

PUBLICise HEALTH

Public Health Telegram on Vector-borne Diseases

Issue No. 3 – MoBo

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Welcome to the third issue of the EDENext Public Health Telegram, the newsletter from the EDENext project focusing on our vector-borne disease research results with direct or indirect impacts on Public Health issues.

EDENext is investigating the biological, ecological and epidemiological components of vector-borne disease introduction, emergence and spread, and creating new tools to control them.

EDENext comprises five specialised vector groups. In this issue we concentrate on the work of the mosquito-borne diseases (MoBo) group. Future issues will examine culicoides-borne diseases (Diptera, Ceratopogonidae) and sand fly or phlebotome-borne diseases (Diptera, Psychodidae).

EDENext is seeking to make research more visible, comprehensible and applicable to the public and policy makers, embedding the research results from each vector group in the context of Public Health and vector-borne disease control in Europe. The EDENext Public Health Telegram was established to inform interested individuals and institutions about research results on vector-borne diseases with direct or indirect impact on public health issues.

For more details about the project, visit www.edenext.eu



Yellow fever mosquito (*Aedes aegypti*); photograph by James Gathany, CDC

In this issue, research results from the EDENext **mosquito-borne disease (MoBo)** group (06/2012 – 06/2013) include:

1. Usutu virus in Europe
2. First detection of the Asian tiger mosquito in the Czech Republic
3. Updates from mosquito-borne disease research in Spain
4. Experimental West Nile virus infection of large falcons
5. Novel mosquito control concept in urban areas
6. Topical global dengue fever risk mapping
7. Reduced flight performance in genetically-modified yellow fever mosquito
8. Development of a novel diagnostic tool for yellow fever
9. Developing malaria predictive maps in southern Benin



EDENext
Biology and control of vector-borne
infections in Europe

MoBo research results & Public Health

1. Usutu virus in Europe

Usutu virus (USUV) is an emerging zoonotic arbovirus. Originally discovered in Africa, it has spread to Europe, causing significant mortality in European songbirds, in particular blackbirds (*Turdus merula*). It is of Public Health importance due to causing sickness in humans (Pecorari et al 2009, Nickolay et al 2011) and due to its similarity regarding ecology, transmission and vectors to other, more dangerous zoonotic viral diseases such as West Nile fever (WNF) and Japanese encephalitis (JE).



European blackbird (*Turdus merula*); photograph by Andreas Trepte

Below, we represent three EDENext studies dealing with USUV.

While the 2001 Usutu virus outbreak in Vienna, Austria, is generally considered the first occurrence of the disease outside of its original African range, a retrospective analysis by **Weissenböck et al (2012)** indicates a previous USUV outbreak among the local blackbird (*Turdus merula*) population in Italy in 1996. This alludes to the necessity of reassessing the introduction and dispersion of the virus to and within Europe. This finding is remarkable in regard to the absence of documented cases between 1996 and 2001, indicating a “silent” spreading of the disease within European blackbird populations. The latter aspect is also of Public Health importance with regards to the other mentioned comparable diseases, such as WNF, for which such a silent spread among native bird populations might be likely in the future.

The EDENext study by **Scagnoleri et al (2013)** evaluates the sensitivity of USUV to type I and III interferons (IFNs) and its capacity to antagonise IFN production. The results indicate that USUV can replicate in human cell lines from different tissues, stimulating only a weak IFN response. These findings are of high importance in regard to the zoonotic potential of USUV, indicating that the virus is not only harmful to birds, but is well capable of using humans as hosts.

Hubálek et al (2012) report the first documented Czech cases of USUV in two blackbirds (*Turdus merula*). This highlights the need for a regular European surveillance programme to monitor both the virus and transmitting mosquito species throughout western and central Europe to provide a better overview about the current distribution range of the virus in Europe.



Hubálek Z, Rudolf I, Capek M, Bakonyi T, Betášová L, Nowotny N.
Usutu Virus in Blackbirds (*Turdus merula*), Czech Republic, 2011-2012.
Transbound Emerg Dis. 2012 Oct 24. doi: 10.1111/tbed.12025.

Scagnolari C, Caputo B, Trombetti S, Cacciotti G, Soldà A, Spano L, Villari P, Della Torre A, Nowotny N, Antonelli G.:
Usutu virus growth in human cell lines: induction of and sensitivity to type I and III interferons.
J Gen Virol. 2013 Apr;94(Pt 4):789-95. doi: 10.1099/vir.0.046433-0. Epub 2012 Dec 19.

Weissenböck H, Bakonyi T, Rossi G, Mani P, Nowotny N.:
Usutu virus, Italy, 1996.
Emerg Infect Dis. 2013 Feb;19(2):274-7. doi: 10.3201/eid1902.121191.

2. First detection of the Asian tiger mosquito in the Czech Republic

Given the central position of the Czech Republic within mainland Europe, the results of Czech mosquito-borne disease research are of particular importance regarding the distribution of both such diseases and their associated mosquito vectors within Europe. The EDENext study by Šebesta et al (2012) documents the first discovery of the Asian tiger mosquito (*Aedes [Stegomyia] albopictus*) in the Czech Republic and thereby adds another European country to the list of



Asian tiger mosquito (*Aedes [Stegomyia] albopictus*); photograph by James Gathany, CDC

countries where this invasive species has been observed. This mosquito is an important vector for the transmission of a great variety of diseases, among others West Nile, dengue and yellow fever as well as heartworms, and is infamous for its aggressive host-locating behaviour during daytime. Its presence is of great importance to Public Health internationally due to potentially facilitating an expansion of the range and chance of transmission of such highly pathogenic mosquito-borne diseases in so far unaffected areas.

Šebesta O, Rudolf I, Betášová L, Peško J, Hubálek Z.:
An invasive mosquito species *Aedes albopictus* found in the Czech Republic, 2012.
Euro Surveill. 2012 Oct 25; 17(43): 20301.



3. Updates from mosquito-borne disease research in Spain

Host feeding and mosquito blood meal sources, albeit in regard to different diseases and mosquito vectors, are the main focus of the EDENext studies from Spain described below.

The study by **Muñoz et al (2012)** analyses the origin of blood meals in five mosquito species from three different wetlands in south-west Spain to estimate their role as potential West Nile virus (WNV) vectors in these areas. Among others, the results of the study indicate that mosquito diet composition plays a major role in the potential transmission of WNV due to particular mosquito species being more attracted by certain animal species (including humans) as hosts and thus increasing the risk of interspecific disease transmission.

An EDENext study by **Martínez-De La Puente et al (2013)** employs two different methods (the HotSHOT procedure and the QIAGEN DNeasy Blood and Tissue® kit) to evaluate the success of blood meal source determination in the mosquito *Anopheles atroparvus* in respect to different stages of blood meal digestion. All in all, the host identification is less likely in mosquitoes with an advanced stage of blood meal digestion and for blood meals extracted using the HotSHOT procedure. Using the QIAGEN kit improves the identification success.

The second study by **Martínez-De La Puente et al (2012)** analyses the origin of blood meals in mosquitoes on two of the Canary Islands (Gran Canaria and Tenerife) to estimate their role as potential vectors of the heartworm (*Dirofilaria immitis*), a roundworm with zoonotic potential. Of the mosquito species collected, *Culex theileri* presented the greatest capacity to act as *Dirofilaria* vector between different potential host species (including humans).

Martínez-De La Puente J, Moreno-Indias I, Hernández-Castellano LE, Argüello A, Ruiz S, Soriguer R, Figuerola J.:

Host-feeding pattern of *Culex theileri* (Diptera: Culicidae), potential vector of *Dirofilaria immitis* in the Canary Islands, Spain.

J Med Entomol. 2012 Nov;49(6):1419-23.

Martínez-Dela Puente J, Ruiz S, Soriguer R, Figuerola J.:

Effect of blood meal digestion and DNA extraction protocol on the success of blood meal source determination in the malaria vector *Anopheles atroparvus*.

Malar J. 2013 Mar 21;12(1):109.

Muñoz J, Ruiz S, Soriguer R, Alcaide M, Viana DS, Roiz D, Vázquez A, Figuerola J.:

Feeding patterns of potential West Nile virus vectors in south-west Spain.

PLoS One. 2012;7(6):e39549. doi: 10.1371/journal.pone.0039549. Epub 2012 Jun 22.

4. Experimental West Nile virus infection of large falcons

West Nile virus (WNV) is a zoonotic arbovirus transmitted by various mosquito species. Firstly described in Uganda, it has spread globally over the past decades, causing epidemic outbreaks in the USA and other countries. Clinical signs vary, also in accordance with the immune status of the human host, from fever (West Nile Fever, WNF) to severe inflammations, in particular of the neurological system. Besides humans, various species can be affected. Birds in particular play an important role in the transmission of the virus. To investigate the pathogenesis of West Nile virus in birds of prey, **Ziegler et al (2013)**



Gyr falcon hybrid; photograph by David Armer

infected 12 gyr falcons/gyr falcon hybrids (*Falco rusticolus*) with WNV of two different genetic lineages (NY99 (lin. 1) and strain Austria (lin. 2)). Both lineages turned out to be highly virulent for the falcons, and all birds, with varying individual aetiopathology, succumbed to the disease.

Necropsy results for both lineages include severe inflammation of various organs/tissues (among others meningoencephalitis, myocarditis, vasculitis).

Quantitative real-time RT PCR detected WNV in blood, swabs and at necropsy in various organs. The high virus load and long duration of viraemia (> two weeks) indicate falcons to be potentially WNV amplifying hosts and therefore to play an important role in WNV dispersion. This is of particular Public Health interest because these falcons are commonly used in falconry worldwide, thus permitting an increased risk of WNV transmission from the birds to their human handlers and keepers.

Ziegler U, Angenvoort J, Fischer D, Fast C, Eiden M, Rodriguez AV, Revilla-Fernández S, Nowotny N, de la Fuente JG, Lierz M, Groschup MH.:

Pathogenesis of West Nile virus lineage 1 and 2 in experimentally infected large falcons.

Vet Microbiol. 2013 Jan 25;161(3-4):263-73. doi: 10.1016/j.vetmic.2012.07.041. Epub 2012 Aug 3.

5. Novel mosquito control concept in urban areas



Asian tiger mosquito (*Aedes [Stegomyia] albopictus*); photograph by James Gathany, CDC

The EDENext study by **Caputo et al (2012)** deals with an experimental approach for controlling populations of *Aedes [Stegomyia] albopictus*, a potential disease-transmitting mosquito species, in urban areas in Rome, Italy. A juvenile hormone analogue called pyriproxyfen is used to disturb the reproduction cycle of the mosquito. The general idea of the study is that wild adult mosquito females, if exposed to artificial resting sites contaminated with pyriproxyfen, will disseminate it into larval habitats of their

offspring, thus interfering with their adult emergence. The results have been positive, with up to 70% mortality in the mosquitoes. Further testing will be necessary for optimization of the method and its extended application.

Caputo B, Ienco A, Cianci D, Pombi M, Petrarca V, Baseggio A, Devine GJ, della Torre A.:
The "auto-dissemination" approach: a novel concept to fight *Aedes albopictus* in urban areas.
PLoS Negl Trop Dis. 2012;6(8):e1793. doi: 10.1371/journal.pntd.0001793. Epub 2012 Aug 28.



6. Topical global Dengue fever risk mapping

Dengue fever is the most common tropical viral disease transmitted by mosquitoes, with millions of human cases worldwide and is continuously spreading, making it a major global Public Health concern. The EDENext study by **Brady et al (2012)** depicts a formal modelling framework to map the global distribution of dengue risk and compares the resulting risk map with detailed longitudinal information from dengue cohort studies and population surfaces to infer the Public Health burden of dengue in 2010. Based on the results, the authors predict dengue fever to be ubiquitous throughout the tropics in the future and the global dengue burden to be more than double the estimate of the World Health Organization (WHO), underlining its importance for global Public Health.

Brady OJ, Gething PW, Bhatt S, Messina JP, Brownstein JS, Hoen AG, Moyes CL, Farlow AW, Scott TW, Hay SI.:

Refining the global spatial limits of dengue virus transmission by evidence-based consensus. *PLoS Negl Trop Dis.* 2012;6(8):e1760. doi: [10.1371/journal.pntd.0001760](https://doi.org/10.1371/journal.pntd.0001760). Epub 2012 Aug 7.



7. Reduced flight performance in genetically-modified yellow fever mosquito

The yellow fever mosquito (*Aedes aegypti*) is an important vector of yellow fever (a tropical viral haemorrhagic disease, YF), dengue fever and other diseases. Originally from Africa, the mosquito has been introduced by accident to other tropical regions worldwide and can be considered both a pest and a major health risk. Among the various methods of mosquito control, the appliance of artificially sterilised mosquitoes (Sterile Insect Technology, SIT) is one of the most commonly used options.

Bargielowski et al (2012) compare wild-type males of the yellow fever mosquito with males of two genetically modified lines that are used for SIT in regard to flight potential (dispersal ability) and energy reserves. The authors detect significant decreases in the flight capacity of the modified lines in comparison to the wild type. This has to be considered when planning and conducting release projects using such modified lines in order to improve control outcomes.

Bargielowski I, Kaufmann C, Alphey L, Reiter P, Koella J.:

Flight performance and teneral energy reserves of two genetically-modified and one wild-type strain of the yellow fever mosquito *Aedes aegypti*.

Vector Borne Zoonotic Dis. 2012 Dec;12(12):1053-8. doi: 10.1089/vbz.2012.0994. Epub 2012 Jul 26



8. Development of a novel diagnostic tool for yellow fever

Dash et al (2012) use a SYBR Green-1 based qRT-PCR assay for the better detection and quantification of yellow fever (YF). As an additional result, an isolate of YF in the mosquito *Aedes aegypti* from Cameroon revealed a marked variation in susceptibility among different colonies at different days post infection.

Dash PK, Boutonnier A, Prina E, Sharma S, Reiter P.:
Development of a SYBR green I based RT-PCR assay for yellow fever virus: application in assessment of YFV infection in *Aedes aegypti*.
Virology. 2012 Jan 22; 9:27. doi: 10.1186/1743-422X-9-27.

9. Developing malaria predictive maps in southern Benin

Based on data collected from villages in southern Benin, **Moiroux et al (2013)** developed predictive maps showing seasonal and spatial variations of the risk of human-vector contacts for local malaria vector mosquitoes (*Anopheles funestus* as well as M and S molecular forms of *Anopheles gambiae* sensu strictu). For this, binomial mixed-effects models, according to vector control measures and environmental covariates derived from field and remote sensing data, were employed. Such maps are designed to help malaria control programmes to implement more effective vector control strategies by taking into account the dynamics of malaria-transmitting mosquito species.

Moiroux N, Bio-Bangana AS, Djènontin A, Chandre F, Corbel V, Guis H.
Modelling the risk of being bitten by malaria vectors in a vector control area in southern Benin, West Africa.
Parasit Vectors. 2013 Mar 15;6(1):71.



Contributions

Contributions to this issue came from Dr. Nils Kley, Dr. Katja Schmidt and Prof. Dr. Martin H. Groschup (all Friedrich-Loeffler-Institut, Greifswald-Isle of Riems, Germany). We are grateful for critical proofreading by Prof. Dr. Norbert Nowotny (Vetmeduni Vienna). Finally, we'd like to thank Andrew Lewer (Argoat Communications) for editorial assistance.

Imprint

The Public Health Telegram on published vector-borne research results by the EDENext project partners is compiled by the EDENext Public Health group and is published at regular intervals.

For more details about the project, visit www.edenext.eu

Contact information: Prof. Dr. Martin Groschup, Friedrich-Loeffler Institute, Südufer 10, D-17493 Greifswald Isle of Riems, Germany; phone +49-383517-1163; e-mail: martin.groschup@fli.bund.de

If you do not wish to receive this newsletter, please send an email to sylvie.pugin@cirad.fr

EDENext Coordinator: Dr. Renaud Lancelot, CIRAD, TA A-15/B Campus de Baillarguet, 34398 Montpellier Cedex 5, France; phone: +33 4 67 59 37 37; e-mail: renaud.lancelot@cirad.fr

