

# ECE 2018

XI EUROPEAN CONGRESS OF ENTOMOLOGY

2-6 JULY 2018, NAPOLI



Società  
Entomologica  
Italiana



Accademia  
Nazionale Italiana  
di Entomologia

CERESIO FAVORIS VERO  
AB ORIBUS ORIGINE  
TENENT



UNIVERSITÀ DEGLI STUDI  
DI NAPOLI FEDERICO II

DIPARTIMENTO DI  
AGRARIA

## BOOK OF ABSTRACTS

specific expression will facilitate this type of experiments. Juvenile hormone acid methyl transferase (JHMT) is a JH biosynthetic enzyme specifically and highly expressed in the CA. Using the CRISPR/Cas9 system, we have integrated a promoter-less gene encoding the green fluorescent protein (GFP) into the JHMT locus. Transgenic mosquitoes show specific GFP expression in the CA. Analysis of transgene expression and survival of homizogous mosquitoes are revealing exciting data that uncover surprising aspects of CA functions. In this poster we will address two interesting questions: Is mosquito postembryonic development initially independent of JH? Do the two CA glands work always in synchrony? Recently we have integrated the gene SWITCH (inactive form of GAL4) into the JHMT locus. Inducible UAS/SWITCH system will allow conditional expression in CA using RU486. This system will allow the CA-specific and inducible expression of selected genes or dsRNAs.

Keywords: Mosquito, corpora allata, gene editing, CRISPR, Juvenile hormone

#### PO420

### SPATIAL AND TEMPORAL VARIATIONS IN THE ABUNDANCE OF *CULEX (MICROCULEX) PLEURISTRIATUS* LUTZ, 1903 AND *CULEX (MICROCULEX) IMITATOR* THEOBALD, 1903 IN AREAS WITH VARIATION IN PROPORTION OF VEGETATION COVER IN THE CITY OF SÃO PAULO, BRAZIL

Rafael de Oliveira Christe, São Paulo Institute of Tropical Medicine, University of São Paulo, Brazil

Antonio Ralph Medeiros-Sousa, Department of Epidemiology, School of Public Health, São Paulo University, Brazil

Walter Ceretti-Junior, Department of Epidemiology, School of Public Health, São Paulo University, Brazil

Mauro Toledo Marrelli, São Paulo Institute of Tropical Medicine, University of São Paulo / Department of Epidemiology, School of Public Health, São Paulo University, Brazil

Introduction: *Microculex* is a subgenus of mosquitoes (Diptera: Culicidae) belong to *Culex* genus, restricted to the Americas and little studied, their role as pathogen vector is unknown. Their species are typically found in wild environments developing mainly in bromeliads, but some species of this group, such as *Cx. pleuristriatus* and *Cx. imitator*, can be found developing in urban green areas. Objectives: We investigated the spatial and temporal variations in the abundance of *Culex pleuristriatus* and *Cx. imitator* species in three areas located in the city of São Paulo, Brazil. Methodology: The sites selected for the study have different proportions of native vegetation covering a buffer of 1 km around the collection point (60%, 70%, 90%). The collections were carried out monthly, from March 2015 to April 2017. Immature forms were collected in bromeliads, bamboos and artificial containers. The specimens collected were morphologically identified in the laboratory. To evaluate the temporal variation, rainfall and monthly temperature data were obtained. Data analysis was performed using non-parametric statistical tests of Kruskal-Wallis and Spearman's correlation. Results: 418 specimens of *Culex pleuristriatus* and 210 *Cx. imitator* were collected throughout the study. *Cx. pleuristriatus* was more abundant at the site with lower vegetation coverage ( $p=0.04$ ), but did not show temporal relation with temperature and precipitation ( $p>0.05$ ). For *Cx. imitator* we did not observed differences in abundance between environments and no temporal correlation with climatic variables. Conclusion: Our data showed that *Cx. pleuristriatus* abundance was influenced by variations in vegetation coverage, whereas *Cx. imitator* was not affected by such variations. We have not observed a direct relationship between abundance with temperature and precipitation for these species. Our future investigation will try elucidating other aspects of ecology, biology, and taxonomic relations of this subgenus.

Keywords: Microculex, ecology, mosquitoes, vegetation.

#### PO421

### WEST NILE VIRUS IN ROMANIA

Valeria Purcarea-Ciulacu, NIRDMM "Cantacuzino", Buchares, Romania

Alexandru Vladimirescu, NIRDMM "Cantacuzino", Military Medical Research Center, Buchares, Romania

Liviu Prioteasa, NIRDMM "Cantacuzino", Buchares, Romania

Elena Falcuta, NIRDMM "Cantacuzino", Buchares, Romania

Gabriela Nicolescu, NIRDMM "Cantacuzino", Buchares, Romania

The circulation of West Nile virus (WNV) takes place in cycles between mosquitoes and birds as main hosts, and the mammals including humans as tangential hosts. The WNV circulation was documented in Romania beginning with the '50s by serological investigations on healthy humans and domestic animals and the confirmation of this virus as etiological agent of sporadic and epidemic human neurological infections. An outbreak of more than 800 human cases of WNV neurological infections appeared in South Romania in 1996. This was the European signal of the increase of WNV circulation especially because of the global environmental changes including climatic ones. The WNV neurological infections continued to appear yearly after the outbreak in Romania on more extended areas. The multidisciplinary investigation using entomological, immunological, virology and molecular biology techniques have been performed in 2001 – 2017 on large territories in Romania on the main elements of the transmission cycles of WNV involving mosquito vectors, domestic and wild birds and horses in natural and anthropic ecosystems and their variations in correlation with changing environmental factors. The virus was detected in females of *Culex pipiens*, *Coquillettidia richiardii*, *Ochlerotatus caspius* and *Anopheles maculipennis* s.l. species. Males of *Culex pipiens* and also over wintering females of this species have been positive for the virus. The isolated viral strains were molecularly characterized. It has been demonstrated the intensive and permanent circulation of WNV on extended territories in the country and the permanent risk of its transmission to humans. The risk areas have been mapped. The permanent surveillance of West Nile virus endemic circulation and the implementation of integrated mosquito control programmes in the key areas at risk in Romania are adequate decisions for public health.

Keywords: West Nile virus, mosquito vectors, vertebrate hosts, Romania

#### PO422

### USING CODON USAGE BIAS TO INVESTIGATE THE ROLE OF ALTERNATIVE HOSTS IN THE SPREAD OF ZIKA

Andrea Silverj, University of Padua, Italy

Nicola Zadra, Fondazione Edmund Mach, Italy

Lino Ometto, Fondazione Edmund Mach, Italy

Omar Rota-Stabelli, Fondazione Edmund Mach, Italy

In the last years, outbreaks of Zika virus (ZIKV) and Dengue have been reported from both endemic and newly invaded areas of the world. ZIKV is in general associated with, and is well adapted to, primates and mosquitoes vectors, on which it can complete its cycle. There is insufficient information regarding other animal reservoirs and amplification hosts, but there's a concrete possibility that ZIKV can infect other species, including domestic animals both from endemic and newly invaded temperate areas; such knowledge is fundamental to properly describe the epidemiology of ZIKV and plan its management. Unfortunately, large scale screenings of putative alternative vectors are extremely time and cost consuming. We suggest to employ Codon Usage Bias (CUB, the uneven use of synonymous codons) to predict if alternative hosts, in particular those associated with humans, can vehicle ZIKV. This will be performed by contrasting codon usage of ZIKV of hosts deduced from transcriptomes/proteomes, calculating parameters like RSCU (relative synonymous codon usage), CAI (codon adaptation index) and ENC (effective number of codons). Our first results indicate that Zika has putatively poor replication efficiency in *Culex pipiens*. Ultimately, we advocate the analyses of CUB to understand evolutionary dynamics of ZIKV and other flaviviruses and better forecast their future outbreaks.

Keywords: Culex, Zika, viruses, codon usage, vectors