



Leopoldina  
Nationale Akademie  
der Wissenschaften

FRIEDRICH-LOEFFLER-INSTITUT

FLI

Bundesforschungsinstitut für Tiergesundheit  
Federal Research Institute for Animal Health

# Arthropod-borne infectious diseases and arthropods as disease agents in human and animal health

October 1-3, 2015, Berlin, Germany



*Ixodes ricinus*, *Cimex lectularius*, *Ceratophyllus* sp., *Anopheles maculipennis*. Photos: Dr. H. Bellmann. From: Aspöck 2002.

We gratefully acknowledge  
financial support from



Bayer HealthCare



## Thursday, October 1, 2015

1.00 pm - 1.30 pm

### Welcome address

Jörg Hacker (Halle/Saale, Germany)

President of the German National Academy of Sciences Leopoldina

Thomas C. Mettenleiter (Insel Riems, Germany)

President of the Friedrich-Loeffler-Institut,  
Federal Research Institute for Animal Health

Richard Lucius (Berlin, Germany)

Dean of the Faculty of Life Sciences, Humboldt-Universität zu Berlin

### Session I: Taxonomy goes OMICs: Molecular versus morphological methods in taxonomic research

1.30 pm - 2.00 pm

Approaches to infer local vectorial capacity: from rapid assays to population genomics and transcriptomics, a review

6

Dina M. Fonseca (New Brunswick, NJ, USA)

2.00 pm - 2.30 pm

Can Next-Generation-Sequencing help with overcoming the taxonomic impediment in arthropod systematics?

7

Rudolf Meier (Singapore)

2.30 pm - 3.00 pm

The Making of Vectors: Lessons from the *Simuliidae*

8

Peter H. Adler (Clemson, USA)

3.00 pm - 3.30 pm

Coffee Break

3.30 pm - 4.00 pm

Tungiasis - a neglected tropical zoonosis with many facets

9

Hermann Feldmeier (Berlin, Germany)

4.00 pm - 4.30 pm

The red flour beetle *Tribolium castaneum* - a novel model for pest insects

10

Gregor Bucher (Göttingen, Germany)

4.30 pm - 5.00 pm

Towards high-throughput identification of arthropod vectors by mass spectrometry

11

Alexander Mathis (Zürich, Switzerland)

## Plenary Lecture

6.00 pm - 7.00 pm

at the Tieranatomisches Theater

[Welcome address](#)

Klaus Osterrieder (Berlin, Germany)

[Introduction](#)

Theodor Hiepe (Berlin, Germany)

[Die Vielfalt der Arthropoden - eine molekularbiologische Sicht \(in German language\)](#) **12**

Bernhard Misof (Bonn, Germany)

7.00 pm

Welcome Reception at the Tieranatomisches Theater

## Friday, October 2, 2015

### Session II: Vector control as “One health” approach? Arthropod-borne diseases in veterinary and public health

9.00 am - 9.30 am

[Modeling of arthropod-borne diseases](#) **13**

Franz Rubel (Vienna, Austria)

#### Mosquitoes

9.30 am - 10.00 am

[Mosquito monitoring in Germany](#) **14**

Helge Kampen (Insel Riems, Germany)

10.00 am - 10.30 am

[The German Mobovirus Surveillance Program, 2009 - 2015](#) **15**

Jonas Schmidt-Chanasit (Hamburg, Germany)

10.30 am - 11.00 am

[Dirofilariasis - a new emerging vector-borne zoonosis in Central Europe](#) **17**

Egbert Tannich (Hamburg, Germany)

11.00 am - 11.30 am

Coffee break

11.30 am - 12.00 pm

[Genetic structure of \*Aedes albopictus\* population and Chikungunya emergence](#) **18**

Anna-Bella Failloux (Paris, France)

12.00 pm - 12.30 pm

[The impact of biotic and abiotic factors on vectorial capacity of \*Culex\* mosquitoes for West Nile virus](#) **19**

Laura D. Kramer (Albany, NY, USA)

12.30 pm - 1.00 pm	
Evolutionary and ecological insights into the emergence of arthropod-borne viruses	20
Sandra Junglen	
1.00 pm - 2.00 pm	
Lunch Break	

### Biting midges

2.00 pm - 2.30 pm	
<i>Culicoides</i> biting midges and their relevance as vectors: a European perspective.	22
Claudio de Liberato (Rome, Italy)	

### Sandflies

2.30 pm - 3.00 pm	
Targeting phlebotomine vectors for the integrated control of leishmaniasis	23
Paul Ready (London, UK)	

### Ticks

3.00 pm - 3.30 pm	
Infections with Spotted-Fever Group <i>Rickettsiae</i> in man and animals	24
Martin Pfeffer (Leipzig, Germany)	
3.30 pm - 4.00 pm	
Tick-borne viruses	26
Gerhard Dobler (Munich, Germany)	
4.00 pm - 4.30 pm	
Coffee break	

### Prevention and Control

4.30 pm - 5.00 pm	
Novel malaria vector control based on proven historical concepts	27
Bart Knols (Wageningen, Netherlands)	
5.00 pm - 5.30 pm	
The potential use of <i>Wolbachia</i> -based mosquito biocontrol strategies for Japanese encephalitis	28
Thomas Walker (London, UK)	
5.30 pm - 6.00 pm	
Analysis of insecticide resistance in major mosquito vectors: from molecular mechanisms to management.	29
John Vontas (Crete, Athens, Greece)	

## Genetic Models for Vector-borne Diseases

- 6.00 pm - 6.30 pm  
**Insect Biotechnology used for eco-friendly pest control** 30  
Marc F. Schetelig (Giessen, Germany)
- 6.30 pm - 7.00 pm  
***Drosophila* as models for Arbovirus Infection** 31  
Stefanie Becker (Hannover, Germany)

## Saturday, October 3, 2015

### Session III: Sleeping with the Enemy: Bedbugs and other parasitic arthropods

- 9.00 am - 9.30 am  
**Vaccinomics: from systems biology of tick-pathogen interactions to vaccine development** 32  
José de la Fuente (Ciudad Real, Spain)
- 9.30 am - 10.00 am  
**Bed Bugs: the Clinical Implications** 34  
Stephen Doggett (Westmead, Australia)
- 10.00 am - 10.30 am  
**Small hive beetle in Italy** 36  
Franco Mutinelli (Legnaro/Padua, Italy)
- 10.30 am - 11.00 am  
Coffee break
- 11.00 am - 11.30 am  
***Varroa destructor*: from an invasive parasite to a permanent threat** 37  
Peter Rosenkranz (Stuttgart, Germany)
- 11.30 am - 12.00 pm  
***Dermanyssus gallinae*: a never-ending story for the poultry industry and public health** 38  
Annunziata Giangaspero (Foggia, Italy)
- 12.00 pm - 12.30 pm  
**Medical Entomology in the 21st Century: Retrospect and Challenges** 39  
Horst Aspöck (Vienna, Austria)
- 12.30 pm - 1.00 pm  
Coffee Break

### Session IV: Gaps and needs in research, prevention and control

- 1.00 pm - 2.00 pm  
Round table discussion and summary



Dina M. Fonseca

## **Approaches to infer local vectorial capacity: from rapid assays to population genomics and transcriptomics, a review**

Department of Entomology, Ecology & Evolution and Public Health, Rutgers, the State University of New Jersey, New Brunswick, NJ, USA

Variability in vectorial capacity among mosquitoes and other disease vectors is perversely the only clear constant. “Anophelism without malaria”, the observation that malaria transmission varied widely among areas all seemingly inhabited by the same *Anopheles* species, led to the identification of cryptic species. This notion was later expanded to the recognition of cryptic populations. When vector populations with differing vectorial capacity have recognizable genetic signatures rapid assays can be used in the assessment of risk. But hybridization among species or mixing between populations can make rapid-assays insufficient and require more thorough multilocus genotyping. Further, recent studies have shown that prior experiences such as larval crowding, type of food, or the microbiome can also affect vectorial capacity. Surprisingly, considering the fast pace of technology development “Know the vector, know the threat” now seems harder to achieve. I will summarize the relevant literature hoping to stimulate a discussion on current practices, aims, limitations and future directions.

Contact:            [dinafons@rci.rutgers.edu](mailto:dinafons@rci.rutgers.edu)

## **Can Next-Generation-Sequencing help with overcoming the taxonomic impediment in arthropod systematics?**

<sup>1</sup> Lee Kong Chian Natural History Museum and Department of Biological Sciences, National University of Singapore, Singapore

<sup>2</sup> Department of Biological Sciences, National University of Singapore, Singapore

Identifying arthropods to species is important because many closely related species have distinctly different biologies. However, accomplishing this task is difficult because many species are undescribed and/or not included in identification keys that are designed for biologists without specialist training. This has led to a taxonomic impediment that affects all fields of arthropod biology including the study of arthropod vectors. A potential solution is species identification via DNA barcodes which tend to be distinct for ca. 80-90% of all multicellular animal species. Unfortunately, DNA barcodes are very expensive when generated via Sanger sequencing. Here, I will discuss new barcoding techniques based on Next-Generation-Sequencing (“NGS barcodes”) which can reduce the cost of DNA barcoding by more than 90%. Thousands of specimens can be sequenced and detailed information on abundances and distributions can be obtained from either eggs, larvae, pupae, adults or a combination of all life history stages. I will discuss the advantages and disadvantages of the different molecular approaches and illustrate how sequencing environmental DNA (“eDNA”) allows for the detection of taxa based on DNA traces instead of specimens.

Contact:            meier@nus.edu.sg

Peter H. Adler

## **The Making of Vectors: Lessons from the Simuliidae**

Department of Agricultural & Environmental Sciences, Clemson University, Clemson, SC, USA

The Simuliidae are among the world's principal vectors of arthropod-borne diseases. About 98% of the 2177 formally described species of black flies feed on vertebrate blood. More than 30 nominal species of parasites are transmitted by black flies. Genetic studies, however, reveal additional diversity in the parasites and hosts, with the majority of simuliids yet to be screened. Two fundamental requirements for the development of vectors are anautogeny and repeated gonotrophic cycles. A key innovation that enhanced vector efficiency was multivoltinism, which increased the probability of infection and accompanied simuliid movement from the ancestral mountainous habitats into warmer lowlands, extending the geographic reach of the vectors. Of importance in the evolution of vectors was the acquisition of their ability to colonize large rivers capable of producing enormous populations. Further fine-tuning of vector efficiency resulted from selection by the simuliid host's behavioral, physiological, and structural defenses. The wealth of biodiversity that continues to be discovered in simuliid vectors and their parasites highlights the need to understand the historical factors that have promoted this diversification, such as global climate change. Once the key factors responsible for vector competency are identified, the search can begin for the genes responsible for the facilitating traits, potentially enabling proactive vector control to be achieved.

Contact:           padler@clemson.edu

Hermann Feldmeier

## **Tungiasis - a neglected tropical zoonosis with many facets**

Institute of Microbiology and Hygiene, Charité University Medicine, Berlin, Germany

Tungiasis (sand flea disease) is a neglected tropical disease that originated in South America and was introduced into sub-Saharan Africa in the 19th century. It is caused by the penetration of female sand fleas (*Tunga penetrans*) into the skin. Sand flea disease is a zoonosis with a broad spectrum of animal hosts. In a tropical environment, three life cycles coexist: the human cycle, the domestic animal cycle and the sylvatic cycle. In dogs, cats, pigs, ruminants and rodents the infection results in severe disease. In humans, tungiasis predominantly affects marginalized and resource-poor populations. Disease occurrence and the degree of morbidity are associated with poverty. Prevalence may be up to 40% in the general population and up to 70% in children. The inflammatory response around burrowed viable, dead or decaying sand fleas is the basis for the clinico-pathological manifestations. Bacterial superinfection is common and intensifies the inflammation. Treatment options are limited. Control of tungiasis can only be achieved by a transdisciplinary approach using the 'One Health' concept.

Contact:            hermann.feldmeier@charite.de

Gregor Bucher

## The red flour beetle *Tribolium castaneum* - a novel model for pest insects

Dpt. of Evolutionary Developmental Genetics, Johann-Friedrich-Blumenbach Institute of Zoology and Anthropology, Georg-August-University Göttingen, Göttingen, Germany

Research in pest insects is notoriously challenging due to difficulties in stock keeping and limited experimental possibilities. Therefore, research profits from model systems that are more easy to handle in the lab and that have an extensive tool kit. This allows pioneering research, the results of which can subsequently be transferred to the pest species. I want to present the red flour beetle *Tribolium castaneum* as an emerging model system representing Coleoptera, which comprise many important pests.

Experimental tools include a well annotated genome, efficient gene knock-down by systemic RNAi and transgenic methods like gene-misexpression lines or in vivo imaging lines. CRISPR/Cas9 has been established recently. Finally, we have set up *T. castaneum* for large scale screening (“iBeetle screen”), which allows for the first time to systematically screen for novel genes involved in a process outside the well-established *Drosophila* system. I will show the results of the iBeetle screen, including examples for the identification novel genes involved in basic cell biological processes like cell adhesion. Further, I will show how the iBeetle screen and the *Tribolium* model were used for detection and characterization of novel target genes for pest control. Finally, I will discuss the possibility to use *T. castaneum* as screening platform for other questions.

Contact: [gregor.bucher@bio.uni-goettingen.de](mailto:gregor.bucher@bio.uni-goettingen.de)

Alexander Mathis

## **Towards high-throughput identification of arthropod vectors by mass spectrometry**

Swiss National Centre for Vector Entomology, Institute of Parasitology, University of Zürich, Zürich, Switzerland

Accurate and high-throughput identification of vector arthropods is of paramount importance in surveillance and control programmes which are becoming more common due to changes in the geographic range and extent of many arthropod-borne diseases, also in Europe. Protein profiling by matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) technically fulfils these requirements for identification, and reference databases have recently been established for some vector taxa by various research groups. However, their approaches greatly vary in terms of sample processing, equipment used, data acquisition and analysis. Furthermore, these databases have typically been generated on a project by project base, are stored on local drives ('in-house databases') and thus are not accessible to the public. In a consortium comprising academic institutions and a private company, we have established the largest database with regard to vector arthropods, and we for the first time showed that spectra obtained on mass spectrometers from different companies can be analysed using this database. Thus, a centralized high-quality database (created by expert taxonomists and experienced users of mass spectrometers), which is easily amenable to customer-oriented identification services, is feasible and should be available in the near future via online platform in a cost-efficient manner.

Contact:           alexander.mathis@uzh.ch

Bernhard Misof

## **Die Vielfalt der Arthropoden - Eine molekularbiologische Sicht**

Zoologisches Forschungsmuseum Alexander Koenig, Center of Molecular Biodiversity Research, Bonn, Germany

Arthropoden stellen, gegeben ihr geologisches Alter, die bei weitem arten- und formenreichste Gruppe vielzelliger Organismen dar. Sehr wahrscheinlich eroberten Arthropoden vielfach terrestrische Lebensräume und sind für die Entwicklung terrestrischer Ökosysteme im Wechselspiel mit Pflanzen bis heute verantwortlich. Innerhalb der Arthropoden kommt den Insekten, als eine ursprünglich ausschließlich terrestrische Gruppe, eine besondere Rolle zu. Ihr Artenreichtum, ihre ökologische Vielfalt sucht seinesgleichen. Bis heute wissen wir keine fundierte Hypothese zur Evolutionsgeschichte der Insekten.

In meinem Vortrag werde ich nun zeigen, in welcher Form umfangreiche genomische und transkriptomische Daten uns helfen, etwas zur Evolutionsgeschichte der Insekten abzuleiten. Zusätzlich werde ich an Hand von Beispielen zeigen, dass mit diesen umfangreichen molekularen Daten es nun möglich wird, wesentlich präzisere Aussagen zur Evolution einzelner Gene, Merkmalskomplexe, bzw. Eigenschaften der Tiere zu sagen.

Abschließend werde ich kurz auf das Potential der Genom/Transkriptomsequenzierung bezüglich der Identifikation von bakteriellen bzw. viralen Parasiten der Insekten eingehen.

Contact:           bmisof@uni-bonn.de

## Modeling of arthropod-borne diseases

Climate Change & Infectious Diseases Group, Institute for Veterinary Public Health, University of Veterinary Medicine Vienna, Vienna, Austria

Generally, the transmission cycles of arthropod-borne diseases depend on climate. After introducing the basic ideas and similarities behind climate and epidemic process models, results from recent outbreaks of mosquito-borne diseases are shown. These comprise mass mortality of blackbirds due to Usutu virus (USUV) as well as West Nile virus (WNV) outbreaks. Both models simulate the seasonal cycle by explicitly considering the environmental temperature to determine model parameters responsible for the mosquito population dynamics and the extrinsic incubation period. Once initialized, the models run for the entire period 2001-2005 (USUV) and 2002-2009 (WNV), exclusively forced by environmental temperature. Simulated incidences were determined by host and vector population dynamics, virus transmission and herd immunity. The USUV model (Rubel et al., 2008; Brugger and Rubel, 2009) is used to demonstrate the projection of incidences to future climate scenarios as, for example, depicted by world maps of Köppen-Geiger climate classifications (Rubel and Kottek, 2010). From epidemic models, the basic reproduction number  $R_0$  can be derived. It is a measure for the number of secondary cases caused by one primary case in a fully susceptible population and frequently used to evaluate control measures. It is applied to Bluetongue disease transmitted by *Culicoides spp.* (Brugger and Rubel, 2013). Finally, some examples of statistical models were given. These comprise presence/absence modelling of *Dermacentor spp.*, the vectors of tick-borne diseases such as tularemia and Q-fever. Air temperature, air humidity and CORINE land classification were used to model the spatial distribution of these disease vectors.

Contact: Franz.Rubel@vetmeduni.ac.at

## Mosquito monitoring in Germany

<sup>1</sup> Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Greifswald  
- Insel Riems, Germany

<sup>2</sup> Leibniz-Centre for Agricultural Landscape Research, Muencheberg, Germany

Due to a dramatic decline in mosquito research after the eradication of malaria from Europe in the middle of the last century, up-to-date data on the indigenous fauna are scarce for Germany. However, mosquito monitoring programmes have recently been initiated, following increasing frequencies of outbreaks and autochthonous cases of mosquito-borne diseases, such as chikungunya, dengue, West Nile fever and malaria, in several European countries. Nation-wide mosquito collections, focussing on both the occurrence and geospatial distribution of mosquito species and the screening of mosquitoes for circulating pathogens, started in Germany in 2011, using active and passive approaches.

In total, 41 of the 48 culicid species previously described for Germany, have been found so far, among them several species not reported for decades. In addition, three new, invasive species were detected including the potential vectors *Aedes japonicus* (Asian bush mosquito) and *Ae. albopictus* (Asian tiger mosquito). While the first has become established in Germany with three separate populations, the latter is regularly introduced by vehicle transport from endemic regions in southern Europe. With some species/species complexes identification problems exist since they are not only highly similar morphologically but also genetically in their CO1 DNA barcoding region. In general, however, reliable data are accumulating, thus facilitating species distribution maps and future risk analyses for mosquito-borne diseases.

Contact: Helge.Kampen@fli.bund.de

## The German Mobovirus Surveillance Program, 2009 - 2015

Department of Arbovirology, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

**Introduction:** Human and animal diseases caused by mosquito-borne viruses (moboviruses) are of growing importance in many countries of Europe including Germany. Continuing eco-climatic changes and globalization create suitable conditions for the emergence of moboviruses in Germany. Up to now, four different moboviruses have been found in Germany. In 1968, Tahyna virus (TAHV) was isolated from mosquitoes that were trapped around Baunach in Bavaria. TAHV is the causative agent of Valtice fever, an influenza-like illness occurring in summer and early autumn. Therefore, TAHV is the first human pathogenic mobovirus that was isolated from mosquitoes in Germany. Since these early discoveries in the late 60s of the last century, mobovirus surveillance in mosquitoes, humans and animals was not performed regularly and therefore, longitudinal data sets are missing, especially from Germany. Thus, we initiated a program that compiles and analyses mobovirus and vector data collected over a number of successive years. This provided a solid base to determine the underlying causes of the seasonal fluctuations in mobovirus activity and the relative abundance of the mosquito vector species. This information can be used as a basis for vector control programs and might provide an early warning of the presence of moboviruses in Germany.

**Results:** Since 2009, mobovirus surveillance was performed mostly in south-west Germany. So far, more than 350.000 mosquitoes were captured and assayed for the presence of moboviruses. In 2009, Sindbis virus (SINV) was isolated from *Culex* and *Anopheles* mosquitoes that were exclusively trapped in the city of Weinheim, south-west Germany. SINV is the causative agent of a febrile illness in humans associated with maculopapular rash and joint pain. Consequently, a study was initiated to investigate the medical importance of SINV in that area. Only four out of 3389 investigated blood donor samples were tested positive for SINV-specific-IgG antibodies and all samples from 355 patients with clinically suspected acute SINV infections were tested negative for SINV-specific antibodies or SINV RNA, thus demonstrating the low medical importance of SINV in south-west Germany. In 2009, Batai virus (BATV) was isolated from *Anopheles maculipennis* mosquitoes trapped around the village of Waghäusel. BATV may cause a mild

illness among sheep and cattle. Thus, more than 500 serum samples from cattle's around the village of Waghäusel were investigated for BATV-specific-IgG antibodies and 3 samples were tested positive, demonstrating past BATV infections. In 2010, Usutu virus (USUV) was isolated from *Culex pipiens pipiens* mosquitoes trapped in the city of Weinheim. Since June 2011, considerable mortality in wild and captive bird species was observed in south-west Germany. Consequently, 168 dead birds were tested for the presence of USUV and USUV RNA was detected in 80 individuals from 6 species. Therefore, the mortality of birds was shown to be associated with the emergence of USUV. In addition, in January 2012, 4,200 serum samples from healthy blood donors from south-west Germany were collected and analysed for USUV-specific antibodies. One IgG- and IgM-positive blood donor was confirmed to have been infected by USUV. The blood donor reported no history of vaccination and did not have a fever during a period of three months before the blood donation. In addition, he had not been abroad during this period. These findings, taken together with the serological results corroborate the hypothesis of a pauci- or asymptomatic and autochthonous USUV infection of the blood donor during late summer 2011.

**Conclusion:** The early discovery of USUV in mosquitoes followed by the recent epidemic proof the importance and predictive value of our mosquito based monitoring program for zoonotic moboviruses. Moreover, public health authorities, blood transfusion services and clinicians in Germany should be aware of the risk of USUV infection in humans, especially during late summer.

Contact:           jonassi@gmx.de

Egbert Tannich

## **Dirofilariasis - a new emerging vector-borne zoonosis in Central Europe**

Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany

Dirofilariasis due to infections with the filarial nematode *Dirofilaria repens* is considered a new emerging zoonosis in Central Europe. The main reservoirs for the parasite are dogs and other carnivores. As with other filarial species, mosquitoes transmit infectious stage 3 larvae (L3), which develop into fertile macrofilariae in their definitive vertebrate hosts. Humans may become infected as aberrant hosts and in most cases the worms remain infertile. Infections in humans usually manifest as subcutaneous nodules, which are caused by macrofilariae that are trapped by immune mechanisms. Subcutaneous migration of the worm may result in local swellings with changing localization. In addition, severe organ manifestations have been reported, which may affect various organs including the brain, the lung, or the eye. The latter is found in particular during the migratory phase of the parasite. Transmission of *D. repens* is found in various regions of the “Old World” including Africa, Asia and Europe. Main endemic areas in Europe are countries of the Mediterranean region, where appropriate warm temperatures allow development of infectious L3 larvae in the mosquito. However, during the last decade the disease has spread to countries further north as autochthonous cases of canine and human dirofilariasis have been reported from Austria, the Czech Republic, Poland or Germany and vector-screening projects revealed *D. repens*-positive mosquitoes in various Central European countries up to the Baltic Sea.

Contact:            tannich@bni-hamburg.de

Marie Vazeille and Anna-Bella Failloux

## **Genetic structure of *Aedes albopictus* population and Chikungunya emergence**

Department of Virology, Institut Pasteur, Arboviruses and Insect Vectors, Paris, France

Emergence of the *Aedes albopictus*-adaptive mutation E1-226V of chikungunya virus (CHIKV) was reported for the first time in Congo in 2011, shortly after the introduction in 2006 of the mosquito *Ae. albopictus*. To determine whether the selection of this mutation follows a scenario similar to the CHIKV emergence in the Indian Ocean in 2005, we performed experimental selection by passaging the CHIKV East-Central-South African genotype isolated in 2000 in DRC (Democratic Republic of Congo) between local mosquito populations and human cells mimicking host alternation. We found that after 10 passages, *Ae. albopictus* from Congo did not better transmit the CHIKV E1-226V as observed for *Ae. albopictus* from the Indian Ocean. We demonstrated using genotyping with 11 microsatellites that *Ae. albopictus* Congo were highly differentiated from *Ae. albopictus* La Réunion. These results indicate that CHIKV emergence in Central Africa probably does not follow the Indian Ocean scenario underlining the key role of mosquito genetics in CHIKV emergence.

Contact:           anna-bella.failloux@pasteur.fr

Laura D Kramer

## **The impact of biotic and abiotic factors on vectorial capacity of Culex mosquitoes for West Nile virus**

Wadsworth Center, New York State Department of Health, and School of Public Health, State University of New York at Albany, Slingerlands, NY, USA

West Nile virus (WNV; Flavivirus; Flaviviridae) is the cause of the most widespread arthropod-borne viral disease in the world and the largest outbreak of neuroinvasive disease ever observed. Mosquito-borne outbreaks are influenced by intrinsic (e.g., vector and viral genetics, vector and host competence, vector life-history traits) and extrinsic (e.g., temperature, rainfall, human land use) factors that affect virus activity and mosquito biology in complex ways. The concept of vectorial capacity integrates these factors to address interactions of the virus with the arthropod host, leading to a clearer understanding of their complex interrelationships, how they affect transmission of vector-borne disease, and how they impact human health. Vertebrate factors including host competence, population dynamics, and immune status also affect transmission dynamics. The complexity of these interactions are further exacerbated by the fact that not only can divergent hosts differentially alter the virus, but the virus also can affect both vertebrate and invertebrate hosts in ways that significantly alter patterns of virus transmission. This presentation will focus on selected components of the virus-vector-vertebrate interrelationship, specifically on how interactions between vector, virus, and environment shape the patterns and intensity of WNV transmission.

Contact:            [laura.kramer@health.ny.gov](mailto:laura.kramer@health.ny.gov)

## Evolutionary and ecological insights into the emergence of arthropod-borne viruses

Institute of Virology, University of Bonn Medical Center, Bonn, Germany

The prevalence of vector-borne diseases is increasing worldwide. A large part of these diseases are arthropod-borne viral diseases (arboviroses) that undergo cyclic transmission between arthropod and vertebrate hosts. In order to understand the emergence of arboviroses, we need more insight into the biodiversity and ecology of viruses that are carried by arthropods but do not, or not yet, undergo arboviral dual-host transmission.

In studying the biodiversity of mainly insect-associated viruses, we have detected an extremely wide spectrum of previously unknown RNA viruses. These viruses establish novel genera within known virus families, or even novel virus families such as the first insect-associated nidovirus Cavally virus, the type species of the family *Mesoniviridae* (order *Nidovirales*; 1,2). Within the family *Bunyaviridae*, which is considered the most diversified family of RNA viruses, we identified four proposed novel viral genera that all seem to be restricted to insects and are in sister relationship to major pathogenic arboviral genera (3-5). Because we have been able to isolate several novel insect-associated viruses in cell culture, we obtained further insight into phenotypic properties such as host cell tropism. Combining phenotypic and phylogenetic studies of live insect-specific bunyaviruses, we found evidence for the hypothesis that arboviruses within the family *Bunyaviridae* have evolved from arthropod-specific progenitors (5). It becomes increasingly clear that insects carry a huge biodiversity of RNA viruses that may exceed and antedate the diversity of pathogenic vertebrate viruses (6).

Arbovirus evasion from primary habitat may be driven by ecological change. Analyses of virus diversity and infection rates studied along disturbance gradients in Ivory Coast and Mexico showed a decrease in genetic diversity of viruses from natural to modified habitat types. Interestingly, infection rates of mosquitoes with specific viruses from several different families increased along disturbance gradients. Knowledge on the interplay between vector

diversity and virus infection rates could provide innovative approaches for epidemic risk assessment and intervention strategies.

Contact: [junglen@virology-bonn.de](mailto:junglen@virology-bonn.de)

References: 1. Zirkel et al mBIO 2011; 2. Zirkel et al J Virol 2013; 3. Marklewitz et al J Virol 2011; 4. Marklewitz et al J Virol 2013; 5. Marklewitz et al PNAS 2015; 6. Junglen et al Curr Op Microbiol 2014

Claudio De Liberato

## ***Culicoides* biting midges and their relevance as vectors: an European perspective.**

Istituto Zooprofilattico Sperimentale del Lazio e della Toscana “M. Aleandri”, Rome, Italy

*Culicoides* spp. (Diptera: Ceratopogonidae) are worldwide distributed vectors of many viruses, some of which of paramount veterinary relevance (e.g. bluetongue and African horse sickness). In EU countries, their economic impact became devastating with the bluetongue epidemics started first in Italy in 2000 and then in central Europe in 2006, epidemics whose effects are still ongoing and that involved most part of Europe, extending up to southern UK. At present, 9 (more?) BT serotypes have been recorded in Europe. In 2011, a new *Culicoides* transmitted virus, Schmallenberg virus, causing an other economically relevant disease of ruminants, first appeared in Germany and the Netherlands, quickly spreading to UK, France, Italy, Luxembourg, Spain, Denmark and Switzerland.

In this scenario, *Culicoides* study in Europe deserved more and more interest in the last two decades, focusing on all the aspects of their taxonomy, biology, ecology, distribution and possible control strategies. Until Italian epidemic, *C. imicola* was considered the only old world BT vector, nowadays it is well known that the responsible of BT circulation in Europe are mainly species belonging to the *C. obsoletus* complex, and many studies aimed at clarifying this complex taxonomy and the different role of its species as vectors have been carried out. The same species group was demonstrated to be the vector of Schmallenberg virus too. Many models trying to predict the geographical distribution of the more relevant species in order to assess BT spread risk have been produced.

Notwithstanding this remarkable study effort, involving researchers all over the EU, many questions about *Culicoides* spp. biology, ecology and role as vectors have still to be addressed.

Contact:            claudio.deliberato@izslt.it

Paul D Ready

## Targeting phlebotomine vectors for the integrated control of leishmaniasis

Department of Disease Control, Faculty of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom

Blood feeding females of phlebotomine sand flies (Phlebotominae) are the only proven natural vectors of *Leishmania* species (Trypanosomatidae), the parasitic protozoans that are the causative agents of the neglected tropical disease leishmaniasis (Ready PD. 2013. Annu Rev Entomol 58:227-250). This presentation considers the best ways of managing sand fly populations as part of the integrated control of leishmaniasis. Examples will be given for transmission cycles in Africa, Asia and South America, and related to what has been achieved in the Mediterranean region of Europe. In southern Europe, the domestic dog is usually considered to be the main reservoir host of zoonotic visceral leishmaniasis (ZVL), which causes mortality and morbidity in human populations (Alvar J et al. 2012. PLoS One 7e:35671). The domestic cat is frequently infected, although it may not be a reservoir host. Therefore, ZVL is both a veterinary and a medical problem in Europe, although the veterinary challenge is currently the greater. Clearly then, the management of these vectors and the integrated control of ZVL would benefit from a one health approach. Most transmission is believed to be by the bites of female sand flies of *Phlebotomus* (*Larroussius*) species, which remain abundant and widespread in rural Mediterranean areas. Integrated control will benefit from transmission modelling, for which informative entomological indices are required (Bates PA et al. 2015. Parasit Vectors 8: 131).

Contact: Paul.Ready@lshtm.ac.uk

## Infections with Spotted-Fever Group *Rickettsiae* in man and animals

Institute of Animal Hygiene and Veterinary Public Health, Center of Veterinary Public Health, University of Leipzig, Leipzig, Germany

Spotted Fever Group (SFG) *Rickettsiae* can cause febrile diseases with or without rash in humans worldwide and they are globally considered emerging disease pathogens. Emergence is thereby based on the continuing discovery of new *Rickettsia* species, the new geographic occurrence of known *Rickettsia* species as well as the medical importance of *Rickettsia* species previously thought to be not pathogenic for man. Still, this group of pathogens is neglected and knowledge of their distribution, vector- and host-association, abundance and transmission patterns is scarce. For most of the *Rickettsia* spp. we have a rough idea on their geographical distribution based on their primary vector appearance, mostly a particular tick species. *Rickettsia felis* is the only known SFG *Rickettsia* where the cat flea (*Ctenocephalides felis*) was long thought to be the sole arthropod vector transmitting this pathogen, but frequent findings in *Ixodes ricinus* ticks as well as recent studies demonstrating *Anopheles* mosquitoes to function as biological vector show that we have a great deal to learn about the epidemiology of this group of bacteria. Using serology to detect antibodies against rickettsiae is only of limited help to further elucidate transmission patterns, as serological tests usually only distinguish between SFG and Typhus Group (TG) *Rickettsiae* because of strong cross-reactivities within the groups. Nevertheless, pet animals may be of use as surrogates for the human exposure to the *Rickettsia* species. Attempts for a differentiation of the antibody reaction together with seroprevalence rates in such animals could serve as possible sentinels and indicator for the distribution of different *Rickettsia* species.

Contact:           pfeffer@vetmed.uni-leipzig.de

## Tick-borne viruses

Bundeswehr Institute of Microbiology, partner of DZIF Munich, Munich, Germany

There are more than 900 species of ticks world-wide and ticks as vectors of pathogens exhibit the broadest spectrum of transmitted pathogens, ranging from metazoan and protozoa, to bacteria, rickettsia, viruses and shedding of toxins. Regarding the viruses there are at least six virus families which have more than 160 viruses which are transmitted by ticks and the detection of new emerging viruses in ticks using modern detection methods has just started.

Among the tick-borne viruses the tick-borne sero-group in the genus *Flavivirus* of the family Flaviviridae shows the most medical and veterinary importance. Within this group there are 16 registered viruses, among them viruses causing encephalitis and hemorrhagic fever forms. From a medical point the most important virus is the Tick-borne encephalitis virus (TBEV). TBEV is occurring on the Eurasian continent and is restricted to the deciduous and coniferous tree zones. This restriction seems mainly due to the occurrence of the main vectors, *Ixodes ricinus* and *Ixodes persulcatus*, and of the presumed major vertebrate vectors, rodents of the genera *Apodemus* and *Myodes*. But also the transmission via contaminated milk from infected animals (goat, sheep, cattle) has been seen since decades in parts of Europe. There are an estimated 3.000 to 10.000 human cases per year in Europe and Asia and therefore it is the tick-transmitted viral disease with the highest number of human cases world-wide. The TBEV can be divided into at least three subtypes, the European subtype, the Siberian subtype and the Far Eastern subtype. The TBEV and the closely related Louping ill virus stand at the end of an evolution, which according to recent genetic analyses (Heinze et al. 2014) took its origin in Africa and evolved over more than 30.000 years through Asia until reaching the current distribution of the viruses of the Tick-borne sero-group. The possible ways of dispersal are unclear but there is increasing evidence that birds may play an important role in the spread of TBEV. The recent genetic analysis of more than 250 E genes of the European TBEV subtype supports the hypothesis that TBEV is spread on long and on short distances by birds. Furthermore the genetic analysis of the European TBEV strains imply that TBEV has been and still is

introduced continuously into Central Europe during the last few hundred years and that it spreads from each introduction to new sites. Also in Austria during the last 40 years of observation there seems to be a drift of the area of distribution of TBEV from east to west (Heinz et al., 2015). The reasons for this drift are unknown and also the mechanisms of movement are only poorly understood. However, it seems, that this spreading is not mainly driven by climatic changes.

Among the other tick-borne viruses some emerging viruses of veterinary and medical importance, like Crimean-Congo Hemorrhagic Fever virus (CCHFV) are found. Ticks of the genus *Hyalomma* mainly transmit this virus. There is also a tendency of recent emergence in some areas in the world, like in Turkey or in India. The virus may cause a fatal disease and can also be transmitted from humans to humans, e.g. in nosocomial settings.

In the last few years some novel tick-borne viruses have been detected causing severe human disease, like the Huayjangshan virus (severe fever with thrombocytopenia syndrome) in Eastern Asia, the Heartwater virus in Middle Western USA, and very recently Bourbon virus also in the Middle Western region of the USA. Only starting recently to use modern detection techniques some new virus nucleic acids of unknown viruses and virus genera can be found. However the medical and veterinary importance of these putative virus candidates warrants further studies.

Contact:            gerharddobler@bundeswehr.org

Bart GJ Knols

## **Novel malaria vector control based on proven historical concepts**

In2Care BV, Wageningen, The Netherlands

The tools currently in use to prevent transmission of malaria by anopheline mosquitoes remain limited and are mostly based on old concepts. In Africa, these tools are mostly based on the use of biocides either indoors on walls or on bednets. Both resistance to insecticides and adaptive behaviours to avoid contact with biocides (outdoor or early feeding) are rendering these tools less efficient.

We present an entirely novel way of exposing mosquitoes to insecticidal agents, based on powder formulations that adhere to netting laced with an electrostatic coating. This method results in much higher transfer of insecticidal particles to mosquitoes than materials impregnated with insecticides. This improvement even results in highly pyrethroid-resistant strains of *An. gambiae* s.s succumbing to exposure with pyrethroids at concentrations >90% lower than used on bednets.

Subsequently, and based on proven concepts, we developed a novel delivery system in which we can use this netting, the so-called eave tube. Combined with window screening, this offers both house improvement and a killing effect. We have so far installed eave tubes in more than 1800 houses in southern Tanzania and our experiences to date will be shared. The research leading to these results has received funding from the European Community's Seventh Framework Programme under grant agreement #306105.

Contact:            bart@in2care.org

## The potential use of *Wolbachia*-based mosquito biocontrol strategies for Japanese encephalitis

Department of Disease Control, Faculty of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, UK

Japanese encephalitis (JE) is a zoonotic arboviral disease, predominantly transmitted by *Culex tritaeniorhynchus* mosquitoes in Asia. Japanese encephalitis virus (JEV) exists in an enzootic transmission cycle with mosquitoes transmitting JEV between birds as reservoir hosts and pigs as amplifying hosts. Irrigated rice fields provide an ideal breeding ground for mosquitoes and attract migratory birds, maintaining the transmission of JEV. Although vaccines have been developed, they are expensive and require multiple doses to maintain efficacy and immunity. As humans are a 'dead-end' host, vaccines are unlikely to result in eradication. Current vector control includes intermittent irrigation of rice fields and space spraying of insecticides during outbreaks. However, *Cx. tritaeniorhynchus* is subject to heavy pesticide exposure in rice fields so insecticide resistance has developed. Significant advancements have recently been made using the bacterial endosymbiont *Wolbachia* for mosquito biocontrol. Transinfection of novel *Wolbachia* strains into *Aedes* mosquitoes has resulted in dengue virus (DENV) refractory mosquito lines. *Wolbachia* strains have now been established in wild *Aedes aegypti* populations through open releases. JEV and DENV are both Flaviviruses and the successful establishment of *Wolbachia* strains in *Cx. tritaeniorhynchus* is predicted to significantly impact JEV transmission. We established colonies of both Greek and Indian *Cx. tritaeniorhynchus* populations and have shown the Greek population is a highly efficient vector of JEV. Embryo and adult microinjection experiments are also ongoing to establish stable *Drosophila Wolbachia* infections in *Cx. tritaeniorhynchus*.

Contact: Thomas.Walker@lshtm.ac.uk

## **Analysis of insecticide resistance in major mosquito vectors: from molecular mechanisms to management**

<sup>1</sup> Institute Molecular Biology and Biotechnology, Foundation for Research and Technology (IMBB-FORTH), Herakleion, Crete, Greece

<sup>2</sup> Pesticide Science, Agricultural University of Athens, Athens, Greece

<sup>3</sup> Department of Biology, University of Crete, Heraklion, Greece

<sup>4</sup> Vector Biology, Liverpool School of Tropical Medicine, Liverpool, UK

The intense use of insecticides have resulted in a selection of insecticide resistance in major mosquito vectors, to such an extent that their control becomes challenging in several cases. We investigate the incidence and the mechanisms of insecticide resistance, by using a variety of approaches, including transcriptomics, functional proteomics, immunohistochemical approaches, and *in vivo* ectopic expression in drosophila, aiming to understand the physiological basis of insecticide resistance, and elucidate the role and contribution of individual genes and mutations in the phenotype.

Subsequently, we develop molecular diagnostics, to monitor the spread and distribution of resistance alleles in field populations and support decisions for resistance management strategies, as well as tools for screening novel active ingredients and resistance breaking compounds.

Examples from our most recent studies include, the analysis of pyrethroid resistance mechanisms in the major malaria vector *Anopheles gambiae* and the characterization of temephos resistance in *Aedes albopictus*.

Contact:           vontas@imbb.forth.gr

Marc F. Schetelig

## **Insect Biotechnology used for eco-friendly pest control**

Justus-Liebig-University Giessen, Giessen, Germany

Environmentally friendly pest control is a requirement for sustainable agriculture in the world. Integrated pest management (IPM) programs within area-wide control strategies have demonstrated the best cost-benefit ratio in terms of economics and sustainability. One important component of IPM programs has been the Sterile Insect Technique (SIT) that is a biologically based strategy relying on over-flooding of field populations with sterile males for successive generations, thus rendering females in the field non-reproductive and suppressing the targeted pest species. The most important prerequisite for successful SIT programs is the availability of male-only populations for release. These can be created by conventional breeding, classical genetics, or transgenic technology. Nevertheless, so called sexing strains have only been available for a limited amount of agricultural relevant species.

For the Mediterranean fruit fly, a mutant-based sexing system has been developed throughout the last 25 years. This system has been optimized and refined for many years and the Vienna-7 and Vienna-8 strains are now used in large-scale SIT programs around the world. Sexing systems recently developed by the use of “insect biotechnology”, from the overexpression of toxic tTA molecules killing larval and pupal stages to embryo-specific female lethality systems, will be compared. These include systems for the Mediterranean fruit fly, the Caribbean fruit fly and the Mexican fruit fly. State-of-the-art systems will be compared with their risks and benefits evaluated in respect to their sustainability and new genome engineering possibilities.

Contact:            Marc.Schetelig@agrar.uni-giessen.de

Stefanie Becker

## **Drosophila as model for Arbovirus infection**

Institute for Parasitology, University of Veterinary Medicine Hannover, Hannover, Germany

Many pandemics caused by RNA viruses have been attributed to the ability of these agents for zoonanthroponotic transmission. Athrophod-borne viruses (arboviruses), which are transmitted by insects to mammals and vice versa are the causative agents of metazooses. They include a wide variety of RNA virus taxa, but the three major families are Flaviviridae, Togaviridae (genus Alphavirus) and Bunyaviridae. Arboviruses can efficiently replicate in evolutionary distinct hosts, such as mosquitoes and humans; yet they seem to depend on the insect vectors for transmission. Competent vectors must not only allow virus infection and dissemination, but must also control the adverse effects of virus replication. Because of the variety of mosquito vectors and the paucity of genetic tool for those, studies of virus-vector interactions are sometimes difficult. The fruit fly *Drosophila melanogaster* can be a useful tool to overcome some problems since it is the best characterized insect concerning its genome and genetic manipulation possibilities. From studies in *Drosophila*, it is known that the insect immune response to viruses mainly relies on the RNAi mechanism and that this mechanism is involved in the control of all viruses tested so far (Flaviviridae, Togaviridae and Bunyaviridae). In addition to RNAi the Toll, Imd and Jak-STAT pathways as well as the induced Vago protein have been shown to act antivirally but the range of viruses controlled by each pathway is more restricted. The insights gained with the *Drosophila* model can be used to inspire and guide new studies in vector insects and help to shed light on basic virus-vector interaction mechanisms.

Contact: Stefanie.Becker@tiho-hannover.de

## **Vaccinomics: from systems biology of tick-pathogen interactions to vaccine development.**

SaBio. Instituto de Investigación en Recursos Cinegéticos IREC (CSIC-UCLM-JCCM), Ciudad Real, Spain  
Department of Veterinary Pathobiology, Center for Veterinary Health Sciences, Oklahoma State University, Stillwater, OK, USA

Ticks are blood feeding arthropod ectoparasites that transmit pathogens causing diseases in humans and animals worldwide. Tick-host-pathogen interactions have evolved through dynamic processes involving genetic traits of hosts, pathogens and ticks that mediate their development and survival. New approaches for tick control are dependent on defining molecular interactions between hosts, ticks and pathogens to allow for discovery of key molecules that could be tested in vaccines for intervention of tick-pathogen cycles. Tick vaccines offer the important advantages of being a cost-effective and environmentally friendly alternative with a dual effect reducing tick infestations and preventing ticks from transmitting disease-causing pathogens. The challenge of developing improved tick vaccines arises from the need to understand the complex molecular relationship between vertebrate hosts, ticks and pathogens which requires a systems biology approach that will allow the integrated analysis of metabolomics, transcriptomics, proteomics and other omics data for discovery of key pathways molecules that mediate tick-pathogen interactions. A vaccinomics approach could then be used to identify and fully characterize candidate protective antigens and validate vaccine formulations, including development of effective screening platforms and algorithms for analysis and validation of data produced by the systems biology approach to tick research. New candidate protective antigens will most likely be identified by focusing on abundant proteins with relevant biological function in tick feeding, reproduction, development, immune response, subversion of host immunity and pathogen transmission. Additionally, the evolution of similar strategies for some pathogens such as *A. phagocytophilum* to infect vertebrate and tick cells suggest the possibility of developing strategies to control pathogen infection in both vertebrate hosts and tick vectors. Tick vaccines that affect both tick infestations and pathogen infection and

transmission could then be developed and used to vaccinate human and animal populations at risk for disease prevention and also reservoir host species in order to reduce tick infections and their vector capacity for pathogens that affect human and animal health worldwide.

Contact:        jose\_delafuente@yahoo.com

## Bed Bugs: the Clinical Implications

Department of Medical Entomology, Westmead Hospital, Westmead, Australia

Since the late 1990's, there has been a worldwide resurgence from bed bugs (Hemiptera: Cimicidae), involving both the common, *Cimex lectularius* L. and the tropical bed bugs, *Cimex hemipterus* F.

Bed bugs are blood sucking insects that readily bite humans and in the process inject range of proteinaceous compounds, some of which have known antigenic properties. Around 50% of people unexposed to the bite of the common bed bug will develop no clinical reaction, however this increases to over 90% upon subsequent exposure. Following the bite, cutaneous reactions may occur almost immediately and can start out with small macular lesions that can develop into distinctive wheals of around 5cm in diameter, often with accompanying papules. These are typically intensely itchy, often leading to disturbed sleep patterns as a result of the victim waking up to scratch the site. In some cases, bullous lesions may erupt. If bed bugs are numerous then the patient can present with widespread urticaria or erythematous rashes. Often bites occur in lines along the limbs, which is a diagnostic indicator that bed bugs are present. Systemic reactions to the bite have been poorly documented, although we are aware of two recent cases involving bed bug researchers who developed systemic and erythrodermic reactions following feeding bed bugs in the laboratory. In both cases, the researchers were taken to Emergency Departments for treatment.

Over forty pathogens have been detected from bed bugs, and recent evidence suggests that bed bugs are capable of transmitting in the laboratory *Trypanosoma cruzi*, the aetiological agent of Chaga's disease. Despite this finding, there is no epidemiological evidence to suggest bed bugs transmit the agent in the field and in fact there is no definitive evidence that they transmit any disease-causing organisms to humans.

Anemia may result when bed bugs are numerous and their allergens can trigger asthmatic reactions, although the latter has not been widely reported.

The misuse of chemicals and other technologies for controlling bed bugs has the potential to have a deleterious impact on human health, and one human death has been implicated with the over use of insecticides.

Bed bugs can be the source of significant psychological trauma and in one sad case of a patient with underlying psychoses, the presence of bed bugs was the final trigger that led to their suicide.

Contact: [stephen.doggett@health.nsw.gov.au](mailto:stephen.doggett@health.nsw.gov.au)

## Small hive beetle in Italy

Istituto Zooprofilattico Sperimentale delle Venezie, NRL for beekeeping, Legnaro (Padova), Italy

*Aethina tumida* Murray (small hive beetle, SHB) was firstly reported in Italy on 5 September 2014. Three nuclei containing honey bees (*Apis mellifera*) and located in a clementine (citrus) orchard near the Gioia Tauro port in the Calabria region (southern Italy) were heavily infested with adult and larval *A. tumida*. *A. tumida* infestation is a notifiable disease of honey bees in the European Union as well as an OIE listed disease. The importation of honey bees is strictly regulated in the European Union (Commission Regulation (EU) No. 206/2010) to prevent its introduction. Early reaction measures adopted in Italy require immediate notification of *A. tumida* discovery to the local veterinary services and cannot move their colonies. Furthermore, a protection area (20 km radius) and surveillance (100 km radius) zone were established. The surveillance zone includes the whole territory of Calabria and Sicily region, following SHB detection in a single municipality of the latter one at the beginning of November 2014. Compulsory visits to all apiaries in the protection zone with georeferentiation and visual colony inspection according to 5% expected prevalence (95% CI) are applied. In Calabria region 60 positive sites were detected and destroyed. Destruction of infested apiaries is compulsory and the soil under the infested colonies must be ploughed and treated with pyrethroids. If apiaries in the protection zone are found to be negative, traps are placed. In the surveillance zone, apiaries are selected according to a risk analysis (migration in infested areas, honey bee or materials exchange) or randomly and colonies are inspected according to 2% expected prevalence (95% CI). Furthermore, a SHB surveillance program was also initiated at national level.

Contact: fmutinelli@izsvenezie.it

Peter Rosenkranz

## **Varroa destructor: from an invasive parasite to a permanent threat**

Apicultural State Institute, University of Hohenheim, Stuttgart, Germany

Originally *Varroa destructor* is a haemolymph sucking mite of the Eastern honey bees *Apis cerana*. On the new host, the Western honey bee *Apis mellifera*, the mite has spread worldwide during the past 50 years. Meanwhile, *V. destructor* is considered the main reason for honey bee colony losses in temperate regions caused by a nearly unlimited population growth of the mite in the new host and the transmission of pathogenic honey bee viruses. After an overview of the life cycle, population dynamic and pathogenesis of *V. destructor* a “historical” review on the Varroa treatments performed by the beekeeper during the past decades will be given. The focus of the presentation will be on those factors in the host parasite relationship that are crucial for the extraordinary reproductive success of the parasite. Recent approaches have revealed new details on the activation and triggering of the reproduction of Varroa females. It will be demonstrated how the disturbance of the mite reproduction could be used (i) for selective breeding and (ii) for future control strategies.

Contact: peter.rosenkranz@uni-hohenheim.de

Annunziata Giangaspero

***Dermanyssus gallinae*: a never-ending story for the poultry industry and public health.**

Dipartimento di Scienze Agrarie, degli Alimenti e dell’Ambiente, Università di Foggia, Foggia, Italy

The poultry red mite, *Dermanyssus gallinae*, is a blood-sucking mite of domestic, wild and synanthropic birds. It poses a significant threat to poultry industries and hen health worldwide, particularly in Europe. *D. gallinae* is increasingly suspected of being a disease vector, and attacks on alternative hosts, like humans, are becoming more common. This is especially the case for poultry workers, but ordinary city residents living close to birds’ nests are coming under attack, therefore it is emerging as a public health problem.

For the poultry industry, the economic importance of this pest has greatly increased. As poultry production moves from conventional cage systems towards a more welfare-oriented breeding system in many parts of the world, *D. gallinae* is likely to become more abundant and difficult to control. Control remains dominated by the use of synthetic acaricides, although resistance and treatment failure are widely reported. Furthermore, there are also worrying reports of collateral effects on human health.

Alternative control measures are beginning to penetrate the market, although most candidate products are still at the pre-commercial stage. Correct identification of the red mite is the first requirement before control methods are applied. Significant advances in *D. gallinae* control are most likely to come through an integrated approach adopting recent research into both existing and novel control strategies; this is now being combined with improved monitoring and modeling in order to better inform treatment interventions.

Contact: [annunziata.giangaspero@unifg.it](mailto:annunziata.giangaspero@unifg.it)

## Medical Entomology in the 21st century: Retrospect and Challenges

Institute of Specific Prophylaxis and Tropical Medicine, Medical Parasitology, Medical University of Vienna, Vienna, Austria

Diseases caused by arthropods directly or - by the transmission of pathogens - indirectly have accompanied the hominids throughout the whole evolution and have led to hundreds of millions of deaths. However, until the 19th century the striking and enormous medical importance of arthropods - particularly as vectors - was entirely underestimated or not even recognised at all.

The first confirmation of the transmission of a pathogen by an arthropod succeeded as late as in 1884, when Sir Patrick MANSON (1844-1922) showed that *Wuchereria bancrofti* was transmitted by mosquitoes. In 1880 Charles Louis Alphonse LAVERAN (1845-1922) discovered the organism causing malaria, but only at the end of the 19th and the beginning of the 20th century the transmission of *Plasmodium* species by mosquitoes was uncovered in brilliant experiments. The last two decades of the 19th century and the whole 20th century until now, the beginning of the 21st century, brought an impressive progression of discoveries in the field of medical entomology. Today we certainly know most arthropods causing diseases and we know most pathogens transmitted by arthropods. Moreover, most life-cycles have been clarified. Nevertheless, new discoveries of relevant arthropods as well as of pathogens so far unknown or neglected are to be expected in our century, although in very limited numbers.

None of us knows what the next 85 years will bring - certainly many new discoveries, inventions, new methods, but unfortunately certainly also many negative developments like wars, epidemics..., but hopefully no terrestrial or extraterrestrial catastrophes. However, among the events to be expected with certainty there are three grave developments in this century which are clearly linked with diseases caused by arthropods:

1) Climate change and global warming. An increase of temperature by 2°C until the end of the century is unavoidable, an increase by 3°C may be likely and even higher values cannot be excluded.

2) The excessive increase of the world population. The present world population is 7.3 billions, it may reach 10.9 billions (or even more and hardly less) until 2100.

3) Further increase of globalisation in numerous forms by voluntary or forced migrations of humans (e.g. more than one billion of travellers per year; about 60 millions of refugees presently) by transport of animals, plants, goods etc.

All these factors imply numerous ways of active and passive dispersal of arthropods, in particular of vectors, as well as of pathogens. All pathogens will remain of importance, however, today effective drugs are available against (almost) all Bacteria, Protozoa as well as all helminths transmitted by arthropods so that gradually the number of fatalities due to such pathogens (Rickettsiales spp. and other bacterial infections, Trypanosoma spp., Leishmania spp., Plasmodium spp. ...) will gradually and continuously decrease - despite the fact that only few (commercially available) vaccines (typhus, plague) are available nowadays.

A completely different situation concerns arboviruses. There are about 150 arboviruses pathogenic for humans, and further ones will be detected. Unfortunately there are practically no effective drugs and only few vaccines (TBE, Yellow Fever, Japanese Encephalitis).

Another risk concerning arbovirus infections results from the importation, dispersal and amplification of exotic vectors, in particular mosquitoes, as it has happened in the recent past. Some of them have high vector capacities for a number of arboviruses causing serious diseases. We have effective tools of monitoring, but actually no really satisfactory ways of specific mosquito control. Most probably the effective control of certain mosquito vectors will base upon genetic manipulations of mosquitoes (introduction of lethal genes into a population). Similar challenges may result from dispersal of other bloodsucking arthropods, particularly sand flies and ticks.

It can hardly be questioned that arboviruses and their vectors will represent the most important challenges of medical entomology in the 21st century.

Contact: horst.aspoeck@meduniwien.ac.at

## Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health

Headquarters Insel Riems

Südufer 10

D-17493 Greifswald - Insel Riems

Phone +49 (0) 38351 7-0

Fax +49 (0) 38351 7-1151

Press Office

Phone +49 (0) 38351 7-1244

Fax +49 (0) 38351 7-1151

E-Mail: [Presse@fli.bund.de](mailto:Presse@fli.bund.de)

Photos/Source: Amöben, Bandwürmer, Zecken ... : Parasiten und parasitäre Erkrankungen des Menschen in Mitteleuropa / Horst Aspöck. - Linz, 2002

Content: Ed. B.M. Bußmann, Friedrich-Loeffler-Institut