identified as “main”, “dominant”, or “principal” in major reviews of *Anopheles* distribution and biology and confirmed as DVS by experts from the different regions. Data have been collected through an exhaustive and systematic search of formal and informal literature and only information collected after 31 December 1984 was searched to map contemporary distribution of the DVS based on modern taxonomic species concepts. Because abundance data have not been reported using methods that can be readily standardized across entomological surveys, only presence and absence data were used to generate the maps.

The maps show the species hypothesised range, encompassing expert opinion and occurrence records. Expert opinion was also substantially modified with consideration to known species-specific habitat requirements as revealed by elevation surfaces, satellite imagery and land cover maps. For Europe, 5 species have been included: *Anopheles atroparvus*, *An. labranchiae*, *An. messeae*, *An. sacharovi* and *An. superpicus*.

Important is that maps are not definitive. A note in each legend highlights areas where it would be particularly relevant to augment the occurrence records to provide the best “training data” and thus increase chances of accurately mapping the geographical distribution. On the other hand, increasing accuracy will also imply deleting ancient data (prior to 31 December 1984) especially when the species is not present anymore, as for example the presence data of *An. labranchiae* in Spain, where the species was not recorded since 1946.

A 2-Year Entomological Study of Potential Malaria Vectors in Central Italy

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Vector-Borne and Zoonotic Diseases. December 2009, 9(6): 703-711

Europe was officially declared free from malaria in 1975; nevertheless, this disease remains a potential problem related to the presence of former vectors, belonging to the *Anopheles maculipennis* complex. Autochthonous introduced malaria cases, recently reported in European countries, together with the predicted climatic and environmental changes, have increased the concern of health authorities over the possible resurgence of this disease in the Mediterranean Basin. In Italy, to study the distribution and bionomics of indigenous anopheline populations and to assess environmental parameters that could influence their dynamics, an entomological study was carried out in 2005–2006 in an at-risk study area. This model area is represented by the geographical region named the Maremma, a Tyrrhenian coastal plain in Central Italy, where malaria was hyperendemic up to the 1950s. Fortnightly, entomological surveys (April–October) were carried out in four selected sites with different ecological features. Morphological and molecular characterization, blood meal identification, and parity rate assessment of the anophelines were performed. In total, 8274 mosquitoes were collected, 7691 of which were anophelines. Six *Anopheles* species were recorded, the most abundant of which were *Anopheles labranchiae* and *An. maculipennis* s.s. *An. labranchiae* is predominant in the coastal plain, where it is present in scattered foci. However, this species exhibits a wider than expected range: in fact it has been recorded, for the first time, inland where *An. maculipennis* s.s. is the most abundant species. Both species fed on a wide range of animal hosts, also showing a marked aggressiveness on humans, when available. Our findings demonstrated the high receptivity of the Maremma area, where the former malaria vector, *An. labranchiae*, occurs at different densities related to the kind of environment, climatic parameters, and anthropic activities.

Link to the article: <http://www.liebertonline.com/doi/pdfplus/10.1089/vbz.2008.0129>

Key words: Malaria, Mosquito-borne diseases, Epidemiology, Field studies

VBORNET comment: 2010-02-24

This interesting field study conducted in a former malaria-endemic region confirms that native malaria vectors are still present in Italy, including the primary vector *An. labranchiae* which is not reported nowadays from Spain and continental France. The relative abundance of anophelines compared to the total amount of collected mosquitoes is not indicative, as used trapping method aimed anophelines (light trap, catches in resting site, human bait collection during night). *Anopheles* species were identified using the state-of-the-art morphological and molecular methods. Results show interestingly that both *An. labranchiae* and *An. maculipennis* s.s. are anthropophilic, but there is also an indication that they have hardly access to human hosts (probably due to a limited dispersal and a nocturnal host seeking). Human bait collection indicates a nocturnal host seeking activity, from 20:00h till 24:00h. Unfortunately, the applied field protocol gives no indication on the start of the biting activity, as the catches started only at 20:00h. High densities of *An. labranchiae* was mainly found in rice field areas and evidence of high receptivity to malaria is restricted to such areas. While reintroduction of endemic malaria is unlikely, there is a possibility, if presence of gametocyte carriers, of occurrence of sporadic locally acquired *P. vivax* cases in such areas.

The World Malaria Report 2008

World Health Organization

World Health Organization, Geneva, Switzerland

WHO publications, 2009; ISBN 978 92 4 156390 1 ;pp. x+66

The 2009 *World Malaria Report* summarizes information received from 108 malaria endemic countries and other sources and updates the analysis presented in the 2008 *Report*. It highlights progress made in meeting the World Health Assembly (WHA) targets for malaria to be achieved by 2010 and 2015, and new goals on malaria elimination contained in the Global Malaria Action Plan (2008). [Complete summary on page viii of the report]

Link to the article: http://whqlibdoc.who.int/publications/2009/9789241563901_eng.pdf

Key words: Malaria, Mosquito-borne diseases

VBORNET comment: 2010-02-23

The WHO report provides updated data for 2008 and analyses the progress and the impact of the malaria control strategies, including prevention, diagnostic and treatment, control and elimination, and financing.

In the WHO European Region, locally acquired malaria cases were reported in 6 of the 53 Member States: Azerbaijan, Georgia, Kyrgyzstan, Tajikistan, Turkey and Uzbekistan. Transmission of *Plasmodium falciparum* is confined to Tajikistan, with only two cases reported in 2008; in other countries, transmission is due exclusively to *P. vivax*, although imported cases of *P. falciparum* may occur. In all affected countries, malaria transmission is seasonal, occurring between June and October, and shows a marked focal distribution. The number of reported cases of malaria in the Region has been reduced substantially, from 32,474 in 2000 to 660 in 2008, only Kyrgyzstan failing to register a decrease of >50% in the number of cases since 2000. In this last country, the number of cases rose from 12 in 2000 to 2744 in 2002, before falling to 18 in 2008. Tajikistan and Turkey accounted for 80% of the reported cases in the Region in 2008. Whereas Armenia has not reported any cases since 2005, the Russian federation reports indigenous cases since that year.

Intensive control activities are implemented throughout the Region. Indoor residual spraying is the primary means of vector control in all countries and is applied with strict total coverage of all residual and new foci of malaria, with a view to interrupting transmission over the target area as soon as possible and preventing its re-establishment. Insecticide-treated mosquito nets are also used for protection, particularly in Tajikistan. The use of larvivorous *Gambusia* fish is promoted by almost all affected countries in rice-growing areas. Blood slides are taken from clinically suspected malaria cases for active and passive case detection. All cases detected are treated, and information on their origins is obtained to facilitate epidemiological classification of malaria foci. Particular attention is given to situations in which there is a risk for spread of malaria between neighbouring countries and regions. In 2005, all nine malaria-affected countries in the region endorsed the Tashkent Declaration, the goal of which is to interrupt malaria transmission by 2015 and eliminate the disease within the region. Since 2008, national strategies on malaria have been revised to reflect the new elimination challenges. In summary, all the malaria-endemic countries in the European Region have active malaria control programmes, which make the Region the most successful, as almost all countries have reduced their case loads.

Are *Aedes albopictus* or other mosquito species from northern Italy competent to sustain new arboviral outbreaks?

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Medical and Veterinary Entomology 2010; 24(1):83-87; Doi : 10.1111/j.1365-2915.2009.00853.x

The Asian tiger mosquito *Aedes albopictus* (Skuse) (Diptera: Culicidae), native to Southeast Asia, has extended its geographical distribution to invade new temperate and tropical regions. This species was introduced in 1990 to Italy and has since become the main pest in urban settings. It was incriminated as a principal vector in the first European outbreak of chikungunya virus (CHIKV) in the province of Ravenna (Italy) in 2007. This outbreak was associated with CHIKV E1-226V, efficiently transmitted by *Ae. albopictus*. The occurrence of this outbreak in a temperate country led us to estimate the potential of *Ae. albopictus* to transmit CHIKV and dengue virus (DENV), and to determine the susceptibility to CHIKV of other mosquito species collected in northern Italy. Experimental infections showed that *Ae. albopictus* exhibited high disseminated infection rates for CHIKV (75.0% in Alessandria; 90.3% in San Lazzaro) and low disseminated infection rates for DENV-2 (14.3% in San Lazzaro; 38.5% in Alessandria). Moreover, *Ae. albopictus* was able to attain a high level of viral replication, with CHIKV detectable in the salivary glands at day 2 after infection. In addition, the other three mosquito species, *Anopheles maculipennis* Meigen, *Aedes vexans vexans* (Meigen) and *Culex pipiens* L., showed variable susceptibilities to infection with CHIKV, of 0%, 7.7% and 0–33%, respectively. This information on vector competence is crucial in assessing the risk for an outbreak of CHIKV or DENV in Italy.

Link to the article:

<http://www3.interscience.wiley.com/journal/123282824/abstract?CRETRY=1&SRETRY=0>

Key words: *Aedes albopictus*, Chikungunya, Dengue, Vector competence, Italy

VBORNET comment: 2010-02-24

This paper completes the assessment of the vector competence of the *Ae. albopictus* populations spreading in Europe. The studied populations show high competence for CHIK virus infection for a variant isolated from a patient in La Reunion island, and phylogenetically close related to the isolates of the Italian strain. CHIKV was detectable in the salivary glands from 2 days after the ingestion of an infectious bloodmeal which support previous data (Vazeille et al., 2007, 2008; Moutailler et al., 2009)

and highlights the risk of a rapid spread of an infection. Other tested species were no or less susceptible to CHIKV, but curiously for the first time a strain of *Culex pipiens* show a certain susceptibility, contrarily to those from southern France (Vazeille et al., 2008). Once more, *Ae. albopictus* shows a high potential of transmitting CHIK virus, and also a potential albeit lower to transmit DEN virus. Therefore surveillance of viraemic humans coming back from endemic areas appears relevant, particularly in areas where vector density and longevity are high.

Effects of Temperature and Rainfall on the Activity and Dynamics of Host-Seeking *Aedes albopictus* Females in Northern Italy

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Vector-Borne and Zoonotic Diseases. 2010; Ahead of print. doi:10.1089/vbz.2009.0098.

The Asian tiger mosquito, *Aedes albopictus*, has colonized nearly all the regions of Italy as well as other areas of Europe. During the summer of 2007 the tiger mosquito was responsible for an outbreak of Chikungunya in Italy, when this virus was brought in by a tourist of Indian origin returning from an endemic area. To increase the knowledge of tiger mosquito population dynamics, a survey was carried out from April to November 2008 in the municipalities of Arco and Riva del Garda (northern Italy) through a Biogents Sentinel™ (BG)-trap sampling. In particular, the aim of the study was to evaluate the influence of temperature and rainfall on the activity and dynamics of *Ae. albopictus* host-seeking females. The seasonal emergence of host-seeking females was strongly influenced by the minimum temperature, and a lower threshold of 13°C was identified. In addition, the threshold for the end of adult activity was found at a minimum temperature of 9°C. Host-seeking female abundance was positively affected by the accumulated temperatures over the period 3 and 4 weeks before the sampling week, possibly as a consequence of the positive effect of accumulated temperatures on larval density. Instead, accumulated precipitation over 1–4 weeks before sampling was negatively correlated with host-seeking female abundance. Finally, the activity of host-seeking females, estimated by the weekly increment in female abundance, was positively affected by the total abundance of females and by mean weekly temperatures. Our study provides useful information for predicting the dynamics of host-seeking *Ae. albopictus* females in northern Italy and for designing control strategies for preventing arbovirus outbreaks in areas colonized by *Ae. albopictus*.

Link to the article: <http://www.liebertonline.com/doi/abs/10.1089/vbz.2009.0098>

Key words: *Aedes albopictus*, Field study, Italy

VBORNET comment: 2010-02-24

This study shows that the dynamics of *Ae. albopictus* is similar in Northern Italy to those noted for other regions of Europe, but the length of the reproductive season is considerably shorter than of more southerly latitudes, such as Rome, presumably due to differences in temperature and photoperiod. Highest adult densities were reported from weeks 31 to 37 (August to Mid-September). Original temperature thresholds correlated with start and end of adult female activity are assessed. For the first time thresholds are identified for European female *Ae. albopictus* populations in the field. The temperature threshold for the start of activity (13°C) is found consistent with other used threshold values (11°C) for the hatching of eggs (Hawley 1988, Kobayashi et al. 2002, Toma et al. 2003) and with recent studies that have modelled the distribution of *Ae. albopictus* and have reported that 81% of the municipalities where this vector was found have a minimal annual mean temperature above 11°C (ECDC, 2009). A temperature threshold (9°C) is also given for the end of adult activity. However, mosquitoes can extend their reproductive season when the outdoor temperature decreases by seeking out a favourable microclimate, e.g. in urban environments where adult mosquitoes could find sheltered resting and breeding locations inside or near human habitations. This very good study shows that the dynamics of *Ae. albopictus* is strongly influenced by temperature, rainfall, and female abundance. With respect to the study area, the authors propose that to predict *Ae. albopictus* host-seeking female abundance and dynamics, the accumulated temperatures of the third and fourth weeks prior to sampling and the accumulated rainfall of the first to fourth weeks prior together with the mean weekly temperature should be monitored. These data should be useful for preventing arbovirus outbreaks in northern Italy, and for designing more effective control campaigns against this mosquito, but also for improving models on distribution of *Ae. albopictus* and on related arboviruses transmission risk.

3. SCIENTIFIC ADVANCES: TICKS

Dissemination of spotted Fever rickettsia agents in Europe by migrating birds.

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PLoS One. 2010; 5(1): e8572.

Migratory birds are known to play a role as long-distance vectors for many microorganisms. To investigate whether this is true of rickettsial agents as well, we characterized tick infestation and gathered ticks from 13,260 migratory passerine birds in Sweden. A total of 1127 Ixodes spp. ticks were removed from these birds and the extracted DNA from 957 of them was available for analyses. The DNA was assayed for detection of *Rickettsia* spp. using real-time PCR, followed by DNA sequencing for species identification. *Rickettsia* spp. organisms were detected in 108 (11.3%) of the ticks. *Rickettsia helvetica*, a spotted fever rickettsia associated with human infections, was predominant among the PCR-positive samples. In 9 (0.8%) of the ticks, the partial sequences of 17kDa and ompB genes showed the greatest similarity to *Rickettsia monacensis*, an etiologic agent of Mediterranean spotted fever-like illness, previously described in southern Europe as well as to the *Rickettsia* sp.IrITA3 strain. For 15 (1.4%) of the ticks, the 17kDa, ompB, gltA and ompA genes showed the greatest similarity to *Rickettsia* spp. strain *Davousti*, *Rickettsia japonica* and *Rickettsia heilongjiangensis*, all closely phylogenetically related, the former previously found in *Amblyomma tholoni* ticks in Africa and previously not detected in *Ixodes* spp. ticks. The infestation prevalence of ticks infected with rickettsial organisms was four times higher among ground foraging birds than among other bird species, but the two groups were equally competent in transmitting *Rickettsia* species. The birds did not seem to serve as reservoir hosts for *Rickettsia* spp., but in one case it seems likely that the bird was rickettsiemic and that the ticks had acquired the bacteria from the blood of the bird. In conclusion, migratory passerine birds host epidemiologically important vector ticks and *Rickettsia* species and contribute to the geographic distribution of spotted fever rickettsial agents and their diseases.

Link to the article:

<http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=20052286>

Key words: *Rickettsia*, Ticks, Migratory birds

VBORNET comment: 2010-01-19

Rickettsial infections have been reported to represent the third most common vector-borne disease acquired during international travel (O'Brien et al. 2001). In North-Eastern Europe, local rickettsial infections caused by *R. helvetica* are also emerging and strictly correspond to the distribution range of *Ixodes ricinus*, its main tick vector in this region (Parola et al. 2005). While tick vectors are well identified for many Rickettsial agents, little information is available on natural vertebrate reservoirs and the existence of a "sylvatic" cycle. The present paper aims to elucidate the role of migratory birds in the epidemiology of *Rickettsia* spp. in Sweden through indirect examination in ticks infesting birds. Mean prevalence of infections in *Ixodes* ticks (11.3%) is similar to those classically reported in Europe (Nijhof et al. 2007). The results provide several evidences suggesting that birds may play an important role as disseminators of *Rickettsia* spp. infected tick vectors but not as competent reservoirs for *Rickettsia* spp. They confirm a previous survey published in 2006 by Santos-Silva from wild birds in Portugal. To better precise bird-pathogen interactions, it would have been interesting to have direct information on bird status instead of predictions based on tick status. However, experimental trials on captive birds seem too difficult and not representative of epidemiological processes in the nature. In addition, there was not any standardized and sufficiently sensitive PCR detection method to directly detect and identify *Rickettsia* spp. from wild birds or any other vertebrate host until recently (Boretti et al. 2009).

The feasibility of developing a risk assessment for the impact of climate change on the emergence of Crimean-Congo haemorrhagic fever in livestock in Europe: a Review.

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Crimean-Congo haemorrhagic fever virus (CCHFV) is one of the most widespread of all medically important arboviruses with ticks of the *Hyalomma* spp. serving as the main vectors. Infection of livestock by CCHFV serves as a route of exposure to humans, as a reservoir of disease and as a route of importation. This study discusses the pathways and data requirements for a qualitative risk assessment for the emergence of CCHFV in livestock in Europe. A risk map approach is proposed based on layers that include the potential routes of release (e.g. by migrating birds carrying infected ticks) together with the main components for exposure, namely the distributions of the tick vectors, the small vertebrate host reservoirs and the livestock. A layer on landscape fragmentation serves as a surrogate for proximity of livestock to the tick cycle. Although the impact of climate change on the emergence of CCHF is not clear, comparing the distribution of risk factors in each layer currently with those predicted in the 2080s with climate change can be used to speculate how potential high-risk areas may shift. According to the risk pathway, transstadial and/or transovarial transmission in the tick vector are crucial for CCHFV spread. Vector competence and tick vector switching, however, remain critical factors for CCHFV colonization of new regions in Europe. The species of migratory bird is also an important consideration in the release assessment with greater abundance and biodiversity of ground-dwelling birds in southern Europe than in northern Europe.

Link to the article:

<http://www3.interscience.wiley.com/journal/123193629/abstract?CRETRY=1&SRETRY=0>

Key words: Climate change, Crimean-Congo haemorrhagic fever, Risk assessment

VBORNET comment: 2010-01-19

In this paper, the authors aimed to characterize environmental factors such as habitat and climatic features that might be associated with the occurrence of Crimean-Congo haemorrhagic fever cases that were reported during the period 2003-2008 in Turkey. The author found that habitat fragmentation constituted the principal factor that impacts on the report of disease in this period. Based on this finding, the authors suggested that increasing fragmentation would increase the contact between vector ticks and humans, thereby increase disease transmission dynamics of this vector borne disease. Particular attention was carried out by the author to homogenize the quality of the spatial predictors, in term of spatial resolution and temporal variability, which is of great importance when comparing longitudinal information. Although one could not agree with the use of "environmental niche" when predicting spatial distribution in non yet stable ecological system, the paper was well written and correspond to the actual needs for better understanding of vector-host-pathogen relationship and particularly tick-borne disease. However, some concerns might be risen regarding case definition. First, positive cells were defined under the condition that at least one reported positive case was resident in that cell. Second, negative cells were defined such as no records of positive cases would necessary means that there is no disease circulation. Both of these assumptions may create problems when interpreting the outcomes of the analysis. As such despite being coherent with the literature and the ecological knowledge of CCHF, further study would be required to confirm the outcomes.

Ecology of the Crimean-Congo Hemorrhagic Fever endemic area in Albania.

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Vector Borne Zoonotic Dis. 2009 Dec;9(6):713-6.

Crimean-Congo hemorrhagic fever virus (CCHFV) is endemic in Albania. Ticks collected from cattle grazing in the endemic areas of Albania were tested for presence of CCHFV RNA, while serum samples collected from goats, cattle, hares, and birds were tested for the presence of specific IgG antibodies to CCHFV. One of the 31 pools prepared, consisting of four female *Hyalomma* spp. ticks, was found to carry CCHFV RNA with 99.2-100% homology to sequences detected in patients from the same region. Antibodies were not detected in cattle, hares, and birds, but 2/10 goats presented high titers of IgG antibodies. The shepherd of that flock was a member of a family affected by CCHF 10 days before the collection of goats' sera, and he presented a mild form of the disease.

Link to the article:

<http://www.liebertonline.com/doi/abs/10.1089/vbz.2008.0141>

Key words: Crimean-Congo haemorrhagic fever, Albania

VBORNET comment: 2010-01-24

This paper aims to provide information on the ecology of CCHF endemic area in Albania. 338 ticks were collected from animals (cattle) and sera from cattle, goats, hares and birds from the CCHF endemic areas of NE Albania and were analysed for IgG antibodies. Surprisingly only 1/31 pools of ticks were positive, and although the most abundant tick collection was *Rhipicephalus* spp., the positive ticks were *Hyalomma* spp., as we might expect. Ticks were not identified to species level. 2/10 goats were positive for IgG. All birds were negative and presumably also the cattle and hares. The latter is surprising as these are generally considered the main reservoir of infection, although the sample size was low. This paper adds very little to our knowledge of the ecology of CCHF, however it does provide some information on the seroprevalence of CCHF in goats and the diversity of ticks on cattle and goats in CCHF endemic areas in Albania. Follow up studies with greater numbers of *Hyalomma* and sera from hares would be worthwhile.

Detection of *Anaplasma phagocytophilum* and *Borrelia burgdorferi* in dogs in the Czech Republic.

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Vector Borne Zoonotic Dis. 2009 Dec;9(6):655-61.

The aim of this study is to present molecular, serologic, and clinical findings for dogs that were naturally infected with *Anaplasma phagocytophilum* or *Borrelia burgdorferi* sensu lato (s. l.) in the Czech Republic. This data can provide information relevant to human infection. In total, blood samples from 296 dogs and 118 engorged ticks were examined. Samples were tested for *A. phagocytophilum* using polymerase chain reaction (PCR) amplification, nested PCR, and direct sequencing of the 16S rDNA, and for *B. burgdorferi* s. l. using PCR amplification of the 16S rDNA and restriction fragment length polymorphism analysis of the 5S-23S rDNA intergenic spacer. In addition, blood samples were screened for antibodies to these bacteria. Ten (3.4%) dogs were PCR-positive for *A. phagocytophilum*. Morulae of *A. phagocytophilum* in granulocytes were found in two of these dogs. Nine of the PCR-positive dogs had clinical signs related to anaplasmosis. Statistically significant differences in the PCR detection rates were found between breeds and between symptomatic and asymptomatic dogs. Infection with *Borrelia garinii* was detected by PCR in a dog with meningoencephalitis. DNA of *A. phagocytophilum* and *B. burgdorferi* s. l. (*B. garinii* or *Borrelia afzelii*) was detected in 8.5% and 6.8% of ticks, respectively. Immunoglobulin (Ig) G seropositivity to *A. phagocytophilum* was 26%. Significant differences were found with respect to breed and gender. IgM and IgG antibodies to *B. burgdorferi* s. l. were detected in 2.4% and 10.3% of dogs, respectively. Our findings suggest that the exposure to *B. burgdorferi* s. l. exists in dogs in the Czech Republic, and exposure to *A. phagocytophilum* is common.

Link to the article:

<http://www.liebertonline.com/doi/abs/10.1089/vbz.2008.0127>

Key words: anaplasmosis, Lyme disease, Czech republic

VBORNET comment: 2010-01-24

This paper provides new and important information on the prevalence of *A. phagocytophilum* and *B. burgdorferi* s.l. in ticks and dogs in the Czech Republic. Results suggest that exposure to *A. phagocytophilum* is common in dogs. The majority of PCR positive dogs also had clinical signs of anaplasmosis. This paper adds to our growing knowledge of this pathogen in ticks and dogs and highlights the need for greater understanding of the public health implications of AP and the possible use of dogs as sentinels of infection. For *A. phagocytophilum*, finding positive PCR in animals with specific symptoms shows that clinical signs may be a useful tool to assess the risk for human related to dogs. Conversely, serology only reflects the past circulation of the pathogen in the dog population. For *B. burgdorferi* s.l., such relationships could not be demonstrated but the present results showed that two species of *B. burgdorferi* s.l. actually circulate in ticks: *B. garinii* and *B. afzelii*. Such study does not propose major enhancements on the epidemiology of *A. phagocytophilum* and *B. burgdorferi* s.l. but it provides clear and synthetic results on the local situation in a domestic animal host, the dog, in Czech Republic.

Detection of antibodies against *Anaplasma phagocytophilum* in Algerian mice (*Mus spretus*), Portugal.

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Vector Borne Zoonotic Dis. 2009 Dec;9(6):663-9.

The recent detection of *Anaplasma phagocytophilum* in Portugal stimulated further research on the agent's enzootic cycle, which usually involves rodents. Thus a total 322 rodents belonging to five species, including 30 *Apodemus sylvaticus* (wood mouse), 65 *Mus musculus* (house mouse), 194 *M. spretus* (algerian mouse), 5 *Rattus norvegicus* (brown rat) and 28 *R. rattus* (black rat), were studied by indirect immunofluorescent assay (IFA) and/or polymerase chain reaction (PCR) for *A. phagocytophilum* exposure in four sampling areas of mainland and two areas of Madeira Island, Portugal. Overall, 3.6% (7/194) of *M. spretus* presented with IFA-positive results. Seropositive mice were detected in all three mainland sampling areas where this species was captured, with prevalence of 5.2% (5/96) and 5.0% (1/20) for the Ixodes-areas of Arrábida and Mafra, and 1.3% (1/78) for Mértola, a difference that was not statistically significant ($p > 0.05$). The majority of IFA-positive mice were detected in spring when considering either Arrábida alone ($p = 0.026$) or all *M. spretus* sampling areas together ($p = 0.021$), although the significance of this association was not evident after Bonferroni correction. Nevertheless, neither the seropositive *M. spretus*, nor additional samples of 10% seronegative rodents from mainland, and 16% of rodents collected in Madeira Island showed evidence of *A. phagocytophilum* active infections when spleen and/or lung samples were tested by PCR. Either the *M. spretus* results represents residual antibodies from past *A. phagocytophilum* infections, present infections with limited bacteremia, or cross-reactions with closely related agents deserves more investigation.

Link to the article:

<http://www.liebertonline.com/doi/abs/10.1089/vbz.2008.0066>

Key words: anaplasmosis, Portugal

VBORNET comment: 2010-01-24

The paper proposes to investigate the potential role of Portuguese rodent species in the maintenance of *A. phagocytophilum* enzootic cycles. In this country, *A. phagocytophilum* has been previously detected in two Ixodes species and an active infection has been recently reported in a horse, as well as presence of antibodies against this agent in Ixodes-exposed patients. 3.6% of *M. spretus* present IFA-positive results, suggesting the exposure of this species to the pathogen. Seropositive animals were detected in the whole country and the highest seroprevalences were observed in the areas where Ixodes is present. However, although all the other rodent species were found negative, no significant difference exists between these ones and *M. spretus*; this result denies the hypothesis of peculiar species sensitivity. Moreover, the rodents that were positive in IFA were not positive in PCR, suggesting that *M. spretus* may not be a reservoir of *A. phagocytophilum*. Other explanations are also proposed such as the low level of bacteria resulting in the lack of detection using PCR or the possibility of cross-reactions of the serological test with agents that share antigenic similarities with *A. phagocytophilum*. This final discussion from authors shows the high importance to continue investigations and resolve such issues.

4. SCIENTIFIC ADVANCES: PHLEBOTOMINAE

The Potential Effects of Global Warming on Changes in Canine Leishmaniasis in a Focus outside the Classical Area of the Disease in Southern France.

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Vector Borne Zoonotic Dis. 2009 Dec;9(6):687-94.

In 1994, an ecoepidemiologic study was carried out in the mid-Ariège valley (French Pyrenees) where autochthonous cases of canine leishmaniasis had been previously reported. Serologic samples were

collected from 336 dogs in two groups of villages. The seroprevalences were 11.67% in the valley villages and only 1.43% in the foothill villages. Five lymph node biopsies were taken from serologically positive dogs, and resultant isolates were identified as *Leishmania infantum* zymodeme MON-1. Phlebotomine sandflies were collected in five locations by CDC light traps. Both of the known French vectors, *Phlebotomus ariasi* and *P. perniciosus*, were identified. Bioclimatic and floristic studies showed that this area is an enclave of the supra-Mediterranean climatic zone, containing a typically xerothermophilic Mediterranean flora. The Pyrenees Mountains are usually considered to be outside of the endemic range of leishmaniasis in southern France, and so our demonstration of a microfocus of canine leishmaniasis in the northern foothills is noteworthy.

A second serologic survey carried out in 2007 (216 dogs) showed an inversion of the seropositive rates between the two groups of villages compared with those of 1994: only 2.72% in the valley villages and 11.32% in the foothills villages. The decrease of seroprevalence in the first area (valley villages) can be related to a considerable use of deltamethrin collars during the transmission season. The increase of seroprevalence of the foothill villages could be related to climatic conditions, since there was an increase of about 1°C in the mean annual temperature.

Link to the article:

<http://www.liebertonline.com/doi/pdfplus/10.1089/vbz.2008.0126>

Key Words: Leishmaniasis, Ecoepidemiology, Bioclimatology, Dogs, Pyrenees, Ariège, Global warming.

VBORNET comment: 2010-02-25

This paper reports very interesting results concerning the effect of global warming on canine leishmaniasis in a **focus outside** of the formerly recognized area of the disease in the midvalley of the Ariège River between Ax-les-Thermes to Tarascon-sur-Ariège in southern France. Since the study area is oriented in the north by the Tabè massif and in the south by the Pyrenees chain, obtained findings has become more interesting. Pyrenees Mountains are usually considered to be **outside** of the endemic range of leishmaniasis in southern France. The demonstration by the authors of a microfocus of canine leishmaniasis in the northern foothills is considerably noteworthy as well as the demonstration of the continuous geographical extension of two vector populations, *Phlebotomus ariasi* and *Ph. perniciosus* from the Mediterranean baseline to inland. This situation indicates that previously determined distribution border of sand fly populations is changing through the inland and higher altitudes. Such geographical extension has already been documented in Turkey and Italy, where a northward spread of leishmaniasis has been reported (Aytekin et al. 2007, Simsek et al. 2007, Svobodova et al. 2008, Maroli et al. 2008, Aytekin et al. 2009). The study has two main objectives: 1) to verify the existence of canine leishmaniasis outside the Mediterranean area in southern France and to analyze the bioclimatic and ecological conditions that could ensure the maintenance of such a microfocus, 2) to assess the expected impact of global warming on the increase the canine leishmaniasis enzootic area (Rodhain 2000), given the presence of the sand fly vector for which the distribution is closely correlated with specific climate (Rispaïl et al. 2002). The evolution of the enzootic disease has been investigated in time and correlated with climatic and environmental changes. Results from two different time period (1994 and 2007) were compared to find out the differences of leishmaniasis situation between the periods and between sub localities (lower and higher altitude). The authors used practical methodology such as Gussen's ombrothermic diagram, Emberger's climatogram, Land-sat images covering the area were acquired, georeferenced, radiometrically referenced, and classified to investigate and then to understand the possible effect of the overall vegetation, bioclimatic features, temperature changes in time on extension of leishmaniasis and vector species. Significant differences in leishmaniasis prevalence were observed between two locations from 1994 to 2007; while the prevalence was appreciably higher in lower location in 1994. On the contrary the situation changed towards to northern foothills. According to the results of this study, two factors may mainly influence this extension in time: 1) the widespread use of deltamethrin collars on dogs during the transmission season of the disease in lower locality in contrast to higher locality, 2) more importantly, the increase in the average of mean annual temperature (0.97 °C) between 1997 and 2006. In addition, higher focus may be classified as "ectopic" and could possibly be considered as a surviving relict of an old larger focus from a time when the temperature were higher. In this context, it could be considered as a "sentinel focus" of particular interest for the study of leishmaniasis extension or emergence in relation to global warming. On the other hand, even several previous studies fully support to these statements, some others insistently contend the importance of effect of humidity fluctuations than that of temperature on sand fly and leishmaniasis distribution (Erisoz and Alten 2005,2006; Erisoz, 2009). However, no definitive conclusions can be drawn at the moment and further studies are required to confirm and explain the results.

5. VECTOR BORNE DISEASE EVENTS

ARBO-ZOONET International Network for Capacity Building for the Control of Emerging Viral Vector Borne Zoonotic Diseases WORKSHOP ON WEST NILE VIRUS DIAGNOSTIC TECHNIQUES

Dates: 2010-04-27/29 – Teramo, Italy

Objectives

1. Increasing knowledge and preparedness for West Nile Virus (WNV) throughout Europe
2. Harmonizing methods for WNV diagnosis
3. Learning how to undertake the following diagnostic techniques for WNV:
 - Preparation and storage of RNA from tissue samples
 - RT-PCR including pan-flavivirus PCR
 - Virus isolation in vitro and calculation of virus titre by plaque reduction neutralization test
 - Virus isolation in vivo (discussion only)
 - Antibody detection by serum neutralization (plaque reduction neutralization test and microtiter technique)
 - Measurement of Flavivirus IgG by ELISA
 - Measurement of WNV-specific IgM by ELISA

At the end of the workshop participants will be able to undertake molecular and serological methods to correctly diagnose WNV.

Link to the website: http://www.arbo-zoo.net/events-projects_4/workshop-on-west-nile-virus-diagnostic-techniques_305.htm

Contact name: formazione@izs.it

Joint Tropical Veterinary Parasitology and EVPC Annual Congress 2010

Dates: 2010-04-29/30 – Munich, Germany

Open to all scientists interested in the area of Tropical Veterinary Medicine

Link to the website:

<http://www.tropa.vetmed.uni-muenchen.de/aktuelles/news/evpc/index.html>

Organizing Committee:

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17th EUROPEAN SOCIETY for VECTOR ECOLOGY CONFERENCE

Dates: 2010-09-13/17 – Wroclaw, Poland

The Society for Vector Ecology (SOVE) serves the interests of public health scientists including vector ecologists, medical entomologists, academia and operational staff and aims to promote the exchange of research and pertinent information in the field of vector ecology and vector-borne diseases in its broader sense.

The Society was established in 1968 in California. Soon after its establishment, SOVE attracted scientists from all over North America as well as Europe, and currently include members also from Australia, and many Asian, African and South American countries. Our World-wide Society organizes the main USA annual conference, bi-annual meetings of the European Branch of SOVE and the international Congress of SOVE every four years which is held alternatively overseas and in the USA.

The SOVE conferences attract scientists and other professionals from all over the World working on vectors, vector-borne pathogens, their ecology, biology, taxonomy, control and related disciplines.

The 17th European Society for Vector Ecology Conference will be held in Wroclaw (Poland) on September 13-17, 2010. Our goal is to provide ample opportunities for world renown scientists to present the latest results of their research, discuss emerging topics, make new friends and meet with old ones, and at the same time enjoy learn more about the new exciting research.

Link to the website: <http://www.esove.microb.uni.wroc.pl>

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