

VBORNET Newsletter 6, May 2010

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1. VBORNET STATUS

Dear VBD Expert,

As this issue goes to press we are making the final preparations for our first Annual General Meeting (AGM) in Antwerp. VBORNET has now reached the symbolic age of nine months and during that period we conducted many activities. These will all be reviewed at the AGM in the presence of sixty VBORNET representatives from Europe and beyond. In addition we will ask all present to make a critical assessment of our achievements and to suggest ways to improve VBORNET in the future. Finally proposals will be made for the objectives of the second VBORNET year. A summary report of this major event will be disseminated to the entire VBD community in the next News Letter.

We are looking forward to your inputs!

The VBORNET consortium

2. SCIENTIFIC ADVANCES: VECTOR-BORNE DISEASES

The past and present threat of vector-borne diseases in deployed troops

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Clin Microbiol Infect. 2010, 16: 209–224

From time immemorial, vector-borne diseases have severely reduced the fighting capacity of armies and caused suspension or cancellation of military operations. Since World War I, infectious diseases have no longer been the main causes of morbidity and mortality among soldiers. However, most recent conflicts involving Western armies have occurred overseas, increasing the risk of vector-borne disease for the soldiers and for the displaced populations.

Link to the article: http://www.afpmb.org/bulletin/vol30/Vector_Troops.pdf

Key words: vector-borne disease, risk communication

VBORNET comment: 2010-05-25

Recently, vector borne diseases (VBDs) are regularly reviewed for their potential threat of emergence in new areas due to changing climatic, ecological and environmental factors. This paper approaches the subject from a slightly different angle, namely from the threats of VBD on deployed troops moving into endemic areas. Of course, VBDs' impact on war and *vice versa* are not novel topics, but the authors have been able to bring past and recent statistics together resulting in an interesting review. While most data presented concern military personnel, similar threats are posed to other non-immunes, such as people displaced by conflicts. Even, as stated by Dr G. White in an interview, everything we do to protect the military from vectors in the desert or the jungle may be applicable for protecting the public as

well (Vector Borne Zoonotic Dis. 2009 Dec; 9(6):755-8). Irrespective of someone's view on war, major past and present scientific progress in the understanding VBDs and their control can be attributed to the efforts from departments of defence.

The arrival, establishment and spread of exotic diseases: patterns and predictions

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Nature reviews. Microbiology. April 2010, doi:10.1038/nrmicro2336

The impact of human activities on the principles and processes governing the arrival, establishment and spread of exotic pathogens is illustrated by vector-borne diseases such as malaria, dengue, chikungunya, West Nile, bluetongue and Crimean-Congo haemorrhagic fever. Competent vectors, which are commonly already present in the areas, provide opportunities for infection by exotic pathogens that are introduced by travel and trade. At the same time, the correct combination of environmental conditions (both abiotic and biotic) makes many far-flung parts of the world latently and predictably, but differentially, permissive to persistent transmission cycles. Socioeconomic factors and nutritional status determine human exposure to disease and resistance to infection, respectively, so that disease incidence can vary independently of biological cycles.

Link to the article:

<http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=20372156>

Key words: West Nile fever, Crimean Congo haemorrhagic fever, viral hemorrhagic fever, predictive model

VBORNET comment: 2010-05-28

Largely based on the experience gained with the other partners of the EDEN project, Emerging Diseases in a changing European Environment, Sarah Randolph and David Rogers review the factors underpinning the arrival, establishment and spread of exotic diseases. Here exotic has to be taken in its most strict sense which is 'introduced from another country, not native to the place where found', and therefore not systematically assimilated to 'tropical'. As recently pointed out in a special report in *New Scientist* (NS2760, 35-45) there is a major difference between climate change skeptics and deniers. Each scientist has the duty to remain skeptical of any evidence provided. In this paper the authors systematically evaluate claims one by one carefully considering evidence and also clearly pointing out when evidence is still missing or point of views are conflicting and not avoiding complexity. As a result the paper is one of the better recent reviews of ongoing global changes taken as a whole and their impact on the emergence of vector borne diseases.

A point of discussion which may remain is the content of box three addressing the issue of risk mapping to identify areas prone to invasion. The example chosen by the authors is the spatial modeling of *Culicoides imicola* in the Mediterranean basin and temperate Europe based on 87 sampling points in Portugal. In doing so two important aspects are underestimated: (a) the eco-climatic conditions prevailing in Portugal may not be representative for the entire area for which modeling outputs have been provided, and (b) *C. imicola* as an invasive species(*) may not have reached its full spread range in Portugal at the time of the sampling. Therefore predictions made with this type of modeling approach based on presence/ absence records at a given point in time, and in a very limited area, though interesting from a scientific point of view (see discussion Tatem *et al.* 2003) may nevertheless be very misleading for decision makers. Whilst the proposed modeling approach certainly is valid to model the potential distribution of resident species provided the samples taken are representative of the entire modeled area, other methods need to be adopted to predict future spread in other areas

Finally whilst in their conclusions the authors correctly stress the fact that risk mapping can be an important prerequisite for planning active surveillance, it may have been helpful to also briefly address the issue of responsiveness. Recent experiences with invasive mosquito species in Europe (see VBORNET NL2, special issue on mosquitoes) have shown that in many cases countries are not legally prepared to eliminate invasive mosquitoes in a natural environment. Knowledge in itself may therefore not be enough to solve a problem!

(*) It is interesting to note that the issue of *C. imicola* as an invasive species has recently been questioned at least for Italy, by A. Conte *et al.* (2009, *Journal of applied Ecology*, 28, 1751-1760). Ironically, the reported situation in Portugal may thus reflect stable distribution limits.

Challenges in predicting climate and environmental effects on vector-borne disease episystems in a changing world

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Journal of Experimental Biology. 2010, 213(6): 946-954, doi:10.1242/jeb.037564

Vector-borne pathogens cause enormous suffering to humans and animals. Many are expanding their range into new areas. Dengue, West Nile and Chikungunya have recently caused substantial human epidemics. Arthropod-borne animal diseases like Bluetongue, Rift Valley fever and African horse sickness pose substantial threats to livestock economies around the world. Climate change can impact the vector-borne disease epidemiology. Changes in climate will influence arthropod vectors, their life cycles and life histories, resulting in changes in both vector and pathogen distribution and changes in the ability of arthropods to transmit pathogens. Climate can affect the way pathogens interact with both the arthropod vector and the human or animal host. Predicting and mitigating the effects of future changes in the environment like climate change on the complex arthropod-pathogen-host epidemiological cycle requires understanding of a variety of complex mechanisms from the molecular to the population level. Although there has been substantial progress on many fronts the challenges to effectively understand and mitigate the impact of potential changes in the environment on vector-borne pathogens are formidable and at an early stage of development. The challenges will be explored using several arthropod-borne pathogen systems as illustration, and potential avenues to meet the challenges will be presented.

Link to the article:

<http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=20190119>

Key words: climate change, Chikungunya Fever, West Nile fever

VBORNET comment: 2010-05-27

This paper discusses at great length the difficulty in predicting the effects of climate change on vector-borne disease. It does this by providing examples in relation to complex episystems associated with West Nile virus in North America, Bluetongue virus in Europe and yellow fever virus. The author argues that considering that these complex episystems are so poorly understood current climate-based models are just simple tools that cannot be used to predict realistic future consequences, and their use has often led to dire predictions. The author concludes by making arguments that work should focus, not on trying to predict the future, but by significantly reducing vector-borne diseases now by 1) ensuring better health care, 2) instituting better surveillance and 3) eliminating poverty to reduce exposure to humans.

Rift Valley fever - a threat for Europe?

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Eurosurveillance, March 2010, 15(10):pii=19506, 18-28

Rift Valley fever (RVF) is a severe mosquito-borne disease affecting humans and domestic ruminants, caused by a *Phlebovirus* (Bunyaviridae). It is widespread in Africa and has recently spread to Yemen and Saudi Arabia. RVF epidemics are more and more frequent in Africa and the Middle East, probably in relation with climatic changes (episodes of heavy rainfall in eastern and southern Africa), as well as intensified livestock trade. The probability of introduction and large-scale spread of RVF in Europe is very low, but localised RVF outbreaks may occur in humid areas with a large population of ruminants. Should this happen, human cases would probably occur in exposed individuals: farmers, veterinarians, slaughterhouse employees etc. Surveillance and diagnostic methods are available, but control tools are limited: vector control is difficult to implement, and vaccines are only available for ruminants, with either

a limited efficacy (inactivated vaccines) or a residual pathogenic effect. The best strategy to protect Europe and the rest of the world against RVF is to develop more efficient surveillance and control tools and to implement coordinated regional monitoring and control programmes.

Link to the article: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19506>

Key words: Rift valley fever, Hemorrhagic fevers

VBORNET comment: 2010-05-27

This paper provides a comprehensive review and risk assessment of the potential for RVFV introduction and outbreaks in Europe, although it provides little new information on the ecological and entomological dynamics of such RVFV outbreaks should they occur in Europe. More than 30 mosquito species globally have been found infected with RVFV including species in 7 genera: *Aedes*, *Ochlerotatus*, *Anopheles*, *Culex*, *Eretmapodites*, *Coquillettidia* and *Mansonia*. In Europe the main competent vectors are *Aedes vexans vexans*, *Oc. caspius*, *Cx. theileri*, *Cx. pipiens* and *Cx. perexiguus*. They conclude that *Cx. pipiens* and possibly *Ae. albopictus* would be the main candidate vectors. Additional summaries and discussion are given on the clinical features of RVFV (in animal and humans), diagnostic methods, vaccines, current geographic distribution and factors for change. They conclude that the greatest risk to Europe is likely to come from illegally imported RVFV-infected ruminants.

3. SCIENTIFIC ADVANCES: MOSQUITOES

Putative New Lineage of West Nile Virus, Spain

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Emerging Infectious Diseases, Mar 2010, 16(3), doi:10.3201/eid1603.091033

To ascertain the presence of West Nile virus (WNV), we sampled mosquitoes in 2006 in locations in southern Spain where humans had been infected. WNV genomic RNA was detected in 1 pool from unfed female *Culex pipiens* mosquitoes. Phylogenetic analysis demonstrated that this sequence cannot be assigned to previously described lineages of WNV.

Link to the article: <http://www.cdc.gov/eid/content/16/3/549.htm>

Key words: West Nile fever

VBORNET comment: 2010-05-24

Nowadays different viral lineages of WNV are considered. Lineage 1 is largely diffused in New World and several European countries, whereas lineage 2 outside of Africa has been detected only in Austria (2008) and in Hungary (2004 and 2005) in wild birds. A new virus isolated in Czech Republic from *Culex pipiens* in 1997 and 1999 (named Rabensburg virus) as well as another isolate from *Dermacentor marginatus* ticks in Russia in 1998 were proposed as members of lineage 3 and 4 respectively. The study presented in this paper was carried out in 2006 when 1,641 mosquitoes pools collected in 2 distinct Spanish wetlands were tested by a generic nested reverse transcription PCR. Approximately 11% of the pools (191 pools) tested positive, but WNV was identified only in 1 *Culex pipiens* pool. The genome of the isolated virus did not match with any genetic sequence of known lineages, albeit more similarities are observed with lineage 4. A complex of WNV lineages is currently circulating in Europe and the results of this study confirm the existence of multiple virus within vector and wild bird populations. The epidemiological implication of the interactions among different lineages and the differences of these various viruses in their pathogenesis for horses and humans are still under study.

Surveillance of Arboviruses in Spanish Wetlands: Detection of New Flavi- and Phleboviruses

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Vector-Borne and Zoonotic Diseases. March 2010, 10(2): 203-206. doi:10.1089/vbz.2008.0188.

The presence of viruses in arthropods in Spain has been studied over 5 years. Flaviviruses similar to cell-fusing agent, sequences of a flavivirus related to those transmitted by mosquitoes, and a phlebovirus similar to Naples and Toscana viruses were detected. Their potential human or animal pathogenicity should be studied.

Link to the article: <http://www.liebertonline.com/toc/vbz/10/2>

Key words: Flavivirus, West Nile fever, phlebovirus

VBORNET comment: 2010-05-24

The paper presents the results of a study carried out from 2001 to 2004 in Spain, during which 4,300 insects (mosquitoes and sandflies) pools were analyzed by PCR. Among them 102 pools (94 mosquitoes and 8 sandflies pools) were positive for the flaviviruses, whereas five sandflies pools were positive for phleboviruses. The analysis of viral sequences resulted in the identification of apparently new flaviviruses, similar to cell-fusing agent (CFA) and to other related viruses (Kamiti river virus [KRV] and other *Culex* Flavivirus). The sequences of the detected phleboviruses were also different from those already known, albeit similar to Naples and Toscana viruses. It is currently not clear the epidemiological importance of these viruses in non-insect species or, even, for the public health. Further studies should be performed to better assess the zoonotic potential of these viruses currently circulating in the Mediterranean.

Malaria imported into Réunion Island: is there a risk of re-emergence of the disease?

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Transactions of the Royal Society of Tropical Medicine and Hygiene 2010, 104 (4): 251-254, doi:10.1016/j.trstmh.2009.10.008

After a long period of endemicity until the 1950s, the World Health Organization considered autochthonous malaria eliminated from Réunion in 1979. To prevent secondary transmission and re-emergence of autochthonous malaria, permanent epidemiologic and entomological surveillance and vector control measures are conducted.

The objective of this study is to report sociodemographic characteristics of imported malaria patients and incidence rates from 2003–2008 using mandatory notification with the aim of identifying risk groups and destinations.

During this period, 684 imported malaria cases were reported. Median age of patients was 34.4 years and 22.1% were children ≤ 15 years. Men represented 67.7% of cases and 59.1% of patients reported having taken chemoprophylaxis based on chloroquine alone. Incidence of malaria was considerably different by country destination. For Comoros, incidence was stable and high during the period accounting for 1481 cases per 100 000 travels in 2008. The rate was lower for travels to Madagascar, South Africa and Mayotte and decreased over the period to 37, 19 and 3 per 100 000 respectively, by 2008.

To avoid re-emergence of malaria on the island and to protect themselves, travelers should reduce their risks of acquisition and importation of parasites by using adequate preventive measures. A special preventive program and social mobilisation should be a priority, essentially for the Comorian community in Réunion.

Link to the article: <http://www.sciencedirect.com/science/journal/00359203>

Key words: Malaria, La Reunion

VBORNET comment: 2010-05-18

La Réunion island is a French tropical overseas department where autochthonous malaria has been eliminated in 1979. However, the endemic malaria vector *Anopheles arabiensis* remains, and 684 imported malaria cases were reported from 2003–2008, mainly from surrounding Indian Ocean islands

and from south-east Africa. Risk of malaria re-emergence in La Réunion then depends on malaria importation, on contact of human beings with *An. arabiensis* and on vectorial capacity of populations of this mosquito. This paper deals only with the risk of imported malaria and with the risk for travellers to get contaminating during stays in malaria endemic countries. Among the 684 imported malaria cases, 84.5% were *Plasmodium falciparum*, and men represented 67.7% of cases. The more "at risk" country is Comoros, with 1481 cases per 100 000 travels in 2008 (1.48 % of travellers from la Réunion to Comoros). The rate was much lower for travels to Madagascar, South Africa and Mayotte. The authors recommend protection against mosquito bites and adequate chemoprophylaxis (mefloquine, atovaquone-proguanil or doxycycline and chloroquine-proguanil or atovaquone-proguanil depending on destinations) for decreasing the risk of importing malaria parasite.

What is not discussed in this article is the actual risk of re-emergence of malaria on the island and that there is an efficient vector control agency in La Réunion which conducts permanent control of larval stages of *An. arabiensis* in breeding sites, using Bti (*Bacillus thuringiensis israelensis*), and makes surveillance and control of *An. arabiensis* populations 500m around every imported (or autochthonous) malaria case using Bti and deltamethine spraying when mosquitoes are present. There is also no comment on parameters of vectorial capacity of *An. arabiensis* such as longevity, trophic behaviour, distribution, density which are key factors as important as parasite importation in assessing the risk of re-emergence. Information on these variables can be found in the cited reference 9: Girod et al. 1999. *Bull Soc Pathol Exot*, 92: 203–209.

MosquitoMap and the Mal-area calculator: new web tools to relate mosquito species distribution with vector borne disease

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International Journal of Health Geographics, 2010, 9: 11, doi:10.1186/1476-072X-9-11

Mosquitoes are important vectors of diseases but, in spite of various mosquito faunistic surveys globally, there is a need for a spatial online database of mosquito collection data and distribution summaries. Such a resource could provide entomologists with the results of previous mosquito surveys, and vector disease control workers, preventative medicine practitioners, and health planners with information relating mosquito distribution to vector-borne disease risk.

Results

A web application called MosquitoMap was constructed comprising mosquito collection point data stored in an ArcGIS 9.3 Server / SQL geodatabase that includes administrative area and vector species x country lookup tables. In addition to the layer containing mosquito collection points, other map layers were made available including environmental, and vector and pathogen/disease distribution layers. An application within MosquitoMap called the Mal-area calculator (MAC) was constructed to quantify the area of overlap, for any area of interest, of vector, human, and disease distribution models. Data standards for mosquito records were developed for MosquitoMap.

Conclusion

MosquitoMap is a public domain web resource that maps and compares georeferenced mosquito collection points to other spatial information, in a geographical information system setting. The MAC quantifies the Mal-area, i.e. the area where it is theoretically possible for vector-borne disease transmission to occur, thus providing a useful decision tool where other disease information is limited. The Mal-area approach emphasizes the independent but cumulative contribution to disease risk of the vector species predicted present. MosquitoMap adds value to, and makes accessible, the results of past collecting efforts, as well as providing a template for other arthropod spatial databases.

Link to the article: <http://www.ij-healthgeographics.com/content/9/1/11/abstract>

Key words: Malaria, distribution

VBORNET comment: 2010-05-25

The authors have developed a web based spatial database of mosquito collections records and distribution models worldwide. Specimen records include voucher material, observations and published literature data and it takes not only presence/absence data but also abundance into account. They have also worked out a method (Mal-area calculator) to identify zones at risk for vector disease transmission implementing different abiotic and biotic factors which could affect vector competence. Both methods are very promising and could be relevant to many authorities and decision makers employed in medical entomology, vector disease control and many more. However, as for many online applications the success and long-term sustainability of this initiative depends on its continued support, development, and refinement; which could be a difficult task to accomplish. It is the aim of the authors to expand the

currently used layers and to include other relevant factors, which could make these tools better and more accurate. Furthermore they would like to use this method also for other important vectors as sandflies, fleas and ticks. Overall, it is a very important and helpful initiative that, with the correct collaboration could grow to be a major help for understanding vector distribution and possible vector disease transmission worldwide. It would be interesting that other initiatives like the Malaria Map project could co-operate to create a standardised and uniform tool that can be used for predicting, assessing and controlling vector disease transmission.

Le zanzare Italiane: Generalita' e identificazione degli adulti (Diptera, Culicidae) [Identification of the adult stages of the Italian mosquitoes (Diptera, Culicidae)]

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Fragmenta entomologica. 2009, 41(2): 213-372

This work contains information on the taxonomy and bionomics of the adult stages of the Italian Culicidae. At present the Italian fauna comprises 64 species of mosquitoes belonging to two subfamilies: Anophelinae and Culicinae.

The subfamily Anophelinae only includes the genus *Anopheles* Meigen, 1818, with 16 species. The subfamily Culicinae is represented by 47 species belonging to 7 genera: *Aedes* Meigen, 1818 (6 species), *Ochlerotatus* (20 species), *Coquillettidia* Dyar, 1905 (2 species), *Culex* Linnaeus, 1758 (12 species), *Culiseta* Felt, 1904 (6 species), *Orthopodomyia* Theobald, 1904 (1 species) and *Uranotaenia* Linch Arribalzaga, 1891 (1 species).

The species considered are: *Anopheles algeriensis* Theobald, 1903, *An. atroparvus* Van Thiel, 1927, *An. claviger* (Meigen, 1804), *An. hispaniola* (Theobald, 1903), *An. hyrcanus* (Pallas, 1771), *An. labranchiae* Falleroni, 1926, *An. maculipennis* Meigen, 1818, *An. marteri* Sevenet and Prunelle, 1927, *An. melanoon* Hackett, 1934, *An. messaeae* Falleroni, 1926, *An. petragrani* Del Vecchio, 1939, *An. plumbeus* Stephens, 1828, *An. sacharovi* Favre, 1903, *An. sergentii* (Theobald, 1907), *An. subalpinus* Hackett and Lewis, 1935 and *An. superpictus* Grassi, 1899; *Ae. aegypti* (Linnaeus, 1762), *Ae. albopictus* (Skuse, 1894), *Aedes cinereus* Meigen, 1818, *Ae. geminus* Peus, 1970, *Ae. vexans* (Meigen, 1830), *Ae. vittatus* (Bigot, 1861); *Ochlerotatus echinus* (Edwards, 1930), *Oc. geniculatus* (Olivier, 1791), *Oc. annulipes* (Meigen, 1830), *Oc. atropalpus* (Coquillett, 1902), *Oc. berlandi* Seguy, 1921, *Oc. cantans* (Meigen, 1818), *Oc. caspius* (Pallas, 1771), *Oc. cataphylla* Dyar, 1916, *Oc. communis* (De Geer, 1776), *Oc. detritus* Haliday, 1833, *Oc. dorsalis* (Meigen, 1830), *Oc. mariae* Sergent & Sergent, 1903, *Oc. pulcritarsis* (Rondani, 1872), *Oc. pullatus* (Coquillett, 1904), *Oc. punctator* (Kirby, 1837), *Oc. rusticus* (Rossi, 1790), *Oc. sticticus* (Meigen, 1838), *Oc. surcoufi* (Theobald, 1912), *Oc. zammitii* (Theobald, 1903), *Oc. refiki* Medschid, 1928; *Coquillettidia buxtoni* (Edwards, 1923) and *Cq. richiardii* (Ficalbi, 1889); *Culex brumpti* Galliard, 1931, *Cx. hortensis*, Ficalbi, 1889, *Cx. impudicus* Ficalbi, 1890, *Cx. laticinctus* Edwards, 1913, *Cx. martinii* Medschid, 1930, *Cx. mimeticus* Noé, 1899, *Cx. modestus* Ficalbi, 1889, *Cx. univittatus* Theobald, 1901, *Cx. pipiens* Linnaeus, 1758, *Cx. territans* Walzer, 1856, *Cx. theileri* Theobald, 1903 and *Cx. torrentium* Martini, 1925; *Culiseta annulata* (Schrank, 1776), *Cs. fumipennis* (Stephens, 1825), *Cs. litorea* (Shute, 1928), *Cs. longiareolata* (Macquart, 1838), *Cs. morsitans* (Theobald, 1901), *Cs. subochrea* (Edwards, 1921); *Orthopodomyia pulchripalpis* (Rondani, 1872) and *Uranotaenia unguiculata* (Edwards, 1913).

Fully illustrated Italian and English keys and morphological diagnoses are provided for adult identification of the individual species. Notes on biology and distribution are included for all taxa. A bibliography includes a complete list of references published since 1960, as well as selected references published before such date.

Link to the article: Email: francesco.severini@iss.it

Key words: mosquito species, Italy

VBORNET comment: 2010-05-17

This booklet (in Italian) provides summarized information on the morphology, the biology and the distribution of the 64 mosquito species recorded from Italy. Invasive species like *Ae. aegypti*, *Ae. albopictus* and *Ae. atropalpus* are also included. Well done dichotomic identification keys are provided (also in English) for both adults females and males. However in some cases, diagnostic characters for sibling species are not given in the key but in the text or in foot notes (*Ae. mariae/zammitii*, *Cx. pipiens/torrentium*). Species of the tribe Aedini are presented here as members of genera *Aedes* or *Ochlerotatus*. This classification is based on Reinert et al, 2000 (JAMCA 16(3):175-188) but *Ae. rusticus* should be assigned to subgenus *Rusticooidus* (Reinert, 1999, Europ. Mosq. Bull. 4:1-7) and *Ae. vittatus* to genus *Fredwardsius* (Reinert, 2000, Europ. Mosq. Bull. 6:1-7). This classification also ignores the more recent papers (Reinert et al., 2004, 2006, 2008) which split again the tribe in several genera, i.e. genus *Dahlia* for *Ae. (Finlaya) geniculatus* and *Ae. (Fin.) echinus*, genus *Georgecraigius* for *Ae.*

(*Ochlerotatus atropalpus*, genus *Stegomyia* for *Ae. (Stegomyia) albopictus* and *Ae. (Stg.) aegypti*. However, editors of several scientific journals suggested that more research (including molecular evidence) and interpretation are needed to develop a consensus on the reclassification of Aedini and authorise authors to maintain usage of the traditional names (i.e. genus *Aedes*). Therefore it would have been simpler to use the genus *Aedes* for all these species.

4. SCIENTIFIC ADVANCES: TICKS

Effects of prolonged exposure to low temperature on eggs of the brown dog tick, *Rhipicephalus sanguineus* (Latreille, 1806) (Acari: Ixodidae).

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The widespread geographical distribution of the brown dog tick *Rhipicephalus sanguineus* (Acari: Ixodidae) is related to the cosmopolitan distribution of its primary host and to its adaptability to different environments, under variable climate conditions. Field studies have suggested that temperature is the most important factor driving the population dynamics of this tick species. In order to investigate the effects of prolonged exposure to low temperature on eggs of *R. sanguineus*, nine groups (II-X) of five egg batches each were maintained at 8±2 degrees C (70±10% RH, and scotophase) for 15, 30, 45, 60, 75, 90, 105, 120, and 135 days. One group (group I) was maintained in the incubator (26±1 degrees C, 70±10% RH, and scotophase) and used as control. The mean egg incubation period from group I was 11.6±0.5 days, with an egg hatch rate of 99.5±0.5%. Conversely, no egg hatched at 8 degrees C. Exposure to cold showed a strong positive correlation with egg incubation period ($r=0.99$) as well as a strong negative correlation with egg hatch rate ($r=-0.95$) and larval longevity ($r=-0.99$). Overall, the present results points out that *R. sanguineus* eggs are sensible to prolonged exposure to low temperature, which is definitely a major limiting factor for the establishment of populations of this tick in cold temperate regions.

Link to the article:

<http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=20381253>

Key words: tick, *Rhipicephalus*

VBORNET comment: 2010-05-25

This paper investigated the effects of prolonged exposure to low temperature on eggs of *R. sanguineus*, the most widespread tick species in the world parasitizing domestic dogs and transmitting several pathogens such as the spotted fever to humans. The exposure to cold was positively correlated to egg incubation period and negatively correlated to egg hatch rate and larval longevity. Such results are always interesting when they are correctly collected (e.g. without omitting to control the relative humidity during the experiment as suggested by the authors) because they allow better understanding the observed geographical distributions of tick vectors. However, it would have been interesting to collect additional information on nymphal and adult stages instead of limiting the study to egg survival and fitness. Such data already existed but without any information on their quality. The authors did not explained why they chose 8°C as the threshold for their study and they should have tested different temperatures as a gradient for the same number of days. Finally, the verification of these experimental results through targeted field investigations on various local populations of *R. sanguineus* would be useful, especially because the authors indicated some doubts concerning the morphological identification of this tick species and the possible existence of a *R. sanguineus* group of species.

Potential for tick-borne bartonellosis.

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Emerging Infectious Diseases, Mar 2010, 16 (3): 385-391, doi:10.3201/eid1603.091685

As worldwide vectors of human infectious diseases, ticks are considered to be second only to mosquitoes. Each tick species has preferred environmental conditions and biotopes that determine its geographic distribution, the pathogens it vectors, and the areas that pose risk for tick-borne diseases. Researchers have identified an increasing number of bacterial pathogens that are transmitted by ticks, including *Anaplasma*, *Borrelia*, *Ehrlichia*, and *Rickettsia* spp. Recent reports involving humans and

canines suggest that ticks should be considered as potential vectors of *Bartonella* spp. To strengthen this suggestion, numerous molecular surveys to detect *Bartonella* DNA in ticks have been conducted. However, there is little evidence that *Bartonella* spp. can replicate within ticks and no definitive evidence of transmission by a tick to a vertebrate host.

Link to the article: <http://www.cdc.gov/eid/content/16/3/385.htm>

Key words: *Bartonella*, tick

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Infectious diseases caused by *Bartonella* spp. have been described for more than 1000 years. To date, more than 20 different *Bartonella* species have been found in a wide variety of mammals and half of them have been recognized as responsible for zoonotic diseases. They are transmitted by different vectors: fleas, lice and sand flies. Transmission by ticks has been also suggested because of many indirect evidences: detection of *Bartonella* spp. DNA in ticks, demonstration of the competence of ticks for *Bartonella* sp. using artificial feeding technique, and numerous case reports of *Bartonella* spp. infection within days or weeks of a tick bite. The last one, published in the February issue of Clinical Infectious Diseases, links presence of *B. henselae* DNA in a tick removed from a patient infected with *B. henselae*. Nevertheless, controversial opinions on the potential role of ticks as vector for *Bartonella* still exist. The March issue of the Emerging Infectious Disease journal illustrated perfectly this "fight" opposing the pro and the cons of *Bartonella* as a tick-borne pathogen.

In this issue, two manuscripts including the one of Angelakis *et al.*, review the evidence for and against tick transmission and conclude that transmission of any *Bartonella* spp. by ticks to human or animals has not yet been directly established. However, as many indirect evidences of potential tick *Bartonella* spp. transmission to humans exist, and considering the medical relevance of the genus *Bartonella*, Angelakis *et al.* recommend new experimental transmission studies, using infected ticks placed on live animals to definitively establish or not, *Bartonella* transmission by ticks.

5. SCIENTIFIC ADVANCES: PHLEBOTOMINAE

Arthropod-borne viruses transmitted by Phlebotomine sandflies in Europe: a review

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Eurosurveillance, March 2010, 15 (10):pii=19507

Phlebotomine sandflies are known to transmit leishmaniasis, bacteria and viruses that affect humans and animals in many countries worldwide. These sandfly-borne viruses are mainly the *Phlebovirus*, the *Vesiculovirus* and the *Orbivirus*. Some of these viruses are associated with outbreaks or human cases in the Mediterranean Europe. In this paper, the viruses transmitted by Phlebotomine sandflies in Europe (Toscana virus, Sicilian virus, sandfly fever Naples virus) are reviewed and their medical importance, geographical distribution, epidemiology and potential spreading discussed. Data on vertebrate reservoirs is sparse for sandfly fever viruses. The factor currently known to limit the spread of diseases is mainly the distribution areas of potential vectors. The distribution areas of the disease may not be restricted to the areas where they have been recorded but could be as wide as those of their vectors, that is to say *Larroussius* and *P. papatasi* mainly but not exclusively. Consequently, field work in form of viral isolation from sandflies and possible reservoirs as well as laboratory work to establish vectorial competence of colonised sandflies need to be encouraged in a near future, and epidemiological surveillance should be undertaken throughout the European Union.

Link to the article: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19507>

Key words: Sandfly Fever virus, Toscana virus, Europe

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Although the Phlebotomine sandflies are mainly known to be the vectors of Leishmaniasis, they also play an important role in public health by transmitting some bacterial and viral diseases. This manuscript is a brief but thorough and in-depth review about viruses transmitted by Phlebotomine sandflies. In addition to well-known phleboviruses causing sandfly fever (Sandfly Fever Sicilian Virus, SFSV and Sandfly Fever Naples Virus, SFNV) or aseptic meningitis (Toscana Virus, TOSV) which are endemic in the

Mediterranean basin; agents such as Chandipura virus, Changuinola virus and Corfou, Massilia and Arbia phleboviruses are included. Of special interest is the discussion on sandfly vectors and possible reservoirs, as well as risks for the future. Other review articles on Sandfly Fever Viruses and Toscana Virus can also be of interest (Dionisio D. et al. 2003, *Curr Opin Infect Dis* 16: 383–388; Charrel R. et al. 2005, *Emerg Infect Dis* 11: 1657-1663). Additionally, a novel variant of SFSV, provisionally named the Sandfly Fever Turkish Virus (SFTV), was identified recently in patients from an outbreak of fever of unknown etiology in Turkey (Carhan et al., in press), and TOSV as well as SFSV and SFNV exposure have been revealed in Central Anatolia, with identified cases of aseptic meningoencephalitis due to TOSV (Ergunay et al, submitted). The paper shows also distributions maps at country level of the main vector species in Europe: *Phlebotomus papatasi*, *P. perniciosus*, *P. ariasi*, and *P. perfiliewi* s. s.; these maps serve as a basis for Vbornet's vector distribution maps which are done at province level (NUTS3) and will be regularly updated.

6. SCIENTIFIC ADVANCES: OTHER VECTORS

***Bartonella quintana* in body lice and head lice from homeless persons, San Francisco, California, USA**

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Bartonella quintana is a bacterium that causes trench fever in humans. Past reports have shown *Bartonella* spp. infections in homeless populations in San Francisco, California, USA. The California Department of Public Health in collaboration with San Francisco Project Homeless Connect initiated a program in 2007 to collect lice from the homeless to test for *B. quintana* and to educate the homeless and their caregivers on prevention and control of louse-borne disease. During 2007–2008, 33.3% of body lice–infested persons and 25% of head lice–infested persons had lice pools infected with *B. quintana* strain Fuller. Further work is needed to examine how homeless persons acquire lice and determine the risk for illness to persons infested with *B. quintana*–infested lice.

Link to the article: <http://www.cdc.gov/eid/content/15/6/912.htm>

Key words: *Bartonella*, lice

VBORNET comment: 2010-05-06

In their article, Bonilla *et al.* highlight the potential for the human head louse, *Pediculus humanus capitis*, to serve as a vector for the bacterium *Bartonella quintana*. Among the ~3,000 louse species that are currently known, only three are human parasites. These include the crab louse, *Phthirus pubis*, the body louse, *Pediculus humanus humanus* (*P. h. humanus*) and the head louse *P. h. capitis*. The taxonomic status of the latter two lice is uncertain, as they are either considered as distinct subspecies from the same species, or, as proposed by Li *et al.* (Li *et al.* Genotyping of human lice suggests multiple emergences of body lice from local head louse populations. *PLoS Neglected Tropical Diseases*. 2010, 4: e641), a single *Pediculus* population, with body lice evolving from head lice. *Pediculus h. humanus* is the vector of three human pathogens, including *Rickettsia prowazekii*, the agent of epidemic typhus, *Borrelia recurrentis*, the agent of relapsing fever, and *B. quintana*. The latter species, currently considered as a re-emerging pathogen, is the only louse-transmitted disease in Europe. It causes Trench fever, endocarditis, bacillary angiomatosis and chronic bacteremia. The impact of *B. quintana* infections in Europe is limited by the strict association of *P. h. humanus* with homeless populations. In contrast, *P. h. capitis* infestation is endemic in school children worldwide. The discovery of *B. quintana* in head lice in homeless, combined with the easy spread of these parasites among human populations, may expose human populations to a new bacterial threat, not only in the USA but also in Europe, as recently demonstrated by unpublished results demonstrating the presence of *B. quintana* in head lice (P.E. Fournier, unpublished data).