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1. SCIENTIFIC ADVANCES: VECTOR-BORNE DISEASES

Interventions Against West Nile Virus, Rift Valley Fever Virus, and Crimean-Congo Hemorrhagic Fever Virus: Where Are We?

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ARBO-ZOONET is an international network financed by the European Commission's seventh framework program. The major goal of this initiative is capacity building for the control of emerging viral vector-borne zoonotic diseases, with a clear focus on West Nile virus, Rift Valley fever virus, and Crimean-Congo hemorrhagic fever virus. To evaluate the status quo of control measures against these viruses, an ARBO-ZOONET meeting was held in Istanbul, Turkey, from 19 to 20 November 2009. The symposium consisted of three themes: (1) vaccines: new and existing ones; (2) antivirals: existing and new developments; and (3) antivector vaccines. In addition, a satellite workshop was held on epidemiology and diagnosis. The meeting brought together foremost international experts on the subjects from both within and without the ARBO-ZOONET consortium. This report highlights selected results from these presentations and major conclusions that emanated from the discussions held.

Link to the article: <http://www.liebertonline.com/doi/abs/10.1089/vbz.2010.0040>

Key words: West Nile Fever, Rift Valley Fever, Crimean Congo Haemorrhagic Fever

VBORNET comment: 2010-12-28

Among vector-borne diseases (VBDs), the viral zoonotic ones receive increasing attention in Europe. There are good reasons for this, besides the emergence of VBD's in general due to globalisation and environmental changes. Not only do viruses make up the majority of vector borne pathogens, zoonotic agents are of concern for both the public and veterinary health providing both opportunities and challenges. Despite growing support for the One Health initiative, implementation of this concept in everyday practice has proven to be challenging. The European commission recognized this and decided to finance (FP7) ARBO-ZOONET, an international network that aims at capacity building for the control of emerging viral vector-borne zoonotic disease focusing on West Nile virus (WNV), Rift Valley fever (RVF) and Crimean-Congo hemorrhagic fever (CCHF). On the basis of presentations of international experts during their meeting in November 2009, Turkey, comprehensive technical report on the state of the art of control of viral zoonotic VBD's by means of development of vaccines and antivirals is given here. The meeting (and the network) focused on achievements but also the research gaps with respect to these control measures for the three diseases. For WNV the lack of effective antiviral agents was identified as the most important challenge for the future. This also holds for RVFV but here focus should also be on the establishment of vaccine efficacy in the target species of RVFV. For CCHFV the authors report on the recent achievements of an animal model and a minigenome system, both important tools for the evaluation of vaccine candidates and antiviral agents. Future efforts should be made to optimally exploit these valuable systems. ARBO-ZOONET, together with many other European initiatives such as VBORNET, VECMAP, ENIVD, EMCA are complementary efforts to challenge the complex task of the prevention and control of endemic and emerging VBDs in Europe.

Pathogenic landscapes: interactions between land, people, disease vectors, and their animal hosts.

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International Journal of Health Geographics, 2010, 9: 54, doi:10.1186/1476-072X-9-54

BACKGROUND: Landscape attributes influence spatial variations in disease risk or incidence. We present a review of the key findings from eight case studies that we conducted in Europe and West Africa on the impact of land changes on emerging or re-emerging vector-borne diseases and/or zoonoses. The case studies concern West Nile virus transmission in Senegal, tick-borne encephalitis incidence in Latvia, sandfly abundance in the French Pyrenees, Rift Valley Fever in the Ferlo (Senegal), West Nile Fever and the risk of malaria re-emergence in the Camargue, and rodent-borne Puumala hantavirus and Lyme borreliosis in Belgium.

RESULTS: We identified general principles governing landscape epidemiology in these diverse disease systems and geographic regions. We formulated ten propositions that are related to landscape attributes, spatial patterns and habitat connectivity, pathways of pathogen transmission between vectors and hosts, scale issues, land use and ownership, and human behaviour associated with transmission cycles.

CONCLUSIONS: A static view of the "pathogenecity" of landscapes overlays maps of the spatial distribution of vectors and their habitats, animal hosts carrying specific pathogens and their habitat, and susceptible human hosts and their land use. A more dynamic view emphasizing the spatial and temporal interactions between these agents at multiple scales is more appropriate. We also highlight the complementarity of the modelling approaches used in our case studies. Integrated analyses at the landscape scale allows a better understanding of interactions between changes in ecosystems and climate, land use and human behaviour, and the ecology of vectors and animal hosts of infectious agents.

Link to the article: <http://www.ij-healthgeographics.com/content/9/1/54>

Key words: Haemorrhagic Fevers, Climate Change

VBORNET comment: 2010-01-07

This very nice paper presents an analysis integrating multidisciplinary research results obtained during the EDEN EU-funded (FP6) project throughout Europe. This clearly shows the added value of multidisciplinary team collaboration to address the complex issue of vector-borne diseases in a changing environment. VBORNET is looking forward to further results which will be obtained during EDENext (FP7) and which started on January 1st, 2011.

2. SCIENTIFIC ADVANCES: MOSQUITOES

Mosquitoes in Malta: Preliminary entomological investigation and risk assessment for vector-borne diseases (Diptera: Culicidae).

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Bulletin of the Entomological Society of Malta, 2010, 3: 41-54

At the request of Malta's Infectious Disease Prevention and Control Unit (IDCU), the European Centre for Disease Prevention and Control (ECDC) organized an expert mission in Malta in 2009 to provide support for a vector-borne disease (VBD) risk assessment. As these diseases are clearly related to the

presence of competent and efficient vectors, and as little information was available on the local mosquito fauna (Diptera: Culicidae), a field study was implemented during the mission. The aim was to determine the presence and relative abundance of potential vectors, and to assess the risk of transmission of mosquito-borne diseases. From April 6th to May 1st, 2009, a total of 114 among 513 investigated putative larval habitat units contained mosquito immature stages. Artificial habitats and coastal saltwater rock pools predominated among the larval habitats. Also, 1,150 female mosquitoes were caught with dry-ice baited light traps. Seven species among the nine known to occur in Malta at the time of the study were observed and *Culex theileri* is reported here for the first time. The most commonly encountered species were *Culiseta longiareolata* and *Culex pipiens*. *Culex hortensis* was only found on the island of Gozo. The mosquitoes of the Mariae complex have been identified in the past as *Aedes zammitii* but all except four of the specimens collected showed morphological characters corresponding to *Aedes mariae*. Neither *Anopheles* spp. nor *Aedes albopictus* were found despite the investigation of suitable larval habitats and the use of CO₂-baited light traps and a few ovitraps. However, these species are known to be more abundant during the summer months and further investigations are needed to confirm their absence or their presence and distribution on the islands. The mosquito-related risk of disease for humans in Malta is discussed and West Nile fever appears to be the most probable mosquito-borne disease that could appear in Malta. The eventual finding of *Aedes albopictus* after this study was completed further strengthens the need to survey both Chikungunya and dengue infections.

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

Request of reprint to the corresponding author: fschaffner@avia-gis.be

Key words: West Nile Fever, Chikungunya

VBORNET comment: 2010-12-24

The islands of Malta have an interesting geographic location, bridging northern Africa to mainland Europe. The authorities of Malta requested the ECDC to carry out a risk assessment of their island regarding vector-borne diseases and this paper addresses risk related to mosquitoes. The basis for such an assessment is finding out what mosquito vector species are present and/or absent, and in what type of area/habitat they occur, or could occur. The authors describe the set-up and results of an entomological surveillance in springtime, show pictures of the type of habitats where particular mosquitoes were encountered, or could have been encountered, and describe for each encountered species what is known about their role as vector of mosquito-borne diseases. Special attention was given to the result that, despite extensive searching, *Aedes albopictus* was not found. This exotic invasive species is present in many areas in southern Europe and is a known vector for dengue and chikungunya viruses. Especially because the surveillance was carried out quite early in the season, the 'not finding' of this species could not rule out absence of the species at the islands. Therefore, the risk assessment team suggested to carry out specific survey for *Aedes albopictus* in the summer. A note at the end of the manuscript describes that later that summer, *Ae. albopictus* was indeed found in several cities and villages and apparently spreading southwards. The manuscript shows that a relatively small entomological survey can form the basis for a mosquito-borne disease risk assessment. Moreover, it shows that a team of experts can indicate how, where, and when to set up appropriate entomological surveillance to pick up particularly important vector species such as *Ae. albopictus*. With the acquired knowledge and expertise, the authorities of Malta have gained in their preparedness for potential mosquito-borne disease outbreaks.

Introduction and control of three invasive mosquito species in the Netherlands, July-October 2010

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Euro Surveillance, 2010,15(45): 4pp. pii=19710.

In July 2010, during routine mosquito surveillance inspections at companies that import used tires, three invasive species were found at five locations in the Netherlands: the yellow fever mosquito (*Aedes aegypti*), the Asian tiger mosquito (*Ae. albopictus*), and the American rock-pool mosquito (*Ae. atropalpus*). This is the first time that *Ae. aegypti* is reported from the Netherlands. Mosquito control was

initiated one week after the first invasive mosquito was found, using adulticides and larvicides. The available data suggest that the implemented control measures have been effective for this season.

Link to the journal: <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19710>

Key words: Mosquito-borne diseases

VBORNET comment: 2011-01-04

This paper details the significant findings of *Aedes aegypti* imported into the Netherlands on used tyres, and the first occurrence of *Aedes albopictus* in the outdoor environment (previous populations have related to glasshouses), in the Netherlands. It also illustrates the continued importance of the trade in used tyres in the importation of exotic species into and throughout Europe. The Netherlands should be commended for their pro-active surveillance of mosquitoes at imported tyre depots and other EU countries could learn much from their approach and their swift control strategies. One of the challenges in identifying potential foci of exotic mosquitoes is access to documentation related to imported tyres and this requires collaboration across a range of sectors: medical entomology, public health and most importantly the tyre-business industry. The authors correctly promote an EU-wide collaboration that brings all these sectors together.

3. SCIENTIFIC ADVANCES: TICKS

Geographical distribution and surveillance of Crimean-Congo hemorrhagic fever in Iran

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Vector-Borne and Zoonotic Diseases. September 2010, 10(7): 705-708. doi:10.1089/vbz.2009.0247.

Crimean-Congo hemorrhagic fever (CCHF) is viral hemorrhagic fever caused by CCHF virus, which belongs to the family Bunyviridae and the genus *Nairovirus*. The virus is transmitted to humans via contact with blood and tissue from infected livestock, a tick bite, or contact with an infected person. Since 2000, we have shown the disease to be prevalent in 23 out of 30 provinces of Iran. Among those, Sistan-va-Baluchistan, Isfahan, Fars, Tehran, Khorasan, and Khuzestan demonstrated the highest infection, respectively. Notably, Sistan-va-Baluchistan province, southeast of Iran, has the highest prevalence of CCHF, and has shown to be present since at least 2000. Phylogenetic study of the CCHF virus genome isolated from Iranian patients showed a close relationship with the CCHF Matin strain (Pakistan). Our epidemiological data in the last decade have implied that the severity and fatality rate of the disease has ranged variably in different provinces of Iran. More pathogenesis and phylogenetic studies should therefore be investigated to clarify these differences.

Link to the article: <http://www.liebertonline.com/doi/abs/10.1089/vbz.2009.0247>

Key words: Crimean Congo Haemorrhagic Fever

VBORNET comment: 2010-12-22

This article provides a timely update on the current status of Crimean-Congo haemorrhagic fever in Iran and clearly demonstrates the wide distribution of CCHF cases across the country. Of particular interest is the reported lack of transmission via ticks to humans. Even in countries with a high rate of nosocomial transmission or where there are many cases through direct contact with infected blood a proportion of cases are attributable to either crushing of ticks or tick bites. It is briefly mentioned that ticks are collected from livestock in high risk areas however no further discussion is given to the identification of tick species or their host preference which may elucidate why humans are not infected via this route and the authors themselves acknowledge this area requires further investigation. All cases discussed were reported between June 2000 and December 2009 with a total of 635 confirmed of which 89 were fatal (14.5%). More males (77.5%) than females (22.5%) were infected and in keeping with findings from other CCHF countries professions involving the handling of blood and organs of potentially infected livestock were identified as a risk factor. A considerable proportion of cases (141) however were in unrelated professions including carpenter, cook, baker, barber and mason; further discussion of the potential sources of their infection would have added much value to the paper.

Detection of spotted fever group *Rickettsia* spp. from bird ticks in the U.K.

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Medical and Veterinary Entomology, 2010, 24(3): 340-343

Migratory birds are known to play a role in the long-distance transportation of microorganisms. To investigate whether this is true for rickettsial agents, we undertook a study to characterize tick infestation in populations of the migratory passerine bird *Riparia riparia* (Passeriformes: *Hirundinidae*), the sand martin. A total of 194 birds were sampled and ticks removed from infested birds. The ticks were identified as female *Ixodes lividus* (Acari: *Ixodidae*) using standard morphological and molecular techniques. Tick DNA was assayed to detect *Rickettsia* spp. using polymerase chain reaction and DNA was sequenced for species identification. A single *Rickettsia* spp. was detected in 100% of the ticks and was designated *Rickettsia* sp. IXL11. Partial sequences of 17-kDa and *ompA* genes showed greatest similarity to *Rickettsia* sp. TCM1, an aetiological agent of Japanese spotted fever-like illness, previously described in Thailand. Phylogenetic analysis showed that *Rickettsia* sp. IXL11 fitted neatly into a group containing strains *Rickettsia japonica*, *Rickettsia* sp. strain Davousti and *Rickettsia heilongjiangensis*. In conclusion, this research shows that U.K. migratory passerine birds host ticks infected with *Rickettsia* species and contribute to the geographic distribution of spotted fever rickettsial agents.

Link to the article:

<http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2915.2010.00886.x/abstract>

Key words: Rickettsial infection

First detection of spotted fever group rickettsiae in *Ixodes ricinus* and *Dermacentor reticulatus* ticks in the UK

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Epidemiology and Infection, 2010 Nov 19, 6 pp. doi: 10.1017/S0950268810002608 [Epub ahead of print]

A preliminary study was conducted to determine the presence of spotted fever rickettsiae in two species of British tick (*Ixodes ricinus* and *Dermacentor reticulatus*). The 16S rRNA gene of *Rickettsia* spp. was detected in 39/401 (9.7%) of ticks tested, including 22/338 (6.5%) *I. ricinus* and 17/63 (27%) *D. reticulatus*. Some positive *I. ricinus* samples showed 100% homology with *Rickettsia helvetica* (10/22), and most positive *D. reticulatus* showed 100% homology with *R. raoultii* (13/17). Five other *Rickettsia* spp. were detected exhibiting 96-99% homology. Ticks positive for rickettsiae were collected from various hosts and from vegetation from eight counties across Great Britain. The distribution of *R. helvetica* in various engorged and unfed stages of *I. ricinus* suggests that *R. helvetica* is widespread. *R. raoultii* was found in questing adult *D. reticulatus* in Wales and England. This is the first evidence of potentially pathogenic spotted fever rickettsiae in British ticks.

Link to the article:

<http://journals.cambridge.org/action/displayAbstract?fromPage=online&aid=7926105>

Key words: Rickettsial infection

VBORNET comment: 2011-01-11

These two papers report two small-scale studies aiming at detecting *Rickettsia* spp. in tick species commonly found in the UK, for a better knowledge of pathogen distribution, and risk assessment regarding human infection. The first study was specifically designed to investigate the prevalence of rickettsiae bacteria carried by ectoparasites of a common migratory bird in the UK: sand martins (*Riparia riparia*). The second exploited tick collections made from different hosts (deer, dog, and human) and from vegetation (dragging), in different places of UK, and at different periods between 2006 and 2009. Both studies revealed moderate to high prevalence rates of *Rickettsia* infections in investigated ticks, all these bacteria having a zoonotic potential, with no previous record of human cases in the UK. Though humans are not usual hosts for *Ixodes lividus*, this tick may also infest peri-domestic bird species, and some of these birds may harbour other competent ticks for *Rickettsia*, such as *I. ricinus*. Moreover, results of the second paper seem to show that *Rickettsia* infection is common in British *I. ricinus* and

Dermacentor reticulatus ticks, which are often hosted by domestic animals and humans. Therefore, the risk of human infection by *Rickettsia* spp. should be better acknowledged in the UK. Obviously, more research is needed to assess the geographical distribution of these emerging pathogens, as well as their spatial and temporal dynamics, and the health risk for human populations, in the UK and elsewhere in Europe. Such studies, coordinated at the European scale, are planned in the EDENext project (Biology and control of vector-borne infections in Europe, funded by FP7, European Commission) which has started on January 1st, 2011.

***Borrelia burgdorferi* sensu lato in *Ixodes ricinus* ticks collected from migratory birds in Southern Norway.**

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Acta Veterinaria Scandinavica, 2010, 52:59, 6 pp. doi:10.1186/1751-0147-52-59

BACKGROUND: *Borrelia burgdorferi* sensu lato (s.l.) are the causative agent for Lyme borreliosis (LB), the most common tick-borne disease in the northern hemisphere. Birds are considered important in the global dispersal of ticks and tick-borne pathogens through their migration. The present study is the first description of *B. burgdorferi* prevalence and genotypes in *Ixodes ricinus* ticks feeding on birds during spring and autumn migration in Norway.

METHODS: 6538 migratory birds were captured and examined for ticks at Lista Bird Observatory during the spring and the autumn migration in 2008. 822 immature *I. ricinus* ticks were collected from 215 infested birds. Ticks were investigated for infection with *B. burgdorferi* s.l. by real-time PCR amplification of the 16S rRNA gene, and *B. burgdorferi* s.l. were thereafter genotyped by melting curve analysis after real-time PCR amplification of the hbb gene, or by direct sequencing of the PCR amplicon generated from the rrs (16S)-rrl (23S) intergenetic spacer.

RESULTS: *B. burgdorferi* s.l. were detected in 4.4% of the ticks. The most prevalent *B. burgdorferi* genospecies identified were *B. garinii* (77.8%), followed by *B. valaisiana* (11.1%), *B. afzelii* (8.3%) and *B. burgdorferi* sensu stricto (2.8%).

CONCLUSION: Infection rate in ticks and genospecies composition were similar in spring and autumn migration, however, the prevalence of ticks on birds was higher during spring migration. The study supports the notion that birds are important in the dispersal of ticks, and that they may be partly responsible for the heterogeneous distribution of *B. burgdorferi* s.l. in Europe.

Link to the article: <http://www.actavetscand.com/content/52/1/59>

Key words: Lyme Disease

VBORNET comment: 2010-12-22

This paper adds to the evidence for the involvement of migratory birds in the distribution of ticks with a focus on those carrying *Borrelia burgdorferi* sensu lato, the causative agent of Lyme borreliosis. Ticks were collected from birds trapped in mist nets during spring and autumn migration in 2008. In addition flagging for questing ticks was performed during the same time period. Only *Ixodes ricinus* ticks were identified, 822 in total, of which all were immature (499 larvae and 323 nymphs). It is worth noting that morphological identification of ticks was performed to species level using Hillyard (1996) however these particular keys do not allow for identification of larvae which constituted the majority of ticks which were collected and subsequently identified.

Similar to other studies an overall infestation prevalence of host-collected ticks of 3.3% was found with a higher rate in spring (6.18%) compared to autumn (2.74%). Of particular interest is the difference in prevalence rates between questing nymphs and those removed from birds, the former being 24.1% and the later 5.4% (spring) and 7.5% (autumn). The authors indicate such a difference may be due to the sensitivity of *B. afzelii* spirochetes to avian complement. To complete the readers understanding of the role in which avian complement may play it would have been useful to include the breakdown of *Borrelia* genospecies in questing ticks in addition to the ticks removed from birds. A final finding of importance was the detection of *B. burgdorferi* s.l. in 3.4% of larvae which could indicate reservoir host competence of certain bird species or trans-ovarial transmission.

4. SCIENTIFIC ADVANCES: PHLEBOTOMINAE SAND FLIES

Occurrence and genetic variability of *Phlebotomus papatasi* in an urban area of southern Italy

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Parasites & Vectors, 2010, 3: 77, 5 pp. doi: 10.1186/1756-3305-3-77

Background: A phlebotomine sand fly was noticed in the second floor of an old building in a highly urbanized area of southern Italy. A short-term entomological survey was carried out in the subsequent weeks to this event, allowing the collection of additional phlebotomine sand flies that were later identified as *Phlebotomus papatasi*. We assessed the genetic variability among *P. papatasi* sequences obtained in this study and those available from Italy using a mitochondrial DNA (mtDNA) fragment (from *cytochrome b* gene to NADH1) and the internal transcribed spacer 2 (ITS2) as genetic markers.

Results: From 9 June to 19 July, eight males and seven females (two blood-fed) of *P. papatasi* were collected in the old town of Bari (southern Italy). The insects were found near the bed and in the bathroom and potential blood sources (e.g., pigeons and dogs) for them were common in the neighbourhood. Again, five females of *P. papatasi* collected in Valenzano, another urban area in the province of Bari, were also identified and included in the genetic study. The mtDNA sequences (945 bp) obtained from Bari and Valenzano were identical except for a single transition (T ↔ C) at the 793 nucleotide residue. Pairwise comparison of the last 440 bp of the mtDNA fragment analyzed herein with other sequences of *P. papatasi* from Italy revealed a nucleotide variation ranging from 0.2 to 1.3%. Three ITS2 sequence types were detected within specimens collected in Valenzano, one of them identical to that from Bari. Pairwise comparison of ITS2 sequences of *P. papatasi* from Italy revealed a nucleotide variation up to 1.8%.

Conclusions: This study reports the occurrence of *P. papatasi* in an urban area of southern Italy and shows a low nucleotide difference among ITS2 and mtDNA sequences of this species available from Italy. The presence of *P. papatasi* in urban areas might represent a risk for human health, particularly for the potential transmission of sandfly fever viruses.

Link to the article: <http://www.parasitesandvectors.com/content/3/1/77>

Key words: Leishmaniasis

VBORNET comment: 2010-12-16

Phlebotomus papatasi is the type-species of the genus *Phlebotomus*, which include all phlebotomine sand fly vectors of *Leishmaniasis* parasites in old World. Moreover, this species is a vector of *Leishmania major*, the agent of zoonotic cutaneous leishmaniasis in North Africa and Middle East, and has been implicated in the transmission of viruses in Europe. It shows a wide-spread distribution pattern in Old World. Even though the reduced abundance of *P. papatasi* due to the control campaigns against malaria in the past century diminished the perceived relevance of this sand fly in Mediterranean countries, the species is represented by abundant and well-established populations in most of the countries. Beside the actual risk for public health in Europe is probably underestimated. For example studies conducted in central and southern Italy from 70s onwards indicated an increase in abundance of this sand fly, especially in urban areas. In contrast of its widespread distribution, data on public health significance of *P. papatasi* in the Mediterranean countries is scant. This study reports the occurrence of *P. papatasi* in an urban area of southern Italy and shows low genetic difference among ITS2 and mtDNA sequences of two populations of this species. The presence of *P. papatasi* in urban areas might represent a risk for human health in the Mediterranean and Europe, particularly for the potential transmission of sand fly fever viruses.

Phlebotomine sand fly population dynamics in a leishmaniasis endemic peri-urban area in southern Italy.

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A 2-year survey was carried out from May to November 2008 and 2009 to study the sand fly species composition, its seasonal phenology and density in Apulia region (southern, Italy). The study was conducted in a dog shelter located in a new residential urban district where *Leishmania infantum* is endemic. Sand flies were collected using sticky traps from May to November, at about 7-day intervals.

Temperature and relative humidity were recorded daily. In December 2008, general environmental improvements (e.g., the ground was covered with gravel and the vegetation present inside the cages was removed to facilitate cleaning) were made in the study area. The most diffused species during the whole study period were *Phlebotomus perniciosus* (2008, n = 248, 49.4%; 2009, n = 254, 50.6%) followed by *Phlebotomus neglectus* (2008, n = 76, 39.8%; 2009, n = 115, 60.2%) and *Phlebotomus papatasi* (2008, n = 5, 50.0%; 2009, n = 5, 50.0%). Four specimens of *Phlebotomus perfiliewi* were collected only in the first year. The number of *Sergentomyia minuta* specimens collected increased considerably in the second (n = 548, 86.2%) in comparison to the first year (n = 88, 13.8%). The highest number of phlebotomine sand flies was collected in July and August when a mean temperature from 27.09 to 28.02 °C and mean relative humidity from 47.28 to 56.36% were recorded. The variations in phlebotomine sand fly species diversity and abundance recorded in this study were related to climatic and environmental factors. Data here presented confirm that sand flies easily adapt to the urban environments and that they may represent a public health concern for *L. infantum* and other pathogen transmission also in similar urban environment of southern Europe.

[Link to the article: doi:10.1016/j.actatropica.2010.08.013](https://doi.org/10.1016/j.actatropica.2010.08.013)

Key words: Leishmaniasis

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This study reports the seasonal population dynamics and phenology of four important sand fly species, *Phlebotomus perniciosus*, *Phlebotomus neglectus*, *Phlebotomus papatasi* and *Sergentomyia minuta*, in Apulia Region (southern Italy). The data collected shows that population density of these species begins to increase in April; it reaches the highest peak in July and August and decreases in September or October in south Italy. This unimodal seasonal dynamism clearly demonstrates that south of Italy is quite suitable for breeding of all these species in terms of its climatic and ecological properties. In this condition, the species may re-establish its strong populations with high population size during long-term period in south Italy, may easily extend its distribution area, and may diffuse to other areas, which have similar conditions in Italy and in other Mediterranean countries. In population biology, one of the most valuable applications of the “intrinsic rate of increase, r_m ” concept is the delineation of the livable environment of a species. When we consider the r_m values that were obtained for different temperature conditions alongside R_0 and T in the studies performed in different countries, we can conclude that 28° C is the optimal condition for populations of the most of the sand fly species to reach high population densities. According to climatological data of this study, mean monthly temperature increases to 28 °C in July and August. Considering the studies on degree-day developmental requirements of *Ph. papatasi* (Erisoz Kasap and Alten, JVE, 2005), results of this study clearly show that populations of these species seem to produce at least two generations in a year in south Italy. Effects of different temperature conditions on r_m may have important consequences on the distribution of the species in temperate regions. According to the population dynamics theory, the probability of successful colonization of an empty site increases with increasing r_m , since a rapid population increase enables a colonizing population to grow quickly. Based on this theory, we may say that higher temperatures could increase both the geographic and seasonal distribution of these species in the Mediterranean Region in the near future. Therefore, the explanations of this study are important to display the potential risk of the species for public health in Europe.