VBORNET Newsletter Year 2 Issue 4, April 2011

VBORNET USEFUL LINKS

Project description:
http://ecdc.europa.eu/en/activities/diseaseprogrammes/emerging_and_vector_borne_diseases/Pages/VBORNET.aspx

VBORNET newsletter archive:
http://ergodd.zoo.ox.ac.uk/eden/index.php?p=82

VBORNET Vector Questionnaire to be downloaded for reporting data:
http://edendatasite.com/ 'VBORNET' menu

VBORNET vector maps:
http://ecdc.europa.eu/en/activities/diseaseprogrammes/emerging_and_vector_borne_diseases/Pages/VBORNET_maps.aspx

CONTENTS

1. VBORNET STATUS

VBORNET AGM

The second Annual General Meeting (AGM) of VBORNET was held at the Institute of Tropical Medicine in Antwerp from 18 to 20 April. As last year 60 delegates were invited to participate. Since this year's focus was on vector-borne diseases and public health (PH) invited delegates mainly included experts who contributed in the VBORNET-PH questionnaire study. As last year the meeting was a great success. As a VBORNET trademark ample time was devoted to questions and discussions.

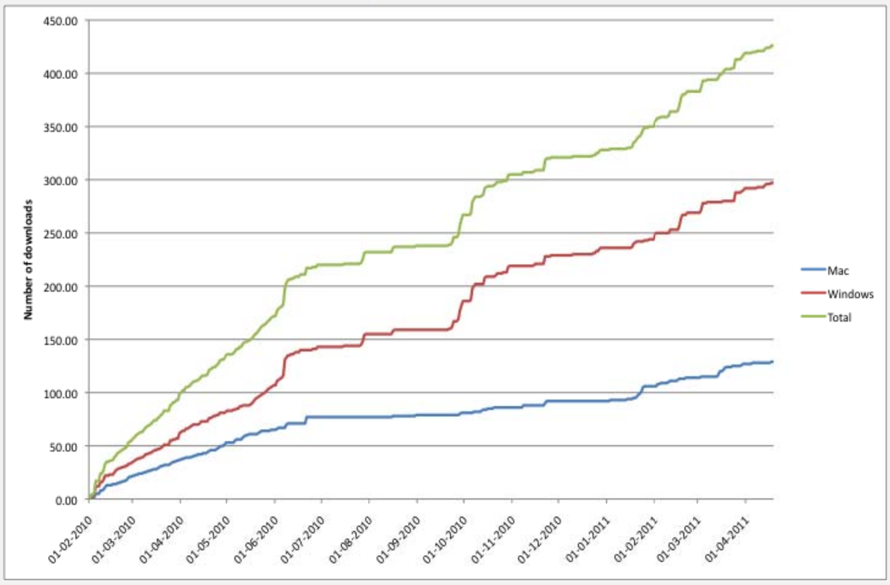

Figure1 - VBORNET Distribution Tool downloads

On the first day the progress made was discussed for each work package. As seen in the graph (Fig.1), interest in joining VBORNET is still growing. Thanks to many expert contributions VBORNET distribution map updates are now published every three months and species covered have been expanded. VBORNET also gained access to some large databases (e.g. EFSA tick distribution database) and validation is ongoing. Whilst information on vector surveillance activities is collected for all species, for the time being only a map of surveillance for invasive mosquito species is published. A web-based map server is under construction and will enable to query information on map content per administrative unit.

VBORNET Distribution Maps in progress can be downloaded from:
http://www.ecdc.europa.eu/en/activities/diseaseprogrammes/emerging_and_vector_borne_diseases/pages/vbornet_maps.aspx

This year's VBORNET factsheets and risk assessments focus on ticks. Specific focus is given to driving forces for change in distribution *of Ixodes ricinus* in Europe, and an understanding of the ecology, habitats and biology of *Hyalomma marginatum* in Europe. During the first half of the year, work on *I. ricinus* has been progressed. All VBORNET tick experts were consulted and invited to take part in a review of the current consensus and evidence for changes in distribution of *I. ricinus* in Europe. Twenty four partners contributed, and along with a thorough literature review, produced more than 100 pieces of evidence or scientific opinion. Results will be published soon.

Whilst during the first year one Newsletter was produced each month, this has been reduced for practical reasons to one issue every two months. This Newsletter is the fourth of this year and all Newsletters can be downloaded from: http://edendatasite.com/ and then clicking the TAB VBORNET/Newsletters.

The second plenary day was a public event focussing on Public Health in vector-borne diseases. First a detailed overview was given of the replies VBORNET obtained from national PH representatives to the VBORNET-PH questionnaire. This was the first large scale effort of its kind. Despite the complexity of the questionnaire more than half of the countries replied and we are looking forward to receive replies from the missing countries. Preliminary results will be published soon, and an in-depth analysis with conclusions and recommendations is planned for the next VBORNET term. A detailed account of the first PH strategic paper was also provided and a published version will be available for summer.

Figure 2 - VBORNET AGM2 Participants

In the afternoon of the plenary day the following issues were addressed by invited speakers:

- Disease mapping in PH: from theory to practice. (David Rogers, Zoology Oxford, UK)
- Burden of Disease assessments: the experience of BCoDE. (Cheryl Gibbons, University of Edinburgh, UK)
- PH impact of WNV outbreaks in Europe in 2010. (Zdenek Hubalek, IVB, Czech Republic)
- PH impact of Lyme disease in Temperate Europe. An example from The Netherlands (Kees van den Wijngaard, RIVM, the Netherlands)
- PH impact of leishmaniasis in Mediterranean Europe. (Luigi Gradoni, ISS, Italy)

During the last day collaboration with other networks and VBD-groups was discussed with particular attention to EMCA, ESOVE and EDENext. Finally the conclusions of the AGM were presented and discussed. These will be published on the VBORNET websites soon.

The VBORNET Coordination Team

2. SCIENTIFIC ADVANCES: VECTOR-BORNE DISEASES

Using Geographic Information Systems and Decision Support Systems for the Prediction, Prevention, and Control of Vector-Borne Diseases

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Annu. Rev. Entomol. 2011. 56:41–61.

Emerging and resurging vector-borne diseases cause significant morbidity and mortality, especially in the developing world. We focus on how advances in mapping, Geographic Information System, and Decision Support System technologies, and progress in spatial and space time modeling, can be harnessed to prevent and control these diseases.
Major themes, which are addressed using examples from tick-borne Lyme borreliosis; flea-borne plague; and mosquito-borne dengue, malaria, and West Nile virus disease, include (a) selection of spatial and space-time modeling techniques, (b) importance of using high-quality and biologically or epidemiologically relevant data, (c) incorporation of new technologies into operational vector and disease control programs, (d) transfer of map-based information to stakeholders, and (e) adaptation of technology solutions for use in resource-poor environments. We see great potential for the use of new technologies and approaches to more effectively target limited surveillance, prevention, and control resources and to reduce vector-borne and other infectious diseases.

Link to the article: http://www.annualreviews.org/doi/pdf/10.1146/annurev-ento-120709-144847

Key words: Geographic Information Systems, Vector-borne diseases

VBORNET comment: 2010-04-29

Spatial-time risk models are increasingly used to understand and anticipate disease emergence and predict the time, size and spatial spread of an ensuing epidemic. Eisen L and RJ provide an excellent review on the different aspects of using geographic information systems and decision systems for the prediction, prevention and control of vector borne diseases. The review starts with introducing the basic concepts, but quickly moves to providing insight into the different kind of models and their advantages and drawbacks. It continues by elaborating on the operational use and the transfer of map based information for vector-borne diseases to the stakeholder community. Subsequently, the available technologies for collection, management, analysis and display of vector and disease data are discussed. By considering the complete chain, from collecting data to utilizing the results, the authors produced a comprehensive guide in this rapidly developing discipline for everyone that is faced with the emergence of vector-borne disease.

3. SCIENTIFIC ADVANCES: TICKS

Argas (Persicargas) persicus (Oken, 1818) (Ixodida: Argasidae) in Sicily with considerations about its Italian and West-Mediterranean distribution.

Pantaleoni RA [1,2], Baratti M [1], Barraco L [3], Contini C [4], Cossu CS [1], Filippelli MT [1], Loru L [1], Romano M [5]
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Parasite Dec. 2010.17(4): 349-55.

Recently, in the province of Trapani (Western Sicily), some overwintering specimens of the argasid tick *Argas (Persicargas) persicus* (Oken, 1818) were observed and collected. Morphological and genetic analysis were utilized in order to reach a definitive identification. The species was found in two semi-natural sites where, having been found repeatedly, its presence does not appear accidental. Moreover the characteristics of the Sicilian findings seem to exclude a human-induced spread. This record, the first regarding Sicily and South Italy, is discussed together with the previous doubtful citations for Italy. These findings revalue not only all the old citations for Italy but also the hypothesis that the Mediterranean distribution of this argasid is of a natural origin.

Link to the article: http://parasite-journal.org/P3V174R11.html

Key words: Ticks distribution

VBORNET comment: 2011-05-17

Pantaleoni et al. provide an update on the distribution of *Argas persicus* in Italy. Until now, this species was considered absent from this country, except for a historical record in Trieste very near to the oriental boundary with the Balkans. All other records were attributed to misidentifications, considering the large changes in the *Argas* taxonomy during these last fifty years. The recent finding of *Argas persicus* in Sicily and its presence in other neighbouring countries confirm that its Mediterranean distribution is of natural origin and not only due to human-induced spread. Considering the revival of more biological agricultural practices in many industrial countries, this tick species could be more frequently encountered in the next future. However, this might have minor consequences for public health since *A. persicus* is only known to transmit avian pathogens and is considered rather a pest for human through irritant and hurting tick bite.

Differences in Questing Tick Species Distribution between Atlantic and Continental Climate Regions in Spain.

Barandika JF [1], Olmeda SA [2], Casado-Nistal MA [2], Hurtado A [1], Juste RA [1], Valcárcel F [3], Anda P [4], García-Pérez AL [1,5]

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Journal of Medical Entomology 48(1):13-19. 2011 doi: 10.1603/ME10079

Climate and vegetation in Spain vary from north to south, affecting tick distribution and consequently the presence of tick-borne diseases. The aim of this study was to investigate throughout a 2-yr study the distribution of the different exophilic questing tick species present in 18 areas: eight located in central and 10 in northern Spain. The same methodology was used in both areas, sampling vegetation on a monthly basis by blanket dragging for 20- to 30-min intervals. A total of 12 species belonging to the genera *Ixodes, Haemaphysalis*, *Rhipicephalus*, *Dermacentor*, and *Hyalomma* was identified. Differences in species distribution and prevalence were dramatically different. The most frequent and abundant species in northern Spain were *Ixodes ricinus* (67% of adult ticks) and *Haemaphysalis punctata* (8%), whereas *Hyalomma lusitanicum* (86%) and *Dermacentor marginatus* (12%) were the most abundant in central Spain. There were important differences in the monthly seasonal patterns for the different tick species. These results highlight important differences in tick distribution in neighboring areas and underline the need for ongoing surveillance programs to monitor tick population dynamics and the prevalence of tick-borne pathogens.

Link to the article: http://www.bioone.org/doi/abs/10.1603/ME10079

Key words: Ticks distribution

VBORNET comment: 2011-05-17

Barandika et al. examine tick species diversity and abundance in two distinct climatic regions of Spain along a two year-monitoring. They highlight that *Ixodes ricinus* and *Hyalomma punctata* are more frequent and abundant in the north oceanic part with mild temperatures and humid conditions while *H. lusitanicum* and *Dermacentor marginatus* are predominant in central Spain with drier continental conditions. This is a clear update of tick presence in Spain and should be extended to other regions to implement tick and tick-borne disease surveillance systems.

4. SCIENTIFIC ADVANCES: PHLEBOTOMINE

First surveys to investigate the presence of canine leishmaniasis and its Phlebotomine vectors in Hungary.

Farkas R [1], Tánczos B [1], Bongiorno G [2], Maroli M [2], Dereure J [3], Ready PD [4].

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4 Department of Entomology, Natural History Museum, London, United Kingdom.

Vector-Borne and Zoonotic Diseases Jan. 2011. [Ahead of print.] doi:10.1089/vbz.2010.0186.

Hungary is regarded as free of leishmaniasis because only a few imported cases have been reported. However, southern Hungary has a sub-Mediterranean climate, and so it was included in the EU FP6 EDEN project, which aimed to map the northern limits of canine leishmaniasis (CanL) in Europe. The numbers of traveling and imported dogs have increased in the last decade, raising concerns about the introduction of CanL caused by *Leishmania infantum*. Serum samples were collected from 725 dogs (22 localities, 6 counties) that had never traveled to endemic countries, as well as from other potential reservoir hosts (185 red foxes and 13 golden jackals). All sera were tested by the indirect fluorescent antibody test, but they were sero-negative using the OIE cut-off of 1:80 serum dilution except for those of two dogs resident since birth in southern Hungary. These had not received a blood transfusion, but the mode of transmission is unclear because no sandfly vectors were caught locally. From 2006 to 2009, phlebotomine sandflies were sampled in the summer months at 47 localities of 8 counties. They were trapped with castor-oil-impregnated sticky-paper, light, and CO(2)-baited traps. Small numbers of two vectors of *Leishmania infantum* were found. *Phlebotomus neglectus* occurred in three villages near to Croatia and one in north Hungary at latitude 47°N, and *Phlebotomus perfiliewi perfiliewi* was trapped at two sites in a southeastern county close to the sites where it was first found in 1931-1932. Our report provides baseline data for future investigations into the northward spread of CanL into Hungary, which we conclude has yet to occur.

Link to the article: http://www.liebertonline.com/doi/pdf/10.1089/vbz.2010.0186

Key words: Leishmaniasis

VBORNET comment: 2010-04-12

Farkas et al. aimed to investigate the presence of canine leishmaniasis (CanL) and its phlebotomine vectors in Hungary. A serological study was performed by indirect fluorescent antibody test (IFAT) on dogs that had never traveled in endemic focus and on other potential reservoirs hosts (foxes and golden jackals). Phlebotomine sand flies were collected from July to September during a 4-year period (2006-2009) by sticky-paper, light and CO_2-baited traps. Two healthy dogs out of 705 dogs were found to be a borderline IFAT positive for *Leishmania*. Nevertheless, these dogs were found IFAT negative for *Leishmania* after one year. The serum samples of the 185 foxes and 13 jackals were identified as IFAT negative. According to surveys of veterinarians, up to now all the declared CanL cases have been imported from Mediterranean basin countries. Two of the three known vectors of *L. infantum* in the southeastern Europe, *Phlebotomus perfiliewi perfiliewi* and *P. neglectus* were found in low numbers (513 specimens in four summer sampling) during the study. It is worth noting that no sand fly vectors were caught around the two transitory seropositive dogs. A new record for Hungary was the finding of *P. mascittii* in three out of eight surveyed counties, particularly in the northern part of Hungary. The results of this study show that there is no evidence of the presence of CanL in Hungary. Nevertheless, since two main vectors of *L. infantum* are present in nearby countries in which the CanL already occurs, such as Croatia and Serbia, there is a potential risk of northward spread of CanL into Hungary.

Characterization of a sandfly fever Sicilian virus isolated during a sandfly fever epidemic in Turkey.

Carhan A [1], Uyar Y [1], Ozkaya E [1], Ertek M [1], Dobler G [2], Dilcher M [3], Wang Y [3], Spiegel M [3], Hufert F [3], Weidmann M [3].

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Journal of Clinical Virology Aug. 2010. 48(4): 264-9.

BACKGROUND: Phleboviruses cause sandfly fever but isolates are rare.
OBJECTIVES: To analyse samples from concurrent outbreaks of suspected sandfly fever in the Mediterranean provinces of Adana, Izmir and the central province of Ankara, Turkey.
STUDY DESIGN: Samples from acute cases were analysed by immunofluorescence assay (IFA). Virus isolation was attempted and pyrosequencing performed.
RESULTS: In IFA 38% of 106 samples tested scored IgM positive for sandfly fever Sicillian virus (SFSV), 12% for SFSV/sandfly fever Cyprus Virus (SFCV) and only 4% for SFCV. A sandfly fever Sicilian type virus designated sandfly fever Turkey virus (SFTV) was isolated. The S-segment sequence of SFTV had a homology of 98% to that of SFCV. The M-segment sequence showed a 91.1% homology to the only SFSV sequence available. The L-segment sequence showed a homology of 58% and 60.3% to Toscana virus and Rift Valley Fever virus sequences, a partial 201nt sequence showed 95.5% homology to the SFSV Sabin strain.
CONCLUSION: A new phlebovirus related to sandfly fever Sicilian virus, SFTV was isolated and characterized from acute patient material. The sandfly fever Sicilian virus activity seems to be changing in Turkey. Entomological studies are needed.

Link to the article: http://www.sciencedirect.com/science/article/pii/S1386653210002246
Key words: Sand fly fever

VBORNET comment: 2010-04-12

Carhan et al. report the identification and genomic characterization of a novel variant of sand fly fever Sicilian virus (SFSV), provisionally named the Sandfly Fever Turkish Virus (SFTV), during the investigation for outbreaks of febrile diseases associated with sandfly bites in Izmir (Aegean coast), Adana (Mediterranean coast), and Ankara (Central Anatolia) provinces in 2007-2008. Sandfly fever viruses (SFVs) comprise three major serotypes; SFSV, SFNV and Toscana virus (TOSV). 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. The S segment of the novel SFTV displayed 98% homology to that of SFCV Cyprus whereas M and partial L segments also showed 91.1% and 95.5% homology to SFSV, respectively. It is generally accepted that SFVs have the capacity to display significant diversity in the sandfly vectors and variants/recombinants, some of which may be capable of inducing human disease which may emerge in the endemic regions. In addition to Carhan et al.'s identification of the SFSV variant in Turkey, another report to support this hypothesis was recently published by Collao et al. who identified in Spain a new member of the phlebovirus genus in sandflies, tentatively named Granada virus (*Am J Trop Med Hyg,* 83(4): 760–765, 2010). Human exposure to this agent is also demonstrated, although association with a clinical syndrome could not be proven. Interestingly, the genomic analysis of Granada virus revealed that it is likely to be a natural reassortant of the recently described Massilia virus (donor of the long and short segments) with a yet unidentified phlebovirus. See also Ergünay et al., 2011 and Hamarsheh, 2011.

Distribution of *Leishmania major* zymodemes in relation to populations of *Phlebotomus papatasi* sand flies

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Parasites & Vectors Jan. 2011. 4: 9. doi:10.1186/1756-3305-4-9

Phlebotomus papatasi (Scopoli) (Diptera: Psychodidae) is the main vector of *Leishmania major* Yakimoff & Schokhor (Kinetoplastida: Trypanosomatidae), the causative agent of zoonotic cutaneous leishmaniasis in the Old World. Multilocus enzyme electrophoresis (MLEE) was extensively used to type different *L. major* stocks allover the world. Multilocus microsatellite typing (MLMT) has been recently used to investigate *P. papatasi* sand flies at population and subpopulation levels. In this article, the association between geographical distribution of *L. major* zymodemes and the distribution of populations and subpopulations of *L. major* vector; *P. papatasi* are discussed.

Link to the article: http://www.parasitesandvectors.com/content/pdf/1756-3305-4-9.pdf
Key words: Leishmaniasis

VBORNET comment: 2010-04-12

Hamarsheh reviews the association between geographical distribution of *Leishmania major* zymodemes and the distribution of *Phlebotomus papatasi*, the proven vector of *Leishmania major,* in the east Mediterranean region. Three main *L. major* zymodems, MON 23, MON 25 and MON 26 and several variants of MON 26 were reported. Two of them, MON 25 and MON 26, appear predominant and widespread. Authors detailed the results obtained using multilocus microsatellites for *Phlebotomus papatasi*. Two main populations A and B and 6 subpopulations (A1 to A4, B1 and B2) were identified. The main conclusion of this review is that the wide distribution range of *P. papatasi*, limited to a certain number of populations and subpopulations, is in correlation with the wide distribution of *L. major* also limited to a certain group of main zymodemes like MON 25, MON 26 and MON 23, and to other less prevalent variants.

Canine leishmaniasis surveillance in a northern Italy kennel.

Baldelli R [1], Piva S [1], Salvatore D [1], Parigi M [1], Melloni O [2], Tamba M [3], Bellini R [4], Poglayen G [1].

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Veterinary Parasitology Feb. 2011. doi:10.1016/j.vetpar.2011.01.052 [Epub ahead of print]

An epidemiological survey on canine leishmaniasis (CanL) was performed during a 3-year period (2007-2009) in a public kennel of the Bologna province. The presence of the disease was shown in the canine population for the first time in 2007 by indirect fluorescent antibody test (IFAT). The parasite circulation was confirmed also by direct diagnostic tools, as PCR, cytology and cultural method, performed on different bioptic materials. The parasite was isolated and identified as *Leishmania infantum* zymodeme MON 1. The serological monitoring was performed also in 2008 and 2009 on animals that previously showed negative or uncertain results. The incidence values calculated by significant seroconversions in IFAT titre ≥1/160, ranged between 4.9% and 6.6%, indicating a stable focus of leishmaniasis. The entomological survey, performed by sticky and CO(2)-baited traps in 2008, showed the presence of the vector *Phlebotomus perfiliewi*. This study allowed us to identify a stable focus of CanL in an area that was not considered eco-compatible with the presence of the vector and infection. Our results confirm the northward spread of CanL towards areas not previously affected by autochthonous foci.

Link to the article: http://www.sciencedirect.com/science/article/pii/S0304401711000860

Key words: Leishmaniasis

VBORNET comment: 2010-04-12

Bardelli et al. demonstrate the presence of canine leishmaniasis in dog of a kennel in northern Italy, based on serological monitoring and confirmed by direct diagnostic tools (PCR), parasitological and molecular methods. The authors report responsible parasite, *Leishmania infantum* zymodeme MON1, and vector sand fly species, *Phlebotomus perfiliewi*. Although the kennel is not a good epidemiological observatory in low endemic areas because of collection of roaming dogs with uncertain geographic origin, the surveillance allowed to identify an active focus of infection due to a zymodeme known as the most common in the Mediterranean Basin and the main VL responsible. The high incidence observed, together with the presence of the vector support the authors' hypothesis of a stable focus of *L. infantum* at the kennel. This study contains three important results in terms of public health: 1) The results confirm the northward spread of CanL towards areas not previously affected by autochthonous foci; 2) This study may represent an example of the outcome of a leishmaniasis monitoring activity in a public health perspective, starting from a group of confined dogs easy to manage. It could be seen as a model for other areas considered at low risk for implementation of regional surveillance programs; 3) Additionally this kind of studies may represent a good trial of the "one medicine": physicians and veterinarians working together on an important zoonosis in order to manage both human and animal health and wellness.

Spatial distribution of phlebotomine sand flies in the Aydin Mountains and surroundings: the main focus of cutaneous leishmaniasis in western Turkey.

Ozbel Y [1], Balcioğlu IC [2], Olgen MK [3], Simsek FM [4], Töz SÖ [1], Ertabaklar H [5], Demir S [6], Alkan MZ [1].

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Journal of Vector Ecology Mar. 2011. 36(Suppl 1): S99-S105. doi: 10.1111/j.1948-7134.2011.00118.x.

An entomological survey was conducted to determine the spatial distribution of phlebotomine fauna and understand the effect of environmental factors. The entomological survey was carried out during 2006-2007 in a study area in the rural area of Aydin province, near the Kusadasi town where VL, CL, and canine leishmaniasis (CanL) are endemic. In 2006 and 2007, 132 locations were sampled using sticky traps mainly on embankments. Detailed environmental and meteorological information was also collected for each location. The results of entomological studies indicated that the probable vectors are *Phlebotomus tobbi* and *P. neglectus* for VL and CanL, and *P. similis* for CL in this western leishmaniasis focus. The data revealed a correlation between their presence and spatial variables such as altitude, sampling site location, and humidity. The distribution areas of probable vector species in this study area allowed the identification of risk levels, which may provide useful information to guide the leishmaniasis research in endemic regions.

Link to the article: http://onlinelibrary.wiley.com/doi/10.1111/j.1948-7134.2011.00118.x/pdf
Key words: Leishmaniasis

VBORNET comment: 2010-04-12

The Journal of Vector Ecology has edited an interesting special issue on sand flies and sand fly transmitted diseases, of which several are related to public health in Europe. Among these, Ozbel et al. report an entomological survey carried out to determine the spatial distribution of sand fly fauna in a human and canine leishmaniasis endemic area of Turkey and analyses were done to understand effect of environmental factors on sand fly's distribution. Only sticky paper traps were used and environmental and meteorological information was obtained for each location. Results suggest as probable vectors *Phlebotomus tobbi* and *P. neglectus* for VL and CanL, and *P. similis* for CL in this endemic focus. The authors pinpoint that altitude, humidity and sampling site location are significantly important spatial variables for the distribution of sand fly species. Meteorological data, remotely sensed images and vector distribution areas are used for identifying risk levels which is an important issue in terms of public health. Identification of risk levels and/or preparation of risk maps can guide policy makers and public health authorities for leishmaniasis control program. Moreover, analysis of different environmental factors without leishmaniasis or vector distribution data may also allow the prediction of potential risks.