

VBORNET Newsletter 5, April 2010

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1. VBORNET STATUS

Dear VBD Expert,

VBORNET is now operational since September last year and it is time for planning (the organization of) the first annual meeting, which will be held at the Institute of Tropical Medicine (ITM) in Antwerp, Belgium, from June 1st to June 3rd, 2010.

VBD experts from several European countries were invited to attend this first VBORNET Annual General Meeting (AGM). This meeting will represent the first real opportunity to gather the VBORNET network, discussing on activities of interest.

As the number of participants is limited to 60 VBD experts, we faced the difficult task to select a group of participants representative for all the European countries (and beyond) as well as for the three main group of vectors dealt with under VBORNET: mosquitoes, ticks and phlebotomines, from our list of over 300 VBD experts. In this process priority was given to experts who responded positively to our request to join the VBORNET network. Nevertheless in some cases choices had to be made and we therefore apologize to anybody who feels he or she should have been included in "the list". Finally it should be clear that the VBORNET network includes all experts who wish to contribute to VBORNET and that the participants invited to the AGM are considered representatives of this VBORNET network. In the next annual meetings care will be taken to invite other members of the network. Don't hesitate to contact us should you have problems with this approach.

We would like to thank all people answering to our invitation and all persons who are working for the organization of this event.

2. SCIENTIFIC ADVANCES: VECTOR-BORNE DISEASES

Applying the Theory of Island Biogeography to Emerging Pathogens: Toward Predicting the Sources of Future Emerging Zoonotic and Vector-Borne Diseases

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Vector-Borne and Zoonotic Diseases. March 2010, 10(2): 105-110. doi:10.1089/vbz.2008.0208.

Emerging infectious diseases are recognized as increasing threats to public and animal health, global economy, and social and political stability. Climate change, environmental changes, changes in human demographics and behaviors, and the rise of global trade and travel are most-often-cited drivers for the emergence of infectious diseases in human and animal populations (Schrage and Wiener 1995, Daszak et al. 2001, Dobson and Foufopoulos 2001, May et al. 2001, Taylor et al. 2001, Antia et al. 2003, IOM 2003, Kuiken et al. 2003, Weiss and McMichael 2004, Wolfe et al. 2005, Woolhouse and Gowtage-Sequeria 2005, Chomel et al. 2007, Woolhouse and Gaunt 2007, Jones et al. 2008). Emerging pathogens are more likely to be zoonotic or vector-borne with a broad host range (Daszak et al. 2000, Taylor et al. 2001, Woolhouse and Gowtage-Sequeria 2005, Jones et al. 2008). Emerging pathogens

are also more frequently RNA viruses (Woolhouse and Gowtage-Sequeria 2005), which may better adapt to and establish in novel host species (Antia et al. 2003, Andre and Day 2005, Woolhouse et al. 2005). Determining the factors driving disease emergence eventually aims at assisting the prediction of the future emergence of infectious diseases. However, because of the multifactorial nature of the drivers involved (IOM 2003), our ability to predict which pathogens may arise in human or animal populations in the future remains limited (WHO/FAO/OIE 2004). In particular, the ability to identify the animal reservoirs where the greatest risks to human health will originate was deemed improbable (WHO/FAO/OIE 2004). Applying the theory of island biogeography (MacArthur and Wilson 1967) to emerging pathogens identifies (i) interactions between recipient host species and species sources of pathogens (including vector species), (ii) interactions within species sources of pathogens, and (iii) interactions within recipient host species, as mechanisms directly driving disease emergence. Most identified drivers for disease emergence correspond to changes in one or more of these three sets of interactions. Importantly, applying the theory of island biogeography to emerging pathogens assists in predicting from which animal species future zoonotic and vector-borne pathogens will most probably emerge. Identifying known and unknown pathogens such species harbor may bring us one step forward toward predicting which pathogen will next emerge in human populations.

Link to the article: <http://www.liebertonline.com/doi/pdfplus/10.1089/vbz.2008.0208>

Key words:

VBORNET comment: 2010-05-02

Prior to the publication of The Theory of Island Biogeography (MacArthur and Wilson, 1967) the field of biogeography was seen as a primarily historical one and as such the field was seen as a purely descriptive one. The publication changed this perception, and showed that the species richness of an area could be predicted in terms of source-island distance factors, island-area like factors and source area like factors. As stated in the abstract, this article makes a case for applying the theory of island biogeography to emerging pathogens to assist predictions from which animal species future zoonotic and vector-borne pathogens will most probably emerge. Here, hosts are considered as islands for pathogens, that can successfully be colonized provided that introduced pathogens cause infection (establish) and transmit between hosts (avoid extinction). Further, this balance is principally affected by the rate of parasite colonization, and the level of interactions between sources of parasites and recipient hosts (source-island distance-like factors) and the rate of parasite extinction, through host body size and lifespan but also through interactions of newly colonized hosts (source- and/or island-area like factors). The authors state that changes in these factors resulting in changes in rates of pathogen colonization and/or extinction may explain the increase in the number of novel pathogens in human (or animal) population. With recently published ecological drivers for emergence of infectious diseases, the author illustrates its case and is convincing. The island theory analogue is smart and might be helpful to categorize identified drivers. The author identifies four categories of animal species that should be targeted by active surveillance. Unfortunately, this subset does not effectively narrow the number of animal species down. Consequently, doubts arise whether this theory can assist predictions of pathogen emergence. While the factors in the original theory were easily operationalized, this is not the case for the many known and unknown pathogens in the world.

3. SCIENTIFIC ADVANCES: MOSQUITOES

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

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Medical and Veterinary Entomology, March 2010, 24(1): 83-7

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: 2010-05-02

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 (A226V mutation observed in Réunion in 2006, as well as in Italy in 2007) that has been shown to be more easily transmitted by this species than the previous circulating virus strains (Schuffenecker et al., PLoS Medicine, 2006, Vazeille et al., PLoS One, 2007). Results support previous data obtained on other European populations (Vazeille et al., Trop. Med. & Int. Health, 2008; Moutailler et al., Trop. Med. & Int. Health, 2009), the Italian populations of *Ae. albopictus* showing very high dissemination rates of CHIKv and a rapid infection of the salivary glands, only days 2 after the ingestion on infectious bloodmeal. Among the other tested mosquito species, only *Ae. vexans* showed a low susceptibility to infection with CHIKv, both *Cx. pipiens* ('biotype' not specified) and *An. maculipennis* s.l. (species complex member not specified and probably not identified) tested populations being found to be refractory (susceptibility of 33% refers to another study). These results demonstrate the likely key role of *Aedes albopictus* as a vector of CHIKV in the province of Ravenna during the summer of 2007. Therefore, CHIKv transmission risk in Europe could be considered as real in areas where the species is proliferating. However, transmission will occur if the virus is introduced by viraemic hosts coming back from endemic areas, and if other parameters of its biology such as density, longevity, and duration of gonotrophic cycle are suitable.

4. SCIENTIFIC ADVANCES: TICKS

New localities of *Dermacentor reticulatus* tick (vector of *Babesia canis canis*) in Central and Eastern Poland.

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Polish Journal of Veterinary Sciences, 12(4): 549-555.

Dermacentor reticulatus tick is a vector and final host of *Babesia canis canis*, protozoan parasite of the dog. In Poland and other European countries, endemic regions for canine babesiosis caused by *B. canis canis* are the same as endemic regions for *D. reticulatus*. In many of these regions, canine babesiosis is the most prevalent tick-borne disease in dogs. In Europe, increasing range of geographical distribution of *D. reticulatus* is observed. A consequence of this fact may be increasing range of canine babesiosis. *D. reticulatus* is one of the most common ticks occurring in Poland, however, it occurs mainly in the north-eastern and eastern part of the country, and there are many areas in which this species has not been reported yet. In this study, *D. reticulatus* ticks were collected from March 2007 to November 2008 in central and eastern Mazowsze region, and in some localities in Bialystok and Lublin regions. Twenty four new sites for *D. reticulatus*, mainly in central and eastern regions of Mazowsze Province have been found. 18 localities are placed on banks of the fishing ponds or in river valleys and 6 are forests borders or barren lands and meadows, not situated near rivers or other water reservoirs. All tick-rich sites are localized in river valleys or on pond banks. However, statistical analysis showed that there were no differences in the density of ticks between groups of areas. These results show that the occurrence of *D. reticulatus* in newly detected areas has become endemic. Probably woodless, unregulated river valleys are important migration tracts for this species of tick and enable them to penetrate new territories. It seems likely that geographical range of *D. reticulatus* is widening from east to west of Poland what can induce an increase in the number of canine babesiosis cases in areas non-endemic for *B. canis canis* and its vector.

Link to the article:

<http://www.ncbi.nlm.nih.gov/sites/entrez?cmd=retrieve&db=pubmed&dopt=genpept&uid=20169932>

Key words: *Dermacentor reticulatus*, canine babesiosis

VBORNET comment: 2010-04-26

This paper provides updated data on the distribution of *Dermacentor reticulatus*, the tick vector of *Babesia canis canis*, in Poland. While the tick has been reported in North-eastern and Eastern Poland from 1990 to 2000, it seems to have recently expended its geographical range to Central and Western Poland. The authors do not think that it is concomitant to recent climate changes but probably likely due to unregulated river valleys, which are peculiar suitable habitat for *D. reticulatus* and may act as important migration tracts for this species to penetrate new territories. Changes of main vertebrate hosts may also influence the modifications of its distribution range. Such surveillance results are always interesting because they allow updating tick distribution and giving information on the risk of emergence of associated animal and human tick-borne pathogens in a priori free regions. However, it is damage that tick examinations have not been conducted in the whole Poland, in order to provide detailed and exhaustive information at the national level and screen even low probable zones for this tick vector. In addition, the authors do not clearly show such extension on a map and do not indicate the names of regions cited in the text as locations infested by ticks, which may lead to confusion for foreigner scientists who do not know the geography of Poland.

5. SCIENTIFIC ADVANCES: PHLEBOTOMINAE

Flavivirus RNA in Phlebotomine Sandflies

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Vector-Borne and Zoonotic Diseases. March 2010, 10(2): 195-197. doi:10.1089/vbz.2008.0216.

Sandfly-transmitted phleboviruses, such as Toscana, sandfly fever Sicilian, and sandfly fever Naples, can cause human disease and circulate at high rates in Mediterranean countries. Previous studies have also established that viruses other than phleboviruses may be detected in and isolated from sand flies. The recent detection and isolation (in a large variety of mosquito species) of insect-only flaviviruses related to cell fusing agent virus has indicated that the latter is not an evolutionary remnant but the first discovered member of a group of viruses, larger than initially assumed, that has high genetic heterogeneity. Insect-only flaviviruses have been detected in and/or isolated from various species of mosquitoes, but nevertheless only from mosquitoes to date; other dipterans have not been screened for the presence of insect-only flaviviruses. The possible presence of flaviviruses, including insect-only flaviviruses, was investigated in sand flies collected around the Mediterranean during a trapping campaign already underway. Accordingly, a total of 1508 sand flies trapped in France and Algeria, between August 2006 and July 2007, were tested for the presence of flaviviruses using a PCR assay previously demonstrated experimentally to amplify all recognized members of the genus *Flavivirus*, including insect-only flaviviruses. Two of 67 pools consisting of male *Phlebotomus perniciosus* trapped in Algeria were positive. The two resulting sequences formed a monophyletic group and appeared more closely related to insect-only flaviviruses associated with *Culex* mosquitoes than with *Aedes* mosquitoes, and more closely related to insect-only flaviviruses than to arthropod-borne or to no-known-vector vertebrate flaviviruses. This is the first description of insect-only flaviviruses in dipterans distinct from those belonging to the family Culicidae (including *Aedes*, *Culex*, *Mansonia*, *Culiseta*, and *Anopheles* mosquito genera), namely sand flies within the family Psychodidae. Accordingly, we propose their designation as phlebotomine-associated flaviviruses.

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

Key words:

VBORNET comment: 2010-04-17

The authors present a very interesting finding, the presence of insect-only flavivirus RNAs in Phlebotomine sand flies. Insect-only flaviviruses propagate only in mosquito cells and may represent a basal lineage of the genus that diverged from other flaviviruses before the separation of the mosquito- and tick-borne groups. In this group, Cell Fusing Agent Virus (CFAV) and Kamiti River Virus (KRV) were initially isolated from *Aedes aegypti* and *Aedes macintoshi*, respectively. *Culex*-only flavivirus were isolated from *Culex pipiens* in Japan and Indonesia and from *Culex quinquefasciatus* in Guatemala. Proposed members of insect-only flaviviruses continue to be identified in mosquitoes. Flavivirus-related sequences, closely related to NS1-NS4A genes of the CFAV and KRV have been discovered in the

DNA genome of *Aedes albopictus* and *Aedes aegypti* mosquitoes, demonstrating for the first time integration into a eukaryotic genome of a multigenic sequence from an RNA virus that replicates without a recognized DNA intermediate. The authors have shown the presence of insect-only flaviviral sequences in field-collected *Phlebotomus perniciosus* sandflies from Algeria employing a PCR assay that was demonstrated experimentally to amplify all recognized members of the Flavivirus genus. The identified sequences formed a monophyletic group and appeared more closely related to insect-only flaviviruses associated with *Culex* mosquitoes and more to insect-only flaviviruses than to vertebrate flaviviruses. The evolutionary implications of the insect-only flaviviruses and possible interactions with mosquito/sandfly and tick-borne viruses will probably turn out to be a hot topic in the upcoming years.

Molecular and Serological Evidence for the Presence of Novel Phleboviruses in Sandflies from Northern Algeria

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The Open Virology Journal, 2010, 4: 15-21

During summer 2007, a total of 785 phlebotomine flies were trapped in northern Algeria, identified morphologically, organised as monospecific pools and tested for the presence of phlebovirus RNA using degenerate primers. Three pools were positive, and the corresponding PCR products were cloned and sequenced. Viral sequences corresponding to two phleboviruses distinct from each other were detected in sandflies circulating in two close locations (140 km apart) in Northern Algeria. The 3 sequences were aligned with homologous polymerase sequences retrieved from the Genbank database, in order to examine their phylogenetic relationships. One viral sequence (from *Phlebotomus papatasi*) was closely related to but distinct from a sequence obtained from *Phlebotomus ariasi* sandflies trapped in Algeria in 2006. The two other viral sequences (from *Phlebotomus longicuspis*) were genetically distantly related to sequences corresponding to virus members of the Sandfly fever Naples virus species and although falling within the same group, this clearly represents a second distinct novel lineage. These results are indicative of a high genetic heterogeneity within sandflies trapped in a relatively small geographic area. Seroprevalence studies conducted on sera from populations living in the same areas indicated that humans can be infected by these viruses.

Link to the article: <http://www.bentham.org:80/open/tovj/openaccess2.htm>

Key words: Sandflies, Phlebotomine, Phlebovirus

VBORNET comment: 2010-05-01

In this study, the authors provide molecular and serological evidence that novel phleboviruses distinct from but related to Sandfly Fever Sicilian Virus (SFSV) and Sandfly Fever Naples Virus (SFNV) are present in Algeria, and can infect humans. They have previously reported the molecular evidence for the presence of a phlebovirus closely related to SFSV in Algeria and a new phlebovirus, named the Massilia Virus, which was proposed as a member of the SFNV complex from southern France. Sandfly Fever Viruses (SFV) are transmitted to humans by the bite of phlebotomine sandflies and comprise three major serotypes; SFSV, SFNV and Toscana Virus (TOSV). SFNV and SFSV serotypes cause a self-limited febrile disease called as phlebotomus, papatacci, or sandfly fever. Sandfly Fever Cyprus Virus (SFCV), a variant of Sicilian serotype, is also responsible for acute febrile disease and TOSV may cause aseptic meningitis/encephalitis in the infected individuals. Recently, a novel variant of SFCV, provisionally named the Sandfly Fever Turkish Virus (SFTV), was identified in patients from an outbreak of fever of unknown etiology in Turkey (Carhan et al., in press). These data imply that the virus diversity is broad in the sandfly vectors and variants/recombinants that are capable of inducing human disease may emerge/identified in the endemic regions. These findings may also have implications for the current laboratory diagnosis of Phlebovirus-associated infections, which relies mostly on serologic or nucleic acid assays which may be drastically influenced by the nucleotide/antigenic variations of the causative agent. As further supported by the findings in this work, field studies and environmental surveillance is vital for a better understanding of the circulating virus populations in endemic regions to predict threats and challenges for public health.

Toscana Virus Epidemiology: From Italy to Beyond

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The Open Virology Journal, 2010, 4: 22-28

Toscana virus (TOSV) is an arthropod-borne virus which is transmitted to humans by *Phlebotomus* spp sandflies. Infection is the cause of brain injuries, such as aseptic meningitis and meningoencephalitis, in

Italy mainly during the summer. More recently some unusual clinical manifestations due to TOSV with severe sequelae, such as ischemic complications and hydrocephalus, have been reported. TOSV represents an important emerging pathogen and its presence is being investigated in several European countries on the Mediterranean basin, including Italy, France, Spain, Portugal and Cyprus. Phylogenetic analysis has distinguished two genotypes of TOSV, A and B; the first is circulating mainly in Italy and the second in Spain, indicating a different geographic distribution possibly related to the vector. This distribution, evolving with the climate, globalization and habitat modification, has implications for the epidemiology of TOSV.

Link to the article: <http://www.bentham.org:80/open/tovj/openaccess2.htm>

Key words: Toscana virus, phleboviruses, vectors, epidemiology, meningitis

VBORNET comment: 2010-05-01

Toscana virus (TOSV) infections account for a proportion of human aseptic meningitis cases in endemic regions, such as countries in the Mediterranean basin. Although the clinical picture is mild, with symptoms of mild meningitis, usually without encephalitic symptoms and frequent recovery without sequelae, severe outcomes, as indicated in this report, can also be observed. Turkey lies in the endemic zone for TOSV as well as other Phleboviruses and the activity of various species of Phlebotomine sandflies have been observed in Mediterranean, Aegean and Central Anatolian regions in Turkey, including *P.papatasi* and *P.perfiliewi*, well-known vector species for Sandfly Fever Phleboviruses. In Turkey, TOSV exposure in humans has been initially demonstrated by Y. Ozbel et al. (3rd Balkan Conf. of Microbiol. Sept. 2003) in the Aegean region. Recently, K. Ergunay et al. (Hacettepe University, Ankara, Turkey, submitted) revealed TOSV as well as other Sandfly Fever Virus exposure and identified cases of aseptic meningoencephalitis due to TOSV in Central Anatolia. In endemic regions, genetically divergent TOSV strains are known to co-circulate and at least two geographically distinct TOSV populations are suggested to be present in the Mediterranean basin. Based on the current data, existence of two lineages of TOSV was proposed for Spain and France. The phylogenetic analyses of the Turkish isolates displayed highest homologies to TOSV sequences from Italy and France and the Turkish TOSVs are placed in the group A of TOSV. Virus detection studies in sandflies are planned to determine the extent of TOSV and other Phlebovirus activity in Turkey.

6. SCIENTIFIC ADVANCES: OTHER VECTORS

First record of *Oestrus ovis* Linnaeus, 1758 from Malta, and case reports of myiasis from the Maltese Islands (Diptera: Brachycera)

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Bulletin of the Entomological Society of Malta, 2008, 1: 5-10

Oestrus ovis is reported for the first time from Malta. An account is given of four cases of myiasis in Malta, one nasopharyngeal in a sheep host involving *O. ovis*, and three cutaneous in a human host and in domestic cats, the latter all involving *Lucilia sericata*.

Link to the article: <http://www.entomologicalsocietymalta.org/>

Key words: *Oestrus ovis*, myiasis, Malta

VBORNET comment: 2010-05-01

This article reports the first occurrence in Malta of *Oestrus ovis* myiasis, and rare cases of *Lucilia sericata* infestations. Myiasis is the infestation of animal or human tissues with fly larvae, commonly referred to as maggots. Myiasis is widespread in tropical and subtropical areas of Africa and the Americas. In Europe, myiasis is common in animals but rare in humans. Although the infestation is most often subcutaneous and produces a furunculoid lesion, it may also develop in wounds and certain body cavities in both humans and animals. In Europe, myiasis is mostly endemic in the Mediterranean area. *Oestrus ovis* (Family *Oestridae*) infestation has been reported in sheep in Malta (this article), France, Germany, Great Britain, Greece, Hungary, Italy, Spain and the Netherlands, in goats in France, Greece and Spain, and in humans in France, Germany, Italy, and Spain; *Hypoderma* sp. (Family *Oestridae*) infestation is known in cattle and deers in Belgium, France, Greece, Italy, Poland and Spain, and in humans in the Netherlands; *Gasterophilus* sp. (Family *Gasterophilidae*) infestation in horses are described in Great Britain, Italy, and the Netherlands; *Wohlfahrtia magnifica* (Family *Sarcophagidae*) infestation has been reported in dogs, horses and sheep in Hungary, in sheep in Greece, and in humans

in France and Italy; *Lucilia sericata* (Family *Calliphoridae*) is described in this manuscript in cats and humans in Malta and has been identified in geese in Hungary; finally, unique cases of human infestation with *Cordylobia* sp., *Calliphora vicina* (Family *Calliphoridae*) and *Eristalis tenax* (Family *Syrphidae*) have been described in Portugal, France and Belgium, respectively, whereas *Przhevalskiana silenus* (Family *Oestridae*) has been identified in goats in Italy. In addition to its agro-economic impact on livestock, as outlined by the authors, another point of concern with myiasis is that it may be the vector of bacterial infections. In France, a *Wohlfartia magnifica* infestation in a homeless woman was complicated by a *Wohlfahrtiimonas chitinoclastica* bacteremia (Rebaudet *et al.* *Wohlfahrtiimonas chitinoclastica* bacteremia in homeless woman. *Emerg Infect Dis.* 2009; 15: 985–987). To date, control programs for myiasis have proven to be efficient for cattle in several European countries (Boulard *et al.* A successful, sustainable and low cost control-programme for bovine hypodermosis in France. *Vet Parasitol.* 2008; 158:1-10).

7. VECTOR BORNE DISEASE EVENTS

7th International Symposium on Phlebotominae Sand Flies (ISOPS 7)

Dates: April 25-30, 2011 – Pine Bay Hotel, Kuşadası, Turkey

The 7th International Symposium on Phlebotomine Sandflies will be held on 25-30 april 2011 in Kusadasi, Turkey.

Kusadasi is one of the endemic sites of human and canine leishmaniasis (*L. infantum*) in western Turkey. It is 80 km from Izmir city centre and one of the most popular holiday resorts on west coast of Turkey. The town is close to the remains of many archeological and natural sites.

The programme is not yet available.

Abstracts sent by participants can be published as supplement of Turkish Journal of Parasitology (This journal is covered by Index Medicus and other international databases – www.tparazitolderg.org).

Link to the website: www.isops7.org

Contact: Prof. Dr. Yusuf Özbel, yusuf.ozbel@ege.edu.tr

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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