9th International Congress of Dipterology

Abstracts Volume

25–30 November 2018
Windhoek
Namibia

Organising Committee:

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Burgert S. Muller
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Michael Osae
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Edited by:
Ashley H. Kirk-Spriggs
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Front cover image: Tray of micro-pinned flies from the Democratic Republic of Congo (photograph © K. Pannecoucke).

Cover design: Craig Barlow (previously National Museum, Bloemfontein).

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Preface

Every four years, dipterists from around the globe meet up at the International Congresses of Dipterology to discuss scientific progress in the various disciplines of dipterology, present research findings, liaise with colleagues and forge future research collaborations. The 9th International Congress of Dipterology (ICD9) is the first such Congress to be held on the African continent and the first in a developing country. The overall theme of the Congress was "Afrotropical dipterology", but all themes and regions were represented. A total of 273 full delegates and students from 51 countries, attended the Congress, including 61 delegates from 13 African countries.

This volume contains 321 abstracts of oral and poster presentations submitted to the Organising Committee of ICD9 for the Congress held in Windhoek, Namibia, in November 2018. This collection of abstracts serves as a snapshot of the range and quality of scientific activity in the international dipterological community and this publication is a permanent record, summarising presentations at the Congress, serving an important purpose both for those who attended the meeting and those who did not.

The table of contents is arranged according to the 23 symposia, arranged alphabetically, to facilitate location of abstracts in specific topic areas. For the purposes of ICD9, poster presentations do not form part of symposia and are listed separately. Abstracts in the volume are arranged alphabetically by first author and the names of presenting authors (if more than one) are underlined. The footer for each abstract indicates to which symposium an oral presentation belongs or whether a plenary, keynote or poster presentation. Two indexes are included at the back of the volume, one comprising the names of all abstract authors, the other key words (as provided by the authors) and used in the titles.

Abstracts were edited to a certain extent for consistency of style and formatting in collaboration with the authors and the various symposia Convenors, but the content of abstracts remains the sole responsibility of the authors. Spelling of words follows British rather than American orthography and all abstracts are edited to apply the passive voice. Presenting author names are underlined and an asterisk (*) indicates corresponding author.

We take this opportunity to thank all ICD9 delegates and symposium Convenors, who assisted with arrangements and made the Congress possible. We also thank the various sponsors who gave financial support (as indicated on the back cover of this book), the Government of the Republic of Namibia and the people of Namibia for their friendly and helpful support.

Ashley H. Kirk-Spriggs & Burgert S. Muller

October 2018

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9th International Congress of Dipterology

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Abstracts

In celebration of Roger Ward Crosskey (1930–2017) – a life well spent

Zoe J. Adams[1]* & Adrian C. Pont[2]

[1]Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, United Kingdom. *z.adams@nhm.ac.uk
[2]Oxford University Museum of Natural History, Oxford, United Kingdom.

Keywords: Afrotropical, catalogue, celebration, Crosskey, Simuliidae, Tachinidae.

The 9th International Congress of Dipterology (ICD9) is dedicated to the memory of the late Roger Ward Crosskey (1930–2017), a former Honorary Member of ICD, in recognition of his substantial contribution to Afrotropical dipterology specifically and to dipterology in general. In this presentation an account is given of his exemplary life and career, with particular emphasis on his fieldwork in Africa with onchocerciasis control, his taxonomic work at the Natural History Museum in London on Afrotropical Simuliidae and Tachinidae and his editorial achievement, with the inception and management of the monumental "*Catalogue of the Diptera of the Afrotropical Region*", published in 1980.

A review of Nearctic *Saropogon* Loew (Asilidae: Dasypogoninae), with the description of a new species from Arizona, U.S.A.

Charlotte H.E. Alberts[1]* & Eric M. Fisher[2]

[1]Department of Entomology and Nematology, University of California, Davis, U.S.A.
*ceherbert@ucdavis.edu
[2]El Dorado Hills, California, U.S.A.

Keywords: Assassin flies, Nearctic, new species, robber flies, taxonomy.

Saropogon Loew is a distinctive genus of Dasypogoninae robber flies, currently with 130 described species globally. About half of the species are distributed in the Palaearctic Region and 10 species are known from the Afrotropical Region. A review is provided of the Nearctic fauna, which comprises 19 species, for which the taxonomy, distribution and biology are discussed, along with a new identification key. A new species is described from Tucson, Arizona, based on specimens collected by D.R. Miller and J.E. Lauck in 1968.

Electrophysiological and behavioural responses of Corn silk flies (Ulidiidae) to colour

Sandra A. Allan

Center for Medical, Agricultural and Veterinary Entomology, United States Department of Agriculture, 1700 SW 23rd Dr, Gainesville, Florida, U.S.A. Sandy.allan@ars.usda.gov

Keywords: Behaviour, *Chaetopsis*, Corn silk flies, ecology, *Euxesta*, vision.

The family Ulidiidae contains a broad range of species, most of which are saprophagous as larvae. Several species known as Corn silk flies oviposit on fresh or damaged vegetables, with a strong preference for ovipositing on corn silk. The subsequent larval damage to the developing cobs results in their designation as primary pest of fresh market sweet corn, particularly in south Florida, where over 60 % of the United States' fresh market sweet corn in produced. Using *Chaetopsis massyla* (Walker) and *Euxesta eluta* Loew, electroretinograms and behavioural assays were used to determine and compare the spectral sensitivity and colour preferences of the flies, respectively. This information can provide the foundation for development of standardised surveillance methods for these species to guide management strategies.

Poster

Empodia of *Corethrella* Coquillett (Corethrellidae) and their value for the taxonomy of the family

André Amaral* & Luiz C. Pinho

Universidade Federal de Santa Catarina, Centro de Ciências Biológicas, Depto. de Ecologia e Zoologia, CEP 88040-901, Florianópolis – SC, Brazil. *ap.amaral@outlook.com

Keywords: Culicomorpha, empodia, morphology, systematics, taxonomy.

The taxonomy of the monobasic family Corethrellidae is largely based on female colouration patterns, which in many cases may present difficulties in recognising species and reconstructing the phylogeny of the group. This study suggests the use of the empodia as a source of characters useful for the taxonomy and possibly the phylogeny of *Corethrella* Coquillett. Thirty Brazilian species (of the 108 species known globally), had their empodia analysed based on slide-mounted specimens. It was observed that empodia varied according to thickness, length and number of branches (acantha), with some distinctive patterns among well-defined groups of species. This study demonstrated that empodia are useful in distinguishing some similar species and adding these characters to new cladistic analyses may result in substantial changes in the phylogenetic arrangement of the group, reinterpreting the relationships between some species.

New species and records of Corethrellidae from Brazil

André Amaral* & Luiz C. Pinho

Universidade Federal de Santa Catarina, Centro de Ciências Biológicas, Depto. de Ecologia e Zoologia, CEP 88040-901, Florianópolis – SC, Brazil. *ap.amaral@outlook.com

Keywords: *Corethrella*, diversity, neotropics, new records, new species.

Corethrellidae is a small family known by the vernacular name “frog-biting midges”. They are most diverse in tropical regions, comprising 108 described species globally. Curiously, there are currently only 34 species recognised from Brazil, which is clearly an underrepresentation of the total diversity, as the country comprises some of the most biodiverse regions of the world. This study presents information on eight new records of Corethrellidae for Brazil, 11 records of new distributions within the country and four new species descriptions. New species are described and figured from females and/or males sampled in the Atlantic and Amazon forests. Although these results represents a rise of 35% in the number of species known from Brazil, results are based on very limited sampling (mostly in Santa Catarina State, southern Brazil) and there is clearly much more to discovered about the diversity and biology of the family.

Poster

Morphology based Diptera phylogeny – taxon sampling, character sampling and analytical challenges

Dalton de Souza Amorim

Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *dsamorim@usp.br

Keywords: Cladistics, coding, homology, missing data, ordering, weighting.

Reconstructing a Diptera phylogeny based on phylogenetic methodologies is challenging. Early authors gathered information and explored problems of homology. Formal numerical analyses were made based on morphology and molecular data. Some hypotheses have wide agreement, but there are conflicts at many levels. One of the most complex challenges facing researchers when attempting to achieve a reliable phylogeny of the Diptera is taxon sampling. With *ca* 170 families globally, thorough sampling entails the inclusion of hundreds of genera. For morphology-based phylogenies, good character sampling demands several hundred characters. There are also analytical challenges: homology is one such challenge and is not trivial. Homology mistakes can result in a cascade of misleading phylogenetic signals. Decisions on coding, ordering and weighting expand the complexity. Dealing with missing data requires special attention. In a broad phylogenetic study of Diptera based on morphology, a proper protocol needs to be developed to address these challenges. The goal is to demonstrate the monophyly of families and relationships between them. This demands intense sampling of families, with selection of at least one genus of each tribe/subfamily of all families. An assessment of Diptera classification resulted in 741 genera being selected, which may still be insufficient to deal with more complex groups. Character sampling was addressed in a study of the entire literature: *ca* 10,200 characters were obtained and removal of redundancy will reduce the list to *ca* 4,000 characters. A number of structures had been only superficially studied and a significant number of new characters are included.

The first Opetiidae (Platypezoidea) known from the Southern Hemisphere from Valdivian Forest, Chile

Dalton de Souza Amorim[1]*, Vera Cristina Silva[1] & Brian V. Brown[2]

[1]Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *dsamorim@usp.br
[2]Natural History Museum of Los Angeles County, Los Angeles, U.S.A.

Keywords: Cretaceous, Cyclorrhapha, disjunction, *Nothofagus*, southern temperate fauna.

The first Opetiidae known from the Southern Hemisphere, *Puyehuemyia chandleri* Amorim, Silva & Brown, is reported. This species was described based on the unique female holotype, collected in the Valdivian Forest of southern Chile. Comparisons were made to the Palaearctic species *Opetia nigra* Meigen. The position of the genus in the family is demonstrated, based on features of the antenna, mouthparts, wing and terminalia. Description of this new genus enabled an investigation of the position of the Opetiidae within the Eremoneura. The inclusion of the family in the Platypezoidea (*i.e*., as a true cyclorrhaphan) is strongly corroborated, possibly in a clade also including Lonchopteridae and Phoridae. The 3-articled condition of the stylus-like arista in *Puyehuemyia* corroborates the hypothesis that the 2-articled condition in *Opetia* Meigen was derived independently from the condition apparent in the Empidoidea and in different branches of schizophorans. The female terminalia of *P*. *chandleri* and *Opetia* are similar to that of parasitoid groups, although details of the life history of opetiid larvae remain unknown. The position of platypezoid Cretaceous amber fossils is considered and *Lonchopterites* Grimaldi & Cumming is considered sister to the crown-group Opetiidae. This species of Opetiidae and of other flies (*Archiphora patagonica* Schmitz and *Gondwanamyia chilensis* Cumming & Saigusa), suggest the existence of an Early Cretaceous zoogeographical layer in the Valdivian Forest in Chile associated to other plants and animals disjunct from New Zealand, in the Southern Hemisphere and disjunct from the beech forests in the Northern Hemisphere.

The reverse-sorting sharp tool – an example of the study of Mycetophilidae from Singapore

Dalton de Souza Amorim[1]*, Darren Yeo[2], Sarah Siqueira Oliveira[3], Yuchen Ang[3] & Rudolf Meier[2]

[1]Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *dsamorim@usp.br; [2]National University of Singapore, Singapore; [3]Instituto de Ciências Biológicas, Universidade Federal de Goiás Goiânia, GO, Brazil; [4]Lee Kong Chian Natural History Museum, National University of Singapore, Singapore.

Keywords: Cluster, COI, inventory, Malaise traps, sequencing, tropical forest.

An integrative approach was performed on Singapore Mycetophilidae diversity, including sequencing, imaging, generic identification and formal morphology-based taxonomic descriptions. A total of 23 sites of old and planted mangroves, swamp forest, primary forest, maturing and old secondary forest and forests in urbanised areas were sampled in Singapore, as part of a much larger survey. In this protocol, specimens are sequenced for COI first and then specimens of the clusters are recognised—the reason this is termed reverse sorting. A total of 1,260 specimens from 145 sampling events with Malaise traps were analysed and sequenced for COI. Clusters with 1, 3, and 5% COI divergence were used to delimit taxonomic units, later checked against morphology for intra- and inter-cluster consistency to delimit nominal species. The study rendered 117 species in 19 genera of all seven subfamilies of Mycetophilidae, of which 110 (94.0%) are new to science. Of the total species sampled, 29 species are represented by singletons (24.7%) and 42 from singletons or doubletons (35.9%), suggesting that the fauna is much larger. The species-rich genera were *Epicypta* Winnertz and *Neoempheria* Osten-Sacken, with over 30 species each, *i.e.*, over half of the species diversity was represented by only two genera. The most abundant species was *Epicypta* sp. n. 7, with 112 specimens, 8.9% of the total mycetophilid specimens sampled. Surprisingly, the swamp forest is the richer habitat in terms of number of species and specimens. All species were imaged, produced as a database available for the public. Databased specimens allows rapid and detailed analysis of phenology, geographic distribution and saturation curves. The overlap between cluster composition and geographic disjunction would be able to indicate recent evolutionary events separating the Singapore fauna from nearby areas. The generic composition of the Mycetophilidae Singapore fauna is compared to other tropical areas of the world and its meaning is discussed. The results of this strongly recommends inventory designs based on inverted-sorting strategies.

Assessment of the efficiency of local protein-rich products for mass rearing of *Bactrocera dorsalis* (Hendel) (Tephritidae) and the parasitoid *Fopius arisanus* (Sonan) (Braconidae)

Florence M. Anato[1]*, Mariano Adjamai[1], Désiré Gnanvossou[2], Antonio C. Sinzogan[1], Rosine B. Wargui[1] & Aimé H. Bokonon-Ganta[1]

[1]Faculty of Agronomics Sciences, University of Abomey-Calavi, 03 BP 2819 Cotonou, Benin.
*anatoflorence@yahoo.fr
[2]International Institute of Tropical Agriculture, Cotonou, Benin.

Keywords: *Bactrocera*, cassava diet, *Fopius*, larval artificial diet, mass rearing, protein.

Fopius arisanus (Sonan) (Hymenoptera: Braconidae) is an ovo-pupal parasitoid, used as a biocontrol agent against the Oriental fruit fly, *Bactrocera dorsalis* (Hendel). The effectiveness of this parasitoid in the field depends partly on the quality of its mass rearing system. Preparation of artificial diets results in high costs and their qualities have great impact on performance of larvae and adults of *B. dorsalis* and *F. arisanus*. Some local protein-rich products were evaluated, such as powder of moringa leaves, powder of cassava leaves and soybean flour, as substitute to the expensive imported hydrolysate yeast. Life history parameters of *F. arisanus* and *B. dorsalis* were compared in relation to the diets. Costs of each diet were also evaluated. The results revealed that *B. dorsalis* eggs hatchability on moringa diet was high, while the adult emergence rate was low. Cassava diet did not differ from the deactivated hydrolysate yeast in eggs hatchability, pupal recovery and adult *B. dorsalis* emergence rate. *Fopius arisanus* parasitised *B. dorsalis* egg hatchability on moringa and cassava diet was higher, however, than the other diets. The pupal recovery from cassava, papaya and soybean was lower than from the control. Pupal weight and emergence rate of *F. arisanus* did not differ among treatments. After assessment of the life history parameters of *F. arisanus* and *B. dorsalis*, the best local protein-based diet was considered to be the cassava diet, which offered performances globally closest to the control diet. In contrast, the papaya diet and the moringa diet performance were low.

Flies in the eyes of flowers – the beauty of the beast

Bruce C. Anderson

Department of Botany and Zoology, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa. banderso.bruce@gmail.com

Keywords: Floral divergence, floral diversification, pollination, pollination syndrome, selection.

Second only to bees (Hymenoptera: Apoidea), flies are arguably the most important pollinators on the planet, but compared to other modes of pollination, relatively little is known about the group as pollinators. Perhaps one of the primary reasons for this, is that flies have radiated into a dazzling array of highly divergent functional groups. Many of these groups are as different to one another as bees are to birds, making it difficult to propose any generalisations about flies as pollinators. Herein lies the beauty of the beast: to a flower, these forms represent a multitude of different niches and because of the diversity of flies (to quote Charles Darwin) "… endless forms [of flowers] most beautiful and most wonderful have been, and are being, evolved". This presentation outlines some character traits of flies that make many of them unique agents of selection and demonstrates how some of these traits have generated divergence in the morphology of flowers.

Digital reference collections are efficient tools for fostering large-scale collaborative taxonomy – Biodiversity of Singapore as exemplar

Yuchen Ang[1]*, Jonathan Kit Ian Ho[2], Amrita Srivathsan[2] & Rudolf Meier[2]

[1]Lee Kong Chian Natural History Museum, National University of Singapore, Singapore.
*nhmay@nus.edu.sg
[2]National University of Singapore, Singapore.

Keywords: Collaborative taxonomy, cybertaxonomy, digital reference collection.

Specimen images are fast becoming the standard for present day taxonomy, given their data richness, online accessibility and, unlike physical specimens, resilience against degradation. This has resulted in a boom of digital reference collections (DRCs), functioning as image databases that aid specimen identifications. Beyond that, it is argued that DRCs can also function as tools for fostering collaborative work, especially in large, “open-ended” taxa. The Biodiversity of Singapore (BoS) website is used as an as exemplar: first, an efficient, cost-effective NGS barcoding pipeline is employed to quickly pre-sort large numbers of insect specimens from Singapore into putative species clusters. Representatives from these clusters are imaged and presented on BoS. Taxon experts then use it to remotely preview large numbers of species clusters and decide on what to work on. This has already resulted in speedy scientific collaboration with several taxonomic groups, because specimens are already pre-sorted and have informative habitus images readily available. Additionally, BoS is a nexus that congregates existing natural history literature and presents life stage associations, as well as species interactions, thus evolving from a species index into a virtual ecological web. Finally, the BoS serves as an online platform that allows the general public to appreciate the “tiny” biodiversity that is often hidden from view. DRCs, such as BoS, are designed to be sustainable. They are easily deployed and modular and can easily capitalise on large-scale NGS barcoding-based species discovery projects, helping accelerate the rate of species discovery and description.

Molecular identification of an obligate parasite of amphibians – *Lucilia bufonivora* (Moniez) (Calliphoridae)

Gerardo Arias-Robledo[1, 3]*, Tariq Stark[2], Richard L. Wall[1] & Jamie R. Stevens[3]

[1]Veterinary Parasitology and Ecology, University of Bristol, 24 Tyndall Avenue, Bristol, BS8 1TQ, United Kingdom. *gerardo.ariasrobledo@bristol.ac.uk
[2]RAVON, Nijmegen, the Netherlands
[3]University of Exeter, Exeter, United Kingdom.

Keywords: Amphibian myiasis, blowfly, Calliphoridae, cytochrome c oxidase subunit I.

In Europe, the toad fly *Lucilia bufonivora* (Moniez) is recognised as the only obligate parasite of the genus *Lucilia* Robineau-Desvoidy. This species has a high host-specificity on amphibians, however, its sister species *L. silvarum* (Meigen) has also been reported as causing myiasis in toads and frogs. The marked morphological similarity of both adult and larval stages of these species has led to misidentification and confusion regarding which species is causing amphibian myiasis in Europe. To resolve this, 20 different dipterous larvae were analysed, extracted from 16 live toads presenting nasal myiasis from different localities in England, The Netherlands and Switzerland, together with 8 adult specimens (4 of each) of *L. bufonivora* and *L. silvarum*. Partial sequences of COX1 and EF1-*α* were amplified and sequenced. All larvae isolated from toads were identified as *L. bufonivora* and no specimens of *L. silvarum* were implicated in amphibian myiasis. This study provides unambiguous molecular identification of the toad fly *L. bufonivora* and highlights the differences with the closely related species *L. silvarum*.

Foraging behaviour of a *Calliphora* Robineau-Desvoidy sp. (Calliphoridae) on Castor bean flowers in Cameroon

Michelson Azo'o Ela[1]* & Fernand-Nestor Tchuenguem Fouhouo[2]

[1]Laboratory of Entomology, Department of Biological Sciences, Faculty of Science, University of Maroua, P.O. Box 814, Maroua, Cameroon. *azooela@yahoo.fr
[2]University of Ngaoundere, Ngaoundere, Cameroon.

Keywords: *Calliphora*, Cameroon, Castor bean, cross-pollination, foraging behaviour, pollination biology, *Ricinus*.

Preliminary trials were conducted to record the foraging behaviour of a *Calliphora* sp. (Calliphoridae) on the flowers of Castor bean, *Ricinus communis* (L.) (Euphorbiaceae), in Domayo (Maroua, Cameroon) from September 20 to October 5 2017. Ten plants were flagged and fly visits were recorded daily on male and female flowers. The following activity parameters were studied: frequency of visits; abundance of foragers; rhythm of insect activity; mean duration of individual visits on male and female flowers; and foraging rate. The influence of several other abiotic and biotic factors on foraging activity were also investigated. Results indicated that 11 anthophilous insect species foraged on Castor bean flowers. Among them, a *Calliphora* sp. accounted for 47.80% of the total number of visits. This species foraged throughout the daylight period, with a peak between 12:00–13:00. It was also noticed that the fly foraged for pollen on male flowers and nectar on female flowers. The mean number of foragers simultaneously active was 293/1,000 flowers. The mean duration of flower visits differed significantly between male (5.57 ± 1.67 seconds) and female (8.23 ± 1.84 seconds) flowers. These low duration of flower visits resulted in a foraging rate of > 5 flowers/minute and it is suggested that this behaviour increases the chance of cross-pollination in Castor bean.

Systematics and taxonomy of *Culicoides* Latreille (Ceratopogonidae) in the Afrotropical Region – what are the challenges and what comes next?

Mame Thierno Bakhoum[1]*, Assane Gueye Fall[1], Jérémy Bouyer[2, 3],
Thierry Baldet[2] & Claire Garros[4]

[1]Institut Sénégalais de Recherches Agricoles, Dakar, Sénégal. *thierno.bakhoum@gmail.com
[2]Centre de coopération internationale en recherche agronomique pour le développement, Montpellier, France.
[3]International Atomic Energy Agency, Vienna, Austria.
[4]Centre de coopération internationale en recherche agronomique pour le développement, Clotilde, Réunion.

Keywords: Afrotropical Region, *Culicoides*, DNA barcoding, Senegal, systematics, taxonomy.

In the context of emergence or re-emergence of vector-borne diseases, several species of *Culicoides* Latreille are involved in the transmission of viruses and parasites, affecting animals and humans (respectively) in the Afrotropical Region. Rapid and reliable identification of vector species is required, but morphology based identification requires scarce taxonomic expertise. In addition, systematic and taxonomic classifications are problematic, as authors disagree on placement of certain species into specific subgenera or informal species-groups. Morphological identification of *Culicoides* larvae is also not possible. This study applied an integrative approach, applying both morphological and molecular criteria to revise the systematics and taxonomy of *Culicoides* species occurring in the Afrotropics, using a multi-marker molecular phylogeny and species delineation. DNA barcodes were also established for Afrotropical species and the DNA barcoding was tested for species identifications at the larval stage on a large number of samples collected from the Niayes area, Senegal. Results revealed: 1) a new species to science (provisionally named *Culicoides* sp. #22) and affiliated to the subgenus *Avaritia* Fox; 2) the affiliation of the *C. similis* and *C. neavei* species-groups to the subgenus *Synhelea* Kieffer; and 3) the existence of cryptic species within *C. oxystoma* Kieffer in the subgenus *Remmia* Glukhova. This study proves the efficiency of DNA barcoding for studying *Culicoides* larval diversity. This offers opportunities for the monitoring of *Culicoides* and implementation of in-depth eco-epidemiological studies to better control *Culicoides*-borne diseases, such as African horse sickness in the Niayes Region, Senegal and in sub-Saharan Africa.

Bioecology of three main *Culicoides* Latreille species (Ceratopogonidae), vectors of equine and ruminant virus in Senegal

Mame Thierno Bakhoum[1]*, Assane Gueye Fall[1], Jérémy Bouyer[2, 3], Geoffrey Gimonneau[2], Claire Garros[4] & Thierry Baldet[2]

[1]Institut Sénégalais de Recherches Agricoles, Dakar, Sénégal. *thierno.bakhoum@gmail.com
[2]Centre de coopération internationale en recherche agronomique pour le développement, Montpellier, France.
[3]International Atomic Energy Agency, Vienna, Austria.
[4]Centre de coopération internationale en recherche agronomique pour le développement, Sainte Clotilde, Réunion.

Keywords: Afrotropical Region, *Culicoides*, larval habitat, Senegal, trophic behaviour.

Several species of *Culicoides* Latreille are involved in the transmission of viruses and nematodes in the Afrotropical Region. Vector-borne diseases caused by viruses transmitted by *Culicoides* biting midges have a renewed interest in West Africa, due to recent major outbreaks, including African Horse Sickness in Senegal in 2007, causing a financial loss estimated at €1.37 million. Although of major economic importance, the bioecology of *Culicoides* species still needs to be explored. The aim of this study was to use innovative ecological approaches for describing the trophic behaviour of *C. kingi* Austen, *C. imicola* Kieffer and *C. oxystoma* Kieffer, as well as their larval habitats in equine environments of the Niayes area, Senegal. These *Culicoides* species are vectors of internationally important viruses of livestock and equids. Firstly, blood meal source in these *Culicoides* species were identified. A correlation was then made between blood meal source (identified in engorged *Culicoides* females collected in a suction light trap) and the available vertebrate hosts along four concentric rings (200, 500, 1,000 and 2,000 m) centred at the trap site, to determine the foraging range of the three vector species. Finally, the larval habitats and spatial temporal dynamics of immature populations of these species were studied. This work completes the corpus of bioecological knowledge of *Culicoides* in the Niayes area of Senegal and proposes research needs to better control the immature and adult populations of vector species in order to better anticipate and prevent *Culicoides*-borne disease outbreaks.

Herbivore dung-derived odours as bait for the stable fly *Stomoxys calcitrans* L. (Muscidae)

Bernard Steve Soh Baleba[1, 2]*, Baldwyn Torto[1], Daniel Masiga[1], Christopher Weldon[2] & Merid Getahun[1]

[1]International Centre of Insect Physiology and Ecology, P.O. Box 30772–00100, Nairobi, Kenya. *bbaleba@icipe.org
[2]University of Pretoria, Hatfield, South Africa.

Keywords: Attractants, dung, odour, stable fly, *Stomoxys*, traps.

Combining behavioural, chemical, classification algorithms and field trapping techniques, the oviposition behaviour of the stable fly, *Stomoxys calcitrans* L. (Muscidae) was investigated. *Stomoxys calcitrans* is a virtually cosmopolitan blood-feeding fly that causes significant losses in domestic livestock production. Results from the oviposition bioassay revealed that gravid females preferred to oviposit on donkey and sheep dung rather than that of buffalo, camel, cow, elephant, giraffe or zebra. This preference to oviposit on donkey and sheep dung was related to the higher fitness performance of their larvae in those breeding media. Using gas chromatography, linked to mass spectrometry and random forest classification, the most important semio-chemicals of the precedent herbivores' dung were identified. In the oviposition bioassay, media singly loaded with the most important volatile of donkey (*β*-citronellene) and sheep (carvone) elicited the strongest oviposition attractions. Furthermore, when *β*-citronellene and carvone were used as baits in the field trapping; these volatiles increased the number of *S*. *calcitrans* caught, as compared to the unbaited traps. Interestingly, traps baited with *β*-citronellene significantly caught more gravid females than those baited with carvone. In the context of insect vector-borne disease surveillance, this study highlights the potential use of *β*-citronellene and carvone as attractants for *S*. *calcitrans*. Results indicate the role of olfaction in the selection of suitable oviposition sites by gravid female flies and the potential use of semio-chemicals arising from the preferred oviposition substrate, as attractants for vector surveillance and control.

More than dead males – looking beyond taxonomy and phylogeny in palaeodipterology

Viktor Baranov

LMU Munich Biocenter, Department of Biology II Großhaderner Str. 2, 82152 Planegg-Martinsried Germany and Department of River Ecology and Conservation, Senckenberg Research Institute and Natural History Museum, 63571 Gelnhausen, Germany. baranowiktor@gmail.com

Keywords: Amber, fossil, integrative palaeobiology.

Palaeodipterology turned over 200 years old, marking the description of *Tipula fusca* Bloch, 1776 from Baltic amber, in his work “Beytrag zur Naturgeschichte des Kopals” from 1776. In the wake of this work, together with Ernst Friedrich Germar’s 1837 seminal work “Insectorum protogaeae specimen sistens insecta carbonum fossilium. Fauna Insectorum Europae” and Svatopluk Presl’s “Additamenta ad faunam protogaem, sistens descriptiones aliquot animalium in succino inclusorum”, often credited as a starting point for all fossil insect studies, it is a perfect time to look back on our achievements and attempt to evaluate future priorities. In recent decades, major strides have been made in dipteran palaeobiology, accelerated by technological advancements in the field of high resolution imaging and discoveries of new fossil deposits (especially amber inclusions). Despite substantial progress, in many ways we are still at the same stage as Germar was in 1837 – cataloguing diversity of fossil faunas and describing endless new taxa. Most of palaeodipterology is essentially a description of the adult (male) insect and application of data acquired from fossils to the wider dipteran phylogenies. We can do better, however, and there are a number of excellent examples of integrative palaeodipterological studies, in which palaeoecological and functional morphological studies were built upon detailed examination of the fossil fauna. The next step should be an integration of palaeodipterological studies into the quantitative palaeoclimatic and palaeobiogeographical models, in order to unleash the potential of one of the largest insect orders to tell the stories of the Earth’s past.

Palaeobiology of frog-biting midges (Corethrellidae) – state of the art and future directions

Viktor Baranov[1]* & Gunnar Mikalsen Kvifte[2]

[1]LMU Munich Biocenter, Department of Biology II Großhaderner Str. 2, 82152 Planegg-Martinsried Germany and Department of River Ecology and Conservation and Senckenberg Research Institute and Natural History Museum, 63571 Gelnhausen, Germany. *baranowiktor@gmail.com
[2]Purdue University, West Lafayette, U.S.A.

Keywords: Amber, amphibians, Corethrellidae, fossil record.

Frog-biting midges (Corethrellidae) are a small family of culicomorph Diptera, represented by the single genus *Corethrella* Coquillett. The genus includes 109 species and occurs in all zoogeographical regions, except Antarctica, with the vast majority of extant species restricted to the tropics and subtropics. Being "eavesdropping" micropredators of frogs and vectors for amphibian trypanosomes, Corethrellidae are an important model system in studying acoustic ecology and host/vector-parasite systems. The geological history of corethrellids spans *ca* 130 MY, with the oldest record of the family, *C*. *cretacea* Szadziewski, 1995, originating from Early Cretaceous Lebanese amber. Nine species of fossil *Corethrella* are currently described – two from the Cretaceous, five from the Eocene and two from the Miocene. Two Cretaceous species – *C*. *andersoni* Poinar and Szadziewski, 2007 and *C*. *cretacea* appear to be sister taxa to the remainder of *Corethrella*. The appearance of *Corethrella* in the geological record was preceded by the appearance of their main prey, anuran amphibians from the Triassic of Madagascar. Corethrellidae are notably absent as compression fossils. Even in amber the family is rare, being represented by less than 20 specimens. It is believed that potential compression fossils of *Corethrella* may be overlooked, due to their rarity and to the narrowness of the taphonomic window for Corethrellidae. In this presentation the state of corethrellid palaeobiology is outlined, unpublished fossil records are discussed and the importance of *Corethrella* palaeobiology is emphasised for interdisciplinary behavioural ecology and conservation research.

Temperature dependent lifespan and emergence traits of *Culicoides* Latreille species (Ceratopogonidae) under laboratory conditions

Carlos Barceló[1]*, Ricardo Del-Río[2] & Miguel-Ángel Miranda[1]

[1]Applied Zoology and Animal Conservation Research Group, University of the Balearic Islands (UIB), Cra. Valldemossa Km. 7.5, Palma de Mallorca, Spain. *carlos.barcelo@uib.es
[2]Sant Jordi, Palma de Mallorca, Spain.

Keywords: Breeding sites, *Culicoides*, Obsoletus complex, survival rate.

Bluetongue is a viral disease affecting wild and domestic ruminants that can result in large economical losses, due to direct and indirect costs. The virus is transmitted by some species of *Culicoides* Latreille biting midges. The bioecology of these insects is not yet fully known in order to control their populations before or during outbreaks of the disease. In the current work, the lifespan of several *Culicoides* species, with particular attention to the effect of different temperatures, was assessed. Also, breeding sites were collected and maintained in the laboratory to assess emergence traits, lifespan and diversity of midges. Results indicated that the vector species from the Obsoletus complex was maintained an average of 19.2 ± 18.0 days (maximum = 65 days) at 25°C under laboratory conditions. However, maximum lifespan for this species was observed at 10°C (20.6 ± 26.7 days with a maximum of 98 days). Regarding the breeding sites, it was observed that the larvae or pupae of *C. circumscriptus* Kieffer may delay emergence for up to 76 days, which may have certain implications in the overwintering mechanism. Finally, some aspects regarding the parasitism of mermithids and mites on *Culicoides* species are discussed.

Increasing momentum in the phylogenetics and systematics of Tabanomorpha

Keith M. Bayless

Australian National Insect Collection, CSIRO, Clunies Ross St, Acton, ACT 2601, Australia. Keith.Bayless@csiro.au

Keywords: Comparative methods, hematophagy, phylogeny, phylogenomics, Rhagionidae, Tabanidae, Tabanomorpha, Vermileonidae.

As increased support and training worldwide have staved off the declining taxonomic expertise in Tabanomorpha, we are accelerating into a new era of international collaboration and the capacity to resolve challenges in the group. The *ca* 5,600 species of Tabanomorpha, spanning 7–9 families, display a high level of adult and larval morphological variation. Almost every antennal syndrome found elsewhere in Brachycera is exhibited within Tabanomorpha. The morphologically homogeneous blood-feeding Tabanidae is the most diverse family. While most larvae are predatory, a few are potentially phytophagous and they have conquered arid to aquatic environments. Adults of most families visit flowers and some have exaggerated proboscid morphology. Family level systematics are not settled, particularly the monophyly of Rhagionidae and the Rhagionoidea and the potential placement of Xylophagidae, Vermileonidae and Nemestrinidae. A densely sampled multi-locus approach is used to contextualise the relationships of groups with disparate diversity and ecology. The compelling phylogenetic results suggests that blood-feeding, antennal structure, and larval habit, highly derived and complex character sets, may be subject to repeated convergence or loss. Vermileonidae is resolved within a paraphyletic Rhagionidae *sensu stricto*. The non-monophyly of the largest genus, *Tabanus* L., is impetus for the use of phylogenomic data to resolve outstanding questions in Tabanomorpha. Building on this foundation, several exome capture and transcriptome projects are now in progress to coalesce a robust phylogeny of the group. The era of massive data has arrived, but it must also be concomitant with productive collaborations to truly realise our shared goals as Diptera systematists.

The natural history, diversity and relationships of fern flies in the genus *Auster* McAlpine & Keyser (Teratomyzidae) *et alia* in Australia

Keith M. Bayless

Australian National Insect Collection, CSIRO, Clunies Ross St, Acton, ACT 2601, Australia. Keith.Bayless@csiro.au

Keywords: Biodiversity, insect-plant interactions, phylogeny, taxonomy, Teratomyzidae.

Although many insect lineages have diversified by feeding on angiosperm plants, few successfully inhabit ferns. The only insect family with this ecological specialisation is the poorly studied acalyptrate family Teratomyzidae. Three genera are endemic to South America (Brazil and Chile), three genera are endemic to Australia and *Teratomyza* Malloch is distributed throughout Australia, New Zealand and South-east Asia. Six of the seven genera in the family are monotypic. The endemic Australian *Auster* McAlpine & Keyser is one of the ostensibly monotypic genera, however, it includes dozens of undescribed species. This genus constitutes one of the largest radiations of fern-associated insects. A revision of *Auster* in concert with an internal phylogeny of Teratomyzidae is necessary to contextualise the evolution of this unique trait. Revisionary syntheses will be performed integrating phylogenomics, morphology and ecology. To this end, in concert with the examination of material at the Australian Museum, specimens and host association data were obtained during field expeditions throughout Australia. New host associations of teratomyzids with five genera of polypod ferns, spanning two orders were obtained. Tree ferns host a particularly diverse assemblage. The twenty-five undescribed species of *Auster* can be differentiated morphologically *via* thoracic chaetotaxy and male terminalia. Most species have narrow geographical distributions and high host specificity. Females of some species have a variety of terminalia modifications, potentially related to host oviposition site preference. This critical life history and biodiversity data was incorporated into an ongoing evolutionary study of Teratomyzidae and their relatives.

A phylogenomic approach elucidates the early diverging acalyptrate lineages of Schizophora

Keith M. Bayless[1]*, Michelle D. Trauwein[2], Sujatha Narayanan Kutty[3], Rudolf Meier[3], David K. Yeates[1] & Brian M. Wiegmann[4]

[1]Australian National Insect Collection, CSIRO, Clunies Ross St, Acton, ACT 2601, Australia. *Keith.Bayless@csiro.au
[2]California Academy of Sciences, San Francisco, U.S.A.
[3]National University of Singapore, Singapore.
[4]North Carolina State University, Raleigh, U.S.A.

Keywords: Acalyptratae, phylogeny, phylogenomics, transcriptomics.

Efforts to understand the evolutionary history of flies are obstructed by the challenge to resolve the major lineages among the acalyptrate Schizophora. Half of the superfamilies are likely not monophyletic and their interrelationships remain unclear. Strong support is lacking for branching patterns between families that contain model organisms, such as Drosophilidae, Diopsidae, Sepsidae and Tephritidae and in the placement of Calyptratae. Even the first bifurcation is controversial. Conopidae, Diopsoidea or Calyptratae + Ephydroidea have all been recently proposed to be the sister-group to the remaining Schizophora. This conundrum is approached by analysing combinations of transcriptome and anchored hybrid enrichment exome data, to yield compelling phylogenetic hypotheses of Schizophora. Calyptratae is recovered deep within the acalyptrates, allied with Ephydroidea, rendering the acalyptrates non-monophyletic. A lineage including Sciomyzoidea, Lauxanioidea and Conopidae is resolved to be the sister-group to the rest of the lineage. All other acalyptrate families can be binned into approximately five other major lineages. A reduced Sphaeroceroidea, along with an intriguing new lineage of flies with variously modified oviscapts (Nerioidea, Tephritoidea, Psilidae, Tanypezidae, Megamerinidae, Acartophthalmidae, Opomyzidae and Sepsidae) form a grade with respect to other acalyptrates and Calyptratae. This compelling novel hypothesis is examined in light of natural history and ecologically functional morphology. Sensitivity analyses exploring parameter space and taxonomic subsamples indicate that the relationships between the other major Schizophora lineages continue to be challenging to recover. This project offers a broad and robust view into the evolution of these flies through time and morphological space.

A first phylogenetic analysis of the subfamily Oscinellinae (Chloropidae)

Zeinab Bazyar* & Dalton de Souza Amorim

Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *s.z.e.bazyar@gmail.com

Keywords: Acalyptratae, Chloropidae, morphological characters, Oscinellinae, phylogeny.

The systematics of the subfamily Oscinellinae (Chloropidae) remains largely unresolved. Their small size, high species richness and the number of small, poorly described genera may have contributed to the lack of a consistent system in the group, despite important efforts made in the literature. The Oscinellinae includes 124 genera in 11 tribes. Most representatives of the subfamily are small-sized (1–3 mm in length), rather uniformly coloured flies, with the costal vein (C) extending to vein M_1 and usually with a femoral organ in males. A comparative study was conducted of features of the head, thorax, wing, legs, abdomen and male and female terminalia of 56 oscinelline genera, representatives of the two other subfamilies: Chloropinae and Siphonellopsinae, with the families Carnidae and Milichiidae as out-groups. A total of 214 morphological character were used in the analysis. Although some characters were highly plastic, some appear to be quite unique within the evolution of the subfamily. The use of successive posterior weighting of characters is recommended to prevent highly plastic characters from interfering at the first steps of the construction of the topology. Results recovered some traditionally recognised tribes as monophyletic, while others proved paraphyletic. Some genera remain unplaced and are regarded as *incertae sedis* in the classification. An increase in taxon sampling in the future will help provide additional characters and more stability to larger clades, resulting in a more stable classification of the Oscinellinae.

More than meets the eye – forensic analysis of insect stains from persons suffering from delusional insect parasitosis

Mark Benecke

International Forensic Research and Consulting, P.O. Box 250411, 50520 Cologne, Germany. forensic@benecke.com

Keywords: Delusional parasitosis, forensic examination, insects, psychosis, stains.

Delusional parasitosis, delusional infestation or Ekbom's syndrome; earlier known as "matchbox syndrome", due to the obsessive collecting of small alleged insect parts in matchboxes; is a regular occurrence in forensic consulting offices. Since the office reports on stains, *i.e.*, actual findings, but not about sanity and reason, insect parts were checked in samples provided by persons who have been determined to have psychological problems or are unwell. It was surprising to find that, together with skin and textile fibres, insect parts did regularly occur in several of the samples examined. The reasons for this were, however, not due to direct infestations with insects, but an involuntary carryover from nature and a general lack of hygiene. Over the past twenty years body parts have been examined of Diptera, Coleoptera, Chalcidoidea (Hymenoptera) and other insects that cannot and do not normally occur in or on the human body. Some cases are described, including communication of the results to clients and psychiatrists/psychologist.

Supermassive insect species loss in Germany

Mark Benecke[1]* & Martin Sorg[2]

[1]International Forensic Research and Consulting, P.O. Box 250411, 50520 Cologne, Germany.
*forensic@benecke.com
[2]Entomologische Sammlungen and Entomologischer Verein, Krefeld, Germany.

Keywords: Ecology, food chain, forensic entomology, pollination, species loss.

In the past 28 years, it appears that Germany has lost more than half, possibly more than three-quarters, of its flying insect biomass and flying insect biodiversity. In mid-summer the decline even amounted to 82% in flying insect biomass. Measurements were and will be taken in > 63 nature protection areas in Germany (96 unique location-year combinations prior to 2017), by the Entomological Society of Krefeld and associated individuals. The measurements were largely under reported until 2017 and the reasons for the steep decline are not yet known. As of spring 2018, the cause may not be global warming. During the summer of 2018 in one German county, a 30 million Euro programme was launched to address the topic and to gather further data until the autumn of 2018. Apart from obvious problems for pollination and food chains, there is also a decrease in information pertaining to forensic entomology cases, since it is preferred to use as many fly (and beetle) species as possible for determination of post-mortem interval and in cases of neglect. Recent data is presented here from the scientific evaluation and analysis of all collections, with a focus on the results of the Krefeld group, until the most recent collections from the autumn of 2018.

A review of the sensory challenges confronted by flies that feed on anuran blood

Ximena E. Bernal

Department of Biological Sciences, Purdue University, IN, U.S.A. and Smithsonian Tropical Research Institute, Balboa, Panama. xbernal@purdue.edu

Keywords: Frog-biting midges, hearing, host detection, specialisation.

Finding an appropriate victim is one of the main challenges of obtaining a blood meal. While endothermic vertebrates produce abundant and diverse cues that reveal their location, ectotherms are usually more cryptic. Specialising in feeding on ectothermic vertebrates is thus expected to result in particular sensory adaptations that increase efficiency of long distance detection of potential victims. A review is provided of our current understanding of the sensory ecology of micropredatory flies that bite anurans, in the light of their foraging strategies. Focusing on hematophagous Diptera, this presentation provides a broad perspective on the sensory adaptations that allow flies to detect and localise frogs and toads, in particular, the ability of some flies to exploit the mating calls of anurans. This strategy has evolved multiple times independently across the Diptera, potentially resulting in different solutions to a similar problem, a hypothesis that deserves further consideration. Finally, using frog-biting midges (Corethrellidae) as a study case, an evaluation is proposed of mechanisms for antennal “hearing” in flies. Overall, this presentation aims to provide an overview of the sensory and foraging ecology of flies that feed from anuran blood, highlighting current gaps in knowledge and insightful venues of future research.

Working on familiar ground – when you think you know everything there is to know …

Paul L.Th. Beuk

Natuurhistorisch Museum Maastricht, De Bosquetplein 6-7, NL-6211 KJ Maastricht, the Netherlands.
muscapaul@gmail.com

Keywords: Malaise trap, new records, new species, survey.

Western Europe is where the insect fauna is best known, because it is where “modern” entomological research began and the region enjoys a long tradition of taxonomic and faunistic research. Running a Malaise trap in such an area can still prove interesting and not only for rarely collected species that are bound to turn up. Advances in knowledge are more likely to be applied to recently collected material in need of identification, than to collections housed in museums. Changes in distribution (climatic change) are also likely to emerge. In early 2018, a Malaise trap survey was initiated to monitor the succession of insects on a slope at the ENCI limestone quarry near Maastricht in the Netherlands, that is being allowed to develop into natural chalk downs. As it progresses, results of this survey will be compared to those of Malaise trap surveys conducted in other parts of the same quarry during the last decades of the 20th century. At the halfway stage of the first year, only a few samples have been analysed, but for Diptera it turns out that the results are even more interesting than anticipated. More than 10% of the 200 species currently identified have not been formally recorded in the Dutch fauna. Two were only known from their type localities and two are apparently new to science. Several unrecorded species were also sampled at other Dutch localities, awaiting formal recording. Additionally a taxonomical problem has come to light, involving the naming of an apparently quite widespread species.

The stem-mining dolichopodid genus *Thrypticus* Gerstaecker – insect friend or foe?

Daniel J. Bickel

Australian Museum, 6 College Street, Sydney, NSW 2010 Australia. dan.bickel@austmus.gov.au

Keywords: Biological control, Dolichopodidae, Neotropical, phytophage, plant pests, *Thrypticus*.

Thrypticus Gerstaecker (Dolichopodidae) is a virtually cosmopolitan genus, the larvae of which are stem-miners in aquatic and semi-aquatic monocotyledons. It is possibly the only “orthorrhaphous” genus to become a plant miner, a life habit that probably evolved from the larval subcortical predation characteristic of its subfamily, the Medeterinae. To facilitate oviposition in plants, *Thrypticus* females have evolved a sclerotised blade-like plant piercing oviscapt, a defining synapomorphy similar to that found in Tephritidae, the true fruit flies. Water hyacinth, *Eichhornia crassipes* (Mart.) Solms (Pontederiaceae), is a serious invasive weed, with the potential to choke tropical and subtropical waterways of the world. Like most aquatic invasive plants, it is South American in origin. In its native habitat it supports a rich array of specialised herbivores, including *Thrypticus*, which are left behind when planted or escaped as an exotic ornamental. In 2002, the writer was invited to study the species of *Thrypticus* associated with water hyacinth along the Rio Parana in Argentina and its possible use as a biological control agent. *Thrypticus* also has the potential to affect agricultural plant production. In 2017 a *Thrypticus* species was discovered mining the stems of maize in Lima, Peru. The species is undescribed and probably jumped from native Poaceae to maize.

Unending diversity – open-ended taxa and the limits of taxonomy

Daniel J. Bickel

Australian Museum, 6 College Street, Sydney, NSW 2010 Australia. dan.bickel@austmus.gov.au

Keywords: Open-ended taxa, taxonomy.

The world's biota perhaps includes some 10 million morphospecies, of which some 1.7 million are described. Proposals to describe all life on Earth fail to consider the immensity of open-ended taxa, highly speciose groups that span zoogeographical regions. The true diversity of such groups cannot be accurately estimated, as they are mostly uncollected/unsorted and remain so poorly studied that only rough generic/subfamily identification is possible. Examples of open-ended taxa from the Diptera are presented. Clearly, the taxonomic description of all species is impossible, so we must consider what we are doing. Should all taxa have names and who wants to know? Is a DNA sequence attached to a centrifuge tube as satisfying as a Linnaean binomial on a pinned specimen? Undoubtedly, there are many reasons for studying taxonomy, ranging from practical economic applications (and employment) to pure pleasure (and lifetime avocation). There is no unified view. Despite the somewhat self-serving hype of taxonomists, describing taxa will not help avert environmental catastrophe. So we stumble along our way, going in some vague direction, but each on his own path. More questions might be asked than are answered.

An assessment of Afrotropical craneflies (Tipulidae), with particular focus on the fauna of Cameroon

Pete Boardman

Natural England Field Unit, Natural England, Parkway Court, Telford. TF3 4LR. United Kingdom. Pete.Boardman@naturalengland.org.uk

Keywords: Alexander, Cameroon, Churchill, craneflies, Smithsonian, Tipulidae.

In 2008, the writer was rather unexpectedly presented with some cranefly (Tipulidae) specimens resulting from an entomological expedition to Mt Kupe in Cameroon. The cranefly fauna of Cameroon is poorly understood and the *Catalogue of the Craneflies of the World* lists only 88 species in 27 genera. Most of these species were named and added by Charles Paul Alexander (1889–1981) in papers published between the 1920s and 1950s, with only a few species added subsequently by Herman De Jong in the early 2000s. The above mentioned material from Cameroon was the result of Malaise trapping at one locality and consists of approximately 95 specimens, representing an estimated minimum of forty species, therefore representing an important opportunity to advance our knowledge of the cranefly fauna of Cameroon. Early research identified several new species to Cameroon from very limited comparative material collected in the collections of the Natural History Museum, London. The remainder of the material will be compared to the C.P. Alexander Collection housed in the National Museum of Natural History, Washington D.C. during October 2018, following the award of a travelling bursary from the Winston Churchill Memorial Trust (WCMT). An updated faunal list of the craneflies of Cameroon will be presented and the faunal composition will be discussed.

A new diagnostic technique for the economically important fruit flies, *Bactrocera correcta* (Bezzi) and *Zeugodacus cucurbitae* (Coquillett) (Tephritidae) to benefit international trade

Yuvarin Boontop[1]*, Nutthima Kositcharoenkul[1] & Nopparat Buahom[2]

[1]Plant Protection Research and Development Office, Department of Agriculture, Chatuchak, Bangkok, 1900, Thailand. *yuvarin9320@gmail.com
[2]Department of Agriculture, Bangkok, Thailand.

Keywords: *Bactrocera*, diagnostic, fruit flies, Guava fruit fly, Melon fly, *Zeugodacus*.

The Guava fruit fly, *Bactrocera correcta* (Bezzi) and Melon fly, *Zeugodacus cucurbitae* (Coquillett), are quarantine pest species for many countries. Larvae of fruit flies are intercepted by quarantine inspections, but their morphological similarity makes identification difficult and unreliable. Rapid, precise identifications of immature fruit flies associated with imported/exported fresh produce is essential to ensure appropriate biosecurity decisions at quarantine barriers, or where commodities are inspected prior to export. A multiplex PCR assay was developed to identify these two species simultaneously in a single test. Species-specific primers were designed by amplifying the mitochondrial COX1 gene to differentiate *B*. *correcta* and *Z*. *cucurbitae* in their various life stages. The multiplex PCR assay demonstrated high specificity, sensitivity and reliability for both target species and revealed less than 1% intra-specific divergence for a range of 10 species examined. This study demonstrated the feasibility of using multiplex PCR diagnostic tools for identifying fruit flies of quarantine importance. Such tools will be required by the Thai biosecurity system to respond to regional trade pressures and by many other countries to cope with the ongoing threats of biological invasions.

Seasonal abundance of fruit flies (Tephritidae) on mango orchard and its relation with biotic and abiotic factors in Manica Province, Mozambique

Luis Domingos Bota[1]*, Braine Gilberto Fabião[1], Massimiliano Virgilio[2], Maulid W. Mwatawala[3], Laura Canhanga[4], Domingos Ranquene Cugala[4] & Marc De Meyer[2]

[1]National Fruit Fly Laboratory, Provincial Directorate of Agriculture and Food Security, Chimoio, P.O. Box 42, Manica Province, Mozambique. *luisbota@yahoo.com.br
[2]Royal Museum for Central Africa, Tervuren, Belgium.
[3]Sokoine University of Agriculture, Morogoro, Tanzania.
[4]Eduardo Mondlane University, Maputo, Mozambique.

Keywords: *Bactrocera*, *Ceratitis*, *Mangifera*, mango, Mozambique, population dynamics.

Mango (*Mangifera indica* L.) is a fruit species with high potential for reduction of hunger and poverty in Mozambique. However, the production of this crop is currently threatened by various fruit fly species, including *Bactrocera dorsalis* (Hendel) and *Ceratitis cosyra* (Walker) (Tephritidae). Their occurrence in Mozambique requires assessment. Both fruit flies were monitored over two consecutive mango cropping seasons from September 2014 to August 2016 on 10 ha of a commercial mango orchard in Vandúzi District, Mozambique. Trapping activities were conducted using Chempac Bucket traps baited with food attractant (torula yeast). Temperature and host phenology data were recorded at the orchard, while rainfall data were obtained from a meteorological station located 10 km away. Fruit fly populations were present in the orchard over the entire trapping period (for *B. dorsalis*); or absent at some periods during vegetative stages of the mango (for *C. cosyra*). For both seasons, the population of *B. dorsalis* peaked in January. For *C. cosyra*, the peak was observed in January of the first cropping season, while it was observed in November of the second season. The population of both species varied between the seasons, but in general *B. dorsalis* was more abundant than *C. cosyra* (average relative abundance index RAI = 0.814). The *B. dorsalis* population density had a positive relationship with minimum temperatures and mango phenology stages and a negative relationship with average temperatures, while the population of *C. cosyra* had a positive relationship with minimum temperatures.

Biodiversity and systematics of leaf-miner flies (Agromyzidae) in Costa Rican cloud forests

Stéphanie Boucher

Lyman Entomological Museum, McGill University, Ste-Anne-de-Bellevue, Quebec, H9X 3V9, Canada. stephanie.boucher@mcgill.ca

Keywords. Agromyzidae, biodiversity, cloud forest, Costa Rica, Neotropical Region, systematics.

Cloud forests are recognised globally for their conservation and biodiversity value. These forests are now listed as one of the most threatened ecosystems on Earth and biodiversity research is a priority to help understand this fragile ecosystem. This study investigated the biodiversity and systematics of the leaf-miner flies (Agromyzidae), occurring at three different cloud forest sites, at approximately 1,600 m elevation in Costa Rica. Flies were sampled over a period of one year as part of a larger and intensive biodiversity project, known as the Zurquí All-Diptera Biodiversity Inventory (ZADBI). A total of 976 specimens of Agromyzidae were collected, resulting in the identification of 158 species (or morphospecies). This number is surprisingly high, considering that only 65 species of Agromyzidae were previously recorded from Costa Rica. Of the total of 14 previously known Neotropical genera of Agromyzidae, 12 were sampled at the cloud forest sites, in addition to the genus *Metopomyza* Enderlein, previously unreported from the Neotropical Region. The Agromyzidae fauna of these cloud forest sites were dominated by the genus *Liriomyza* Mik (31 sp.), followed closely by *Melanagromyza* Hendel (30 sp.) and *Phytoliriomyza* Hendel (26 sp.). Distribution patterns, species range extensions and endemism are also discussed.

Taxonomy of *Dasyhelea* Kieffer (Ceratopogonidae) – an Indian perspective

Shubhranil Brahma* & Niladri Hazra

Entomology Research Unit, Department of Zoology, University of Burdwan, Burdwan, West Bengal, India. *shubhra634@gmail.com

Keywords: Biting midges, immature stages, India, Oriental Region, taxonomy.

The nematocerous family Ceratopogonidae, commonly known as “biting midges”, is an extremely diverse group that inhabits a broad range of aquatic, semi-aquatic and terrestrial habitat types. The genus *Dasyhelea* Kieffer is widely distributed and is recorded from all zoogeographical regions, except Antarctica. Prior to this study, there were more than 600 species described globally, including *ca* 127 species from the Oriental Region; with only 21 species recorded from India. The present study reports on 14 additional species from India, comprising nine species new to science and five described from elsewhere. Among the 14 species, nine are recorded as adults and five species resulted from the rearing of immature stages. Pupal morphology and ecology of the respective species are presented here. Prior to this research, there was no knowledge regarding the immature stages of *Dasyhelea* from India. Further samplings of additional localities in the country are required in order to acquire a more comprehensive portrait of the genus. Results of a study of seasonal abundance of species was also undertaken using both UV (8W) and white (15W) light traps in the University of Burdwan campus and these results are also presented here.

Phorid fly diversity – frontiers in species richness, structure and behaviour

Brian V. Brown

Entomology Section, Natural History Museum of Los Angeles County, 900 Exposition Boulevard, Los Angeles, CA, U.S.A. 90007. bbrown@nhm.org

Keywords: Automated identification, bioinventory, Phoridae, tropical, urban, wing venation.

The Phoridae are one of the most species-rich families of flies, with thousands of undescribed species, dozens of undescribed genera and large parts of the world still unsampled. Following a review of some of the most spectacular and bizarre phorid flies, what this diversity means to researchers will be discussed, especially the special difficulties it presents for species inventories. Use of wing venation for semi-automated identification of the largest genus of phorids, *Megaselia* Rondani, is explored and applied to two major inventory projects. A system that provides greater than 95% identification accuracy is presented, along with suggestions about how it could be applied to large-scale projects.

Fossils – what do “Burmese amber” Phoridae tell us about evolution in the family?

Brian V. Brown[1]* & John Hash[2]

[1]Entomology Section, Natural History Museum of Los Angeles County, 900 Exposition Boulevard, Los Angeles, CA, USA. 90007. *bbrown@nhm.org
[2]Smithsonian Institution, Washington D.C., U.S.A.

Keywords: Cretaceous, evolution, fossils, Myanmar, Phoridae.

Newly available Cretaceous amber from Myanmar (“Burmese amber”) contains fossils of the earliest “true” (non-sciadocerine) phorids and hones our understanding of what character states define the group. The sciadocerine phorids are a potential grade group for which no convincing synapomorphies have yet been proposed.

A phylogenomic perspective of the Oestroidea (Calyptratae) using ultraconserved elements and historical museum specimens

Eliana Buenaventura[1]*, John O. Stireman, III[2], Thomas Pape[3], Pierfilippo Cerretti[4], Arianna Thomas-Cabianca[5], Michael W. Lloyd[1] & Torsten Dikow[1]

[1]National Museum of Natural History, Smithsonian Institution, Washington D.C., U.S.A. *elianabuenaventura@gmail.com; [2]Wright State University, Dayton, U.S.A.; [3]Natural History Museum of Denmark, Copenhagen, Denmark; [4]Sapienza Università di Roma, Rome, Italy; [5]Universidad de Alicante, Alicante, Spain.

Keywords: Calliphoridae, Mesembrinellidae, Oestridae, phylogenomics, Rhiniidae, Rhinophoridae, Sarcophagidae, Tachinidae.

The diverse superfamily Oestroidea (~15,000 species) includes blowflies, flesh flies and botflies among other well-known dipteran groups. The Oestroidea exhibit strikingly divergent morphological and ecological traits. Previous phylogenetic studies, including Oestroidea species utilising a variety of data sources and inference methods, have failed to reach a consensus on the relationships among major lineages. Targeted enrichment of ultraconserved elements or UCEs has emerged as a promising tool for resolving difficult phylogenetic problems at varying timescales in many taxa. A UCE probe set was developed to examine the utility of UCEs for reconstructing phylogenetic relationships among families of the Oestroidea. This dataset included ~2,500 UCE loci from 180 representatives of all oestrid families, except Ulurumyiidae and Mystacinobiidae, and six calyptrate out-groups, with a total concatenated length of more than 61 Mb. About 35% of the sampled taxa consisted of museum specimens (0.25–64 years old), of which 80% resulted in successful enrichment. Concatenated analyses using maximum likelihood produced well-resolved and highly supported trees. Most families were recovered as monophyletic (exceptions: Calliphoridae and Oestridae). Oestroidea was recovered as monophyletic, with Mesembrinellidae as sister to the remaining oestroid families. Rhinophoridae was sister to (Luciliinae (Toxotarsinae (Melanomyinae + Calliphorinae))), Phumosiinae sister to Chrysomyinae, Bengaliinae sister to Rhiniidae and Polleniinae sister to Tachinidae. Oestridae was paraphyletic with regard to Sarcophagidae. These results support the ranking of most calliphorid subfamilies as separate families. This phylogenetic hypothesis conflicts with some morphological data, but is largely consistent with recent molecular phylogenies, but with greater branch support.

An anchored hybrid enrichment-based dataset challenges the traditional classification of flesh flies (Sarcophagidae)

Eliana Buenaventura[1]*, Krzysztof Szpila[2], Brian K. Cassel[3],
Brian M. Wiegmann[3] & Thomas Pape[4]

[1]National Museum of Natural History, Smithsonian Institution, Washington D.C., U.S.A. *elianabuenaventura@gmail.com
[2]Nicolaus Copernicus University, Toruń, Poland.
[3]North Carolina State University, Raleigh, U.S.A.
[4]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Anchored phylogenetics, hybrid enrichment, Miltogramminae, Oestroidea, Paramacronychiinae, Sarcophaginae, systematics.

The Sarcophagidae are one of the most specious families within the superfamily Oestroidea. This diversity is represented by three lineages: Miltogramminae, Paramacronychiinae and Sarcophaginae. Historically, the phylogenetic relationships among these lineages have been elusive, due to poorly supported hypotheses, small taxon sets or both. Thus, a dramatic increase in molecular data, a balanced sampling of all three lineages from all zoogeographical regions and a re-assessment of morphological characters using SEM make this the first attempt at elucidating the subfamilial phylogeny in Sarcophagidae from a holistic perspective. This analysis of the largest molecular dataset ever produced for the phylogenetic analysis of an insect family, with 985 loci and 450,759 bp., from 89 species, revealed Paramacronychiinae as sister to Miltogramminae, not to Sarcophaginae, as suggested by morphological characters. Maximum likelihood analysis produced a completely resolved topology with 91% of the nodes receiving strong bootstrap proportions (> 97%). In strong contrast to the molecular data, three out of five morphological characters studied here point to the sister-group relationship of (Sarcophaginae + Paramacronychiinae) and the remaining two characters are either symplesiomorphic or in need of further study. The phylogeny reconciles older and widely used systems of classification with tree-based thinking and sets up a classification of flesh flies to conform to their evolutionary history. With a strong conflict between molecular and morphological characters, this study provides new insights into the evolution of male genitalic traits within the Sarcophagidae and promotes the use of molecular and anatomic data in the systematics of Diptera.

Multigene-phylogeny of the rapidly diversified Palaeogene tribe Exechiini (Mycetophilidae)

Nikola Burdíková[1], Jostein Kjaerandsen[2], Jon Peder Lindemann[2]*, David Kaspřák[1], Andrea Tóthová[3] & Jan Ševčík[1]

[1]Department of Biology and Ecology and Institute of Environmental Technologies, Faculty of Science, University of Ostrava, Ostrava, Czech Republic.
[2]Tromsø University Museum, UiT – The Arctic University of Norway, Tromsø, Norway. *jon.p.lindemann@uit.no
[3]Masaryk University, Brno, Czech Republic.

Keywords: Bibionomorpha, fungus gnats, insect systematics, molecular markers, phylogenetic analysis, Sciaroidea.

According to known fossil records and recent higher-level phylogenies, the fungus gnat tribe Exechiini constitutes the most apomorphic, distinctly monophyletic clade of the family Mycetophilidae. The tribe originated in the Palaeogene and apparently quickly diversified in the Neogene, with an unusually rapid radiation of complex male terminalia. Currently, it comprises *ca* 700 recognised species, placed in 20 described genera, but additional unnamed species certainly count in the hundreds. Earlier attempts to reconstruct the phylogeny of the tribe, based on both morphology and molecular methods, have not yielded reliable hypotheses, either in terms of resolution, nor in terms of support for major clades. Increased taxon sampling and wider gene sampling have been suggested to achieve better phylogenetic resolution. Aiming at this, a new phylogeny is proposed, based on the combined analysis of four nuclear and two mitochondrial gene markers, with all known genera and subgenera of Exechiini represented. While many terminal intergeneric relationships are well supported, most of the major, deeper clades remain poorly supported. It is suggested that a rapid radiation event close to the root may be causing the low resolution at this level in the phylogeny. This contrasts with phylogenies of the older subfamilies and tribes of the family Mycetophilidae, where traditional clades are usually recovered with high support. Further in-depth studies of the evolutionary history of the Exechiini are needed to determine the specific phenomena driving their unique morphological, genetic and phylogeographic histories.

Big data, big challenges – resolving the phylogenetic relationships of the subfamily Syrphinae (Syrphidae) with target DNA enrichment

Trevor O. Burt[1]*, Thomas Pauli[1, 2], Gaby Nottebrock[1], Sandra Kukowka[1], Andrew D. Young[3, 4], Kevin M. Moran[3, 4], Scott Kelso[3], Claudia Etzbauer[1], Ralph S. Peters[1], Alexander Donath[1], Christoph Mayer[1], Kurt Jordaens[5], Gunilla Ståhls[6], Shanlin Liu[7, 8, 9], Xin Zhou[10, 11], Jeffrey H. Skevington[3], Oliver Niehuis[1, 2], Bernhard Misof[1] & Ximo Mengual[1]

[1]Zoologisches Forschungsmuseum Alexander Koenig, Leibniz Institut für Biodiversität der Tiere, Adenauerallee 160, D-53113 Bonn, Germany. *trevburt@gmail.com; [2]University of Freiburg, Freiburg, Germany; [3]Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa, Canada. [4]Carleton University, Ottawa, Canada; [5]Royal Museum for Central Africa, Tervuren, Belgium; [6]Finnish Museum of Natural History, Helsinki, Finland; [7]China National GeneBank-Shenzhen, Shenzhen, China; [8]BGI-Shenzhen, Shenzhen, China; [9]University of Copenhagen, Copenhagen, Denmark; [10]Beijing Advanced Innovation Center for Food Nutrition and Human Health, Beijing, China; [11]China Agricultural University, Beijing, China.

Keywords: Anchored hybrid enrichment, new-generation sequencing, molecular phylogeny, bait design, flower flies, hoverflies.

A transcriptomic library comprising 19 taxa from the 1KITE project was used to design baits specific to the family Syrphidae in an attempt to resolve the phylogenetic relationships of the subfamilies, tribes and genera. Orthographic prediction resulted in more than 2,000 orthologous genes, with > 2,100 features or 2,899,920 base pairs, aligned with the reference genome of *Drosophila melanogaster* Meigen (Drosophilidae). BaitFisher was used to design baits (also known as probes) of 120 bp length and an offset of 60. After applying optimality criteria, the newly designed bait kit, Syrphidae 1.0, has 2,044 features of 1,357 genes, requiring 24,877 baits. The dual-indexed captured library was enriched with Illumina high-throughput sequencing (MiSeq) with guaranteed 25 million reads. Fifty percent of the genes targeted are part of the BUSCO (Benchmarking sets of Universal Single-Copy Orthologs) gene set. Targeted sequences were captured for 192 taxa from all subfamilies with emphasis on Syrphinae with only one fail. The average success rate of the enrichment of the targeted genes was 75%. COI sequences for each specimen were joined with enriched data to form a large-scale molecular matrix to explore the phylogenetic relationships of the subfamily Syrphinae (Syrphidae).

The smelly sex lives of blowflies (Calliphoridae)

Nathan J. Butterworth[1]*, Philip G. Byrne[1], Paul A. Keller[2] & James F. Wallman[1]

[1]Centre for Sustainable Ecosystem Solutions, School of Biological Sciences, University of Wollongong, NSW 2522, Australia. *nb187@uowmail.edu.au
[2]University of Wollongong, Wollongong, Australia.

Keywords: Behaviour, Calliphoridae, hydrocarbon, pheromone, sexual selection.

Blowflies (Calliphoridae) are a biodiverse family that occupy a wide range of ecological niches. In carrion-breeding species, adults aggregate and breed around decaying animal matter, which is an ephemeral and speciose environment. Under these conditions, there is intense competition for mates and a high risk of misguided mating investment. As such, it is likely that blowflies have evolved highly specific sexual signals to mediate mate recognition and sexual attraction. Most observations of blowfly sexual behaviour have focused on visual cues, which appear to be an important aspect of blowfly communication. By contrast, very little attention has been given to chemical communication in blowflies, which is also likely to be important considering the prevalence of pheromones throughout other calyptrate fly groups. One type of pheromone common amongst Diptera are cuticular hydrocarbons (CHCs), which are long-chain hydrocarbons expressed on the cuticle of virtually all insects. Within Calliphoridae, CHCs have been found to be highly species-specific. There is no evidence, however, that they facilitate sexual communication. To assess whether CHCs may have a communicative function in blowflies, behavioural assays, gas-chromatography mass-spectrometry and genetic data were combined to analyse the CHCs of several Australian blowfly species. This presentation reports species- and sex-specific differences and discusses the potential role for CHCs to mediate the sexual behaviour of flies.

General dipterology

The role of host phylogeny in shaping the diversity of bee fly (Bombyliidae) microbiomes

Allan Cabrero[1]*, Aman Gill[1], Kipling Will[1] & Patrick O'Grady[2]

[1]Enviromental Science, Policy and Management Department, Organisms and Environment Division, University of California Berkeley, California 94720, U.S.A.*acabrero@berkeley.edu
[2]Cornell University, Ithaca, U.S.A.

Keywords: Bee flies, Bombyliidae, microbiome, parasitoid, phylogeny.

A growing interest in the field of evolutionary biology has been the study of host-associated microorganisms. Studies have shown that these microbial communities can influence a host's behaviour, development and even speciation. Bombyliidae, or bee flies, are a large family of ~5,000 species. These pollinating flies have a virtually cosmopolitan distribution, with a large amount of diversity found in arid and semi-arid regions. Bee fly larvae are parasitoids of other insects and are an ideal group to study parasitoid evolution within the Diptera, as the family includes species that exhibit ecto-, endo- and hyperparasitic life histories. Given the diverse parasitic life histories, this study sets out to understand how host phylogeny and ecology influence the resident microbial communities. Thirty-four samples were collected representing seven subfamilies, 17 genera of Bombyliidae and two samples representing the sister-group Mythicomyiidae. Bacterial communities of each specimen were characterised using 16s rRNA gene sequencing. Preliminary results indicate that the composition and diversity of resident microbial communities are shaped by both host phylogeny and ecology. These results provide a baseline understanding of the resident bacterial communities across the Bombyliidae, which will help with future studies in understanding how bacterial communities influence host selection and diversification within the Bombyliidae.

A revision of *Aphestia* Schiner (Asilidae: Laphriinae) with the description of nine new species

Alexssandro Camargo da Silveira[1]* & Rodrigo Vieira[2]

[1]Instituto Nacional de Pesquisas da Amazônia-INPA, Campus II, CEP 69067-375, Av. André Araújo, 2936, Petrópolis, Manaus, Amazonas, Brazil. *alexssandroecs@gmail.com
[2]Secretaria de Estado de Educação do Governo do Amazonas-SEDUC, Manaus, Brazil.

Keywords: Assassin flies, Atomosiini, new species, robber flies, revision, terminalia.

A revision of the Neotropical asilid genus *Aphestia* Schiner was undertaken. The genus is characterised by the antennal postpedicel *ca* 2.5 × the length of the scape and pedicel combined and by the mystacal macrosetae covering the entire face. Previously, *Aphestia* comprised three valid species: *A*. *annulipes* (Macquart) and *A*. *nigra* Bigot, with three and two junior synonyms (respectively), which occur throughout the Neotropics, and *A*. *chalybaea* von Roeder recorded from Australia. Since the description of the genus *ca* 150 years ago, it has not been the subject of a dedicated revision and the assignment of the Australian species has not been tested. Moreover, the male and female terminalia of the genus have never been described. Name-bearing types of the three described species were examined, together with 367 additional specimens obtained through loans from national and international collections. *Aphestia brasiliensis* Schiner, previously considered to be a junior synonym of *A*. *annulipes*, was revalidated and nine new *Aphestia* species described. It was also confirmed that the Australian *A*. *chalybaea* is not congeneric with Neotropical species of the genus and this species is transferred to the Australian genus *Cyanonedys* Hermann. *Aphestia* is, as a result, now endemic to the Neotropical Region with 12 valid species. An illustrated dichotomous identification key to *Aphestia* species is presented and the geographical distribution of species is outlined.

Phylogenomic and morphological analysis of *Tabanus* L. (Tabanidae) – Neotropical species-groups divergence times and the identification of monophyletic lineages

Daniel D.D. Carmo[1]*, Augusto Loureiro Henriques[1], Charles M.D. Santos[2] & Brian M. Wiegmann[3]

[1]National Institute of Amazonian Research, Biodiversity Coordination, Manaus, Amazonas, Brazil. *dandorndias@gmail.com
[2]Federal University of ABC, São Paulo, Brazil.
[3]North Carolina State University, Raleigh, U.S.A.

Keywords: Anchored hybrid enrichment, Neotropical Region, phylogenetic analysis.

With *ca* 1,350 valid species, *Tabanus* L. includes nearly one-third of the species of Tabanidae (Brachycera), distributed in all zoogeographical regions of the world, except Antarctica. Despite being well known and economically important flies, there are still no widely sampled, published phylogenetic hypothesis focusing on species of *Tabanus*. Reconstructing phylogenetic relationships of a genus as species-rich as *Tabanus* is not a trivial task. As a first attempt at large scale higher-level analysis, sampling efforts were focused on species-groups of *Tabanus*, especially those distributed in the Neotropical Region. Using anchored hybrid enrichment (AHE), a phylogenomic dataset of 193 loci was obtained for 45 horse fly species, and 54 internal and external morphological characters were scored for 88 terminals. Results show *Tabanus* to be polyphyletic and suggest the existence of at least two Neotropical monophyletic lineages of potentially new generic rank. Bayesian divergence time estimation of the phylogenomic dataset places the origin of *Tabanus* in the Palaeocene, followed by radiations of several Neotropical lineages between the Eocene and Miocene.

Fruit flies (Tephritidae: Tephritinae) from Palmas, Paraná, Brazil – new records of flies and their host-plants

Zenilda F. Carneiro[1], Adriana C. Pereira[2]* & Marcoandre Savaris[3]

[1]Universidade Tecnológica Federal do Paraná-UTFPR, Campus Pato Branco, Setor de Agronomia, Pato Branco, Paraná, Brazil.
[2]Instituto Federal do Paraná, Palmas, Brazil. *adriana.couto@ifpr.edu.br
[3]Escola Superior de Agricultura "Luiz de Queiroz", Piracicaba, Brazil.

Keywords: Asteraceae, Brazil, fruit flies, host-plants, interaction, Paraná.

Tephritidae is represented by 4,911 species in *ca* 500 genera. It is a virtually cosmopolitan family and its wide distribution is probably directly related to the distribution of its host-plants. This study aims to contribute to knowledge of species of the subfamily Tephritinae (Tephritidae) in Palmas, Paraná and its interaction with Asteraceae host-plants. Asteraceae capitula in the pre-anterosis stage were collected in urban and rural areas of Palmas, between February and August 2015, in search of those infested with third-instar larvae and puparia. Capitula were collected and kept for 30 days to allow for the eclosion of adults, being inspected every two days. The identification of adults was performed using identification keys and host-plants were identified in the Botanical Garden, Curitiba. Thirty species of Asteraceae were sampled, but tephritines only emerged from 43.3% of plant species. A total of 110 specimens of Tephritidae emerged, representing the genera *Dioxyna* Frey (*n* = 22), *Paracantha* Coquillett (*n* = 31), *Plaumannimyia* Hering (*n* = 50), *Rachiptera* Bigot (*n* = 1), *Tomoplagia* Coquillett (*n* = 1) and *Xanthaciura* Hendel (*n* = 5). *Plaumannimyia* represented 45.44% of the total number of emerged flies and were reared only from *Baccharis* species. *Paracantha* which represented 28.19% of emerged flies where specifically associated with a single unidentified species of Asteraceae. A graphic representation is provided of all associations between Tephritidae and Asteraceae. *Paracantha australis* Malloch, *Plaumannimyia pallens* Hering and *D*. *peregrina* (Loew) were found to be dominant species in the Palmas area.

Reclustering the cluster flies (Oestroidea: Polleniidae)

Pierfilippo Cerretti[1]*, John O. Stireman III[2], Silvia Gisondi[1, 3] & Thomas Pape[3]

[1]Sapienza University of Rome, Department of Biology and Biotechnologies ‘Charles Darwin’, Entomology - Piazzale Aldo Moro 5, 00185, Rome, Italy. *pierfilippo.cerretti@uniroma1.it
[2]Wright State University, Dayton, U.S.A.
[3]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Evolution, molecular phylogeny, Oestroidea, parasitoids, phylogeny, Polleniidae, Rhinophoridae.

A combination of 70 morphological traits and sequence data were used from three nuclear protein-coding genes (CAD, MAC, MCS) for a selection of 27 oestroid taxa to resolve the phylogenetic position of six taxa previously assigned to the oestroid family Rhinophoridae. These taxa included species of the *carinata*-group, all Afrotropical, originally assigned to the rhinophorid genus *Phyto* Robineau-Desvoidy and *Alvamaja chlorometallica* Rognes, the last named recently described from the Balkans, based on three male specimens. The analyses revealed strong support for placement of these taxa as representatives of the resurrected family Polleniidae (formerly a subfamily of the Calliphoridae). The family Polleniidae is widespread throughout the Holarctic and Palaeotropical realms, including the Australasian Region, with seven genera and 144 species. These results indicate that the clade is also present in the Afrotropical Region. Despite an apparent lack of unambiguous morphological synapomorphies supporting the Polleniidae, the family emerged as monophyletic, with strong statistical support, indicating a robust molecular signal. Moreover, in agreement with most recent phylogenetic reconstructions, polleniids were placed as sister to the Tachinidae.

The invasive gall midge *Litchiomyia chinensis* Yang & Luo (Cecidomyiidae) on Lychee in Taiwan

Yi-Min Chao*, Sheng-Feng Lin & Man-Miao Yang

Department of Entomology, National Chung Hsing University, 145 Xingda Road, South District, Taichung City, Taiwan. *wert6213217@gmail.com

Keywords: Biocontrol agent, Cecidomyiidae, crop, invasive species, IPM, parasitoid, pest.

Lychee, *Litchi chinensis* Sonn. (Sapindaceae), is an important economic crop in subtropical regions of the world, with an annual yield of 2.5 million tonnes globally. Cultivation covers almost 800,000 ha^2 and the crop is grown in Australia, Central and South America, France, Hawaii, India, Israel, Madagascar, Mauritius, Myanmar, South Africa, Taiwan, West Indies and many other countries. Among the pests of the crop, one potentially invasive species, the Lychee gall midge (*Litchiomyia chinensis* Yang & Luo), has received increasing attention in recent years. Its first occurrence in China was noted in 1999 and it was later recorded from the east coast of Australia and from Chiayi County, Taiwan in 2008. Lychee gall midge induces blister galls on leaves, which can cover most of the leaf surface and reduce photosynthesis. After the mature larva exits the gall and drops into the soil to pupate, the resulting exit holes on leaves also enable secondary infections by plant pathogens. In this presentation, a summary is given of a damage evaluation and control study and the latest information is provided on the prevalence of Lychee gall midge in Taiwan. Detailed biological information on Lychee gall midge is also outlined, based on recent studies, including population dynamics, life cycle, gall development, other countries of potential invasive threat and parasitoid associations. Potential biocontrol agents for the midge include five species of Hymenoptera in three families. Results provide fundamental information to improve the control efficiency of integrated pest management on Lychee.

Poster

Phylogeny of the tribe Adramini (Tephritidae) – new insight from combined analysis of morphological and molecular evidence

Xiao-lin Chen[1]*, Allen N. Norrbom[2], Amnon Freidberg[3], Md Sajedul Islam[4] & Chao-dong Zhu[5]

[1]Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China. *xlchen@ioz.ac.cn
[2]ARS-USDA, Washington D.C., U.S.A.
[3]Tel Aviv University, Tel-Aviv, Israel.
[4]Pennsylvania State University, Pennsylvania, U.S.A.
[5]Chinese Academy of Sciences, Beijing, China.

Keywords: Adramini, morphological and molecular evidence, new genera, phylogeny, Tephritidae.

Species of the tribe Adramini (Tephritidae: Trypetinae) are usually slender in general appearance. A few species have the eyes borne at the long ends of stalks. The tribe is mainly distributed in the tropics and subtropics of the Afrotropical, Australasian and Oriental Regions. The phylogeny of Adramini is presented, based on a total evidence analysis of morphology and DNA sequences of nuclear 28S rDNA, the mitochondrial cytochrome c oxidase I (COI), the mitochondrial cytochrome c oxidase II (COII) and the mitochondrial 16S ribosomal (16S rDNA) genes for representative species in a majority of the genera of the tribe. The results recovered good support for the monophyly of Adramini and for most of the genera, although *Euphranta* Loew appears to be paraphyletic. *Sapadrama* Hancock & Marshall, *Celidodacus* Hendel and *Euphranta* are early branching clades and *Coelopacidia* Enderlein, *Soita* Walker and *Trypanophion* Bezzi are closely related to the stalk-eyed fruit flies (*Pelmatops* Enderlein + *Pseudopelmatops* Shiraki). Moreover, two main clades (clade I + clade II) were recovered by the morphological data analysis; meanwhile, four clades (clade I + clade II + clade III + clade IV) were recognised by analysis of the combined dataset of DNA sequences alone and the combined morphological and molecular dataset. A hypothesis of the morphology-functional relationships of clade I and clade II with different evolving probabilities is inferred. Two new genera, *Chloroeuphranta* Chen & Freidberg and *Ichneumonmacula* Chen & Norrbom are described and an identification key to all genera of Adramini of the world is provided.

A pilot study to delimit *tsetse* target populations in Zimbabwe

Gerald Chikowore[1]*, Ahmadou H. Dicko[2], Peter Chinwada[3], Moses Zimba[3], William Shereni[1], François Roger[2], Jérémy Bouyer[4] & Laure Guerrini[2]

[1]Tsetse Control Division, Department of Livestock and Veterinary Services, Ministry of Lands, Agriculture and Rural Resettlement, P.O. Box CY52, Causeway, Harare, Zimbabwe. *gkchikore@gmail.com
[2]Centre de Coopération Internationale en Recherche Agronomique pour le Développement, Montpellier, France.
[3]University of Zimbabwe, Harare, Zimbabwe.
[4]International Atomic Energy Agency, Vienna, Austria.

Keywords: Probability model, species distribution, *tsetse*, Zimbabwe.

Tsetse (Glossinidae) are cyclical vectors of human and animal trypanosomoses currently targeted by the African Union, under the Pan African Tsetse and Trypanosomiasis Eradication Campaign (PATTEC). Elaborate plans to guide intervention are a requirement if effective control of *tsetse* is to be achieved. A model to aid the planning of intervention programmes and assist a fuller understanding of *tsetse* distribution was applied in a pilot study covering 400 km^2 in Masoka, Zimbabwe and targeted two savanna species, *Glossina morsitans morsitans* Westwood and *Glossina pallidipes* Austen. Current data were used to study habitat suitability of both species, based on climatic and environmental data derived from MODIS and SPOT 5 satellite images. Factors influencing distribution were explored, using an Ecological Niche Factor Analysis (ENFA), whilst habitat suitability was predicted using a Maximum Entropy (MaxEnt) model at a spatial resolution of 250 m. Area Under the Curve (AUC), an indicator of model performance, was 0.89 for *G. m. morsitans* and 0.96 for *G. pallidipes*. The probability that flies were really absent from grid cells where they were not captured during the study was then calculated, based on a probability model using a risk threshold of 0.05. Apart from grid cells where *G. m. morsitans* and *G. pallidipes* were captured in the study area, there was a high probability of presence in additional grid cells adding up to 128 km^2 and 144 km^2 respectively. The modelling process promised to be useful in optimising the outputs of presence/absence surveys, allowing the definition of *tsetse* infested areas with improved accuracy.

Taxonomic revision of the subgenus *Apiocera* (*Anypenus* Philippi) (Apioceridae)

Brandon Claridge[1]* & Torsten Dikow[2]

[1]Utah State University, 5305 Old Main Hill, Logan, Utah, 84322, U.S.A.
*brandon.claridge@aggiemail.usu.edu
[2]National Museum of Natural History, Washington D.C., U.S.A.

Keywords: Argentina, Chile, revision, taxonomy, Neotropical Region.

The South American species of Apioceridae are revised. The nominal genus in the family, *Apiocera* Westwood, has been recorded from the Neotropical Region with two subgenera: *A.* (*Anypenus* Philippi) from Chile and *A.* (*Pyrocera* Yeates & Irwin) from southern Mexico. The regional faunas of *Apiocera* have been revised over the years and the Australian (74 species) and North American (68) faunas are the most diverse while the Afrotropical fauna is the most species-poor with only three known species. The South American species were dealt with by Artigas in 1970 who recognised four species. Since then, new material has accumulated in several natural history collections from Chile, as well as for the first time from neighbouring Argentina, thereby initiating the current study. The four previously known species are recognised in this study and ten new species are described, four from Chile for a total of eight from that country and six from Argentina for a total species diversity of 14 South American species. *Anypenus* is, therefore, shown to have a much wider distribution in South America and is not restricted to the narrow strip west of the Andes. Species are also found east of the Andes in western Argentina, such as in Catamarca, La Rioja and Mendoza Provinces, but also from further east in La Pampa and Santiago del Estero Provinces. Additionally, significant aspects of morphology, biogeography and seasonal incidence of *Anypenus* species are discussed.

The old and the new – African Anophelinae (Culicidae) and malaria transmission

Maureen Coetzee[1, 2]*, Ashley Burke[1, 2], Leonard Dandalo[1, 2], Erica Erlank[1, 2], Givemore Munhenga[1, 2], Yael Dahan-Moss[1, 2], Richard H. Hunt[1], Lizette L. Koekemoer[1, 2] & Basil D. Brooke[1, 2]

[1]Wits Research Institute for Malaria, MRC Collaborating Centre for Multidisciplinary Research on Malaria, Faculty of Health Sciences, University of the Witwatersrand, 7 York Avenue, Parktown, Johannesburg 2001, South Africa. *maureen.coetzee@wits.ac.za

[2]Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Johannesburg, South Africa.

Keywords: Anophelinae, malaria, mosquitoes.

Several families of Diptera include species that transmit pathogens to humans and animals. Of these, Culicidae is probably the most extensively studied, because of mosquitoes' involvement in transmission of human parasites (malaria and filaria) and arboviruses around the globe. After it was demonstrated, 120 years ago, that malaria parasites are transmitted to humans by female anopheline mosquitoes, the taxonomic study of this group blossomed. The major African malaria vectors were both described in 1900 (*Anopheles costalis* Loew [later named *An*. *gambiae* Giles] and *An*. *funestus* Giles) and since then, over 140 species have been described from the Afrotropical Region. The presence of species complexes (good biological species that appear morphologically identical, but that may have very different behaviours), was recognised in Europe in the 1920s. With the advent of genetical tools (simple Mendelian inheritance, cytogenetics and molecular biology), it became apparent that species complexes were the rule rather than the exception and the identification of members of these complexes became critical for vector surveillance and control. Today, new species are still being discovered and "old" species are being implicated in malaria transmission, where previously they were thought not to be involved. So, despite almost 120 years of extensive research into the African malaria vector mosquitoes, there is still much we have yet to discover and many hurdles to overcome before the ultimate goal of malaria eradication is reached.

An overview of Australian Dasypogoninae (Asilidae)

Chris Cohen* & Michael Brewer

Department of Biology, East Carolina University, 1000 E 5th St, Greenville, NC 27858, U.S.A. *myelaphus@gmail.com

Keywords: Asilidae, Australia, phylogeny, systematics, UCEs.

Assassin flies or robber flies (Asilidae) are a highly charismatic family of venomous predators, but like many flies, they are remarkably understudied. In the subfamily Dasypogoninae, for example, nearly half of Australia's generic diversity remains to be formally described. This may represent the largest unknown component of a region's fauna in all of Asilidae. The subfamily is traditionally united by the presence of a large spur on the fore tibia, but this trait has been shown to be homoplastic in assassin flies. More work is, therefore, required to evaluate characters useful for delimitation of this group. As a critical step toward understanding the evolution and diversity of Dasypogoninae, the Australian fauna is here reviewed and a roadmap for much needed revisionary systematics is presented. Previous phylogenetic hypotheses are considered and a subset of relationships derived from a UCE family-level phylogeny are discussed in more detail.

Towards an improved classification of robber flies (Asilidae) using ultraconserved elements

Chris Cohen[1]*, Katherine Noble[2], Jeff Cole[1] & Michael Brewer[1]

[1]Department of Biology, East Carolina University, 1000 E 5th St, Greenville, NC 27858, U.S.A.
*myelaphus@gmail.com
[2]University of Utah, Salt Lake City, U.S.A.

Keywords: Assassin flies, Asilidae, phylogenomics, phylogeny, robber flies, systematics, UCEs.

The most recent classification organises robber flies (Asilidae) into 14 subfamilies. Not all workers accept this arrangement, however, and many genera remain unplaced. Previous phylogenetic studies utilising morphology or traditional molecular markers have struggled to provide strong support for many clades, lending further uncertainty to these subfamily relationships. A dataset consisting of hundreds of UCE loci was, therefore, leveraged to infer the best supported comprehensive phylogeny of Asilidae to date. Comparisons of loci recovery, support values, topology and phylogenetic informativeness are made between UCEs and other types of loci. Implications for the subfamily classification and the evolution of select morphological characters are also discussed.

Succulent plant niches and unexplored insect diversity – the gall midges (Cecidomyiidae) of Aizoaceae in South Africa

Jonathan F. Colville[1, 2]*, Stephany Van Munster[3, 4], Cornelia Klak[3], Anthony R. Magee[4, 5], J. Stephen Boatwright[6, 7], Annalie Melin[2, 3] & Netta Dorchin[8]

[1]Kirstenbosch Research Centre, South African National Biodiversity Institute, Private Bag X7 Claremont, 7735, South Africa. *jonathan.colville@gmail.com
[2]University of Cape Town, Rondebosch, South Africa.
[3]University of Cape Town, Rondebosch 7701, South Africa.
[4]South African National Biodiversity Institute, Claremont, South Africa.
[5]University of Johannesburg, Gauteng, South Africa.
[6]University of the Western Cape, Bellville, Cape Town.
[7]University of California, Berkeley, U.S.A.
[8]Tel Aviv University, Tel Aviv, Israel.

Keywords: Aizoaceae, Asphondyliini, host associations, Lasiopterini, new species.

Gall midges are excellent models for studying the importance and context of host shifts in insect speciation, because of the intimate nature of their relationships with their host-plants. Closely related groups of gall midges are known to have diversified through shifts between hosts and shifts between organs within a host-plant. Little to no work, however, has been undertaken on the diversity of the South African gall midge fauna, despite the region having an exceptionally rich and phylogenetically diverse flora. In a recent and ongoing study, a highly interesting, but unexplored gall midge fauna was found associated with the succulent Aizoaceae within the arid biomes of South Africa. This clade of succulent plants includes the highly speciose Ruschioideae with > 1,500 species, which exhibits a very recent and rapid radiation. A first attempt is reported to document the gall midge diversity of South Africa's Aizoaceae and some preliminary results are presented following the first year of surveying. So far, more than 80 new gall midge morphospecies have been found, which were reared from ~20 Aizoaceae genera and > 100 species and the succulent clades on which they are most diverse are indicated. The diversity of gall morphology is also presented and some aspects of possible specialisations and codiversification are discussed.

A provisional checklist of Syrphidae from Kenya, with notes on collections and collectors

Robert S. Copeland[1]* & Kurt Jordaens[2]

[1]Biosystematics Unit, International Centre of Insect Physiology and Ecology, P.O. Box 30772, Nairobi 00100, Kenya.*rcopeland@icipe.org
[2]Royal Museum for Central Africa, Tervuren, Belgium.

Keywords: Afrotropical Region, checklist, Kenya, species accumulation curve, Syrphidae.

Information extracted from published and unpublished sources was used to construct a provisional checklist of Syrphidae known from Kenya. Forty genera have been collected in the country, representing *ca* 180 species. These represent 65% (*n* = 62) of Afrotropical syrphid genera and 30% of the *ca* 610 species known from the Afrotropical Region. Kenya is the type locality for 21 syrphid species, eleven of which were described by Mario Bezzi. Several undescribed species, including new *Afrosyrphus* Curran and *Phytomia* Guérin-Méneville, are known from various collections and many of these will be published shortly. A species accumulation curve for Kenyan syrphids suggests, at first, that few species remain to be collected from the country. The shape of the curve, however, appears to illustrate several pulses in collection activity, separated by flat periods, each of which would have contemporaneously appeared to show the curve reaching an asymptote. These apparent asymptotes probably represent the absence of collection effort over periods of years. It is postulated that the present flattened part of the curve represents such a period of limited collecting in the Afrotropics. Recent increase in the interest in flower flies and other potential Diptera pollinators, such as Bombyliidae and Tabanidae, has already spurred renewed collection effort, likely leading to the discovery of previously undescribed species and a spike in the number of syrphids known from Kenya.

Poster

Phylogenetic complexity, increased diversity and ranking in the Parathalassiinae (Empidoidea: Dolichopodidae *sensu lato*)

Jeffrey M. Cumming* & Scott E. Brooks

Canadian National Collection of Insects, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Ave., Ottawa, ON, K1A 0C6, Canada. *jeff.cumming@canada.ca

Keywords: Classification, genera, morphology, phylogeny, species-groups, subgenera, zoogeography.

Phylogenetic relationships of the subgroups of Parathalassiinae are presented, based on a morphological cladistic analysis. Worldwide, all known extant genera, subgenera, species-groups and newly discovered undescribed lineages are represented in the analysis. Some previously proposed generic relationships are supported by the cladograms, but recognition of several current genera render others, such as *Microphorella* Becker, deplorably paraphyletic. Many included species-groups of *Microphorella* will need to be elevated to at least subgeneric level, while certain currently recognised genera may need to be classified as subgenera. The zoogeographic history of the included lineages of the subfamily based on this new classification will also be discussed.

Flying under the radar – a look at moth midges (Psychodidae) that bite frogs in obscurity

Gregory R. Curler

Mississippi Entomological Museum, Mississippi State University, 100 Old Highway 12, P.O. Drawer 9775, Mississippi State, MS 39762-9775 and Research Collaborator, Smithsonian Institution, National Museum of Natural History, 10th and Constitution NW, Washington D.C. 20560-0169, USA. gcurler@gmail.com

Keywords: Biodiversity, hematophagy, new species, Sycoracinae.

Hematophagous flies have evolved elaborate means to locate and take blood meals from vertebrate hosts, thereby profoundly impacting the behaviour and evolution of their hosts. Consequentially, a significant body of research exists with respect to the biology of biting flies. This is particularly true for groups of flies known to be vectors of disease agents affecting humans and other vertebrates. For this reason, representatives of the psychodid subfamily Phlebotominae have received a great deal of attention. Other blood-feeding psychodids, such as Sycoracinae, have been the topic of fewer studies. Approximately 40 extant and five fossil species of Sycoracinae are described, distributed virtually worldwide, except in North America and Antarctica. The world sycoracine fauna is incompletely known, as new genera and species await description. Although generally regarded as being associated with frogs, only four reports have confirmed this association for a total of five species. Anuran blood-meal hosts of one species, *Aposycorax chilensis* (Tonnoir), have been positively identified based on DNA sequence; all other host associations are based on observational data. In one case, a *Sycorax* Haliday species was reported to have transmitted filarial worms among frogs, although this has not been corroborated. Future research is necessary to demystify Sycoracinae and their association with frogs. Pertinent topics for investigation include determining if sycoracines are obligate blood-feeders, how they locate their frog hosts and whether they are transmitting disease agents among them. Natural history data on the immature stages is also required in order to clarify which species are aquatic or terrestrial.

Assessment of homologies in male terminalia of lower Diptera and phylogenetic implications for Psychodomorpha

Gregory R. Curler[1]*, R. Isaí Madriz[2] & Alexander Mykris[3]

[1]Mississippi Entomological Museum, Mississippi State University, 100 Old Highway 12, P.O. Drawer 9775, Mississippi State, MS 39762-9775 and Research Collaborator, Smithsonian Institution, National Museum of Natural History, 10th and Constitution NW, Washington D.C. 20560-0169, U.S.A.
*gcurler@gmail.com
[2]Casilla #367 Correos Coyhaique. Coyhaique, Chile.
[3]Toronto, Canada.

Keywords: 3D models, Blephariceridae, Psychodidae, synapomorphy, Tanyderidae.

It is well established that male terminalia of Diptera are a rich source of character data for delimiting taxa and inferring phylogeny. A hypothesis of the groundplan in male terminalia has been proposed, based on a study of homologous structures traced across representatives of Diptera. According to this hypothesis, homologies in lower Brachycera, Eremoneura and selected Bibionomorpha were also proposed. Despite these contributions, detailed evaluations of terminalia homologies are lacking for most Diptera. Homologies are here assessed in the male terminalia of lower Diptera, with particular attention given to Blephariceridae, Psychodidae and Tanyderidae. In studies of molecular phylogeny, these families have been hypothesised to constitute Psychodomorpha. By contrast, morphological phylogenetic analyses have resulted in varying placement of all three. Results from this study provide additional evidence supporting a sister-group relationship between Tanyderidae and Psychodidae. Evidence of their relationship to Blephariceridae is, however, less clear due to autapomorphies in terminalia of the last-named. One example of a compelling synapomorphy supporting Tanyderidae + Psychodidae involves the association of their basal gonocoxal lobes to the parameres and dorsal bridge; together these act as a housing around the aedeagus. Colour-coded drawings are applied in two and three-dimensional format to illustrate hypothesised homologies, including this and other complex characters. A thorough evaluation of homologies in the male terminalia and other character systems is required for a broader taxon sample of fossil and extant Diptera. This will facilitate the further establishment of a uniform morphological terminology and framework for testing phylogenetic hypotheses.

Are flies fussy? Comparing fly assemblages attracted to dead pigs and humans

Blake M. Dawson[1]*, Philip S. Barton[2] & James F. Wallman[1]

[1]Centre for Sustainable Ecosystem Solutions, School of Biological Sciences, University of Wollongong, NSW 2522, Australia. *bmd994@uowmail.edu.au
[2]The Australian National University, Canberra, Australia.

Keywords: Australia, decomposition, forensic entomology, succession.

In forensic entomology, pig carcasses have traditionally been used as models for human cadavers, due to the commonly held assumption that pig decomposition mimics that of humans. Recent research, however, has indicated that pigs and humans decompose very differently. Importantly, few studies have assessed this difference in an entomological context and the question of whether pigs are adequate proxies for human cadavers in forensic entomological research, therefore, remains unanswered. To assess the assumption that pig carcasses are reliable human substitutes, the attraction of flies to decomposing pig and human cadavers is being studied at the Australian Facility for Taphonomic Experimental Research (AFTER), the first facility of its kind outside of the United States. This project provides an opportunity to study the fly fauna involved in human decomposition in an ecosystem distinctly different from that of America. Special attention will be given to forensically important species of Calliphoridae, Muscidae and Sarcophagidae that use the remains of decomposing animals to complete their life cycles. The results of a preliminary experiment comparing the fly assemblages of a pig carcass and a human cadaver are discussed and future directions are summarised.

A preliminary study into the correlations between vegetation type and climate conditions with *tsetse* (Glossinidae) distribution and abundance in South Africa

Chantel J. de Beer* & Gert J. Venter

Epidemiology, Parasites and Vectors, Agricultural Research Council-Onderstepoort Veterinary Institute, Private Bag X5, Onderstepoort 0110, South Africa. *debeerc@arc.agric.za

Keywords: *Glossina*, land-cover map, KwaZulu-Natal Province, *tsetse*.

Glossina brevipalpis Newstead and *G*. *austeni* Newstead, the trypanosomosis vectors in South Africa, are present in an area of 16,000 km^2 in the north-eastern part of the KwaZulu-Natal Province. *Tsetse* apparent densities (ADs) were incorporated into a recently updated vegetation map for the area to assess the potential correlation between vegetation and *tsetse* distribution and/or abundance. According to the vegetation map, the main land-cover classes for the infested area were savanna woodland, herbaceous savanna, shrub savanna, dense dry forest, gallery forest, tree plantations, crops, urban areas, swamps, water bodies and bare ground. Similarly, climate data, obtained from permanent weather stations, were mapped and correlated with *tsetse* AD. The highest ADs for both *G*. *brevipalpis* and *G*. *austeni* were obtained in the dense dry forest vegetation class. Sites with moderate temperature ranges and higher relative humidity yielded high ADs for both species. Although vegetation and climate do indeed play a decisive role in determining the distribution and abundance of both *G*. *brevipalpis* and *G*. *austeni*, it does not fully explain their observed distribution patterns. This indicates that factors, such as differential fly mobility or host preference and availability, may also play an imperative role. Changes in the climate, agricultural practises and land use can have a significant and rapid impact on *tsetse* abundance and trypanosome transmission in the area. To manage the trypanosomosis problem successfully it will be essential to monitor *tsetse* burdens constantly at selected sites in the area.

Comparing methods for the assessment of blood meal volume of *Culicoides imicola* Kieffer (Ceratopogonidae) fed on an *in vitro* feeding system

Chantel J. de Beer*, Gert J. Venter & Ben Mans

Epidemiology, Parasites and Vectors, Agricultural Research Council-Onderstepoort Veterinary Institute, Private Bag X5, Onderstepoort, 0110, South Africa. *debeerc@arc.agric.za

Keywords: Hematophagous insects, Hemotek® feeding system, spectrophotometry.

The volume of the blood meal of hematophagous insects will determine the number of infective particles taken up during feeding and may denote the minimum dose needed to infect a competent vector. *Culicoides imicola* Kieffer midges are amongst the smallest hematophagous vectors and determining their blood meal size, and factors that may influence this, may be challenging. The applicability of spectrophotometry and weighing for this purpose were compared. Field collected *C. imicola* females were fed on defibrinated bovine blood using a Parafilm® membrane and a Hemotek® feeding system. Immediately after feeding, the weight of 10 engorged females were compared to that of 10 unfed females to determine blood meal volume. These pools were stored at -20°C until homogenised using a TissueLyser (Qiagen®) in 120 µl distilled water. The samples were transferred to an ELISA plate and absorbance read at 410 nm range using a SpectraMax spectrophotometer. These readings were converted to blood meal volume with a calibration curve, obtained by the dilution of known volumes of the blood used for feeding. Although the mean blood meal volume as determined with spectrophotometry (0.06 µl) was significantly ($P < 0.01$) smaller than that obtained by weighing (0.07 µl) the range in blood meal volume as determined by spectrophotometry (0.03 – 0.08 µl) and weighing (0.01 – 0.11 µl) showed a significant positive correlation ($r = 0.7$, $P < 0.01$). The correlation obtained indicates that both methods can be used to evaluate factors that may influence the volume of blood taken up during artificial feeding.

Poster

Mosquito/anuran interactions and feeding patterns of frog-biting mosquitoes (Culicidae) in Sri Lanka

Priyanka P. de Silva[1]*, Ximena E. Bernal[2, 3], Dilan Chathuranga[1] & Parakrama Karunaratne[1]

[1]Department of Zoology, Faculty of Science, University of Peradeniya, Peradeniya, Sri Lanka. *depriyanka@pdn.ac.lk
[2]Purdue University, West Lafayette, U.S.A.
[3]Smithsonian Tropical Research Institute, Balboa, Panama.

Keywords: Anurans, blood-feeding, *Mansonia*, micropredation, host specificity, *Uranotaenia*.

Blood-feeding behaviour of mosquitoes that are attracted to mating calls of male anurans was studied in two localities in central Sri Lanka. Monthly samplings were conducted to collect frog-biting mosquitoes, environmental data, anuran abundance and activity patterns of both anurans and mosquitoes. Mosquitoes attracted to the four most common anuran species in the study area, namely: *Duttaphrynus melanostictus* (Schneider), *Fejervarya limnocharis* (Gravenhorst), *Polypedates cruciger* Blyth and *Pseudophilautus rus* (Manamendra-Arachchi & Pethiyagoda), were collected separately using aspirators and sound traps broadcasting calls of each anuran species. A total of 1,079 frog-biting mosquitoes of four species in two genera were sampled (*Mansonia uniformis* (Theobald), *Uranotaenia rutherfordi* Edwards, *Uranotaenia* morphotype 1 and *Uranotaenia* morphotype 2). Monthly abundance data of mosquitoes indicate significant fluctuations that correlate with precipitation levels. Of the three *Uranotaenia* species sampled, *Uranotaenia* morphotype 1 fed exclusively on *D*. *melanostictus*, *Uranotaenia* morphotype 2, exclusively on *P crucifer* and *U. rutherfordi* mainly on *P*. *rus*. By contrast, *Mansonia uniformis* was attracted to all anuran species, indicating a wide host range. The feeding patterns of these mosquitoes reveal precedent evidence of host specificity of frog-biting *Uranotania* mosquitoes.

What's eating the grape? A review of African frugivorous Tephritidae research over the past 25 years

Marc De Meyer*, Kurt Jordaens & Massimiliano Virgilio

Department of Biology, Royal Museum for Central Africa, Leuvensesteenweg 13, B3080 Tervuren, Belgium. *demeyer@africamuseum.be

Keywords: Afrotropical, *Bactrocera*, *Ceratitis*, *Dacus*, *Zeugodacus*.

African Tephritidae, and in particular the frugivorous representatives within the family, have been a recurrent research subject for more than a century, due to their economic significance in horticulture and the invasive nature of some pest species. However, the growing importance of fruit production, increased international trade and movement of people and the introduction of invasive species in and out of Africa, has triggered an intensification of this research over the past decades and initiated a number of research programmes focusing on the family. This presentation will review recent progress made through these programmes in the following disciplines: morphological and molecular identification and taxonomy; phylogeny and associations with host-plants; population genetics; biogeography; tracing origin and dispersal pathways; and detection, monitoring and control methods. It highlights the current state-of-the-art and related knowledge gaps and also provides an overview of the major ongoing regional initiatives focusing on tephritid fruit fly research in Africa.

Belgium on the lookout for exotic mosquito species (Culicidae)

Isra Deblauwe[1]*, Katrien De Wolf[1], Nathalie Smitz[2], Ingrid Verlé[1], Anna Schneider[1], Jacobus De Witte[1], Adwine Vanslembrouck[3], Wouter Dekoninck[3], Kenny Meganck[2], Sophie Gombeer[3], Yoo Ree Van Bourgonie[3], Thierry Backeljau[3, 4], Marc De Meyer[2], Wim Van Bortel[1] & Marc Pollet[3, 5, 6]

[1]Medical Entomology Unit, Department of Biomedical Sciences, Institute of Tropical Medicine (ITM), Nationalestraat 155, 2000 Antwerp, Belgium. *ideblauwe@itg.be
[2]Royal Museum for Central Africa, Tervuren, Belgium.
[3]Royal Belgian Institute of Natural Sciences, Brussels, Belgium.
[4]Evolutionary Ecology Group, University of Antwerp, Wilrijk, Belgium.
[5]Research Institute for Nature and Forest, Brussels, Belgium.
[6]Ghent University, Ghent, Belgium.

Keywords: *Aedes*, Belgium, Culicidae, invasion, mosquitoes, surveillance.

Based on the current spread of exotic mosquito species (EMS) in Europe, the number of interceptions in Belgium and suitability models developed for *Aedes albopictus* (Skuse) in Europe, EMS are likely to establish and spread in Belgium. A prerequisite for their control is their early detection. Therefore, the Belgian federal authorities and the federated entities funded a 3-year active monitoring project (MEMO) (July 2017–June 2020). The aims are early detection of EMS in Belgium, quantifying locally established EMS populations, evaluating the EMS import risk at possible points of entry (PoE), expand reference collections and make recommendations for a future, long-term, cost-effective EMS monitoring plan in Belgium. Monitoring activities are implemented at 23 PoE using adult trapping with CO_2 and lure traps, egg sampling with oviposition traps and larval sampling with dipping nets. DNA barcoding is used to validate morphological identifications and to expand the DNA reference database. Specimens are also added to the morphological reference collection at Royal Belgian Institute of Natural Sciences. Since July 2017, four EMS were intercepted. The colonised area of *Ae*. *koreicus* (Edwards) in Belgium increased from 7 to 113 km^2. *Aedes japonicus* (Theobald) was detected again in southern Belgium, from where it was thought to be eliminated. This species has now also been collected on the border with Germany. *Anopheles pharoensis* (Theobald) entered Belgium *via* cargo transport. *Aedes albopictus* was intercepted at four PoE. To conclude, EMS are effectively entering and spreading in Belgium and appropriate control management strategies on the national level are urgently required.

Poster

Asilidae and Mydidae of the central Namib Desert at the Gobabeb Research and Training Centre, Namibia

Torsten Dikow

Department of Entomology, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, MRC 169, Washington D.C., 20013-7012, U.S.A. DikowT@si.edu

Keywords: Afrotropical, Asilidae, Mydidae, Namib Desert, seasonality, species diversity.

The Namib Desert is one of the oldest deserts on Earth and harbours a unique fly fauna. The Gobabeb Research and Training Centre is a research facility dedicated to the study of this Desert and is located in the central Namib in the Namib-Naukluft National Park, approximately 110 km S.E. of Walvis Bay and 300 km S.W. of Windhoek. It is uniquely situated between the ephemeral Kuiseb River, a linear oasis, the Namib Sand Sea, with towering shifting dunes and the desert gravel plains. The plant and animal life is influenced by recurring fog from the Atlantic Ocean, which is approximately 60 km due west. Here, the Asilidae and Mydidae fauna at Gobabeb is summarised, with data obtained from taxonomic revisions, museum collections and fieldwork. To date, 14 Asilidae species from 13 genera, representing six subfamily taxa have been recorded. Of these, two species are endemic to this part of the Namib, one of which is undescribed, while all others have been collected elsewhere in the Namib or the adjacent Nama Karoo and arid savanna. Interestingly, the most diverse and widespread Afrotropical genus, *Neolophonotus* Engel, has not yet been collected at Gobabeb. Currently, seven Mydidae species from seven genera, representing two subfamily taxa have been recorded. Of these, three species have only been collected in the Gobabeb area thus far and represent undescribed species. Furthermore, two of these species belong to undescribed genera. Photographs of the habitats and flies are provided and the seasonality and habitat preferences of species are summarised.

Poster

The online Afrotropical Asilidae Portal

Torsten Dikow

Department of Entomology, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, MRC 169, Washington D.C., 20013-7012, U.S.A. DikowT@si.edu

Keywords: Afrotropical, assassin flies, Asilidae, biodiversity data, open access, robber flies, taxonomy.

The recent publication of the *Manual of Afrotropical Diptera* (MAD) chapter on Asilidae provided a comprehensive review of the Afrotropical robber fly fauna. With some 1,700 species and 148 genera, representing 22% and 27% of the world fauna, respectively, it is one of the richest faunas known to date. It is also one of the best-studied faunas, primarily due to the contributions by Jason G.H. Londt since 1977. He alone has described about 29% of the Afrotropical species and 30% of the generic level taxa, while other authors have also contributed significant revisions in recent decades. The Afrotropical Asilidae Portal (AfroAsilPortal, asiloidflies.si.edu/afroasilportal) is a newly developed website that summarises information on robber flies to serve as a digital, structured and database-driven website. It will host and keep up-to-date the Afrotropical species catalogue and provide information on each species through distribution maps based on specimen occurrence data and images. Through retrospective data capture of the taxonomic revisions by Jason Londt and other recent authors using GoldenGATE, the original descriptions (and potential re-descriptions) of all species and associated illustrations will be made digitally accessible on the portal *via* the open access Plazi TreatmentBank (plazi.org/resources/treatmentbank) platform. The portal will also feature a catalogue of the genera along with a list of their Afrotropical species, a structured generic synopsis as published in the MAD chapter, an updated key to Afrotropical genera and keys to species on the Lucidcentral key server (www.lucidcentral.org).

Shaping our taxonomic legacy – tools to accelerate biodiversity discovery and make data openly accessible

Torsten Dikow

Department of Entomology, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, MRC 169, Washington D.C., 20013-7012, U.S.A. DikowT@si.edu

Keywords: Biodiversity data, cybertaxonomy, open access, revisionary taxonomy.

Taxonomy has a long tradition of describing Earth's biodiversity. For the past 20 years or so, taxonomic revisions have become available in PDF format, which is regarded as a good means of digital dissemination. A PDF document is, however, nothing more than a text document that can be transferred easily among researchers. In today's world, traditional taxonomic techniques need to be met with novel tools to make data dissemination a reality, make species hypotheses more robust and open the field up to rigorous scientific testing. Cybertaxonomic tools provide such methods and are here summarised in the context of revisionary taxonomy. While many of the tools have been around for some time now, very few practicing taxonomists embrace and utilise these tools in their publications. In order to leave a lasting scientific legacy as a taxonomist studying flies, it is argued that not only detailed descriptions and taxon delimitations should be seen as high-quality output, but also the dissemination of the captured and published data in a structured format to data repositories. This presentation will provide information on what kind of data can and should be openly shared (*e.g.*, specimen occurrence data, digital images, names, descriptions and authors) and outline best practices utilising globally unique identifiers for specimens and data. Data standards and the best-suited data repositories, such as GBIF and Zenodo, with its Biodiversity Literature Repository and the Plazi Treatment-Bank, an emerging species portal, are discussed to illustrate retrospective and prospective data capture of taxonomic revisions.

Preliminary results of a comparative morphological study and cladistic analysis of Phasiinae (Tachinidae), based on morphological characters

Rodrigo de Vilhena Perez Dios* & Silvio Shigueo Nihei

Department of Zoology, Institute of Biosciences, University of São Paulo, Rua do Matão, Travessa 14, no. 101, 005508-090, São Paulo, Brazil. *rodrigodios@gmail.com

Keywords: Calyptratae, cladistics, morphology, parasitoid, phylogeny, systematics.

The subfamily Phasiinae has historically been grouped based on the fact that their larvae are mostly parasitoids of the suborder Heteroptera and they were more recently grouped based on male terminalia. Currently, the subfamily is classified into 108 genera and *ca* 640 species, distributed across all zoogeographical regions, except Antarctica. Previously published results of a morphological phylogeny of Tachinidae and a molecular phylogeny of Phasiinae corroborates the monophyly of Phasiinae. More extensive studies are required, however, and there are no published cladistical analyses using morphological data for Phasiinae. The inclusion of taxa from most zoogeographical regions and a broader sampling of global genera in the analysis are necessary, as well as an accurate and detailed analysis of shared morphological structures. A new and exhaustive phylogenetic hypothesis, with a broader taxa sampling can contribute to new phylogenetic and taxonomic studies, further allowing host-parasite evolutionary studies. Thus, the current study will interpret new phylogenetic relationships for Phasiinae tribes and genera, based on morphological characters, as well as analyse the monophyly of subfamilies and tribes. At present, the 193 morphological characters data matrix has been developed with 113 terminals, including 61 genera of Phasiinae from all tribes and all zoogeographical regions. The preliminary results will be presented and discussed.

Unmitigated gallers – specialisation leads to diversification in the Cecidomyiidae

Netta Dorchin

School of Zoology, the Steinhardt Museum of Natural History, Tel Aviv University, 69978 Tel Aviv, Israel. ndorchin@tauex.tau.ac.il

Keywords: Biodiversity, cryptic speciation, gall, host-plant, phylogeny.

Interactions between insects and plants are among the most important drivers of speciation. This is particularly true for endophytic herbivores, which must evolve highly specialised adaptations to enable feeding inside the tissues of their host-plants. Gall midges (Cecidomyiidae) constitute one of the most speciose groups of endophytic insects worldwide and may well be the largest family in the order Diptera. As such, they make excellent candidates for studying the relationships between evolutionary adaptations and speciation patterns. Nevertheless, the tiny size and notoriously difficult taxonomy of cecidomyiids deter most entomologists from studying this family, leaving thousands of species undescribed and entire gall midge faunas in different parts of the world unexplored. A first comprehensive phylogenetic inference is presented for the Cecidomyiinae, the largest and most biologically diverse subfamily of gall midges, which includes all the plant-feeding species. Those clades which are the most rapidly evolving are shown and the possible contribution of host associations and life histories to this pattern are discussed. The evolution of alternative lifestyles in the family is also addressed, such as predation, inquilinism (gall invasion) and herbivory without gall formation. Finally, the challenges of taxonomic work on Cecidomyiidae are discussed, including cryptic speciation and morphological uniformity in many taxa, which make it impossible to provide accurate estimates for their real numbers based on current knowledge.

Insects visiting flowers of Oil palm, *Elaeis guineensis* Jacquin (Arecales: Arecaceae), in Uganda

James P. Egonyu[1]*, Stephen E. Sisye[1], Milton Otema[2], Gabriel Ddamulira[2], Virginia Namagala[1] & Rehema Naluyimba[2]

[1]Department of Zoology, Entomology and Fisheries Sciences, Makerere University, P.O. Box 7062 Kampala, Uganda. *egonyu@gmail.com
[2]National Crops Resources Research Institute, Namulonge, Uganda.

Keywords: Agro-ecological zones, Bugala Island, Diptera, fruit set, natural vegetation, pollinators, weevils.

Fruit set in Oil palm, *Elaeis guineensis* Jacquin (Arecales: Arecaceae), in Uganda is poor, indicating insufficient pollination. Little has been done, however, to ascertain the status of Oil palm pollinators in the country. This survey investigated the diversity of insects visiting Oil palm flowers in Uganda and variation in their abundance across insect groups. To this end, four agro-ecological zones where the crop is cultivated were investigated on the mainland and on Bugala Island in Lake Victoria. Insects were trapped *in situ*, by rapidly enclosing male and female flowers in polyethene bags, from February–March 2018. Insects sampled in order of dominance, were weevils of the genera: *Elaeidobius* Faust and *Prosoestus* Faust (both Curculionidae), other beetles (Nitidulidae, Scarabaeidae and Staphylinidae), Diptera (Muscidae, Drosophilidae and Platystomatidae), ants (Formicidae) and honeybees (*Apis mellifera* L.) (Apidae). Insect abundance varied across agro-ecological zones. Only weevils and Diptera occurred on both sexes of flowers, suggesting that only these may transfer pollen from male to female flowers. Both the weevils and flies were more abundant on male than female flowers – attributable to the stronger anise seed-like odour emitted by male than female flowers. Ants were sampled only on female flowers, while beetles occurred only on male flowers. Dominant weevils from mainland sites differed from those of the island site. Insects were more abundant on Oil palm plants nearer to natural vegetation than on those positioned farther away. Focussed research on ecology and biology of weevils and Diptera and manipulation of natural vegetation is suggested to boost Oil palm pollination in Uganda.

Bee flies (Bombyliidae) and not bees, are the keystone pollinators of spring mass flowering displays in Southern African deserts

Allan G. Ellis

Botany and Zoology Department, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa. agellis@sun.ac.za

Keywords: Bombyliidae, diversity, floral evolution, fly behaviour, Mariobezziinae, phylogeography, pollination, South Africa.

Bees are usually considered to be the most important pollinators of desert floras. This notion is challenged here and it is shown that the spring mass-flowering daisy displays that characterise the Southern African deserts are largely reliant on pollination by flies, particularly small bee flies (Bombyliidae: Mariobezziinae) and that floral diversity in these systems is shaped by selection imposed by these fly pollinators. As many plant species in these displays are self-incompatible annuals, pollination by flies is critical to their persistence in the system. Pollination network approaches were used to highlight the diversity of the fly pollinators involved and the plants that rely upon them, often exclusively and experimental approaches to demonstrate how selection by fly pollinators has shaped the floral diversity that makes the Namaqualand flower displays so special. The focus is on the little we do know about the evolution of the fly pollinators themselves, indicating that their evolutionary history is broadly congruent with the spectacular diversification of the Succulent Karoo flora. More research effort is urgently required to understand the requirements of these underappreciated, and yet critical, keystone pollinators on which the ecological and evolutionary integrity of the economically important mass flowering displays of Namaqualand depends.

Opportunistic blood-feeding behaviour of U.K. *Culicoides* Latreille (Ceratopogonidae) and implications for disease spread in zoo animals

Marion E. England[1]*, Paul Pearce-Kelly[2], Victor A. Brugman[1], Simon King[1], Simon Gubbins[1] & Simon Carpenter[1]

[1]The Pirbright Institute, Ash Road, Woking, GU24 0NF, United Kingdom.
*marion.england@pirbright.ac.uk
[2]Zoological Society of London, London, United Kingdom.

Keywords: Arbovirus, bluetongue, blood-feeding, *Culicoides*, Schmallenberg virus, zoo animals.

Some species of *Culicoides* Latreille biting midges are capable of transmitting bluetongue virus (BTV), Schmallenberg virus (SBV) and African horse sickness virus (AHSV) in northern Europe. Zoos are home to a wide range of "at risk" exotic and native species of animals. Therefore, it is necessary to understand the risk of these viruses to zoo animals, by characterising the *Culicoides* fauna at zoos and determining which potential vector species are feeding on which zoo animals. Using light suction traps at two U.K. zoos, a total of 9,684 individual *Culicoides* were caught, comprising a total of 20 different species. The six putative vectors of BTV, SBV and AHSV in northern Europe were found at both zoos and made up the majority of the total catch. Thirty-five blood-fed midges were processed for blood meal analysis. Vector species of *Culicoides* were found to be biting a wide range of birds and animals, including camels, elephants, rhinoceroses and rhea. This indicates that vector *Culicoides* are opportunistic feeders with little or no host preference. Due to the susceptibility of some zoo animals to *Culicoides*-borne arboviruses, this study demonstrates that preventative measures would need to be taken in the event of a U.K. outbreak of one of these viruses. These findings are of great importance for the protection of zoo animals, which are highly valuable, both in financial terms and in terms of their significant role in international breeding programmes for species conservation.

Trapping and phenology of Tabanidae on a farm in the South of France

Lucas Etienne, Azza Ferjani & Gérard Duvallet*

Centre d’Ecologie fonctionnelle et évolutive (UMR 5175 CEFE), Université Paul-Valéry Montpellier, France. *gerard.duvallet@univ-montp3.fr

Keywords: Control, ecology, horse flies, phenology, trapping methods.

Tabanids are a hematophagous nuisance and potential vectors of pathogens to livestock. The prevalence of besnoitiosis, due to the protozoan *Besnoitia besnoiti* (Sarcocystidae), is dramatically increasing in France. During a survey of horse flies, a hotspot of diversity and abundance was located on a farm near Montelimar, south-eastern France. During the period May to October 2017, using 7 H-traps on a 2.75 ha farm, more than 50,000 specimens of Tabanidae were collected, representing more than 24 different species. Traps were collected on a weekly basis and a phenology diagramme of horse flies has been established, showing species appearing in early spring and later during the summer and autumn periods. In addition to the phenology data, a comparison of different trapping systems, *i.e.*, H-trap, Nzi trap, Vavoua trap and a blue sticky screen trap, is also presented. These results provide some clues on how to better control tabanids and raises questions about the ecology of the different species.

Lumpers, splitters and *mihi*, oh my! The foibles and fancies of dealing with speciose Diptera genera through history

Neal L. Evenhuis

J. Linsley Gressitt Center for Research in Entomology, Bernice Pauahi Bishop Museum, Kaiwiʻula Research Complex, 1525 Bernice Street, Honolulu, Hawaiʻi 96817-2704, U.S.A. NealE@bishop-museum.org

Keywords: Asymptotes, foibles, history, Meigen, Robineau-Desvoidy, Rondani, taxonomy.

Dealing with a seemingly bottomless pit of undescribed flies is not a new problem. Come along on a delightful romp through history as we discover how others have tried (and failed miserably sometimes) to deal with filling the vacuum of taxonomic knowledge of Diptera by various means. We will discover some ignominious record-holders along the way, including the most synonyms ever described by one author for a single species (125!); and most papers co-authored by a professor who had no clue what the students' papers were about (nah, that will just get me in trouble, but we know who you are!). While traveling through space and time, the history of lumpers and splitters will be explained; and examples aplenty of usage of the wonderful terms *mihi* and *nobis* will be bandied about with reckless abandon. Arriving at the present, we will summarise the state of affairs with a brief discussion of the ultimate futility of ever reaching an asymptote in describing new species of Diptera in various speciose or "open-ended" genera of flies. The future is indeed bleak. Have another beer.

A phylogeny of Sarginae (Stratiomyidae) – monophyly, new characters, species-rich genera and the problem of Chrysochlorininae/Hermetiinae

Diego Aguilar Fachin[1]*, Dalton de Souza Amorim[1] & Martin Hauser[2]

[1]Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, São Paulo, Brazil. *diegoafachin@gmail.com
[2]Califonia Department of Food and Agriculture, Sacramento, U.S.A.

Keywords: Chrysochlorininae, Hermetiinae, phylogeny, Sarginae, Stratiomyidae, worldwide.

Sarginae is one of the largest subfamilies of Stratiomyidae, with > 550 described species, representing one-fifth of the family's diversity. Nevertheless, in the past 30 years, the taxonomy of the subfamily has received little attention, especially the fauna of the Afrotropical, Neotropical and Oriental Regions. Furthermore, there is no published cladistical study interpreting relationships between genera in the subfamily, although a few genera (*e.g.*, *Merosargus* Loew and *Sargus* F.) have been considered polyphyletic. The subfamily is usually defined as having five antennal flagellomeres, but in Chrysochlorininae and Hermetiinae there are eight flagellomeres. This study recovered the relationships between genera of Sarginae and addressed the relationships between the Chrysochlorininae, Hermetiinae and Sarginae. The data matrix consists of 204 morphological characters from 150 terminal taxa, representing all 22 genera assigned to Sarginae, 13 of the 14 genera of Chrysochlorininae and Hermetiinae, one genus each of the seven other stratiomyid subfamilies and two of xylomyids as the out-group. The three most parsimonious trees recovered a clade comprising Chrysochlorininae + Hermetiinae + Sarginae. All three subfamilies appear polyphyletic, considering their present limits. A reclassification is proposed delimiting each subfamily based on the synapomorphies identified. A monophyletic Sarginae (exclusive of *Gongrosargus* Lindner) is uniquely supported by a five-segmented flagellum. Some chrysochlorine genera and *Gongrosargus* are now classified under a new subfamily name and all remaining chrysochlorine genera are nested within the Hermetiinae. Within Sarginae, the phylogeny clarifies a number of taxonomic and evolutionary issues in the group.

Biogeographical and allometric aspects of the Diopsidae of Madagascar

Hans R. Feijen[1], Frida A.A. Feijen[1, 2] & Cobi Feijen[1]

[1]Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, The Netherlands.
*hans.feijen@naturalis.nl
[2]ETH Institute of Integrative Biology, Zürich, Switzerland.

Keywords: Allometry, biogeography, dimorphy, Diopsidae, endemism, Madagascar.

Twelve Diopsidae species are known to occur in Madagascar, while more species remain to be described. They belong to *Cladodiopsis* Séguy (3 species), *Diopsis* L. (1), *Gracilopsina* Feijen, Feijen & Feijen (2), *Madagopsina* Feijen, Feijen & Feijen (5) and *Sphyracephala* Say (1). Eleven of these 12 species are endemic to Madagascar and only *Sphyracephala beccarii* (Rondani) occurs more widely in the continental Afrotropical Region. *Cladodiopsis* is a near-endemic genus with (besides the Malagasy species), one undescribed species from Comoros. *Cladodiopsis* forms the sister-genus of *Sphyracephala*, which has a virtually worldwide distribution. *Cladodiopsis* is moderately to highly dimorphic with regard to eye span, but *Sphyracephala* species are mainly homomorphic, with some species having low dimorphy. The genera *Gracilopsina* and *Madagopsina* are both endemic. The moderately dimorphic *Madagopsina* is assumed to be the sister-group of the homomorphic Oriental genus *Eurydiopsis* Frey. The phylogenetic position of the moderately to highly dimorphic *Gracilopsina* is not yet known, but it is also likely to be related to the basal homomorphic genera of the irrorated-wing group. *Diopsis nigrosicus* Séguy is an endemic species belonging to a genus distributed in the Afrotropical and Oriental Regions. The moderately dimorphic *D. nigrosicus* is a distant representative of the uniformly homomorphic Afrotropical *Diopsis ichneumonea* species-group. All endemic Madagascan diopsids are shown to be dimorphic, while their sister-groups in other regions are homomorphic. This appears a special case of the disputed Foster’s rule and may form an additional argument that eye-stalk dimorphy in Diopsidae is not only determined by sexual selection.

Advances in the taxonomy of Neotropical *Pholeomyia* Bilimek (Milichiidae)

Heloísa F. Flores* & Dalton de S. Amorim

Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *heloisa.flores@usp.br

Keywords: Milichiidae, Neotropical Region, *Pholeomyia*, taxonomy.

Pholeomyia Bilimek (Schizophora: Milichiidae) comprises 39 described species, 27 of which are known from the Neotropical Region, seven from the Nearctic, one from the Afrotropics and one from the Oriental. There is no complete taxonomic review of the genus and a large number of species are still expected to be described. There are no phylogenetic studies for the relationships between the species. This study represents an effort to organise the knowledge of the taxonomy and systematics of the genus. To date 11 described and three undescribed Neotropical species of the genus have been identified. Habitus photographs and illustrations of the male and female terminalia of these species are made available for the first time. In the long run, the intension is to study non-Neotropical species for reconstruction of phylogenetic relationships within *Pholeomyia* and to interpret the biogeographical evolution of the genus, *e.g.*, whether Neotropical diversity corresponds to a single clade, or if tropical species belong in a separate clade from temperate species, *etc*.

Poster

First insights in Odiniidae phylogeny

Heloísa F. Flores*, Gabriela Pirani & Dalton de S. Amorim

Departamento de Biologia, FFCLRP, Universidade de São Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *heloisa.flores@usp.br

Keywords: Neotropical Region, Odiniinae, phylogeny, Traginopinae.

Odiniidae is a small family of acalyptratae flies, with 71 described species globally, ascribed to 16 genera. The family has received reasonable attention in the past 10 years, with publication of a catalogue to world species, description of new species, new genera and an identification key to genera. Nevertheless, a global approach to study of the group is still wanting and aspects of male terminalia sclerite homology remain unclear. The Odiniidae have been divided into the subfamilies Odiniinae and Traginopinae, but no cladistic study of the family has been undertaken to support such a division. This study of the relationships between genera of Odiniidae has some bias in terms of taxon sampling of the Neotropical fauna, but actually intends to contribute to a general understanding of the evolution of the family. The data matrix consists of 53 morphological characters, from 35 terminal taxa, representing 13 of the 16 genera of Odiniidae. It also includes three genera of Agromyzidae and one genus of Clusiidae as out-groups. *Pradomyia* Gaimari, a genus previously ascribed to the Traginopinae, was surprisingly recovered as belonging to the Odiniinae. Two major clades are particularly well supported: (*Inpaeuma* Limeira-de-Oliveira, Marques, Reis & Rafael + *Helgreelia* Gaimari) and ((*Traginops* Coquillett + *Neotraginops* Prado) + *Paratraginops* Hendel). In addition to comments on the relationships between genera, a discussion is developed on the morphology of the group and on problems of homology of the male terminalia.

A remarkable new muscid genus (Coenosiini) from Colombian Páramos, with phylogenetic position inference

João Manuel Fogaça[1]*, Márcia S. Couri[2], Marta Wolff[3] &
Claudio José Barros de Carvalho[1]

[1]Departamento de Zoologia, Universidade Federal do Paraná, Caixa Postal 19020, 81531-980, 19020, Curitiba, PR, Brazil. *fogacabio@gmail.com
[2]Museu Nacional, Rio de Janeiro, Brazil.
[3]Universidad de Antioquia, Medellín, Colombia.

Keywords: Highlands, morphology data, Muscidae, new genus, Páramos, ultrastructure.

The Páramo, located in the Andes at elevations of 2,800–4,700 m, is cited as a centre of high endemism and as a biodiversity hotspot. However, this region is poorly known, especially considering its Diptera fauna. Muscidae occur in almost all habitats, except the most arid areas and muscid species form an important proportion of the Diptera fauna of the Andean highlands. In the entomological collections of the Universidad de Antioquia, Colombia, were located specimens from the Colombian Páramos, which cannot be identified to any known Neotropical muscid genera. The unusual morphology of head and mouthparts, in combination with several characters of the male terminalia demonstrated that these specimens represent a new genus of the tribe Coenosiini, which has been established as a monophyletic group. The new genus is characterised by the modified and well-developed labellum, the wide gena and parafacial, the short palpus and the prestomal teeth weakly developed. The new genus is morphologically close to the endemic genera *Apsil* Malloch and *Reynoldsia* Malloch from southern Chile and Patagonia. They share the enlarged gena, one seta on the median third of the posterior surface of mid tibia and the hind tibia with median, supramedian and preapical posterodorsal setae. The new genus differs from these described genera by the prestomal teeth being weakly developed, the labellum well-developed, the fronto-orbital plate bare, the scutum virtually bare, the presence of one presutural dorsocentral seta, the lower calypter elongate and the cercus of the male terminalia without a posterior concavity.

Pollinator body size influences stigmatic pollen print, irrespective of the evaluation method used – a meta-analysis

Rita Földesi[1]*, Bradley G. Howlett[2], Ingo Grass[3] & Péter Batáry[3]

[1]Institute of Crop Science and Resource Conservation, Agroecology and Organic Farming, University of Bonn, Auf dem Hügel 6, 53121-Bonn, Germany. *foldesri@gmail.com
[2]New Zealand Institute for Plant and Food Research Ltd., Christchurch, New Zealand.
[3]Georg-August-University Göttingen, Göttingen, Germany.

Keywords: Approach, flies, honeybee, pollinator efficiency, wild pollinators.

Many insect species provide essential pollination services, however, their pollen print (amount of pollen deposited onto a stigma when flower visiting) can vary greatly between taxa. Yet, studies assessing the relationships between the insects pollen print, body size and the type of method employed to measure prints remain limited to a small number of plants and pollinating species. To gain a more comprehensive understanding of how pollen prints vary between pollinating species, a meta-analysis was conducted using data from 27 studies. These contained pollen print data for 108 wild pollinator taxa across 30 species of plants. The western honeybee was used as a comparator species from each study. It was found that wild pollinators deposited more pollen on stigmas than honeybees and body size had a significant positive effect on the amount of deposited pollen: if body length increased with 1 cm, pollen print also increased by over 70%. Pollen print of bees was significantly larger compared to honeybees, while flies had a smaller pollen print. However, data for flies was much more limited, as only nine “fly studies” could be involved. No significant difference was found between the two methodological approaches, “static” *versus* “active”, regarding pollen print size. This study demonstrates the importance of wild pollinator species in delivering pollen to many crop and non-crop plant species. These findings also point to the need to further quantify the pollination effectiveness of non-bee pollinators as studies have largely focused on managed and wild bee pollinating species.

Influence of abiotic factors on occurrence and seasonality of fruit flies (Tephritidae) attacking cucurbits in three localities of Cameroon

Mokam Didi Gaëlle[1]* & Djiéto-Lordon Champlain[2]

[1]University of Ngaoundéré, P.O. Box 454, Ngaoundéré, Cameroon. *tawogaelle@yahoo.fr
[2]University of Yaoundé I, Yaoundé, Cameroon.

Keywords: Attack rate, horticulture, infestation rate, occurrence, seasonality.

In Central Africa, horticulture is seriously impaired by some economically important tephritid fruit flies. Knowledge on the impact of abiotic factors on abundance and seasonality of these pests is vital information for the implementation of control strategies. The current study was undertaken in experimental plots situated at three localities in southern Cameroon: Ngoa-Ekelé, Olembé and Koutaba, from 2009–2011. Four species infesting Cucurbitaceae were recorded: *Dacus bivittatus* (Bigot), *D*. *ciliates* Loew, *D*. *punctatifrons* Karsch and *D*. *vertebratus* Bezzi. Based on monthly presence/absence data, occurrence of these tephritids varied. *Dacus bivittatus* was observed at the three localities throughout the year. Similar observation were reported for *D*. *ciliatus* and *D*. *punctatifrons* at Ngao-Ekelé and Koutaba. *Dacus ciliatus* was absent from June to August and May to October at Olembé. *Dacus vertebratus* occurred less frequently. Strong correlations were found between attack rates of these tephritids and three abiotic factors: temperature, humidity and rainfall. At Ngao-Ekelé, the attack rate of *D*. *bivittatus* was negatively correlated with temperature (r = -0.52; P = 0.007) and positively correlated with humidity (r = 0.49; P = 0.01); while for *D*. *ciliatus*, the reverse phenomenon was observed. At Koutaba, attack rate of *D*. *bivittatus* and *D*. *ciliatus* were positively (r = 0.5; P = 0.01) and negatively (r = -0.3; P = 0.01) correlated with rainfall, respectively. Thus attacks of *D*. *bivittatus* were more important during the wet period and those of *D*. *ciliatus* during the dry season. Independent of climatic season the infestation rate did not vary.

The family Celyphidae in the New World and remarks on the world genera

Stephen D. Gaimari

California Department of Food and Agriculture, Plant Pest Diagnostics Branch, 3294 Meadowview Road, Sacramento, California 95832, U.S.A. sgaimari@gmail.com

Keywords: *Atopocelyphus*, *Chamaecelyphus*, French Guiana, *Hemiglobus*, Lauxanioidea, *Paracelyphus*, *Spaniocelyphus*.

The family Celyphidae (Lauxanioidea) was long considered as a strictly Old World group, despite the 1844 description of one species from French Guiana by P.J.M. Macquart. This species, *Celyphus ruficollis* Macquart, was rarely mentioned in subsequent literature, despite having been the third species of *Celyphus* Dalman described. The identity and type locality of this species were verified by examination of Macquart's 1844 work, his type specimen, labels and the 1826–1834 accession book in Muséum national d'Histoire naturelle (Paris) and a second specimen recently collected from the same country in the Natural History Museum (London). As the species possesses unique characteristics relative to other celyphid genera, indicating a separate lineage from the Old World celyphids, the new genus *Atopocelyphus* Gaimari was described. In addition to this New World genus, the Old World genera of celyphids are reviewed, including discussion of the synonymy of *Chamaecelyphus* Frey under *Spaniocelyphus* Hendel and the elevation in rank to genus of *Hemiglobus* Frey and *Paracelyphus* Bigot.

Homologisation of sclerites and musculature of male terminalia of Diptera “Aschiza” (Platypezoidea, Syrphoidea) and Schizophora Acalyptratae (Nerioidea, Diopsoidea, Tephritoidea, Lauxanioidea) with a phylogenetic perspective

Tatiana V. Galinskaya[1]*, Anatole I. Shatalkin[2] & Olga G. Ovtshinnikova[3]

[1]Entomology Department, Biological Faculty, Lomonosov Moscow State University, Leninskie gory 1-12, Moscow 119234, Russia. *nuha1313@gmail.com
[2]Zoological Museum of Lomonosov Moscow State University, Moscow, Russia.
[3]Zoological Institute of Russian Academy of Sciences, St Petersburg, Russia.

Keywords: Abdomen, pregenital sclerites, terminalia.

Sclerites and musculature of the male abdomen and terminalia were studied for several families of brachycerous Diptera. The following representatives of the “Aschiza” were studied: Platypezoidea (Platypezidae and Phoridae), Syrphoidea (Syrphidae), plus the following representatives of Schizophora Acalyptratae: Nerioidea (Micropezidae), Diopsoidea (Nothybidae, Diopsidae and Psilidae), Tephritoidea (Tephritidae, Ulidiidae and Platystomatidae) and Lauxanioidea (Celyphidae). Based on a series of morphological characters, parallelisms and homologisation of pregenital and genital structures were revealed. It is assumed that the sclerites connected with the hypandrium and having a musculature connecting them to the hypandrium (*i.e.*, pregonites, postgonites, parameres, postgonital arms, parameral arms, lateral sclerites, *etc.*), appeared in the evolutionary history of Cyclorrhapha independently several times in different groups. This process is here termed the “hypandrium division syndrome”. Since the process took place in parallel, the characters of the appendages of the hypandrium can be used for phylogenetic constructs within the “Aschiza” and Schizophora Acalyptratae, at a taxon level not higher than the rank of the family. Characters of the pregenital sclerites and muscles can, however, be used for phylogenetic constructions at family level and also for higher taxon ranks.

Modifications in the skeleton and musculature of the male abdomen and terminalia in Psilidae and implications for phylogeny

Tatiana V. Galinskaya[1]*, Anatole I. Shatalkin[2] & Olga G. Ovtshinnikova[3]

[1]Entomology Department, Biological Faculty, Lomonosov Moscow State University, Leninskie gory 1-12, Moscow 119234, Russia. *nuha1313@gmail.com
[2]Zoological Museum of Lomonosov Moscow State University, Moscow, Russia.
[3]Zoological Institute of Russian Academy of Sciences, St Petersburg, Russia.

Keywords: Body size, *Chamaepsila*, *Chyliza*, *Imantimyia*, *Loxocera*, *Psila*, *Psilosoma*, terminalia.

The musculature of the male abdomen and terminalia were studied in the following species of Psilidae: *Chamaepsila humeralis* (Zetterstedt), *Chyliza vittata* Meigen, *Imantimyia nigrifrons* (Macquart), *Loxocera aristata* (Panzer), *Psila nigripalpis* Shatalkin and *Psilosoma audouini* (Zetterstedt). These were compared to equivalent musculature in the family Diopsidae and it was demonstrated that Psilidae are characterised by secondary symmetry of the pregenital and genital sclerites and muscles and by reduction of syntergosternite 7+8, which is correlated to reduction of the ejaculatory apodeme. The family exhibits pregenital and genital compaction, which is, however, expressed in different ways. The clades [*Chyliza*], [*Imantimyia* + *Loxocera*] and [*Chamaepsila* + *Psilosoma* + *Psila*] are supported by several synapomorphies.

Molecular phylogeny of the subfamily Asilinae (Asilidae) based on mitochondrial 16S and 12S rDNA and nuclear 18S rDNA

Tatiana V. Galinskaya[1]*, Dmitry M. Astakhov[2], Dmitry M. Schepetov[1, 3, 4],
Tatiana V. Neretina[5] & Anatole I. Shatalkin[5]

[1]Entomology Department, Biological Faculty, Lomonosov Moscow State University, Leninskie gory 1-12, Moscow 119234, Russia. *nuha_1313@list.ru
[2]Institute of Natural Sciences, Volgograd, Russia.
[3]National Research University Higher School of Economics, Moscow, Russia.
[4]Koltzov Institute of Developmental Biology RAS, Moscow, Russia.
[5]Lomonosov Moscow State University, Moscow, Russia.

Keywords: Assassin flies, Asilinae, divergence time, phylogeny, robber flies, systematics.

The robber fly family, Asilidae comprises over 7,500 species in 556 genera. There are over 67 genera in the subfamily Asilinae (including Apocleinae) in the Palaearctic Region and their phylogenetic relations are of considerable interest. Contemporary data clarifies to some extent subfamily level relationships, but at the same time affiliation of some genera to tribes remains an unresolved issue. This study focused on reconstruction of the phylogeny of Palaearctic Asilinae, based on molecular data. One of its purposes was to determine consistency of taxa described by P.A. Lehr in light of re-evaluated phylogenetic relationships. An attempt was also made to reveal the systematic position of the Palaearctic genera *Albicoma* Lehr, *Neoepitriptus* Lehr and *Odus* Lehr within Asilinae and a number of others from the list of "unplaced genera", based on molecular data. The current study provides strong evidence supporting validity of Apocleini as a tribal level taxon and composition of the tribes Machimini, Neomochtherini and Philonicini proposed by Lehr.

Population genetics and morphological variation of eastern European *Lucilia sericata* (Meigen) (Calliphoridae)

Tatiana V. Galinskaya[1]*, Anna V. Diakova[2], Dmitry M. Schepetov[2, 3, 4], Nadezhda Y. Oyun[2, 5, 6] & Anatole I. Shatalkin[2]

[1]Entomology Department, Biological Faculty, Lomonosov Moscow State University, Leninskie gory 1-12, Moscow 119234, Russia. *nuha_1313@list.ru
[2]Lomonosov Moscow State University, Moscow, Russia.
[3]National Research University Higher School of Economics, Moscow, Russia.
[4]Koltzov Institute of Developmental Biology RAS, Moscow, Russia.
[5]Vavilov Institute of General Genetics, Moscow, Russia.
[6]Martsinovsky Institute of Medical Parasitology, Moscow, Russia.

Keywords: Blowfly, forensic entomology, genetic structure, microsatellite, population.

The population structures of different species of Calliphoridae are highly diverse at different locations. Populations of the eastern European blowfly *Lucilia sericata* (Meigen) were investigated, using chaetotaxy and eight microsatellite loci. Results of a genetic analysis indicated that there is a panmictic population of *L. sericata* in the area studied, with putatively a high rate of gene flow within this population. It is assumed that the ability of *L. sericata* to migrate long distances and their high fertility outweighs existing genetic drift and effects of geographical distances. The assumption that genetic drift is relatively negligible is also supported by the results of the effective population size estimations, *i.e.*, the “infinite” number of breeders. It is also possible, however, that overlapping generations or a sampling error could have led to similar results. The chaetotaxy analysis also strongly supports this panmictic population hypothesis.

Poster

Prospects for South American Simuliidae studies

Leonardo H. Gil-Azevedo

Departamento de Entomologia, Museu Nacional, Universidade Federal do Rio de Janeiro, Cep 20940-040, Parque Quinta da Boa Vista s/n, São Cristóvão, Rio de Janeiro, RJ, Brazil. lhgazevedo@mn.ufrj.br

Keywords: Biogeography, blackfly, diversity, Neotropical Region, systematics.

Simuliidae is a family distributed virtually worldwide, with 2,204 species in 26 genera. Knowledge on the taxonomy of South American blackflies has improved over the past 50 years and there are now 247 valid species distributed in eight genera in the region. In the past 15 years, 91 papers and two extensive manuals have been published, which resulted in the discovery of 25 species. Most species in South America are well described and are well represented in collections. Due to the accumulated published knowledge on species, lack of data is not the main issue, but other systematic challenges have arisen: 1) the supraspecific relationships within *Simulium* Latreille, a genus that contains 80% of all species in the family, are poorly understood and the diagnoses of most South American subgenera are unsatisfactory; 2) the delimitation of species from homogeneous groups is unclear, as they are differentiated by limited features, which are variable and/or have many intermediate states, therefore *ca* 30% of all species names proposed in South America were synonymised; and 3) there is a large amount of distributional data on species in the literature and in collections that, with very few exceptions, have never been discussed from a biogeographical perspective. Many questions regarding the distribution of South American blackflies await answers, such as: how is the fauna on the continent composed; what is the correlation between lineage distributions and their phylogeny; and why are there species with wide distribution and other that are much more restricted?

A major step back for Neotropical dipterology – the impact of the fire at the National Museum, Brazil

Leonardo H. Gil-Azevedo*, Cátia Antunes Mello-Patiu, Valéria Cid-Maia & Márcia S. Couri

Departamento de Entomologia, Museu Nacional, Universidade Federal do Rio de Janeiro, Cep 20940-040, Parque Quinta da Boa Vista s/n, São Cristóvão, Rio de Janeiro, RJ, Brazil. *lhgazevedo@gmail.com

Keywords: Collection, fire, Neotropical Region, primary types.

On 2 September 2018, staff watched helplessly as a catastrophic fire consumed wing by wing of the Palace of National Museum (Federal University of Rio de Janeiro, Rio de Janeiro, Brazil), in the very same year the institution, the first house of Science in Brazil, celebrated its 200 year anniversary. The Entomological Collection, as well as the Entomological Department facilities (laboratories and other rooms), were almost entirely destroyed in this tragedy. The Entomological Collection of the National Museum was one of the largest and most representative in Latin America, with *ca* five million specimens, including 3,500 primary types of 10 different orders of Hexapoda. For more than a century the collection was built, through the concerted efforts of hundreds of entomologists. Currently, the Department has four active dipterists and most of the material of Diptera was stored in the Palace and the remainder in the annex Alípio de Miranda Ribeiro building, which is located beside the Palace and was thankfully unaffected. Consequently, only material of the families Agromyzidae (18 types), Bombyliidae (3), Cecidomyiidae (111), Fanniidae (25) and Muscidae (151) were unaffected, plus undetermined material resulting from recent fieldwork and material on loan from other institutions. The numbers of specimens destroyed of other families of Diptera is estimated at *ca*. 150,000 specimens, including more than 300 primary types. The loss is incalculable, but human patrimony of the museum is preserved and the hard work has begun of reconstruction. The Museum is alive!

Abundance of forensically related flies from greater Johannesburg, South Africa

Allison E. Gilbert[1, 2]*, Richard H. Hunt[1] & Maureen Coetzee[1, 2]

[1]Wits Research Institute for Malaria, School of Pathology, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa. *Allison.e.gilbert@gmail.com
[2]Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Johannesburg, South Africa.

Keywords: Abundance, forensic Diptera, Gauteng, South Africa.

Numerous species of Diptera are of forensic importance. An understanding of the biology and distribution of the appropriate flies aids in numerous forensic aspects, such as determination of post-mortem interval. For this to be accurately assessed, an understanding of the species shifts that occur over the seasons is crucial and these data are lacking for the Gauteng Highveld region, South Africa. Furthermore, the effect of urbanisation on the species shift is also poorly understood. Seasonal abundance of forensically related flies was examined within the greater Johannesburg area over a one-year period. Samples were collected for seven days fortnightly from each site: an urban, rural and industrial area of the city. Samples were collected using a modified RedTop Fly Trap™ baited with pork liver. The dominant Diptera families were the Calliphoridae, Sarcophagidae and Muscidae. In the Calliphoridae, the dominant genera were *Calliphora* Robineau-Desvoidy, *Chrysomya* Robineau-Desvoidy and *Lucilia* Robineau-Desvoidy. Comparisons were made regarding the species diversity and presence for each season and each location. This study provides information on population diversity of forensically important flies in Johannesburg and determines whether urbanisation affects population distribution.

Phylogenetic relationships of spider flies (Acroceridae) – discordance, uncertainty and the perils of phylogenomics

Jessica P. Gillung

Bohart Museum of Entomology, Department of Entomology and Nematology, University of California Davis, One Shields Avenue, CA 95616, U.S.A. jpg.bio@gmail.com

Keywords: Anchored hybrid enrichment, Bayesian inference, Brachycera, conflict, systematic error.

Spider flies (Acroceridae) are a monophyletic group of lower Brachycera currently classified into three subfamilies, 55 genera and *ca* 530 species. The group has long been considered a rogue taxon and its placement within the Diptera tree of life remains uncertain. Phylogenetic relationships among lineages of spider flies are by contrast relatively well established, with hypotheses proposed based on molecular data from both Sanger and high-throughput sequencing. Phylogenomic estimation of spider fly relationships yields different topologies, depending on whether data is coded and analysed as nucleotides or as amino acids. The most significant difference among the two data types is in the monophyly of Panopinae; a morphologically and ecologically recognisable group, that is recovered as monophyletic only in the analyses of nucleotides. This study uses Acroceridae as a system to explore the effects of potential confounding factors in phylogenomic reconstruction. This research takes advantage of modern and powerful statistical approaches, including posterior predictive simulation, to understand the effects of conflict, uncertainty and systematic error in the estimation of evolutionary relationships using the standard phylogenomic toolkit.

Phylogeny of Rhinophoridae and Polleniidae – toward the evolution of Oestroidea

Silvia Gisondi[1, 2]*, Thomas Pape[2] & Pierfilippo Cerretti[1]

[1]Department of Biology and Biotechnologies 'Charles Darwin', Sapienza University of Rome, Piazzale Aldo Moro 5, 00185, Rome, Italy. *silvia.gisondi@uniroma1.it
[2]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Evolution, molecular phylogeny, Oestroidea, parasitoids, phylogeny, Polleniidae, Rhinophoridae.

Calyptrates are a megadiverse, actively radiating group of dipterans, including the oestroid clade. Recent attempts at resolving the oestroid phylogeny, employing few taxa seem converging in retrieving monophyly for most of the families and subfamilies, but deep relationships among these still have very low support, as for two very interesting and relatively unexplored families of parasitoid flies: Rhinophoridae and Polleniidae. Rhinophorids are the only insects exploiting crustaceans (Crustacea: Isopoda: Oniscidea) as hosts and their adult stages are difficult to separate from other oestroids, due to the lack of autapomorphies. Polleniids have traditionally been considered a subfamily of the Calliphoridae, but there is growing evidence supporting the view that this clade has evolved separately from "core" calliphorids and is the extant sister taxon to the Tachinidae. A careful taxon sampling is employed for the first time in the current project: a good number of worldwide distributed samples are already present and stored in alcohol thanks to fieldwork (hand collecting and Malaise traps) and help from other research groups. Both Sanger sequencing using three informative nuclear markers (CAD, MAC, MCS) and an anchored hybridisation approach will be employed together in order to shed light on the generic phylogeny of Rhinophoridae and Polleniidae. These molecular results will be analysed and compared with morphological data in a total evidence analysis and included in a more general context of calyptrate phylogeny.

Review and phylogeny of *Dolichophaonia* Carvalho (Muscidae) – is it a monophyletic group?

Lucas Roberto Pereira Gomes* & Claudio José Barros de Carvalho

Universidade Federal do Paraná, Dept. of Zoology, P.O. Box 19020, 81531-980, Curitiba, Paraná, Brazil. *lucaspergos@gmail.com

Keywords: House flies, molecular and morphology analysis, Neotropical Region, taxonomy.

Muscidae is a highly diverse family of Diptera occurring in all zoogeographical regions, except Antarctica. *Dolichophaonia* Carvalho comprises 30 species, including 28 from the Neotropics and two from the Nearctic. It can be recognised by wing vein M_1 straight or slightly curved toward the apex; the hind tibia with a posterodorsal seta (calcar) twice as long as the width of the tibia; and the wing without cilia, except on the costal vein (*C*). Two characters from the female proboscis support the monophyly of the group: the hook-like tip to the anterior region of the clypeus and strong sclerotisation of the prementum. The main aims of this project were: to review *Dolichophaonia* species; to provide an identification key; and to reconstruct the phylogenetic relationships among species of the genus, using morphological evidence. As a result, three new species were described from Brazil, São Paulo, Cananéia; Costa Rica, Punta, Monteverde and Peru, Madre de Dios, Boca Colorado. The most parsimonious tree supported *Dolichophaonia* as a monophyletic group by two synapomorphies (the hook-like tip to the anterior region of the clypeus and strong sclerotisation of the prementum) and three homoplasies (radial sector (*Rs*) bare; a median anterodorsal seta on the hind tibia; and calcar twice as long as tibia width). The phylogenetic position using molecular data of *Dolichophaonia* and its related genera *Phaonia* Robineau-Desvoidy and *Helina* Robineau-Desvoidy, indicated the genera as separated groups by Bayesian inference analyses.

Description of a remarkable new species of *Neodexiopsis* Malloch (Muscidae) from southern Brazil, using ultrastructural morphology and DNA barcoding analysis

Lucas Roberto Pereira Gomes*, João Manuel Fogaça & Claudio José Barros de Carvalho

Department of Zoology, Universidade Federal do Paraná, Rua Francisco H. dos Santos, Jardim das Américas, 81531-980, Curitiba, PR, Brazil. *lucaspergos@gmail.com

Keywords: Biodiversity, molecular, Neotropical Region, Palmas-PR, taxonomy.

Neodexiopsis Malloch is one of the most speciose genera of the Neotropical tribe Coenosiini, with 97 valid species, including 48 species recorded from Brazil. Adults are small- to medium-sized predatory flies, which inhabit forests or pastures. The taxonomy of the genus remains unclear; several species are known only from the unique female holotypes and no phylogenetic analysis of species of *Neodexiopsis* has been undertaken. A new species is described from southern Brazil (Palmas, Paraná), illustrated using photographic images, line drawings and ultrastructural morphology of the proboscis and male terminalia. This new species superficially resembles Scathophagidae, while the male terminalia are typical of Coenosiini. A DNA barcoding analysis of the new species and six other *Neodexiopsis* species is provided, using neighbour-joining confirmed that the new species belongs to the genus *Neodexiopsis*.

Richness and abundance of Anthomyiidae in a Conservation Unit of Paraná, Brazil

Lucas Roberto Pereira Gomes[1]*, João Manuel Fogaça[1], Josiane Kempka[2] & Adriana C. Pereira[2]

[1]Department of Zoology, Universidade Federal do Paraná, Rua Francisco H. dos Santos, Jardim das Américas, 81531-980, Curitiba, PR, Brazil. *lucaspergos@gmail.com
[2]Instituto Federal do Paraná campus Palmas, Palmas, Brazil.

Keywords: Ecological succession, ecology, highland grasslands, Neotropical Region.

Anthomyiid flies (1,941 species and 53 genera) are distributed virtually worldwide. Adults are found in a wide range of habitats. A few species are synanthropic and others are agricultural pests. In Brazil, 26 species are known in 12 genera. This study was conducted over a two-year period in a federal conservation unit (Campos de Palmas wildlife refuge) in the state of Paraná, southern Brazil, at an elevation of 1,100 m. Two bi-weekly collections were undertaken in four sites with a different floristic composition: a fragment of indigenous forest (area A); a forest margin (area B); a native grassland field (area C); and a forest site with *Pinus taeda* L. removed (area P). Sampling was conducted using two concomitant Malaise traps in each area. The total Diptera yield during the study comprised 92,864 specimens, with Anthomyiidae represented by 549 individuals (0.6%). The Anthomyiidae material included 16 species in eight genera. *Anthomyiia* Meigen was the most speciose genus, with eight species, three of which were new to science. The other genera were represented by only one or two species each. The most abundant species was *Coenosopsia ferrari* Nihei & de Carvalho (*n* = 205; 37.3%). In relation to defined areas sampled, area P exhibited the greatest abundance (*n* = 321; 66.9%) and species richness (15), followed by area C. This study was the first survey of its kind in the region. A list of sampled species is presented and it is concluded that the family seems to prefer open environments.

Integrative study of Iberian flightless ant flies (Hybotidae: Tachydromiini) unveils an overlooked diversity

Ana Gonçalves[1]*, Eduardo Marabuto[1], Rui Andrade[2], Patrick Grootaert[3], Ximo Mengual[4] & Octávio Paulo[1]

[1]Computational Biology and Population Genomics Group, cE3c – Centre for Ecology, Evolution and Environmental Changes, Universidade de Lisboa, Portugal. *anagoncalvesm@gmail.com
[2]Porto, Portugal.
[3]Royal Belgian Institute of Natural Sciences, Brussels, Belgium.
[4]Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany.

Keywords: Brachyptery, Hybotidae, Iberian Peninsula, geographic distribution, phylogenetics, *Tachydromia*, taxonomy.

Within the widespread family Hybotidae, there is a cluster of species endemic to the Atlantico-Mediterranean area, especially on the Iberian Peninsula. They share strong similarities with the speciose and widely distributed genus *Tachydromia* Meigen, but owing to extreme reduction in the wings and the absence of halteres, they were originally assigned to different genera. These are minute predaceous flies, *ca* 2 mm in length, which occupy microhabitats among grass and in leaf litter of deciduous forests, often under *Quercus* (Fagaceae). Numerous populations are isolated from each other, as their habitats tend to be severely fragmented. Until recently, most species have not been collected since the time of their original descriptions and several aspects of their biology and evolution remained unknown. An integrative study was undertaken to resolve their relationships, infer their evolutionary history and understand their biology. It included the analysis of molecular and morphological data, as well as behavioural and ecological observations. Knowledge of their distribution was significantly enhanced and their behaviour (mainly courtship and feeding) and habitat preferences, were recorded and described. Based on the recovered phylogenetic relationships and morphological analysis, it was necessary to describe additional species. While there are still many aspects to be studied, these data obtained are an important step towards further conservation measures.

Phylogeny of *Ischnotoma* (*Icriomastax* Enderlein) (Tipulidae)

Jéssica Gouvêa Ferreira[1, 2]* & Leonardo H. Gil-Azevedo[2]

[1]Programa de Pós-graduação em Zoologia, Universidade Federal do Rio de Janeiro.
*jgouveabio@gmail.com
[2]Museu Nacional, UFRJ, CEP 20940-040, Quinta da Boa Vista s/n, São Cristóvão, Rio de Janeiro, RJ, Brazil.

Keywords: Craneflies, *Ischnotoma*, Neotropical Region, subgenera.

The family Tipulidae comprised 3,743 species in 32 genera globally. The genus *Ischnotoma* Skuse is divided into three subgenera: *I*. (*Icriomastax* Enderlein) with ten species, occurring in Brazil and northern Argentina; *Ischnotoma sensu stricto* with 40 species, occurring in Australia and southern South America (Argentina and Chile); and *I*. (*Neotipula* Alexander) with four species, occurring from Peru to Guatemala. *Ischnotoma* is recognised in having a 12-segmented antenna, a filiform to serrate antennal flagellum, the radial sector (*Rs*) longer than crossvein *m–cu* (except in *I*. (*Icriomastax*), in which it is subequal), the anal lobe moderately developed and the calypter commonly bare. Revisions of the Australian and Chilean species of *Ischnotoma*, as well as identification keys have already been made. The same cannot be said for *I*. (*Icriomastax*) species however. Also, no previous phylogenetic analysis was performed to investigate the relationships between *I*. (*Icriomastax*) species, this study aimed to test the monophyly of *I*. (*Icriomastax*) applying morphological characters of the adult and to propose hypothesis of relationship among species of the subgenus. For the phylogenetic analysis, all nine species of *I* (*Icriomastax*), four species of *I*. (*Ischnotoma*), two species of *Holorusia* Loew and two species of *Zelandotipula* Alexander were included, where 51 morphological characters were obtained. This analysis indicated that *I*. (*Icriomastax*) is monophyletic and has six synapomorphies: rostrum with light dorsal region; rostrum with dark lateral region; dark maculae on cells *bm*, r_2, r_{4+5} and *cua*.

Studying the sensory ecology of frog-biting midges (Corethrellidae) and their frog hosts using ecological interaction networks

T. Ulmar Grafe[1, 2]*, Hanyrol Ahmad Sah[2], Norhayati Ahmad[2], Art Borkent[3], Ivonne Meuche[2] & Oliver Konopik[1]

[1]Faculty of Science and Institute for Biodiversity and Environmental Research, University Brunei Darussalam, Tungku Link, Gadong 1410, Brunei Darussalam. *grafe@biozentrum.uni-wuerzburg.de
[2]University of Würzburg, Würzburg, Germany.
[3]British Columbia Museum, Salmon Arm, Canada.

Keywords: Anura, Borneo, *Corethrella*, ecological networks, frog-biting midges, sensory ecology, specialisation.

The advertisement calls of anurans are subject to “eavesdropping” by illegitimate receivers, such as competitors, predators and biting flies. The selective pressures that act on anuran advertisement calls and calling behaviour are reported on for frog-biting midges (Corethrellidae) from northern Borneo. Frog-biting midges feed on frog blood and are also known to be vectors of trypanosomes and thus must be regarded as having significant influence on the design of frog advertisement calls and calling behaviour. In a ten-year effort, midges were collected directly from calling frogs and with traps broadcasting frog advertisement calls and pure tones in lowland mixed dipterocarp rainforest and peat swamp forest in Brunei Darussalam and Sarawak, Malaysia. Nine species of frog-biting midges were found to bite 23 species of frogs. Frogs with advertisement calls below 4 kHz were bitten more, suggesting a significant cost to calling in these species and an upper limit in the hearing threshold of most midges. In addition, sound traps broadcasting at high rates, high amplitude and placed on the ground versus 4 m above ground were more attractive. Quantitative bipartite host-ectoparasite networks indicated an antagonistic interaction network containing both generalist and specialist relationships with significant specialisation asymmetry. Host defences and parasite offenses varied strongly in different frog and midge species. A significant role of habitat filtering, behaviour and coevolution in shaping network structure is proposed.

Preliminary observations of blood-sucking flies in the genus *Sycorax* Haliday (Psychodidae) and their frog hosts in lowland forests of Borneo

T. Ulmar Grafe[1, 2]*, Hanyrol Ahmad Sah[1] & Zdeněk Mačát[3]

[1]Faculty of Science and Institute for Biodiversity and Environmental Research, University Brunei Darussalam, Tungku Link, Gadong 1410, Brunei Darussalam. *grafe@biozentrum.uni-wuerzburg.de
[2]University of Würzburg, Germany.
[3]Palacký University in Olomouc, Czech Republic.

Keywords: Anura, Borneo, lekking behaviour, moth flies, sensory ecology, *Sycorax*.

Over a period of ten years, numerous observations of moth flies (*Sycorax* Haliday spp.) aggregated on male frogs were made in the lowland rainforests of Borneo. Two of the species were recently described as *S*. *konopiki* Ježek and *S*. *tomkineana* Ježek, but others await formal description. Here a report is given on the lekking behaviour of male *Sycorax* that aggregate on calling male anurans. Flies were collected directly from five frog species at night using suction aspirators: *Ansonia longidigita* Inger, *A*. *leptopus* (Günther), *A*. *minuta* Inger (Bufonidae), *Kalophrynus intermedia* Inger (Microhylidae) and *Leptolalax fritinniens* Dehling & Matsui (Megophyridae). Over 200 *Sycorax* were collected, but only three were females. Two females were captured mating with males near an *A*. *longidigita* male, the other was perched near an *L fritinniens*. All females had ingested blood. On all occasions males were observed running around on the frog's dorsal surface, throat and extremities, most likely in search of females. It is thus suggested that males use frogs to locate females and compete with other males for access to females by scramble competition. Such lekking behaviour is known to occur in other Psychodidae.

Poster

Effect of temperature on development of two forensically relevant species of *Fannia* Robineau-Desvoidy (Fanniidae)

Andrzej Grzywacz*, Kinga Adamska, Marta Niewiadomska & Piotr Olszewski

Department of Ecology and Biogeography, Nicolaus Copernicus University, Toruń, Poland.
*hydrotaea@gmail.com

Keywords: *Fannia*, Forensic entomology, linear model, mPMI, nonlinear model, rate isomoprphy.

Entomological material may be used to estimate the time since death occurred (minimum post-mortem interval, mPMI) in forensically obscure cases. The method that is commonly used to calculate mPMI is application of the thermal summation model. Little is known about the thermal requirements of Fanniidae. To fill this gap, temperature influence was examined on the development period of two fanniids: *Fannia canicularis* (L.) and *F. pusio* (Wiedemann). The experiment was performed under nine ambient temperatures. The thermal summation constants (k) and developmental zeros (Tmin) were calculated for six developmental landmarks. Data were primarily analysed with two linear models and since the relationship between temperatures and the development rate is curvilinear close to the lower and higher developmental thresholds, the relationship was also modelled using three nonlinear models. Ikemoto & Takai model suggests that development from egg to eclosion in *F. canicularis* requires 481.73 ± 9.89 degree-days above a threshold 4.64 ± 0.19°C and in *F. pusio* 199.14 ± 5.79 degree-days above a threshold 11.96 ± 0.18°C. Results obtained from nonlinear models were not satisfactory and could not be considered biologically reliable. A discussion is provided for some unexpected results of this study; for example, the wandering larvae of *F. canicularis*, that proceeded to diapause instead of pupariation at lower temperatures. Usefulness of nonlinear modelling in the light of common Tmin value for all developmental stages within a population of a species (rate isomorphy) is also discussed.

Third time lucky? – A comparison of phylogenetic hypotheses, based on multilocus Sanger sequencing and next-generation sequencing, a case of the family Muscidae

Andrzej Grzywacz[1]*, Paulina Trzeciak[1], Brian K. Cassel[2], Brian M. Wiegmann[2], Krzysztof Szpila[1] & Marcin Piwczyński[1]

[1]Department of Ecology and Biogeography, Nicolaus Copernicus University, Toruń, Poland. *hydrotaea@gmail.com
[2]North Carolina State University, Raleigh, U.S.A.

Keywords: Anchored hybrid enrichment, molecular systematics, Muscidae, RAD sequencing, Sanger sequencing.

Multilocus Sanger sequencing (mS-seq) may fail to reconstruct systematic relationships or receive statistically insignificant branch support values for some nodes of the phylogenetic tree. High-throughput DNA sequencing has become more and more popular in phylogenetic research. For example, Restriction Site Associated DNA (RAD-seq) sequencing enables rapid generation of up to thousands of loci randomly scattered across the genome and is suitable for nonmodel organisms. According to recent studies RAD-seq may be applied to reconstruct relationships between lineages diverged up to 60 MYA. The recent attempts to reconstruct relationships within Muscidae by means of mS-seq did not provide satisfactory results. The beginning of muscid radiation is estimated up to 61 MYA. Thus this family was used as a model group to verify RAD-seq usefulness for phylogenetic inference. As expected, a large amount of missing data was observed and significant dropout of shared loci along with decreasing relatedness of taxa in RAD-seq data. Consequently, some taxa have been randomly scattered throughout obtained phylogenetic tree. Both mS-seq and RAD-seq approaches received poor statistical support for deeper nodes and this corresponds with other studies on muscid molecular phylogeny. Nevertheless, the amount of obtained phylogenetic information allowed successful reconstruction of some intrageneric relationships (*e.g.*, *Ophyra* Robineau-Desvoidy nested within the monophyletic *Hydrotaea* Robineau-Desvoidy) and intergeneric relationships for more recently diverged lineages. RAD-seq failed to reconstruct relationships at deeper phylogenetic levels and thus relations between some muscid lineages remained unresolved. Anchored hybrid enrichment approach could be used as a next step in producing phylogenetic hypotheses for the muscids.

Pollinating Diptera from the community perspective

Jiří Hadrava[1]*, Zdeněk Janovský[2], Michael Mikát[2] & Jan Klečka[3]

[1]Department of Zoology, Faculty of Science, Charles University, Viničná 7, CZ-128 43 Praha 2, Czech Republic and Institute of Entomology, Biological Centre, Czech Academy of Science, Branišovská 31, CZ–370 05 České Budějovice, Czech Republic. *hadravajirka@seznam.cz
[2]Charles University, Prague, Czech Republic.
[3]Czech Academy of Science, České Budějovice, Czech Republic.

Keywords: Central Europe, ecology, pollinators, pollination networks.

Diptera are among the most common pollinators throughout European ecosystems. Even though they are known to be generalist pollinators, they do not visit plants purely at random. Flower-visiting Diptera demonstrate complex foraging behaviour, which determines their dynamic role in the systems of plants and their pollinators. To investigate this subject, several different approaches were applied: 1) a pollination network approach was used to describe the systems of plants and pollinators under natural conditions across European ecosystems; 2) observations in controlled conditions were used to describe the vertical stratification of plant-pollinator interactions; and 3) detailed long-term monitoring of a single locality was undertaken in order to understand the spatio-temporal dynamic of pollination networks.

Poster

The research-casework continuum in forensic dipterology

Martin J.R. Hall

Department of Life Sciences, Natural History Museum, Cromwell Road, London, SW7 5BD, United Kingdom. m.hall@nhm.ac.uk

Keywords: Calliphoridae, casework, climate reconstruction, forensic, minimum post-mortem interval.

Research is a vital component of all forensic sciences, including forensic dipterology. Research can often be stimulated by forensic casework which identifies lacunae in our knowledge. There is a continuum between research and casework and most forensic entomologists are involved in both aspects to a greater or lesser extent. This presentation will discuss the different challenges at either end of the continuum, from the replicated, highly controlled, sometimes esoteric aspects of research to the very individual, sometimes chaotic and disruptive, but highly applied aspects of casework. Casework can vary from the ideal, where the entomologist collects the insect and climate evidence at the scene and produces a robust witness statement based on a full analysis, to situations where samples, if collected at all, are poorly preserved, not representative of the full cadaver fauna available and presented to the entomologist months or years after the event, without local temperature data. Examples of how casework throws up challenges for research will be provided, ranging from the aging of insect samples by a variety of techniques, including micro-CT scanning, to the potential for colonisation of bodies in inaccessible sites, such as suitcases and determination of the developmental origin of adults found at indoor crime scenes. Challenges from cuts to budgets for forensic science and investigation will also be discussed and how these might impact on the ability of a future generation of forensic entomologists to gain casework experience in an environment that also encourages research, as the two should go hand-in-hand.

The identification of hymenopteran parasitoids of fruit flies (Tephritidae) and their specific host relationships using a next-generation taxonomy approach

Julien M. Haran[1, 3]*, Simon van Noort[2], Laure Benoit[1] & Pia Addison[3]

[1]CBGP, Cirad, Montpellier SupAgro, INRA, IRD, Univ. Montpellier 755, Avenue Agropolis, F- 34398 Montpellier, France. *julien.haran@cirad.fr
[2]Iziko Museums of South Africa, Cape Town, South Africa.
[3]Stellenbosch University, Stellenbosch, South Africa.

Keywords: Biocontrol, Braconidae, DNA metabarcoding, fruit flies, parasitoids, species complexes, trophic web.

In Africa, fruit flies (Tephritidae) are pests that cause significant damage in fruit production. Classical biological control using specific coevolved parasitic Hymenoptera is an important and successful component among the strategies currently applied to manage these pests. However, the frequent cases of cryptic diversity of species of fruit flies and their parasitoids constitute an important limitation to the establishment of more efficient biological control programmes. The next-generation taxonomy approach, that combines traditional recognition of species based on morphology and DNA metabarcoding analysis can help to face these challenges. An introduction is given to the recent application of a non-destructive Illumina-sequencing protocol on historical museum specimens of parasitic Hymenoptera of fruit flies. This method allowed reliable barcode data to be obtained from insects identified by experts and the exploration of intra-specific genetic divergences and hosts/parasite associations in a single analysis. This general approach is currently applied more broadly in the Afrotropical Region to study the distribution, host-plant and host insect preferences of parasitic Hymenoptera of fruit flies in the region.

Step right up! Joining the OET circus – sheer madness or scientific altruism?

Emily A. Hartop

Station Linné, Ölands Skogsby 161, 38693 Färjestaden, Sweden. emily.hartop@stationlinne.se

Keywords: *Megaselia*, open-ended taxa, Phoridae, species discovery.

In the study of open-ended taxa (OET) there exists little hope for a satisfying culmination of a life's work ahead. Instead, the best you might hope for is to leave the situation better for the next hapless soul. The current situation for OET *Megaselia* Rondani (Phoridae) is considered. How do thousands of terminalia sketches from Swedish specimens and tens of thousands of NGS barcodes from South-east Asia and Uganda coalesce into something useful? How might butterflies and bacteria become inspiration for a bifurcated approach to the endless chaos? It's time to stop tackling bottomless pits of species with shovels; it's time to step back, look at all the tools we have available and rethink the pit. Joining the OET circus might require madness or altruism (or both), but the three-ring OET spectacle is full of opportunities and challenges for those willing to run away with us.

The after party – where you can take all those fresh new species once they're described

Emily A. Hartop[1]*, Elizabeth Long[2], Carol Bornstein[3], Lisa Gonzalez[3] &
Brian V. Brown[3]

[1]Station Linné, Ölands Skogsby 161, 38693 Färjestaden, Sweden. *emily.hartop@stationlinne.se
[2]University of California Los Angeles, Los Angeles, U.S.A.
[3]Natural History Museum of Los Angeles, Los Angeles, U.S.A.

Keywords: Los Angeles, *Megaselia*, Phoridae, pollinators, Syrphidae, urban.

While taxonomists might be tempted to call it a night after species discovery and descriptions are over, that is when the real fun begins. At the after party for forty-three newly described species of *Megaselia* Rondani (Phoridae) from Los Angeles, fresh taxonomic findings were used in examination of a year's worth of data from the Nature Gardens at the Natural History Museum of Los Angeles and five other sites across the city. Contrasting the poorly known local Phoridae with a diverse grouping of pollinators (bees, butterflies and flower flies) revealed just how targeted urban spaces might be. Are parks and gardens really enhancing city biodiversity, or are they creating targeted "wildlife spectacles" of predictable, charismatic minifauna? Utilising highly diverse and abundant (but often poorly known) groups might just be the future of urban ecology and dipterists are key players. Party on!

New phylogenetic perspectives on Platypezoidea and early lineages of Phoridae based on morphological evidence and dense taxon sampling

John M. Hash[1]* & Brian V. Brown[2]

[1]Department of Entomology, Smithsonian Institution, National Museum of Natural History, 10th and Constitution NW, Washington D.C. 20560-0169, U.S.A.*hashjm@si.edu
[2]Natural History Museum of Los Angeles County, Los Angeles, U.S.A.

Keywords: Amber, fossils, Morphobank, morphology, Phoridae, phylogeny, Platypezidae, systematics.

Inferring the phylogenetic relationships between the families of Platypezoidea has been a decades-long source of confusion. The current consensus is that Platypezoidea is monophyletic and this has been supported by recent molecular studies, but studies attempting to resolve relationships within the superfamily have traditionally relied on limited taxon sampling. The inability to make solid claims about phylogenetic relationships, likely stems from the diverse morphological adaptations that have occurred in tandem with the diversification into a wide range of biological niches. Additionally, wildly uneven taxonomic diversity between sister clades, deep evolutionary history and extinction of intermediary lineages, has left large gaps in phenotypic space. In order to build a more comprehensive understanding of the evolution of Platypezoidea, fossil data is critical, where using extant taxa alone has proven insufficient. A preliminary phylogeny of Platypezoidea is presented, based primarily on 55 adult external characters and over 60 extant and extinct taxa, including out-groups. Morphological evidence for the sister-group relationship between Lonchopteridae and Phoridae is presented. Additionally, the possibility that Ironomyiidae renders Platypezidae paraphyletic and the placement of several Cretaceous amber fossils is discussed.

Novel morphological data to decipher character and life-history evolution in Asiloidea and Nemestrinoidea

John M. Hash[1]*, Torsten Dikow[1] & Bradley J. Sinclair[2]

[1]Department of Entomology, Smithsonian Institution, National Museum of Natural History, 10th and Constitution NW, Washington D.C. 20560-0169, U.S.A. *hashjm@si.edu
[2]Canadian National Collection of Insects and Canadian Food Inspection Agency, Ottawa, Canada.

Keywords: Brachycera, “Burmese amber”, Morphobank, morphology, “Orthorrhapha”, phylogeny, systematics.

“Orthorrhapha” historically includes large, morphologically diverse lineages of lower Brachyceran flies representatives of which are pollinators, honeydew- and nectar-feeders, parasitoids and predators. Despite a long historical interest in the phylogeny of lower Brachycera, no consensus on the relationships between these early diverging lineages has been reached. Recent studies employing morphological and molecular data have similarly been equivocal on the question of whether “Orthorrhapha” is monophyletic or rendered paraphyletic by the Eremoneura. In addition, morphological synapomorphies supporting the monophyly of several families are not available for all taxa. Here, an attempt is made to discover and utilise novel morphological characters to decipher the phylogeny of the lower Brachycera, focusing on Asiloidea and Nemestrinoidea, to understand the evolution of parasitoidism and other morphological and life-history traits. In contrast to past analyses that employed groundplan coding and limited taxon sampling, a specimen-based scoring approach is used, combined with dense taxon sampling that includes rarely sampled and fossil taxa and the traditionally challenging to place *Apystomyia* Melander and *Hilarimorpha* Schiner. Furthermore, the position of several species recently described from fossils from Myanmar (“Burmese amber”), representing stem lineages of extant families will be discussed. Findings from a preliminary dataset of 80 primarily adult, external morphological characters scored for 140 taxa are presented. All matrices, character descriptions, images, and specimen data are being handled in Morphobank (www.morphobank.org), to provide open access and future reusability of these gathered data. Further comment is made on the utility of advanced internal imaging techniques for character exploration and phylogenetics.

The genus *Eumerus* Meigen (Syrphidae) in Madagascar

Martin Hauser

California Department of Food and Agriculture, Plant Pest Diagnostics Branch, 3294 Meadowview Road, Sacramento, 95832, CA, U.S.A. Phycus@gmail.com

Keywords: Afrotropical Region, *Eumerus*, Madagascar.

The genus *Eumerus* Meigen is widespread in the Old World, with 287 valid species of which 72 occur in the continental Afrotropics. From the Island of Madagascar, there are 10 described endemic species and an additional five introduced species. In his unpublished research on *Eumerus* of the Afrotropical Region, Leif Lyneborg recognised 12 additional species. In the extensive material of *Eumerus* housed in the California Academy of Sciences (U.S.A) from Madagascar, an additional four undescribed species are recognised. A first step to revise this genus in Madagascar is presented in this poster.

Poster

Diptera – drivers of diversification in Stapeliinae (Apocynaceae: Asclepiadoideae)

Annemarie Heiduk[1, 6]*, Irina Brake[2], Michael von Tschirnhaus[3], Jean-Paul Haenni[4], Jeff Ollerton[5], Sigrid Liede-Schumann[6], Ulrich Meve[6] & Stefan Dötterl[1]

[1]Department of Biosciences, Plant Ecology, University of Salzburg, Hellbrunnerstraße 34, Salzburg, Austria. *annemarie.heiduk@gmx.net
[2]Natural History Museum, London, United Kingdom.
[3]University of Bielefeld, Bielefeld, Germany.
[4]University of Neuchâtel, Neuchâtel, Switzerland.
[5]University of Northampton, Northampton, United Kingdom.
[6]University of Bayreuth, Bayreuth, Germany.

Keyword: Chemical mimicry, morphological shifts, myiophily, pitfall flower, radiation.

The Stapeliinae (Apocynaceae: Asclepiadoideae: Ceropegieae) is a fascinating example of fly-driven species radiation (> 720 species) with outstanding floral morphologies. This includes the sophisticated pitfall flowers of *Ceropegia*, which exploit small Diptera as pollinators. Recent phylogenetic analyses propose multiple shifts from pitfall (*Ceropegia*) to non-pitfall (*Brachystelma* and stapeliads) flowers. Apparently, these shifts in functional flower morphology are due to selection by flies as sole pollinators; however, the key floral traits involved in fly attraction are hardly known. The flowers of many species emit unpleasant odours and are assumed to mimic food or oviposition sites to attract flies, whereby flower scent seems to play a major role. There is a huge gap in our knowledge of the volatiles involved, the sensory impression they generate in the flies (imitated models) and their function in the biology of the flies. Most data exist for *Ceropegia* pitfall flowers, which are generally specialised on 1–2 pollinating fly families/genera, although some are more generalised. Twenty-five Diptera families are known visitors, 16 are confirmed as pollinators. These studies suggest that pollinator specificity is achieved through species-specific floral chemistry and distinct pollination strategies. Some remarkable strategies were discovered, such as mimicry of injured insects as food source for kleptoparasitic flies and mimicry of yeast. Electroantennographic measurements with scatopsid fly pollinators of *Ceropegia stenantha* K.Schum suggest that novel chemicals identified in this species' scent are of biological relevance for Scatopsidae. Studying floral chemistry in fly-pollinated flowers contributes valuable knowledge to better understand life histories of pollinating Diptera.

Diversity of Mycetophilidae (Bibionomorpha) reared from macrofungi of the high Andean forest, Central Cordillera of Colombia

Carolina Henao Sepúlveda[1]*, Marta Wolff[1] & Dalton de Souza Amorim[2]

[1]Grupo de Entomología, Universidad de Antioquia, Cll. 67 #53 – 108, Medellín, Colombia.
*carolinahenao8@hotmail.com
[2]Universidade de São Paulo, Riberão Preto, Brazil.

Keywords: Central Cordillera, Colombia, diversity, high Andean forest, macrofungi.

The macrofungi constitute an important source of food and shelter for the larvae of flies, including Mycetophilidae. The ecology of most Neotropical species of mycetophilids remains poorly known however. The life cycle of a number of fungus gnat genera (excluding Cecidomyiidae and Sciaridae), are primarily associated with macrofungi. This association largely applies to larval development and dispersion of fungal spores. Reports regarding rearing and host specificity of mycetophilids are best known in the Palaearctic, with only the single record of *Neoempheria punticoxa* Edwards from Brazil in the Neotropics. Records for Colombia are entirely unknown, including temperate ecosystem faunas of the high Andean forest. In this survey, 170 macrofungi were sampled, representing 21 genera in 19 Basidiomycetes families. The study was conducted during the rainy and dry periods of 2016 and 2017 in the high Andean forest of the Central Cordillera. All specimens were reared under laboratory controlled conditions until adult emergence. A total of 849 specimens of Mycetophilidae were reared, representing seven genera in three subfamilies. Specimens of *Mycetophila* Meigen (n = 525) were the most abundant, followed by *Neoempheria* Osten Sacken (n = 132), *Phronia* Winnertz (n = 91) and *Rymosia* Winnertz (n = 77). *Zygomyia* Winnertz, with 16 specimens and *Exechiopsis* Tuomikoski and *Leia* Meigen, with a single specimen each, were the most uncommon genera. Results of host identity of these mycetophilids and some other aspects of their ecology and natural history are presented in the first study of its kind for the high Andean forest of Colombia.

Poster

Diversity of fungus gnats (Mycetophilidae) in Páramos ecosystems of Colombia

Carolina Henao Sepúlveda[1]*, Marta Wolff[1] & Dalton de Souza Amorim[3]

[1]Grupo de Entomología, Universidad de Antioquia, Cll. 67 #53 – 108, Medellín, Colombia.
*carolinahenao8@hotmail.com
[3]Universidade de São Paulo, Ribarão Preto, Brazil.

Keywords: Colombia, diversity, Páramos ecosystems.

The Colombian fauna of Mycetophilidae remains poorly studied, with records of only four genera and twelve known species, for a group potentially extremely diverse in the country. Colombian Páramos provide important ecosystems services as regulators of regional water, storage and capture of carbon dioxide and also as a shelter for a variety of organisms, including fungus gnats. This study addresses the diversity and aspects of the biology of mycetophilids in three vegetation types of Páramos ecosystems: Grasslands, between 2,000 and 2,500 masl; High Andean Forest, between 2,500 and 3,000 masl; and Páramos, between 3,000 and 3,900 masl. Sampling was conducted using floor and canopy Malaise traps and by sweep netting, during rainy, dry and transitional periods between 2016 and 2017. A total of 19,008 specimens of mycetophilids were sampled with floor Malaise traps, 1,937 specimens with canopy Malaise traps and 1,275 specimens by sweep netting. These samples represent species of six of the mycetophilid subfamilies in 38 genera. The High Andean Forest was dominated by species of the genera *Dziedzickia* Johannsen, *Leia* Meigen and *Zygomyia* Winnertz; Transitional Forest mostly by species of *Duretophragma* Borkent; and Páramos included a large number of *Paraleia* Tonnoir and *Procycloneura* Edwards specimens. The study revealed a clear difference in the fauna between the rainy and transitional weather conditions. This is the first study in Colombia on mycetophilid fauna in temperate, highly vulnerable environments, such as the Andean Páramos and represent the first step to include mycetophilid in conservation management in Páramos programmes.

Current entomotoxicology research in the Western Cape, South Africa

Marise Heyns

CapeFORTE, Division of Forensic Medicine and Toxicology, Faculty of Health Sciences, University of Cape Town, P.O. Box 13914, Mowbray, 7705 South Africa. marise.heyns@uct.ac.za

Keywords: Calliphoridae, entomotoxicology, forensic entomology, taphonomy.

No forensic entomotoxicological research has been conducted at the University of Cape Town or in the Western Cape, prior to the writer joining the University in 2012. One aim of the entomological research is to identify the blowfly species (Calliphoridae) that are active in land-based environments in the Western Cape and to determine baseline development rates for these species, which will aid in more accurate post-mortem interval (PMI) determinations. One study investigated the influence of Ritalin (methylphenidate hydrochloride/MPH) on the development of *Chrysomya chloropyga* (Wiedemann). MPH was detected from treated larvae preserved in ethanol and by freezing. Furthermore, MPH could be detected from samples containing as few as three larvae, after 3.5 days incubation at ~30°C. This may be indicative of an improved preservation and stability of MPH in insect specimens, especially given the labile nature of MPH. The influence of MPH on the duration of developmental stages was evident in an expedited larval stage of up to 17 hours and a prolonged puparial stage of up to 16 hours. Another study was to analyse the effect of amitriptyline on the development and growth rate of *C. chloropyga* and *Lucilia sericata* (Meigen). Results indicate that Amitriptyline delays pupariation in blowfly larvae by at least 26 hours and the emergence of the imago by at least 72 hours. Further research should be conducted into areas such as standardised methodology for entomological investigations, bioaccumulation, insect metabolism of drugs and quantitative analyses of insect evidence.

Current research and utility of forensic entomology in the Western Cape, South Africa

Marise Heyns* & Devin Finaughty

Division of Forensic Medicine and Toxicology, Faculty of Health Sciences, University of Cape Town, P.O. Box 13914, Mowbray, 7705, South Africa. marise.heyns@uct.ac.za

Keywords: Calliphoridae, entomotoxicology, forensic entomology, puparia, taphonomy.

Since A.J. Prins described the morphology of six adult blowflies and their immature stages in 1982, no significant records for forensically significant species have been described for the Western Cape, South Africa. No forensic entomological research was conducted in the region prior to 2012 and the practise of forensic entomology has been largely restricted to a limited number of medico-legal death investigations, conducted by Forensic Pathology Services. The teaching of forensic entomology was introduced in the master's programme in Biomedical Forensic Science, launched at the University of Cape Town, South Africa in 2012 and has resulted in some valuable entomological research on local blowfly populations. This presentation will provide an overview of the blowfly species present in land-based environments in the Western Cape, South Africa and their seasonal distribution, abundance and baseline development rates. Research includes barcoding of species, evaluating the effect of climatic conditions (particularly temperature and humidity), entomotoxicology, the geographical distribution of species, identification and aging of puparia and flyspecks or artefacts caused by fly activity at crime scenes. Given the attendant benefits, regional forensic entomology research stands to bring local forensic practice, it is now of critically importance to strategise around the usefulness and the future of forensic entomology in this region.

The Knight Stick sticky stable fly trap

Jerome A. Hogsette

USDA-ARS, CMAVE, 1600 SW 23rd Drive, Gainesville, FL, 32608, U.S.A. jerry.hogsette@ars.usda.gov

Keywords: Attraction, biting fly, livestock, management, Muscidae, traps.

Effective traps for stable flies (Muscidae) first appeared in the literature in the late 1970s, with the development of a series of fiberglass traps. These traps reflect sunlight in wavelengths that make them attractive almost exclusively to stable flies. Flies attracted to the traps are captured on a sticky substrate. In 2001, work began on development of the Knight Stick sticky fly trap, which appeared on the market about five years ago. Initial studies demonstrated its superior rate of catch and that the sticky trap is also attractive when used on objects other than the trap base. These traps are easy to use and easy to move from one location to the next as needed. The need to place traps close to host animals to obtain the best rate of catch was overcome by placing the Knight Stick traps inside of protective perimeters of electric fence. Traps placed close to congregation sites of the host animals captured many more flies than traps placed along the perimeter fences of fields and paddocks. Comparative studies with Knight Stick traps and current national and international projects will be discussed.

Basic biology and host use patterns of stalk-eyed fruit flies (Tephritidae: Trypetinae) breeding in *Rubus* L. (Rosaceae)

Ning Huangfu*, Xiaolin Chen, Yong Wang & Chaodong Zhu

Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China. *819067530@qq.com

Keywords: Basic biology, host use patterns, stalk-eyed fruit flies.

The stalk-eyed fruit flies, comprising the genera *Pelmatops* Enderlein and *Pseudopelmatops* Shiraki, are easily distinguished from other tephritids by their unusual head structure, with the eyes borne at the ends of stalks. In order to understand the general biology and host use patterns of stalk-eyed fruit flies, fieldwork was undertaken at Tianmu Mountain, Zhejiang Province and Zhougong Mountain, Sichuan Province in China, from 2013 to the present. Their feeding, mating and oviposition behaviour were observed in the field and laboratory. The host-plant of *Ps*. *angustifasciatus* Zia & Chen and *Ps*. *continentalis* Zia & Chen was discovered to be *Rubus peltatus* Maxim (Rosaceae) and of *Pe*. *ichneumoneus* (Westwood) to be *Rubus setchuenensis* Bureau & Franch (Rosaceae). The mating process observed, includes pre-mating (approach, chase) and mating. The female of *Ps*. *angustifasciatus* and the male of *Ps*. *continentalis* were observed mating, both in the field and in the laboratory; it is deduced that they belong to conspecific organisms. The female of *Pe*. *ichneumoneus* and the male of *Pe*. *tangliangi* Chen were observed mating in the laboratory; whether it is conspecific or not requires further study. The female oviposition behaviour of *Pe*. *ichneumoneus* includes selecting healthy stems, piercing the stem surface with the ovipositor and laying eggs under it. The larvae of *Pe*. *ichneumoneus* feed and develop in the stems of *R*. *setchuenensis* and begin to feed downwards as they mature and finally chew holes to escape and pupariate in nearby soil.

Effect of temperature on development and reproduction of *Bradysia* sp. and *Bradysia impatiens* (Johannsen) (Sciaridae)

Yuki Ishihara & Yohsuke Tagami*

Faculty of Agriculture, Shizuoka University, Ohya 836, Suruga-ku, Shizuoka, Japan.
*tagamiy@gmail.com

Keywords: *Bradysia*, development, reproduction, temperature.

During 2017, some Welsh onion and carrot fields were damaged by *Bradysia* dark winged fungus gnats. The most notorious agricultural dark winged fungus gnat pest in Japan is *B*. *impatiens* (Johannsen); a species which damages these crops, but to a lesser extent than an underscribed *Bradysia* sp. The effects of temperature on the development and reproduction of *Bradysia* sp. and *B*. *impatiens* were investigated. The developmental period of all life stages of *Bradysia* sp. were longer than for *B*. *impatiens* at all temperature ranges; 112.8 days and 26.6 days were required for development of the female *Bradysia* sp. at 11°C and 25°C, respectively and 115.0 days and 25.7 days at 11°C and 25°C respectively for the male. Female *B*. *impatiens* required 93.3 days at 11°C and 19.3 days at 25°C and the male took 86.1 days at 11°C and 15.8 days at 25.8°C. The intrinsic rate of natural increase rate at 11°C, 16°C, 20°C, 25°C and 30°C of *Bradysia* sp. were 0.002, 0.045, 0.085, 0.138 and -0.011 and for *B*. *impatiens* were 0.016, 0.071, 0.146, 0.154 and 0.087 respectively. These results suggest that *Bradysia* sp. have lower fecundity than *B*. *impatiens* at all temperature ranges.

Pseudeurina de Meijere (Chloropidae) from Australia, New Guinea and the Neotropics

Barbara Ismay[1]*, Zeinab Bazyar[2], Paula Raile Riccardi[3] & John W. Ismay[4]

[1]Schultmay Ltd., 67 Giffard Way, Long Crendon, Aylesbury, Bucks., HP18 9DN, United Kingdom.
*schultmay@insectsrus.co.uk
[2]Universidade de São Paulo, São Paulo, Brazil.
[3]Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil.
[4]Oxford University Museum of Natural History, Oxford, United Kingdom.

Keywords: Australia, Chloropidae, Neotropical Region, New Guinea, new species, *Pseudeurina*, revision.

The tropical and subtropical genus *Pseudeurina* de Meijere has been placed in the subfamily Oscinellinae within the species-rich family Chloropidae. It is only known from three described species, the widespread Oriental *Pseudeurina maculata* de Meijere, the south-east Palaearctic *P*. *miscanthi* (Nartshuk) and the Indian *P*. *indica* Cherian. Further species were discovered by the fourth author in New Guinea and in collections from Australia. Recently, additional species were found by the second and third authors in collections from Brazil and Chile. This genus has not been found in the Afrotropical Region. This presentation is an overview of ongoing revision of this genus. The main characters of eleven new and three described species are illustrated and the generic limits of *Pseudeurina* are discussed. Thus the genus is now known from fourteen species in the Palaearctic, Oriental, Australasian and Neotropical Regions.

Why is the Chloropidae fauna of New Guinea so diverse and high in endemics?

John W. Ismay

Oxford University Museum of Natural History, Parks Road, Oxford OX1 3PW, United Kingdom. schultmay@insectsrus.co.uk

Keywords: Chloropinae, distribution, diversity, endemism, New Guinea, Oscinellinae, Siphonellopsinae.

The speaker worked in Papua New Guinea from 1980 to 1986 and concentrated his efforts on the family Chloropidae. The family exhibits a very high degree of endemism in New Guinea. The subfamily Siphonellopsinae included 50 species mostly endemic to New Guinea, with one species common to Australia. Very few species are known from the islands west of Wallace's Line, but the Australian fauna is even larger with *ca* 100 mostly endemic species. In the subfamily Oscinellinae the genus *Tricimba* Lioy is diverse in all these regions, with 39 species from New Guinea mostly different from those from elsewhere. Two species are also found in the Oriental Region and nine are common with Australia, with a further 57 only occurring there. The genus *Cadrema* Walker is richer in species in New Guinea (> 100) than in the rest of the world and almost all are endemic, with perhaps two species common to Australia and one cosmotropical species. *Gaurax* Loew is also highly diverse, with over 100 almost all endemic species, but is not satisfactorily defined. Finally, *Conioscinella* Duda contains around 100 species, but requires a lot of work at the generic level. The subfamily Chloropinae is poorly represented, but *Chloropsina* Becker contains at least 50 species, a few are common to the Oriental Region, the remainder are endemic. This degree of endemism is also reflected in other chloropid genera and in other taxa such as butterflies and birds.

Phylogeny and biogeographical discussion of *Wiedemannia* Zetterstedt (Empididae: Clinocerinae) with a revision of subgeneric concepts

Marija Ivković[1]*, Emma Wahlberg[2] & Ana Previšić[1]

[1]Division of Zoology, Department of Biology, Faculty of Science, University of Zagreb, Rooseveltov trg 6, 10000 Zagreb, Croatia. *marija.ivkovic@biol.pmf.hr
[2]Swedish Museum of Natural History, Stockholm, Sweden.

Keywords: Biogeography, Empididae, Eocene, Europe, Palaearctic, phylogeny, subgenera, *Wiedemannia*.

The phylogenetic relationships and biogeography within *Wiedemannia* Zetterstedt (Empididae: Clinocerinae) are investigated. The subgeneric division within the genus is poorly defined and problematic. Numerous species are not assigned to a subgenus or have been assigned to a subgenus without clarification. In this study, two mitochondrial (COI and Cyt*β*) and two nuclear (CAD and EF-1*α*) gene fragments were sequenced to reconstruct the phylogenetic relationships within the genus, using both Bayesian inference and maximum likelihood approaches. All subgenera: *Chamaedipsia* Mik, *Eucelidia* Mik, *Philolutra* Mik, *Pseudowiedemannia* Engel, *Roederella* Engel and *Wiedemannia* (*sensu stricto*), were represented. The genus is found to be monophyletic, but most of the subgenera are not found to be natural groups, with species assigned to various subgenera intermixed. It is recommended that the subgeneric divisions within *Wiedemannia* be no longer recognised. Molecular dating using a log normal clock model and calibration with fossil species for the subfamily Clinocerinae and family Empididae indicated that *Wiedemannia* diversified about 48 MYA in the Eocene, while there was still a land connectivity between Europe and Asia with North America. *Wiedemannia* has a worldwide distribution, apart from the Australasian and Neotropical Regions and Antarctica. The highest diversity of *Wiedemannia* occurs in Europe, especially in mountainous areas of the Mediterranean diversity hotspot.

Systematics and ecology of Empidoidea

Two million species of gall midges – who is surprised?

Mathias Jaschhof

Station Linné, Ölands Skogsby 161, 38693 Färjestaden, Sweden. mjaschhof@yahoo.de

Keywords: Biodiversity, Cecidomyiidae, hyper-diverse, open-ended taxa, work methods.

Increasing concern over biodiversity loss is fueling attempts to considerably accelerate our inventory of the Earth's biota and taxa so speciose, that their true size cannot even be accurately estimated, make this a formidable challenge. The term "open-ended taxa" was coined in 2009, to conceptualise what taxonomists often perceive as a quandary of "too many species and too little time". In this race against time, new molecular tools and computer technology are generally believed to bring the breakthrough. Workers on gall midges (Cecidomyiidae) appear to be only marginally affected by this atmosphere, despite the fact that this family is likely the largest of the order Diptera. The handful of scientists currently concerned with cecidomyiid taxonomy, either as a core theme or a spin-off, use a variety of approaches to tackle issues of biodiversity, although to investigate the true number of species of the family is not among their major concerns. A closer look at present-day cecidomyiid research unfolds a mindset that prioritises quality over quantity and intimate knowledge of species (characters) over indiscriminate attraction towards ever new tools. Constantly confronted with an inestimable biodiversity, workers on cecidomyiid content themselves with making reasonable contributions to what they regard as an organically grown classification system; to strive for final answers seems rather strange to them. The Cecidomyiidae offer open-ended opportunities for productive research and additional, dedicated students are welcome to advance the field with novel ideas. That said, it is acknowledged that different taxa, or research priorities, might call for different approaches.

What dirty water means to mosquitoes – the effect of common water pollutants on the life history of the major malaria vector *Anopheles arabiensis* Patton (Culicidae)

Alexander C.S.N. Jeanrenaud, Michael Samuel, Basil D. Brooke & Shüné V. Oliver*

Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Sandringham, Johannesburg and Wits Research Institute for Malaria, School of Pathology, University of the Witwatersrand, Parktown, Johannesburg, South Africa. *Shuneo@nicd.ac.za

Keywords: *Anopheles*, larvae, longevity, mosquitoes, pollution, resistance.

Larval environment is a crucial determinant for adult mosquito success. The breeding sites for representatives of the *Anopheles gambiae* complex, such as *An*. *arabiensis* Patton are defined as clean temporary bodies of water. Human activities, however, are resulting in increased water pollution, and as such, these mosquitoes are adapting to breeding in polluted waters. This is likely to affect life history characteristics, including those of epidemiological importance. Two *An*. *arabiensis* laboratory strains were exposed to a range of water pollutants; heavy metals, herbicides, inorganic fertilizers and cattle manure. The varying effects of these pollutants on larval development rate, adult longevity and insecticide tolerance are discussed in relation to SENN, an insecticide susceptible strain of *An*. *arabiensis* and SENN DDT, a strain selected from SENN and exhibiting multiple resistance phenotypes. SENN DDT showed larval development delays in polluted conditions, an accelerated larval development rate in herbicide polluted water and increased adult longevity, following emerging from herbicide treated water. Larval exposure to all pollutants increased insecticide tolerance in SENN DDT adults. SENN showed larval development delays under conditions of inorganic pollution and also displayed inconsistent insecticide tolerance increases after pollutant exposure. SENN, however, had a marked advantage when breeding in manure polluted water. Significant increases in larval development rate, adult size and longevity were observed in SENN, but not SENN DDT. Cattle manure pollutant exposure resulted in the greatest increase in pyrethroid tolerance in SENN DDT. The significance and context of these findings in terms of malaria transmission will be discussed.

A Hainanese in the haze – a phylogenetically unplaceable Oriental blowfly

Arn Rytter Jensen[1, 2]*, Liping Yan[3], Dong Zhang[3] & Thomas Pape[2]

[1]Sapienza University of Rome, Piazzale Valerio Massimo 6, 00162 Rome, Italy.
[2]Natural History Museum of Denmark, University of Copenhagen, Universitetsparken 15, DK–2100 Copenhagen, Denmark. *arn.jensen@snm.ku.dk
[3]Beijing Forestry University, Beijing, China.

Keywords: Calliphoridae, molecular phylogenetic, morphology, Oestroidea, phylogeny.

A large and colourful blowfly recently collected in the montane forests of southern Hainan Island represents an undescribed species with a surprising mixture of oestroid features. The species is presented and the possible phylogenetic relationships are discussed, based on both morphological and molecular evidence. The species has a distinctive blowfly-like appearance, but morphological data fail to support inclusion of the species within any of the currently accepted calliphoroid families or subfamilies. The large posterior thoracic spiracle, which is non-operculate and possesses a large, continuous ventral fringe, is a striking match to the condition found in the exclusively Neotropical Mesembrinellidae. Even the anterior spiracle, which has a fringe with a tear-shaped dorsal opening, agrees with the Mesembrinellidae. However, the biogeographical disjunction would appear to make this relationship highly unlikely. The stem vein is setose dorsally, as in the Mesembrinellidae, Rhiniidae and the Chrysomyinae (incl. Toxotarsinae), but no other morphological evidence supports an affiliation with either of these taxa. Molecular data based on 18S, 28S, COI, CAD, EF1*α* and TPI are still inconclusive, but point to a sister-group relationship with *Phumosia* Robineau-Desvoidy (Phumosiinae).

Integral integration – a combined morphological and molecular approach delineates cryptic species and evolutionary relationships in Australian Miltogramminae (Sarcophagidae)

Nikolas P. Johnston[1]*, Thomas Pape[2], Krzysztof Szpila[3], Mark Dowton[4] & James F. Wallman[1]

[1]Centre for Sustainable Ecosystem Solutions, School of Biological Sciences, University of Wollongong, NSW 2522 Australia. *npj304@uowmail.edu.au
[2]Natural History Museum of Denmark, Copenhagen, Denmark.
[3]Nicolaus Copernicus University, Toruń, Poland.
[4]University of Wollongong, Australia.

Keywords: Integrative taxonomy, Miltogramminae, phylogenetics.

Integrative taxonomy involves the application of multiple data sources to identify, circumscribe and classify taxa and the relationships between them. This approach is particularly suitable when the taxon of interest contains morphologically indistinct or polymorphic entities or if it is undergoing rapid genetic diversification. One such group are the Miltogramminae. Miltogramminae account for ~20% of global sarcophagid diversity and have largely been neglected in Australian fly research. They are notoriously difficult to identify and, in some cases, much as in other flesh flies, accurate species identification relies heavily upon male terminalia. Furthermore, some genera, such as *Protomiltogramma* Towsend, appear to have radiated rapidly within Australia and species identification, boundaries and relationships are, therefore, difficult to resolve without carefully planned multi-gene molecular approaches. The research presented here documents the first targeted application of integrative taxonomy to the known Australian miltogrammine fauna. This integrative approach has made use of traditional and next-generation sequencing, multi-gene molecular phylogenetics and comprehensive morphological documentation using scanning electron microscopy (SEM) and high-resolution stacking photography. This has resulted in re-descriptions of all previously described Australian Miltogramminae, detailed discrimination and documentation of at least 10 new species, discovery of a genus for the first time in the region and a phylogenetic reconstruction of interspecies relationships.

A conspectus of research on the role of Diptera in plant-pollination in the Afrotropical Region

Kurt Jordaens

Department of Biology, Royal Museum for Central Africa, B-3080 Tervuren, Belgium.
kurt.jordaens@africamuseum.be

Keywords: Afrotropical Region, ecosystem services, plant-pollinator networks, pollination.

An emerging field in the management and conservation of biodiversity is the study of plant-pollinator networks. Moreover, pollination is a key ecosystem service which sustains significant food production. Understanding plant-pollinator interactions is thus critical, especially in the face of environmental change. Surprisingly, most of the efforts to understand plant-pollinator networks has been dedicated to well-known insect groups, such as Hymenoptera (bees and wasps), Lepidoptera (butterflies) and Coleoptera (beetles), whereas the role of Diptera in these networks is strongly neglected and this certainly holds true for the Afrotropical Region. As a result, there is no baseline to describe the current status of the role of Diptera in plant-pollinator networks. Pinpointing the relative role of each of the Diptera groups, or species, in plant pollination is very challenging. An overview is here provided of these challenges and suggestions are made as to how we can increase appreciation of Diptera as important pollinators in the region. Some ongoing or projected research will be outlined that explores the role of Diptera in plant-pollinator networks in the Afrotropics.

Recent advances in the taxonomy and ecology of the hoverflies (Syrphidae) of the Afrotropical Region

Kurt Jordaens[1]* & Marc De Meyer[1]

[1]Department of Biology, Royal Museum for Central Africa, B-3080 Tervuren, Belgium.
*kurt.jordaens@africamuseum.be

Keywords: Afrotropical Region, catalogue, checklist, DNA barcoding, faunal assessments, flower flies, hoverflies, taxonomy.

Syrphidae (hoverflies or flower flies) are one of the most eye-catching, biodiverse and familiar families of flies. Yet, research on syrphids of the Afrotropical Region has lagged behind that of other zoogeographical regions. K.G.V. Smith and J.R. Vockeroth were the first to publish a comprehensive catalogue of Afrotropical Syrphidae in 1980, which H.G. Dirickx updated in 1998, to include 22 species in 54 genera. Since then, a number of new genera and species have been described and currently there are *ca* 610 species in 62 genera known from the region. These figures indicate that progress in syrphid taxonomy is substantial, yet for many genera, especially speciose ones, contemporary taxonomic revisions are lacking and difficulties in identification persist. In 2003, A.E. Whittington outlined the future needs of the taxonomic sector and indicated which genera were most in need of revision. Here the historical progress in Afrotropical syrphid research over the past 100 years is summarised and progress is indicated since Whittington's assessment. An overview is provided of ongoing taxonomic revisions, DNA barcoding activities, phylogenetic studies and faunal assessments. Finally, it is illustrated how progress in these fields has opened research in other biological research fields, such as pollination ecology and life history evolution.

A mitogenomic approach to resolve the phylogeny of Afrotropical hoverflies (Syrphidae)

Kurt Jordaens[1]*, Nele Mullens[2], Gontran Sonet[2], Massimiliano Virgilio[1, 2], Carl Vangestel[2], Georg Goergen[3] & Marc De Meyer[1]

1Department of Biology, Royal Museum for Central Africa, B-3080 Tervuren, Belgium.
*kurt.jordaens@africamuseum.be
[2]Royal Museum for Central Africa, Tervuren and Royal Belgian Institute of Natural Sciences, Brussels, Belgium.
[3]International Institute of Tropical Agriculture, Cotonou, Benin.

Keywords: Afrotropical Region, flower flies, hoverflies, mitochondrial DNA, phylogeny, Syrphidae, taxonomy.

Syrphidae (hoverflies or flower flies), are one of the most biodiverse families of flies globally. Currently available syrphid phylogenies have been reconstructed beginning from a relatively limited number of molecular markers and were largely based on Nearctic and Palaearctic species. The phylogenetic relationships among many Afrotropical syrphids, therefore, remained largely unresolved. The complete mitochondrial genome of >100 Afrotropical samples was sequenced of four target genera (*Eristalinus* Rondani, *Mesembrius* Rondani, *Phytomia* Guérin-Méneville and *Syritta* Le Peletier & Serville) and of a few out-groups, in order to investigate: 1) the mitochondrial DNA (mtDNA) structure of hoverflies; 2) the phylogenetic informativeness (PI) of the protein-coding and ribosomal RNA (rRNA) genes; and 3) the usefulness of mitochondrial genes to resolve species phylogenetic relationships within these genera. The general mtDNA structure of hoverflies is illustrated and it is demonstrated that a few genes show high PI. Using these genes and the entire mtDNA, a highly resolved phylogenetic tree for the four target genera was produced. This study indicates that complete mtDNA, or a subset of selected coding mtDNA genes, can be used to resolve the phylogenetic relationships of hoverflies and thus may contribute to a better understanding of morphological character evolution within this family.

Apical tooth of the third-instar Medfly *Ceratitis capitata* (Wiedemann) larvae (Tephritidae)

Ilya O. Kamayev[1]* & Tatiana V. Galinskaya[2]

[1]All-Russian Plant Quarantine Center, Pogranichnaya st. 32, Bykovo, 140150, Russia.
*ilyaokamayev@gmail.com
[2]Lomonosov Moscow State University, Moscow, Russia.

Keywords: *Ceratitis*, larvae, Medfly, morphology.

The Medfly, *Ceratitis capitata* (Wiedemann), is a quarantine pest, absent on the territory of the Russian Federation. The pest's main pathway is in the transport of fruit in which the larvae develop. The accurate and reliable identification of the third-instar Medfly larvae has major importance for plant quarantine practices. While the absence of an apical (or secondary) tooth on the larval mouthhooks is recognised to be typical of the third-instar larvae of *Ceratitis capitata*, it is present in some individual larvae and is variable in some geographical populations. The presence of the apical tooth in the third-instar Medfly larvae was studied from different geographical populations: Peru (culture for biomethod, 10 examples), Turkey (natural population, 10) and Egypt (natural population, 8). Slides of the cephaloskeleton of individual specimens were prepared and examined. It was ascertained that the presence of the apical tooth varied significantly: the tooth may be well or poorly developed, or entirely absent. It was best expressed in individuals from the cultured population than among natural populations. Fluctuating asymmetry was also noted when the apical tooth is developed only on one of the paired mouthhooks.

Poster

Taxonomic studies of Japanese Limoniinae (Tipulomorpha: Limoniidae)

Daichi Kato* & Takuji Tachi

Kyushu University, 744 Motooka, Fukuoka 819-0395, Japan. *hehemanpuldoa.d4@gmail.com

Keywords: Craneflies, Japan, morphology, species list, taxonomy, Tipulomorpha.

Limoniidae is one of the largest families of Diptera and includes 10,778 species globally, classified into four subfamilies. In Japan, 447 nominal species are recorded and *ca* 90% of these are based on C.P. Alexander's descriptive works, published between 1913 and 1971, as Japanese entomologists of that period sent numerous specimens to him for description. Since there are still abundant undescribed and unrecorded species in Japan and most of the type specimens are preserved in the USA, it is difficult to identify Japanese species. To help solve this problem type specimens of Tipuloidea were examined in the National Museum of Natural History, Washington D.C. and characters of each Japanese species of the subfamily Limoniinae (164 species) were verified. Consequently, 220 Japanese species were identified, including undescribed and unrecorded species, synonyms and misidentifications. An updated list of Japanese species of the subfamily Limoniinae is provided with remarks on different issues, especially taxonomic changes.

Poster

Diptera associated with Hymenoptera in trap-nests in Palmas, Brazil

Josiane Kempka, Laércio Peixoto Amaral-Neto & Adriana Couto Pereira*

Instituto Federal do Paraná campus Palmas, Avenida Bento Munhoz da Rocha, PRT 280, s/n, Trevo Codapar, 85.555-000 Palmas-PR, Brazil. *adriana.couto@ifpr.edu.br

Keywords: Hymenoptera, trap-nests, parasitoids, Phoridae, Sarcophagidae, Bombyliidae.

Trap-nests are used for studying solitary wasps (Hymenoptera) that nest in pre-existing cavities, provisioned with paralysed insects as larval food. Hymenopteran nests have numerous natural enemies, including Diptera. To investigate Hymenoptera/Diptera associations, wooden trap-nests of different diameters (5, 7, 10 and 13 mm) were deployed in an area of cultivated *Pinus* and a fragment of natural *Araucaria* pine forest in Palmas, Paraná, Brazil. In both forest types five sampling stations were established, distanced 25 meters apart from each other in a transect, with 16 wooden trap nests in each. Sample stations were visited monthly from 16th November 2016 to 9th November 2017. Nests were returned to the laboratory and monitored for the emergence insect parasites. One hundred and fourty-nine nests were collected, of which 32 were parasited, seven by Diptera. Thirty-six individuals of three Diptera families: 18 Phoridae, 4 Sarcophagidae and 1 Bombyliidae, emerging from nests of *Pachodynerus* sp. (Vespidae) and 13 Sarcophagidae from nests of *Trypoxylon* sp. (Crabronidae). Phoridae were collected from the forest fragment, while the others were reared exclusively from nests in cultivated *Pinus*. Representatives of these three families are noted in the literature as being hymenoptera parasites, but observed parasitism coincided with rainy periods, which causes fungal development and decomposition of stored insect food. As a result, some of the reared Diptera may have resulted from larvae that feed on decaying matter. Further observations on the biology of nests and species identification of Diptera may help to better comprehend Diptera/Hymenoptera interactions.

Poster

Barcoding dipteran pollinator networks in agroecosystems

Isabel C. Kilian Salas[1, 3]*, Katharina Kurzrock[1], Axel Ssymank[2], Wolfgang. J. Wägele[1], Andrée Hamm[3], Ralph S. Peters[1] & Ximo Mengual[1]

[1]Zoological Research Museum Alexander Koenig, Leibniz Institute for Animal Biodiversity, Adenauerallee 160, D-53113 Bonn, Germany. *I.Kilian@gmx.de
[2]Federal Nature Conservation Agency, Bonn, Germany.
[3]Institute of Crop Science and Resource Conservation, Bonn, Germany.

Keywords: Agroecosystem, Brachycera, DNA barcoding, German Barcode of Life, pollination networks.

Pollination is one of the most important ecosystem services, crucial for human food security and biodiversity. In the past decade, however, a massive decline of insect pollinators has been observed, while the role of one of the largest pollinator groups, the Diptera, has unfortunately been underestimated. In this study, DNA barcoding was applied to study the potential brachyceran pollinators in plant-pollinator networks. The main goal was to elucidate the plant-pollination networks for selected crops and to establish a DNA barcode library for brachyceran flies, pollen and visited plants. This project forms part of the German Barcode of Life programme. The plant-pollinator networks of two different crops (apple and caraway) with and without flowering stripes at the margins were studied. Sampling took place during the vegetation period (March to September) from 2016 to 2018. Specimens were collected with a hand net within 50 m transects for a period of 30 minutes, at three time intervals during each sampling-day. Pollen loads were washed off with glycerine and prepared for morphological and molecular identification *via* metabarcoding. Specimens were identified morphologically and with DNA barcoding. During 2016, a total 1,749 Brachycera were collected in 20 sampling days in the apple orchards and in eight sampling-days in the caraway fields. In 2017, 1,136 brachyceran flies were collected in the caraway fields during 14 sampling-days and *ca* 900 specimens in the apple orchards during 16 sampling days.

Poster

Species delimitation in the *Ochlerotatus communis* (De Geer) complex (Culicidae), a novel mitochondrial DNA (mtDNA) line from Europe

Heli Kirik[1]*, Lea Tummeleht[2], Tobias Lilja[3] & Olavi Kurina[1]

[1]Biodiversity and Nature Tourism, Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Tartu, Estonia. *hekirik@gmail.com
[2]Estonian University of Life Sciences, Tartu, Estonia.
[3]National Veterinary Institute, Uppsala, Sweden.

Keywords: DNA barcoding, mosquito diversity, *Ochlerotatus*, phylogenetics.

The *Ochlerotatus* (*Oc*.) *communis* complex consists of four sibling species: Holarctic *Oc*. *communis* (De Geer) as well as Northern American *Oc*. *churchillensis* (Ellis & Brust), *Oc*. *nevadensis* (Chapman & Barr) and *Oc*. *tahoensis* (Dyar). *Ochlerotatus communis* is considered to be the only European representative in this group of closely related species. However, persistent genetic discrepancies were found among morphologically identical *Oc*. *communis* specimens during routine DNA barcoding in Estonia, as some mosquitoes appeared to be more closely related to *Oc*. *tahoensis* than *Oc*. *communis*, according to the mitochondrial cytochrome c oxidase (COI) region. Therefore, three additional markers were sequenced: internal transcribed spacer 2 (ITS2), 28S rDNA and NADH dehydrogenase subunit 5 (ND5). Resulting sequences were combined with publicly available DNA data from GenBank (National Center for Biotechnology Information, U.S.A.) and used to analyse the genetic differences between *Oc*. *communis*, *Oc*. *tahoensis* and other mosquito species. Results showed the presence of a distinct mtDNA line in Estonian *Oc*. *communis* populations, which is just as different from the parent species as it is from *Oc*. *tahoensis*. However, there were no dissimilarities in the nuclear DNA among different *Oc*. *communis* specimens, but a variation was found between the ITS2 regions of *Oc*. *communis*, *Oc*. *tahoensis* and other mosquitoes. Thus, there is currently not enough evidence to suggest the presents of a new species from the *Ochlerotatus communis* complex in Europe. Yet, an unusual mtDNA line appears to exist in the *Oc*. *communis* populations, leaving the future discovery of novel species possible.

No more Dodo doo doo – Diptera of the Mascarene Islands

Ashley H. Kirk-Spriggs* & Burgert S. Muller

Department of Entomology, National Museum, P.O. Box 266, Bloemfontein 9300, South Africa. *ashley.kirk-spriggs@nasmus.co.za

Keywords: Mascarene Islands, Mauritius, publication, Réunion, Rodrigues, survey.

The Mascarene Islands (Mauritius, Réunion and Rodrigues) are all volcanic in origin formed by the Réunion hotspot. The fauna and flora of these islands are, therefore, the result of various “sweepstake” introductions over millions of years from continental Africa, the Oriental Region and elsewhere. The islands are more famous for their early extinctions (flightless birds, such as the Dodo and Rodrigues Solitaire and various species of giant tortoises – that were previously the major indigenous herbivores), than for their extant faunas. The islands have suffered further alarming deforestation in the recent past, mainly due to clearance for sugarcane production, resulting in further habitat loss and extinctions. Only *ca* 320 species of Diptera are recorded from the islands, but 120 are endemic to specific islands and 11 to all Mascarenes. The National Museum of Bloemfontein recently embarked on a dedicated survey of the Diptera of the islands, beginning with a month long survey of Réunion in 2015, a two-week survey of Mauritius in 2017 and a three-week survey of Mauritius and Rodrigues in 2018. Sampling was mainly conducted using Malaise traps, but selected sites were also sampled by general sweeping. An extensive coastal survey was undertaken of Mauritius and Rodrigues. Sampling is now completed and the material is being processed and distributed to specialists. The project aim is to produce the book: “*Diptera (Insecta) of the Mascarene Islands*”. Each authored chapter will deal with a family and include identification keys to species, species accounts and descriptions of new taxa.

Diptera collection of the National Museum, Bloemfontein – a regional and international resource

Ashley H. Kirk-Spriggs, Burgert S. Muller & Mary K. Kirk-Spriggs*

Department of Entomology, National Museum, P.O. Box 266, Bloemfontein 9300, South Africa. *mary.kirk-spriggs@nasmus.co.za

Keywords: Collection development, Diptera collection, research, resource, South Africa.

In the past 10 years, the Diptera collection of the National Museum, Bloemfontein has developed from a small foundation collection of *ca* 1,500 specimens (mostly spirit-preserved Hippoboscidae), to the largest non-specialised collection of Diptera on the African continent, with over 250,000 specimens. This has been achieved through dedicated sampling using Malaise traps and other passive sampling techniques in South Africa and as part of a larger initiative, *i.e.*, the "International Survey of Afrotropical Diptera", which is targeting the sampling of poorly-collected African countries and oceanic island groups. The collection now comprises recent material from Benin, Burundi, Cameroon, Democratic Republic of Congo, Kenya, Réunion Is., Madagascar, Malawi, Mauritius, Namibia, Rodrigues Is., South Africa (Eastern and Western Cape, Free State, Mpumalanga and KwaZulu-Natal Provinces), Togo and Zambia. The great strengths of the collection are that it is almost all recently generated, there are usually long series of specimens, the dry-pinned specimens are pinned in the field and are rapidly dried using silica gel and all spirit preserved specimens are preserved direct in 96% ethanol, making both suitable for DNA extraction. The collection is an essential research tool for any specialists interested in Afrotropical Diptera and currently over 50,000 specimens are on loan to international researchers. The scope, storage and use of the collection is outlined and illustrated.

Poster

Blockchain technology and other decentralised consensus systems for edge-centric database computing have the potential to vitalise taxonomy

Jostein Kjærandsen

Tromsø University Museum, UiT – The Arctic University of Norway, Tromsø, Norway.
jostein.kjarandsen@uit.no

Keywords: Blockchain, cryptography, open-access, Scienceroot, taxonomic database, token-curated registry.

Blockchain technology and related decentralised consensus systems, also known as “Crypto 2.0”, may enable a new, progressive taxonomic enterprise to run and grow on its own, outside the publishing industry. By creating a secure infrastructure for the Internet of Taxa and Scientific Names (ITSN), the rules for formation of scientific names can be imbedded through so-called “smart contracts”, hashing cryptography will take care of time-stamps and immutability and decentralised P2P-consensus (“proof of stake”, “proof of human”) will replace traditional peer review. An integrated cryptocurrency (TaxaCoins) that tracks individual investments into working up each new and already published taxa with associated descriptions, images and DNA barcodes in a data sheet on ITSN, may drive incentives for collaborative contributions through egalitarian dividend-based token rewards. Token Curated Registries (TCRs), with ownership for individual data sheets with published names on ITSN, enables further incentive mechanisms to add species and drive proper and accurate curation. With proper parametrisation, the token value may even increase proportional to the use (citations) of ITSN data sheets to back up scientific names in publications. A funding proposal to Innovation Norway to develop ITSN in co-operation with Romania-based Scienceroot, one of the first companies developing a blockchainified platform for research communities, is currently in the making. The technology for instant open sharing and worldwide online co-operation is here, are we as taxonomists ready for it?

Building the DNA barcode library of Nordic Sciaroidea – goals achieved, limitations and prospects for an operating Holarctic library on BOLD

Jostein Kjærandsen

Tromsø University Museum, UiT – The Arctic University of Norway, Tromsø, Norway.
jostein.kjarandsen@uit.no

Keywords: BOLDSYSTEMS, DNA barcoding, Holarctic Realm, integrative taxonomy, Mycetophilidae, NorBOL, Nordic Region.

A continuous cooperative effort by taxonomists to build and curate the DNA barcode library on BOLDSYSTEMS is essential, in order to furnish a vouchered reference library of high quality for applied uses in fields such as biomonitoring, ecology and next generation sequencing. Through the initiatives of NorBOL and FinBOL, the Nordic countries have come a long way towards achieving this goal. Currently, some 6,000 submitted samples of Sciaroidea have resulted in nearly 5,000 sequences, representing some 1,000 identified species, classified into more than 1,200 Barcode Index Numbers (BINs). Most cases of discordance between morphological identification and BIN assignment are solved upon careful re-examination of the vouchers, leaving only a handful of species complexes merged into BINs with near identical barcodes. The proportion of morphologically recognised species that split into two or several BINs, however, is higher, with some 150 SPLITs (12%) that remain unresolved at present. Examples will highlight how to proceed with these issues. A summary of the 760 Mycetophilidae species found in Norway reveals 618 (81%) species with one or several assigned BINs, while 5% are pending processing, 5% have so far failed to produce sequences and 9% have not yet been submitted. Currently, 50 species and 1 genus new to science are recognised among these BINs, while another 85 potential OTUs are pending further examination. The taxonomic precision of 30,000 barcodes assigned to some 1,800 BINs of Mycetophilidae from the Holarctic has been improved, through online inspection of voucher images and ID-trees including the Nordic BIN registry.

A surveillance strategy to measure population dynamics of biting Diptera at a horse boarding facility and wildlife refuge in Florida, U.S.A.

Daniel L. Kline

USDA-ARS, CMAVE, 1600 SW 23rd Drive, Gainesville, FL, 32608, U.S.A. Dan.kline@ars.usda.gov

Keywords: Aspirators, Ceratopogonidae, Culicidae, surveillance, Tabanidae, traps.

Arthropod-borne pathogens are responsible for significant global morbidity and mortality in humans, livestock and wildlife. Biting Diptera have played a prominent role as both pests and carriers of pathogens throughout the history of Florida. The ultimate goal of the research reported in this presentation was the development of a biting Diptera management strategy at a horse boarding facility and wildlife refuge located in Levy County, FL, U.S.A, in a manner to achieve human and animal health, while protecting the environment from any adverse effects. The initial step in developing this management strategy was determining which species needed to be targeted for control. A multi-year surveillance programme was conducted, which utilised a variety of techniques, such as landing rates, traps (baited and unbaited), aspirators for collection of resting and nectar seeking adults, resting boxes and sweep nets. It was determined that the major species of biting Diptera at these two locations included several species of Ceratopogonidae, Culicidae and Tabanidae and that no single technique was effective for collecting all the key species, not even within the same family. Therefore, the major finding of this multi-year study was that in order to detect all the key pest/potential pathogen carrying species and to determine their seasonal and spatial distribution patterns, a combination of surveillance techniques needed to be used simultaneously.

The genus *Cheilotrichia* Rossi (Limoniidae) from Ukrainian amber inclusions

Katarzyna Kopeć*, Kornelia Skibińska & Wiesław Krzemiński

Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016, Kraków, Poland. *kopeck1981@gmail.com

Keywords: Baltic amber, Bitterfeld amber, *Cheilotrichia*, fossils, Limoniidae, Ukrainian amber.

The genus *Cheilotrichia* Rossi in the family Limoniidae is represented by more than 130 extant species distributed on all continents, expect Antarctica. This genus is divided into two subgenera, *i.e*., *Cheilotrichia sensu stricto* and *Ch*. (*Empeda* Osten-Sacken). The subgenus *Ch*. (*Empeda*) is more abundant and more diverse in both the extant and extinct faunas. The oldest representative of the genus is *Ch*. (*E*.) *palaeocenica* Krzemiński from Sakhalin amber (Middle Eocene). The richest fauna is known from the slightly younger Baltic amber. Two additional ambers are known from the same period: Ukrainian and Bitterfeld. Only one species has been described from Bitterfeld and five species have been discovered in Ukrainian amber, two of which are new to science. Discussion regarding the origin of Ukrainian and Bitterfeld ambers and their connections with Baltic amber from the Scandinavian Peninsula are of great interest, especially considering their origin in the same geological period, as evidenced by the common species preserved. Some researchers believe that Ukrainian and Bitterfeld ambers are found in primary deposits and are not a redeposition of amber from Scandinavia carried by a glacier. The presence of different species than in Baltic amber indicates a significant ecological diversity of environments in the area of occurrence of “amber forests”.

The case of *Osa* Paramonov (Tephritoidea: Pyrgotidae)

Valery A. Korneyev

I.I.Schmalhausen Institute of Zoology, NAS of Ukraine, B.Chmielnicki St.15, 01030 Kyiv, Ukraine. valery.korneyev@gmail.com

Keywords: Australia, history, *Osa*, taxonomy, Tephritoidea.

The genus *Osa* Paramonov was originally established in 1958 to include five Australian species of the tribe Toxurini (Pyrgotinae), with apically bifurcated claws on all tarsi; a synapomorphy, which is unique among the Pyrgotidae. Sergei Paramonov subsequently prepared descriptions of six additional species and had selected and marked holotypes and paratypes in the Australian National Insect Collection (Canberra), but did not publish the manuscript before his death in September 1967. These specimens have been re-examined and illustrated (by microphotos and SEM) and descriptions of the male and female terminalia prepared and two additional previously unknown species have been recognised in collections, all while revising the Australian Pyrgotidae. These results are now summarised in a paper prepared for publication some 50 years after the first draft was written. Unlike most Toxurini genera, females of *Osa* possess no special structures which could be used for clasping their beetle hosts and ovipositing into their abdomens by piercing the abdominal tergites; instead, they have long oviscapes, which can be curved forward beneath the body while following a host beetle, before darting at it in a manner similar to that of *Frontalia* Malloch and *Prodalmannia* Bezzi, as described by S.J. Paramonov in 1958. The swallowtail-shaped oviscape apex in several *Osa* species is similar in shape to the aedeagus of scarab beetles with parameres and is believed to serve as a “lock pick” when the female fly oviposits into the abdomen of a scarab beetle female by imitating copulation.

First results of genome and transcriptome sequencing in psammorheophilous Chironomidae

Olga Kozlova[1], Oleg Gusev[1], Ivan Pozdeev[2] & Andrey Przhiboro[3]*

[1]Laboratory of Extreme Biology, Kazan Federal University, Parizhskoy Kommuny 9, Kazan 420021, Russia.
[2]State Research Institute on Lake and River Fisheries, Perm Branch, Chernyshevskogo 3, Perm 614002, Russia.
[3]Zoological Institute of the Russian Academy of Sciences, Universitetskaya nab. 1, St Petersburg 199034, Russia. *Dipteran@mail.ru

Keywords: Genome, transcriptome, heat shock proteins, psammorheophilous, river.

Chironomidae is a diverse family, with larvae dominating most aquatic ecosystems, including extreme habitats. Larvae of several chironomid lineages are specialised inhabitants of shifting sand at river bottoms and species in these lineages have independently developed similar adaptations for living under such peculiar conditions. Two such species are compared, “Orthocladiinae acuticauda” (Orthocladiinae; undescribed genus) and *Robackia demeijerei* (Kruseman) (Chironominae) on the genome and transcriptome levels. Following high-throughput DNA and RNA sequencing, genome scaffolds were assembled and RNA-Seq data were used for control and heat-shocked (30°C) larvae were used to perform a differential expression analysis. Based on bioinformatics approach, genome sizes were roughly assessed as 108–138Mb for “Orthocladiinae acuticauda” and 168–200Mb for *Robackia demeijerei*, while final assembly lengths were 107 and 170Mb, respectively. This reflects compact genome structure of midges, while variability between genome sizes in different species is achieved by expansion of repeat regions and introns extension. In order to reveal common and specific genetic features of species under investigation, as well as patterns of their reaction towards heat shock, a promising comparative genomics and transcriptomics approach was used, focusing on number, structure and behaviour of genes, coding for heat shock proteins and other genes with the most drastic changes of expression in heat-shocked samples. Heat shock proteins (HSP) are universal agents for protecting cells and the entire organism from biotic and abiotic stress, which is why changes in number and expression patterns of HSP-coding genes may reveal molecular traits of adaptation of chironomids to extreme and non-stable conditions.

Flowers fuel flies – supply of nectar for long-proboscid flies (*Prosoeca* sp.: Nemestrinidae)

Harald W. Krenn[1]*, Florian Karolyi[1], Annalie Melin[2, 3] & Jonathan F. Colville[3, 4]

[1]Department of Integrative Zoology, University of Vienna, UZA1 Althanstraße 14, 1090 Vienna, Austria. *harald.krenn@univie.ac.at
[2]Compton Herbarium, South African National Biodiversity Institute, Cape Town, South Africa.
[3]University of Cape Town, Rondebosch, South Africa.
[4]Kirstenbosch Research Centre, South African National Biodiversity Institute, Cape Town, South Africa.

Keywords: Insect/flower interaction, mouthparts, nectar-feeding, *Prosoeca*.

Long-tongued flies of the genus *Prosoeca* Schiner are representatives of the long-proboscid fly pollination system of the Greater Cape Floristic Region. They have proboscis lengths up to 42 mm and obtain nectar from long-tubed flowers. A population of a narrow endemic *Prosoeca* species was studied in Nieuwoudtville (Northern Cape Province, South Africa), which feeds on several long-tubed host-plants. At one of these discontinuous study sites, however, isolated by transformed land, *Babiana vanzyliae* L.Bolus (Iridaceae) was the only flowering host-plant and source of nectar. This particular isolated area (*ca* 10,000 m²) gave the opportunity to estimate the total nectar supply that fuels a population of pollinating insects for the first time. Mark/recapture experiments from surrounding host-plant sites (five sites; closest site ~5 km) indicated almost no exchange of individual flies between populations. The mean nectar content *of B*. *vanzyliae* was approximately 1.33 µl per flower (*n* = 52). It is here estimated that during a single flower visit, a *Prosoeca* fly took up approximately 0.80 µl (*n* = 45). The estimated number of flies in this particular area was 84–99 individuals, based on mark and recapture trials conducted in August 2017. Flower and nectar availability was estimated from flower counts (*n* = 407 flowers) providing a total nectar crop of 541.31 µl in the area. These data allow calculation of the resources required by this keystone pollinator, allowing insights into how loss of host-plant habitat may affect fly populations.

Fossils – key to Diptera phylogeny

Wiesław Krzemiński

Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016, Kraków, Poland. wieslawk4@gmail.com

Keywords: “Burmese amber”, evolution, fossil Diptera.

The first 100 million years of Diptera evolution are exclusively documented in sedimentary rocks, making information for that period fragmentarily, both in terms of specimen preservation and evolutionary history. Nevertheless, their preserved morphology is our only source of information, since genetic material is not preserved and not applicable, even that extracted from amber inclusions. The oldest known Diptera are dated to the Anisian (242–247 MYA) and originate from the Middle Triassic of the Vosges Mountains of north-eastern France. Although Triassic Diptera are very scarce and only rarely found, they already represent all the main evolutionary lineages, *i.e.*, Bibiononomorpha, Brachycera, Culicomorpha, Psychodomorpha, Ptychopteromorpha and Tipulomorpha (according to the modern classification, based on molecular data). The Jurassic was a period of evolutionary radiation and domination of the “lower Diptera”, whilst the Brachycera were still poorly represented and were poorly differentiated. The first Diptera preserved tri-dimensionally occur in fossil resins, the oldest being inclusions in Lebanese amber *ca* 145 MYA. The richest assemblages, however, are found in amber from Myanmar (“Burmese amber”) (99 MYA). Preserved specimens allow us to examine the entire body structures of long extinct lineages with accuracy and to compare these to extant Diptera. The Cretaceous was a time of profound change in the dipteran fauna. The Brachycera evolved rapidly, and by the Upper Cretaceous, almost all recent families were represented, while the “lower Diptera” had already undergone complete remodelling. Many families, subfamilies and genera of Triassic and Jurassic origin had disappeared, being replaced by the modern fauna.

Homology of the cubital and anal veins in the Mecoptera and Diptera

Wiesław Krzemiński* & Ewa Krzemińska

Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016, Kraków, Poland. *wieslawk4@ gmail.com

Keywords: “Burmese amber”, fossil Mecoptera, homology, wing venation.

Homology of the cubital and anal veins in Mecoptera and Diptera was correctly resolved by R.J. Tillyard as early as 1919 and later by G.W. Byers in 1989, both of whom based their ideas on comparison of wing venation in the Mecoptera and Diptera. Today, there are two different systems in common use, one proposed in volume 1 of the *Manual of the Nearctic Diptera* (published in 1981) and one in the newly published volume 1 of the *Manual of Afrotropical Diptera* (published in 2017). Further examples are presented here, based on newly discovered material of Mecoptera from Myanmar (“Burmese amber”) and the Lower Cretaceous of England. Diptera have only one cubital vein (*Cu*), homologous with vein *CuA* (or Cu_1) in the Mecoptera. The second cubital vein in Mecoptera, named *CuP* (or Cu_2), had disappeared in the Diptera completely. The first anal vein (A_1) is homologous in the Diptera and Mecoptera and its presence is a plesiomorphic state in the Diptera and cannot be identified with *CuP* of the Mecoptera. The second anal vein (A_2), which is characteristically long in the Tipulomorpha, must have arisen independently (secondarily), since the Tipulomorpha do not constitute sister-group to the remaining Diptera (according to earlier investigations both of fossils and molecular data).

How many more? The genus *Manota* Williston (Mycetophilidae) as an example of open-ended genera

Olavi Kurina[1]* & Heikki Hippa[2]

[1]Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Kreutzwaldi 5 D, 51006 Tartu, Estonia. *olavi.kurina@emu.ee
[2]Zoological Museum, Turku, Finland.

Keywords: Fungus gnats, *Manota*, open-ended taxa, species diversity.

The genus *Manota* Williston (Mycetophilidae) has been cited to illustrate the concept of open-ended genera; they are often virtually cosmopolitan, with unexpected numbers of species. Indeed, the genus exhibits an incredible diversity. Being the subject of cutting edge fungus gnat studies during the past two decades, the number of described species has grown more than ten-fold, from only 25 to 300 species. The majority of species are described from tropical areas, with 102 species described from the Oriental Region, 92 from the Neotropics, 56 from the Afrotropics and 39 from the Australasian/Oceanian Regions, while only 18 species are known from the Holarctic. The number of sympatric *Manota* species is quite remarkable and every substantial sampling effort in a tropical locality yields a mass of new species to be described. Species delimitation is currently based exclusively on the morphology of the male terminalia, while females are morphologically virtually indistinguishable. Only a few species have so far been sequenced, however, and this would certainly speed up discovery of the true diversity worldwide. Moreover, cryptic diversity is also expected. A final prediction of a thousand species worldwide is probably not an overestimation. The main constraint is the availability of suitable material for both morphological and genetic study.

The comparative analysis of the fauna of empidoids (Atelestidae, Brachystomatidae, Empididae, Hybotidae) of Crimea and Western Caucasus

Semen Kustov* & Yulia Kustova

Department of Zoology, Kuban State University, Stavropolskaya 149, Krasnodar, Russia, 350040.
*kustov-semen@mail.ru

Keywords: Caucasus, comparative analysis, Crimea, Empidoidea, fauna.

The Crimean Peninsula and the Western Caucasus are adjacent lands separated by the narrow strip of the Kerensky Strait. Despite the spatial proximity of these regions and the similarity of their main landscape types, there are significant differences in the faunas of these two territories. Currently, the fauna of the Crimea includes two families, 20 genera and 58 species: 28 species in seven genera of Empididae and 30 species in 13 genera of Hybotidae. By contrast, the empidoids of the Caucasus include 31 genera and 180 species in four families: Empididae – 11 genera and 114 species; Hybotidae – 16 genera and 62 species; Atelestidae – 1 genus and species; and Brachystomatidae – three genera and three species. In quantitative terms, the fauna of Crimean empidoids is three times poorer than the fauna of the Western Caucasus. In qualitative terms, the fauna of neighbouring regions also exhibit significant differences: only 31 species are the same in the two regions; the similarity index (the Jaccard coefficient) is 0.15. Some genera and subgenera of empidoids (*Chelifera* Macquart, *Dolichocephala* Macquart, *Drapetis* Meigen, *Empis* (*Xanthempis* Bezzi), *Tachydromia* Meigen, *Trichina* Meigen and *Trichinomyia* Tuomikoski) are characterised by total absence of the species common for the two regions. The reasons for these differences are seen in the geological features of the formation of these regions and in the current location of the main landscape types in the bordering areas of the territories.

Phylogenomic analysis of Calyptratae – resolving a major radiation of Diptera

Sujatha Narayanan Kutty[1]*, Karen Meusemann[2, 3, 4], Keith M. Bayless[4, 5, 6], Marco A.T. Marinho[7], Adrian C. Pont[8], Xin Zhou[9], Bernhard Misof[3], Brian M. Wiegmann[6], David K. Yeates[4], Pierfilippo Cerretti[10], Rudolf Meier[1] & Thomas Pape[11]

[1]Department of Biological Sciences, National University of Singapore, 14 Science Dr 4, Singapore 117543. *sujathank@gmail.com
[2]University of Freiburg, Freiburg, Germany; [3]Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany; [4]CSIRO Australian National Insect Collection, Canberra, Australia; [5]California Academy of Sciences, San Francisco, U.S.A; [6]North Carolina State University, Raleigh, U.S.A.; [7]Universidade Federal de Pelotas, Pelotas, Brazil; [8]Oxford University Museum of Natural History, Oxford, United Kingdom; [9]China Agricultural University, Beijing, China; [10]Sapienza Università di Roma, Rome, Italy; [11]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Molecular phylogeny, phylogenomics.

With more than 22,000 described species, Calyptratae are one of the largest fly clades. They originated and diversified after the K–Pg event and yet exhibit high species diversity and a diverse array of life history strategies. Higher-level relationships of calyptrates still contain considerable uncertainty, which may be due to fast radiation and morphological diversification. Results are presented here of the first phylogenomic analysis of calyptrate relationships, based on 40 exemplar species, representing all calyptrate families. The analyses, based on nucleotide and amino acid data for 1,456 single-copy protein-coding genes obtained from transcriptome shotgun sequencing, yielded overall well-resolved and robust topologies for most families and subfamilies. The topologies are largely congruent across trees obtained with different analytical approaches (maximum parsimony, maximum likelihood, coalescent-based species tree and four-cluster likelihood mapping) and a random addition concatenation analysis (RADICAL) and analyses of a Dayhoff-6 recoded amino acid dataset support and confirm the robustness of many clades. Within the calyptrates, the backbone topology (Hippoboscoidea (Fanniidae (Muscidae (Anthomyiidae + Scathophagidae + (Oestroidea))))) is strongly supported and most families are monophyletic (exceptions: Anthomyiidae and Calliphoridae). Compared to hypotheses based on sequence data from the Sanger era, largely congruent, but much higher clade indicate support for relationships within the muscoid grade. However, even phylogenomic data cannot confidently place certain blowfly subfamilies (Ameniinae, Chrysomyinae, Helicoboscinae). With regard to much of Oestroidea, Sanger and phylogenomic data struggle equally with regard to finding congruent and well-supported hypotheses.

Advances in Diptera phylogenomics

Advantages of a DNA based approach to freshwater biomonitoring illustrated by Chironomidae

Sujatha Narayanan Kutty[1]*, Wan Ting Lee[1], Huei Khee[1], Zhisheng Hou[2] & Rudolf Meier[1]

[1]Department of Biological Sciences, National University of Singapore, 14 Science Drive 4, Singapore 117543. *sujathank@gmail.com
[2]Singapore's National Water Agency, Singapore.

Keywords: Chironomidae, freshwater biomonitoring, metabarcoding, water quality.

Biomonitoring of freshwater ecosystems is often based on assessing macroinvertebrate communities that are closely associated with such an environment and provide information on water quality. Chironomids are one of the most abundant groups in these habitats, hence becoming a key indicator taxon in routine biomonitoring. In general, biomonitoring indices use family-level (or sometimes order-level) morphological identifications and abundance data for water quality assessments. Identifications to species would be desirable, but are difficult, due to manpower constraints and the lack of identification keys, especially for the species occurring in tropical areas, such as South-east Asia. This means that all species are lumped, although we know that chironomid species often have different habitat requirements and important information is lost when the specimens are not sorted to species level. It is demonstrated here that species-level resolution can be obtained *via* DNA metabarcoding of bulk biomonitoring samples from local reservoirs and streams, based on cost-effective high throughput sequencing. To improve DNA based species sorting, a COI barcode reference database for species associated with local reservoirs and streams is being developed concurrently.

Poster

Coevolution of Diptera with anuran amphibians – an overview

Gunnar Mikalsen Kvifte

Department of Biological Sciences, Purdue University, 915 West State St, 47907 West Lafayette, Indiana, U.S.A. gkvifte@purdue.edu

Keywords: Amphibia, Anura, biological interactions, coevolution, micropredation, myiasis, parasitism.

In this presentation, the natural history and evolutionary ecology of the biotic interactions between Diptera and Amphibians are reviewed. Apart from frog predation on flies, for which there has been no evidence of specialised coevolution presented, three main interaction types can be identified: 1) micropredator/host interactions with adult Diptera feeding on amphibian blood; 2) egg predator/prey interactions, where Diptera larvae feed on amphibian eggs; and 3) myiasis interactions, where Diptera larvae develop as ectoparasites or ectoparasitoids of adult amphibians. Each of these interaction types has evolved multiple times within Diptera and there appears to be distinct biogeographical differences in which taxonomic groups of Diptera dominate in their interaction guild. Micropredators occur among representatives of Ceratopogonidae, Corethrellidae, Culicidae and at least two subfamilies of Psychodidae and include behaviours ranging from opportunistic feeding, to closely knit, potentially coevolutionary relationships. Specialised egg predators and parasites of frogs include representatives of the families Calliphoridae, Drosophilidae, Ephydridae and Phoridae, whereas representatives of several families attack frog eggs opportunistically. Myiasis agents include specialised lineages of Chloropidae (in Australia and Papua New Guinea), of Calliphoridae (in the Holarctic) and of Sarcophagidae (in the Neotropics). Knowledge gaps in natural history and evolutionary ecology are discussed, particularly with regards to degrees of specialisation.

Segmental origins of genital appendages in lower Diptera – are surstyli present in the groundplan?

Gunnar Mikalsen Kvifte

Department of Biological Sciences, Purdue University, 915 West State St, 47907 West Lafayette, Indiana, U.S.A. gkvifte@purdue.edu

Keywords: Genitalia, gonopods, homologies, hypopygia, morphology, surstyli, terminalia.

Two major hypotheses have been proposed for the homologies of appendages in the male terminalia of Diptera. The epandrial-surstylar hypotheses suggests that the presence of articulated surstyli (1-segmented jointed appendages of tergite 9), is a synapomorphy for the Eremoneura and that cases of tergite 9 appendages in “Nematocera” and lower Brachycera are independently derived structures. The opposing view is the periandrial hypothesis, which suggests that the surstyli of Eremoneura are homologous with the gonostyli of lower Diptera (part of the gonopods; 2-segmented jointed appendages with affinities to sternite 9). In the present talk a number of cases in nematocerous Diptera (mostly Psychodinae) and lower Brachycera will be discussed, in which tergite 9 possesses appendages or vestiges thereof, in addition to gonopods with gonostyli. It is then argued, that the ubiquity of this character is better explained with a common developmental mechanism than as a series of non-related events. Under this model, it is suggested that tergite 9 appendages form part of the Diptera groundplan, even if they are fused with tergite 9 or reduced in most taxa. This is proposed as the “reverse polarity” version of the epandrial-surstylar hypothesis and this is compared to existing hypotheses for Diptera genital homologies, indicating it to be potentially more parsimonious.

Deploying an army of nuclear genes to resolve the phylogeny of Australian soldier flies (Stratiomyidae) and the discovery of more than 150 new species

Bryan D. Lessard[1]*, Norman E. Woodley[2], Xuankun Li[1], Martin Hauser[3],
Brian M. Wiegmann[4] & David K. Yeates[1]

[1]Australian National Insect Collection, CSIRO Black Mountain, Clunies Ross Street, Acton, ACT, 2601. *bryan.lessard@csiro.au
[2]Smithsonian Institution, Washington D.C., U.S.A.
[3]California Department of Food and Agriculture, Sacramento, U.S.A.
[4]North Carolina State University, Raleigh, U.S.A.

Keywords: Anchored hybrid enrichment, citizen science, NGS, systematics, taxonomy.

Soldier flies (Stratiomyidae) are one of the most morphological diverse families of Diptera, with more than 2,700 species, described from every continent of the world, excluding Antarctica. Larvae are aquatic and terrestrial and used broadly as biological indicators of water quality, alternative proteins for feeding animals and are occasionally pests of agricultural crops. The family is currently divided into 12 subfamilies, with all but three occurring in Australia. The Australian fauna is poorly understood and virtually impossible to identify, with the majority of the taxonomic work ending in the 1920s and a lack of robust identification keys and authoritatively identified material in Australian collections. Despite this, there has been a recent surge of renewed interest in the taxonomy of the Australian soldier flies. Anchored hybrid enrichment was used to sequence up to 600 single copy nuclear genes to reconstruct the phylogenetic relationships of the family, with a focus on the Australian fauna. Results confirmed that the majority of the subfamilies are monophyletic, including Chiromyzinae, Beridinae, Antissinae, Stratiomyinae and Sarginae. Conversely, two subfamilies were resolved as paraphyletic: Clitellariinae and Pachygastrinae, comprised four and two clades, respectively, which is largely congruent with the previous phylogenetic hypotheses based on Sanger data. The Australian fauna is revised at a generic level and new identification keys have been produced for all subfamilies and genera. Also presented are the first Australian records for the subfamily Nemotelinae, an additional 18 extralimital genera, six new endemic genera and the discovery of more than 150 new species.

Distribution patterns of Philippine endemic Diptera

Socrates D. Letana

Bohart Museum of Entomology, Department of Entomology and Nematology, University of California, One Shield Avenue, Davis, 95616, CA, U.S.A and Research Associate, California State Collection of Arthropods, CDFA, PPDB, Sacramento, CA 95832, U.S.A. sdletana@ucdavis.edu

Keywords: Biodiversity, distributions, endemics, Philippines.

Although the Philippines is noted as a tropical biodiversity hotspot, Diptera diversity has not been adequately researched. A review of current knowledge, including knowledge gaps and research priorities (areas and taxa) are presented, assessing 1,748 endemic fly species, mapped in 16 terrestrial biogeographic regions of the country. Records are skewed toward the larger and older islands in the archipelago and potential bias was identified. The smaller under studied islands with potential high endemicity are noted as being vulnerable to various conservation threats. Challenges and the future direction for fly fauna research are also enumerated.

Poster

Taxonomy, phylogeny and evolution of *Portschinskia* Semenov (Oestridae: Hypodermatinae) – a rare genus of bumblebee mimicking botflies

Xin-yu Li[1]*, Thomas Pape[2] & Dong Zhang[1]

[1]Key Laboratory of Non-Invasive Research Technology for Endangered Species, School of Nature Conservation, Beijing Forestry University, Beijing, 100083, China. *136179665@qq.com
[2]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Botflies, Batesian mimicry, colour pattern, distribution, oviposition biology, *Portschinskia*, phylogeny, taxonomy.

Portschinskia Semenov (Oestridae) are bulky and vividly coloured flies that exhibit a striking resemblance to bumblebees in habitus and colour patterns. They are obligate subcutaneous parasites in rodents and pikas in the larval stages, as known from very sparse biological information. Due to their narrow distribution and often remote montane habitats, species of *Portschinskia* are rare in scientific collections and are listed as endangered. Although they are regarded as conspicuous and intriguing species, the scarce material available, a paucity of diagnostic characters and an entirely untouched species-level phylogeny have largely impeded their taxonomic and evolutionary investigation. A taxonomic revision with a new identification key and explicit species-level diagnoses are presented for all 11 known species (including four new to science). A set of 36 morphological characters from all body parts were analysed to produce the first species-level phylogeny. The monophyly of *Portschinskia* was strongly supported based on eight synapomorphies. Three types of colour patterns were classified, which exhibit a strong phylogenetic association, with closely associated species sharing the same patterns. The yellow tail colour pattern was reconstructed as the ancestral state, with independent origins of red and black tails and two reversals. A correlation of colour patterns between sympatric *Portschinskia* and the locally dominant *Bombus* Latreille species (Hymenoptera) is documented. The resemblance in both appearance and behaviour between *P. magnifica* Pleske and sympatric bee *B. pyrosoma* Morawitz is demonstrated, which strongly implies Batesian mimicry. Oviposition behaviour of *Portschinskia* is reported for the first time and the evolutionary implications are discussed.

Morphological phylogeny and biogeography of Bombyliinae (Bombyliidae)

Xuankun Li[1, 2]* & David K. Yeates[1]

[1]Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, ACT 2601, Australia. *xuankun.li@csiro.au
[2]Australian National University, Canberra, Australia.

Keywords: Bee fly, biogeography, cladistics, morphological phylogeny.

The Bombyliinae is one of the largest subfamilies of bee flies (Bombyliidae), comprising over 1,100 described species in 73 known genera distributed globally, except in Antarctica. The first global phylogenetic analysis for the subfamily is presented, based on 157 morphological characters from adults, scored for 123 terminal species, representing 60 genera, belonging to all the tribes of Bombyliinae and the related subfamilies Lordotinae and Toxophorinae. Four most parsimonious trees were generated from the analysis under equal weighted schemes. The monophyly of Bombyliinae is supported and Lordotinae is sister to Bombyliinae. Within Bombyliinae, the tribe Conphorini is sister to the remaining tribes. On the basis of this analysis, five previously recognised tribes are re-defined and four new tribes are erected. In addition, a tribal key to world Bombyliinae is provided, which places almost all genera in the tribal classification based on available character evidence. Using these phylogenetic results, distribution data and a dispersal-vicariance optimisation model (DIVA), the biogeography of the subfamily is explored. The ancestral area reconstruction suggests a global distribution of the common ancestor of Lordotinae and Bombyliinae, as well as the basal lineages of Bombyliinae. A Gondwanan origin is, however, proposed for the other major lineages of Bombyliinae.

Towards a revision of the Bombyliinae (Bombyliidae) of Australia

Xuankun Li[1, 2]* & David K. Yeates[1]

[1]Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, ACT 2601, Australia. *xuankun.li@csiro.au
[2]Australian National University, Canberra, Australia.

Keywords: Bee fly, cladistics, morphological phylogeny, new genera, revision, taxonomy.

The Bombyliinae, one of the largest subfamilies of Bombyliidae, includes 78 genera assigned to four tribes and is distributed on all continents, except Antarctica. Larvae are parasitoids and adults are important pollinators. The purpose of this studies is to establish the phylogeny of the Australian representatives of the subfamily Bombyliinae, including the boundaries and relationships of genera, using morphological characters and revising the Australian species of the subfamily. One maximum parsimony tree was generated from 83 morphological characters, scored for 50 species, representing all recognised genera and some unplaced species that are considered to represent new genera. Phylogenetic analysis recovered the relationships between the recognised Australian genera of Bombyliinae and clarified their generic limits. It was found that *Pilosia* Hull was sister to the remaining Australian Bombyliinae. This ongoing revisionary work has resulted in the description of six new genera and 31 new species and proposed three generic junior synonyms, two specific junior synonyms and 11 new combinations. In addition, all known genera are re-defined and a generic identification key to Australian representatives of Bombyliinae is provided. These current studies provide the basis for a phylogenetic analyses of the world bombyliine fauna and relationships are tested with phylogenomic analyses, using anchored hybrid enrichment data.

Poster

A preliminary phylogeny of Asiloidea using anchored enrichment data (Brachycera)

Xuankun Li[1, 2]*, Luisa C. Teasdale[1], Bryan D. Lessard[1], Keith Bayless[1],
Michelle D. Trautwein[3], Christine L. Lambkin[4], Carlos José Einicker Lamas[5],
Brian M. Wiegmann[6] & David K. Yeates[1]

[1]Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, ACT 2601, Australia. *xuankun.li@csiro.au
[2]Australian National University, Canberra, Australia.
[3]California Academy of Sciences, San Francisco, U.S.A.
[4]Queensland Museum, South Brisbane, Australia.
[5]Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil.
[6]North Carolina State University, Raleigh, U.S.A.

Keywords: Anchored hybrid enrichment, Asiloidea, phylogenomics.

The superfamily Asiloidea includes nine families (Apioceridae, Apsilocephalidae, Asilidae, Bombyliidae, Evocoidae, Hilarimorphidae, Mydidae, Scenopinidae and Therevidae) and forms a major clade of lower Brachycera. Within Asiloidea, the monophyletic therevoid clade (Evocoidae + Apsilocephalidae) + (Therevidae + Scenopinidae), has been strongly supported, with the topology (Asilidae + (Apioceridae + Mydidae)). Bombyliidae, however, is considered to be the sister of the remaining Asiloidea, or sister to the remaining Asiloidea + Eremoneura and the position of Hilarimorphidae has not been firmly established. Anchored hybrid enrichment (AHE) is enabled by next-generation sequencing (NGS), which targets mostly coding regions of the genome and generates data on a large number of nuclear loci (~500 loci) from nonmodel species by using short DNA sequences (~60–120 bp oligonucleotide). This new technology has been applied in several recent studies and showed great potential in solving phylogeny relationships of difficult lineages. This preliminary analysis includes ~40 taxa from five families, the phylogenetic result supports the monophyly of the families and suggests Asiloidea is paraphyletic. An assessment is made of the implications of these results for the evolution of significant morphological character systems in the superfamily.

Review of genera of Sciomyzidae (Acalyptratae) from China, with new records, synonyms and notes on distribution

Zhu Li[1]*, Ding Yang[2] & William L. Murphy[3]

[1]Beijing Museum of Natural History, 126 Tianqiao South Street, Beijing 100050, China.
*bamboo_L@163.com
[2]China Agricultural University, Beijing, China.
[3]Smithsonian Institution, Indiana, U.S.A.

Keywords: biogeography, distribution, key, Oriental, restoration, survey, snail-killing, taxonomy.

The status of the 20 genera comprising at least 60 species of Sciomyzidae known from China are reviewed and ten genera are recorded for the first time. An identification key to all genera known from China is provided, along with illustrations of the main characters. The geographical distribution of each genus known is discussed. Two genera (*Coremacera* Rondani and *Pherbina* Robineau-Desvoidy) and five species (in the genera *Dichetophora* Rondani, *Pherbellia* Robineau-Desvoidy and *Tetanocera* Duméril), are recorded for the first time from the Oriental Region. *Euthycera meleagris* Hendel, previously synonymised with *Dichetophora meleagris* (Hendel), is resurrected as a valid name. *Pherbellia brevistriata* Li, Yang & Gu is placed as a junior synonym of *Pherbellia nana reticulata* (Thomson). The female of *Ph*. *ditoma* Steyskal and the male of *Ph*. *orientalis* Rozkošný & Knutson, both discovered in China during this study, are recorded for the first time.

A taxonomic study of *Odinia* Robineau-Desvoidy (Odiniidae), with the description of eleven new species from Brazil

Francisco Limeira-de-Oliveira[1]*, Dayse Willkenia Almeida Marques[2], Stephen D. Gaimari[3], Geniana A. Reis[1] & José Albertino Rafael[2]

[1]Universidade Estadual do Maranhão, 65604–380, Caxias, Maranhão, Brazil. *limeiraf@gmail.com
[2]Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil.
[3]California Department of Food and Agriculture, Sacramento, U.S.A.

Keywords: *Odinia*, Neotropical, new species, taxonomy.

Odiniidae currently comprises 70 species in 16 genera, occurring in all zoogeographical regions, except Antarctica. More than one-third of these species belong to the genus *Odinia* Robineau-Desvoidy and of these 25 species, six occur in the Neotropical Region, with only two of these known for Brazil, *O. brevitibia* Shewell and *O. surumuana* Prado. When analysing material collected in the north and north-east regions of Brazil, 11 new species of *Odinia* were discovered that are being described and illustrated, representing a significant increase for both the Neotropical fauna of this genus and the Brazilian fauna specifically. These are the first records for the genus in the Brazilian states of Amazonas, Ceará, Maranhão and Piauí. The large number of specimens analysed (447), results from an extensive sampling effort undertaken in various habitats in these states over the past 5 years, which suggests that this group has been neglected and its species richness underestimated.

Revealing odiniid diversity (Odiniidae) with the discovery of thirteen new species of *Helgreelia* Gaimari from Brazil

Francisco Limeira-de-Oliveira[1]*, Geniana Alves Reis[2] & Stephen D. Gaimari[3]

[1]Universidade Estadual do Maranhão, Departamento de Química e Biologia, 65604-380, Caxias, Maranhão, Brazil. *limeiraf@gmail.com
[2]Universidade Estadual do Maranhão, Maranhão, Brazil.
[3]California Department of Food and Agriculture, Sacramento, U.S.A.

Keywords: Brazil, *Helgreelia*, Neotropical, new species, Traginopinae.

Odiniidae is a widely distributed family of small and robust flies, with 70 species distributed in 16 genera and two subfamilies: Odiniinae and Traginopinae. The Neotropical Region is the best represented, with 31 species in 10 genera, of which 18 species in seven genera have records from Brazil, including *Helgreelia* Gaimari, the target group of this work. *Helgreelia* is exclusively Neotropical, with three described species, two from Costa Rica, *H*. *albeto* Gaimari and *H*. *parkeri* Gaimari and one from Brazil, *H*. *gaimarii* Carvalho-Filho, Esposito & Santos. When analysing specimens of odiniids collected in the north, north-east and central regions of Brazil, 13 new species of *Helgreelia* were discovered and are being described and illustrated. This represents the first records of the genus for the Brazilian states of Amazonas, Maranhão and Tocantins. The large number of new species is the result of a large sampling effort undertaken in various habitats in Brazil over the past five years, which has provided significant results and increased knowledge about this family.

Poster

Molecular phylogeny of East Asian *Daphnephila* Kieffer (Cecidomyiidae)

Sheng-Feng Lin* & Man-Miao Yang

Department of Entomology, National Chung Hsing University, 145 Xingda Road, South District, Taichung City, Taiwan. *sflin654@gmail.com

Keywords: Gall midge, mitochondrial DNA, systematics.

The genus *Daphnephila* Kieffer comprises ten described species, that induce galls on *Machilus* (Lauraceae), with a single species inducing galls on *Lindera pulcherrima*. (Nees) Benth. (Lauraceae). This study revealed additional species associated with *Machilus* in Japan, Taiwan and China and further species associated with *Persea* (Lauraceae) in Indonesia. More than 40 *Daphnephila* gall morphotypes occur in Taiwan, but only six species are named, forming seven gall morphotypes. The COI gene was employed to reconstruct the phylogeny of the group and to address the following: what is the diversity of Taiwanese *Daphnephila* at the species level, and secondly, what are divergence processes among regions and between galling positions? A total of 114 specimens, belonging to 16 Taiwanese species and three out-groups, were included in the analysis using Bayesian inference. Monophyly of *Daphnephila* is supported and three clades: leaf-galler clade; East Asia stem-galler clade I; and East Asia stem-galler clade II, were recovered. The East Asia stem-galler clade II is sister to the leaf-galler clade and East Asia stem-galler clade I. This indicates galling of the stem may be the ancesetral condition and leaf-galling the more derived. The leaf-galler clade was further divided into an Indonesian leaf-galler subclade and an East Asia leaf-galler subclade, that are sister taxa to one another. This indicates that geographical isolation could be responsible for divergence. Paraphyly of taxa from each East Asian country indicates that their diversification could be earlier than their geographical isolation. More Asian taxa are needed to study the phylogeny and biogeography *Daphnephila*.

A new flightless marine species of Chironomidae – ancestry, adaptations and taxonomic implications

Xiaolong Lin[1]*, Torbjørn Ekrem[2], Rolf Georg Beutel[3], Xin Qi[4], Chao Song[1], Igor Orlov[5], Chuntang Chen[6] & Xinhua Wang[1]

[1]College of Life Sciences, Nankai University, Tianjin, China. *lin880224@gmail.com
[2]Norwegian University of Science and Technology, Trondheim, Norway.
[3]Friedrich-Schiller-Universität Jena, Jena, Germany.
[4]Taizhou University, Zhejiang, China.
[5]University of Copenhagen, Copenhagen, Denmark.
[6]Xianju Forestry Bureau, Zhejiang, China.

Keywords: Adaptation, flightless, marine, skater, phylogeny.

Insects have invaded marine habitats only rarely and secondarily. Recently, a flightless dipteran species was discovered skating rapidly on the surface of seawater ponds at the Pacific coast of eastern China. Morphological analyses initially suggested an isolated position of the non-biting midge, suggesting the erection of a new genus within Chironomini (Chironomidae). However, an analysis of molecular data revealed that the marine species is in fact nested within the species-rich genus *Dicrotendipes* Kieffer. The apparent conflict between molecular and morphological data can be easily explained. It is likely that the new species has evolved a series of autapomorphic adaptations. These traits clearly distinguish the taxon from other species of the genus, but do not justify the erection of a new supraspecific taxon, which would render *Dicrotendipes* paraphyletic. The switch to marine environments was likely a trigger for various morphological modifications resulting from increased selective pressure. Molecular data suggest that the potential speciation event occurred around 19–29 MYA, linked with a migration from freshwater to seawater ponds along the Pacific Ocean. Considering the results of the analysis, the flightless marine skater is placed in the genus *Dicrotendipes*. All life stages of the new marine species are described, with larvae obtained by rearing or confirmed through association with DNA barcodes. The biology and ecology of the species are outlined based on collection data and *in situ* observations. Evolutionary patterns linked with repeated invasions of marine habitats are discussed.

An integrative taxonomic revision of two species-groups of *Exechia* Winnertz (Mycetophilidae) with a circumpolar distribution

Jon Peder Lindemann[1]*, Geir Søli[2] & Jostein Kjærandsen[1]

[1]Tromsø University Museum, UiT – The Arctic University of Norway, Tromsø, Norway.
*jon.p.lindemann@uit.no
[2]Natural History Museum, University of Oslo, Norway

Keywords: Circumpolar, DNA barcoding, *Exechia*, fungus gnats, Holarctic, taxonomic revision.

With *ca* 170 described species worldwide, *Exechia* Winnertz is the largest among 20 genera currently classified in the tribe Exechiini. The Holarctic *Exechia* fauna is traditionally thought to be largely circumpolar, with 48 out of 62 Palaearctic species also recorded in the Nearctic Region. Yet, the lack of a thorough taxonomical revision comparing species from both continents makes the status and species determinations questionable, due to insufficiently described and illustrated morphological traits. This study aims to revise two species complexes of *Exechia*, the *E*. *cornuta-lunstroemi* group and the *E*. *parva-repanda* group, both with unresolved circumpolar distribution patterns. An integrative approach is applied, based on morphological and molecular delimitation methods combined, to revise the species and identify species limits among the circumpolar populations. The Barcode of Life Data system (BOLD), with its fast-growing database of DNA barcodes automatically clustered into Barcode Index Numbers (BINs) has proved to be a useful tool to organise the groups into a set of putative species (OTUs) and to efficiently localise material crucial in the revision. At present, 33 species are recognised in these two species-groups, of which 19 are regarded as new to science. Preliminary results indicate a lower proportion of circumpolar species and that several cross-continental names have been erroneously applied, based on superficial morphological similarities.

Poster

Male terminalia and their rotation in Tanyderidae (Psychodomorpha) since the Mesozoic

Elena D. Lukashevich[1]*, Olga G. Ovtshinnikova[2] & Tatiana V. Galinskaya[3]

[1]Borissiak Paleontological Institute of Russian Academy of Sciences, Profsoyuznaya St. 123, Moscow 117647, Russia. *elukashevich@hotmail.com
[2]Zoological Institute of Russian Academy of Sciences, St Petersburg, Russia.
[3]Lomonosov Moscow State University, Moscow, Russia.

Keywords: *Araucoderus*, morphology, musculature, *Nothoderus*, sclerites, terminalia.

Male terminalia are reviewed in both extant and extinct genera of Tanyderidae, based on new observations and by reference to the literature. The structure of the gonostyli, parameres and cerci exhibit greater variation among extinct than among extant taxa. The diversity of the tanyderid aedeagus appears to be the most extreme in the Diptera. A bifid aedeagus occurs in representatives of both subfamilies: the extant nannotanyderine *Peringueyomyina* Alexander (and probably Eocene *Coramus* Skibińska) and the extinct tanyderine genera *Macrochile* Loew and *Similinannotanyderus* Dong, Shih & Ren. A common trifid aedeagus and the rarely undivided form both appear to have evolved from it. The Triassic family Nadipteridae, which is supposedly ancestral to Tanyderidae, already displays rotation of the male terminalia, suggesting that such rotation is extremely ancient in the Diptera and was inherited by Tanyderidae. Tanyderid genera vary in the presence and angle of this rotation. The male terminalia of *Araucoderus* Alexander (from Chile) and *Nothoderus* Alexander (from Tasmania) were examined. Both genera have similarly rotated terminalia, although 180° rotation may be either clockwise or counter clockwise. The hypandrial origin of the stripe between the gonocoxites is exnibited in both studied genera (*Araucoderus* and *Nothoderus*). The entire membranisation of tergite 8 and partial membranisation of the hypoproct is exhibited in *Nothoderus*. Tanyderidae are characterised by highly specialised musculature, which differs significantly from previously studied representatives of Blephariceridae, Psychodidae and Ptychopteridae.

Poster

A new family and genus of Mesozoic Simulioidea (Culicomorpha)

Elena D. Lukashevich[1], Mateus Pepinelli[2] & Douglas C. Currie[2]*

[1]Russian Academy of Sciences, Moscow, Russia.
[2]Department of Natural History, Royal Ontario Museum, Toronto, Ontario, Canada and Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Ontario, Canada.
*dc.currie@utoronto.ca

Keywords: Mesozoic fossils, new family, new genus.

Simulioidea are rare in the fossil record, especially from the Mesozoic Era when the Culicomorpha originated. A new family and genus are described from the Cretaceous of Asia. The new family resembles the Simuliidae, but lacks many of the synapomorphies ascribed to blackflies, such as the male eye with a line of discontinuity between the upper and lower facets, hind basitarsus laterally flattened, tergite I with a posterior fringe of setulae, a single spermatheca and probably grooved lobes on the base of the male tarsal claw. Most of these features are known to be present in previously described Mesozoic blackflies. Some characters, such as the basal shift of the *r–m* crossvein and elongation of the radial sector (*Rs*) and the vein M_{1+2} fork, are typical of the Thaumaleidae; however, the extremely long *Rs*, originating at the level of the humeral crossvein is unique to the new family. The new family also exhibits a suite of plesiomorphic character states (long antenna with 12 flagellomeres, both vein *CuP* and A_1 thick and subparallel) that are unknown in the Simulioidea. Other features, such as shortening of the maxillary palp, at least in the male, and a sigmoid pleural suture on the thorax are unknown in the Culicomorpha, but are common in the basal lineages of certain Bibionomorpha. These peculiarities notwithstanding, the overall gestalt of the fossils, the small antennal pedicel in both sexes, the absence of ocelli, the general shape and venation of the wing, point to a close relationship with simuliids.

Insect death metal – taxonomy and phylogeny of the Australian bristle fly genus *Rutilia* Robineau-Desvoidy (Tachinidae)

James Lumbers*, Bryan Lessard, David Rowell & David K. Yeates

The Australian National Insect Collection, CSIRO Canberra 2601 and the Research School of Biology, Australian National University, Canberra 2600, Australia. *james.lumbers@gmail.com

Keywords: Anchored hybrid enrichment, parasitoids, phylogenomics, *Rutilia*.

Bristle flies (Tachinidae) are important insect parasitoids and play a significant role in regulating insect populations in natural and agricultural landscapes. The family is currently recognised to include four subfamilies, the Dexiinae, Exoristinae, Phasiinae and Tachininae, which are further divided into a total of 50 tribes. The impressive metallic-coloured genus *Rutilia* Robineau-Desvoidy (subfamily Dexiinae, tribe Rutiliini), is divided into seven subgenera: *R*. (*Ameniamima* Crosskey), *R*. (*Chrysorutilia* Townsend), *R*. (*Donovanius* Enderlein), *R*. (*Grapholostylum* Macquart), *R*. (*Microrutilia* Townsend), *R*. (*Neorutilia* Malloch) and *Rutilia sensu stricto*. As far as is known, *Rutilia* are parasitoids of scarab beetle larvae in the soil. Roger Crosskey revised the genus in 1973 and recognised 52 species. The genus is largely confined to Australia, but three described species are known from South-east Asia and the Pacific Islands. In recent decades, many undescribed species have accumulated in Australian collections. This PhD project aims to revise *Rutilia* by describing new species and generating a modern identification key to species, test the boundaries of the subgenera and create a robust phylogenetic framework for the genus, using both morphological and phylogenomic (anchored hybrid enrichment) datasets.

Poster

Decomposition and fly-borne *Ignatzschineria indica* bacteria

Dorothy C. Madamba

Natural History Museum of Bulawayo, Corner Park Road and Leopold Takawira Avenue, Centenary Park, Bulawayo, Zimbabwe. madambadc@gmail.com

Keywords: Accumulated degree days, competitive exclusion, decomposition, *Ignatzchineria*, post-mortem interval.

Microbes play a major role from the onset of and throughout decomposition. Studies indicate that a decomposing body supports a necrobiome, a term coined to mean a community of living things associated with decomposition of remains, specifically with reference to micro-organisms. The objective of the current study was to show how *Ignatzschineria indica*, a fly-associated and selected bacteria associated with a decomposing human body affect decomposition under controlled (laboratory) conditions. Results from this experiment indicated that the initial bacterial composition in dead mice does not affect the rate of decomposition under laboratory controlled conditions of temperature and moisture, with the exclusion of vertebrate and invertebrate scavengers. Adding *Ignatzchineria indica* to dead mice specimens under laboratory controlled conditions did not significantly affect the rate of decomposition, but rather affects the pathway of decomposition. This was evident from the different intensities of volatile organic compounds (VOCs) that were collected and assayed from the different samples. These findings lead to the conclusion that the addition of *Ignatzschineria indica* bacteria to decomposing mice does not significantly alter the rate of decomposition. It does alter the chemical pathways of decomposition as evidenced by variant VOCs composition.

Seeing flies from different angles – the utility of interactive, 3D models for research and teaching

R. Isaí Madriz[1]*, Gregory R. Curler[2, 3] & Alexander Mykris[4]

[1]Casilla #367 Correos Coyhaique, Coyhaique, Chile. *rimadriz1@gmail.com
[2]Mississippi Entomological Museum, Starkville, U.S.A.
[3]Smithsonian Institution, Washington D.C., U.S.A.
[4]Toronto, Canada.

Keywords: Animation, illustrations, imaging, morphology, techniques.

In many organisms evolutionary adaptation results in complex morphology. Understanding, interpreting and describing such complexity is a challenge, especially for those who study Diptera. Two-dimensional illustrations are adequate in some applications, such as wing venation, but are limited in their effectiveness for explaining more complex characters, such as male terminalia. Digital sculpting software can be used to convert 2D or 3D illustrations and images to accurate 3D models of whole or partial specimens. Sculpting structures individually and subsequently combining them as a visually seamless model, allows for the creation of custom animations, involving some or all parts. The models can be used as research and teaching tools to communicate complex information, including hypotheses of homology and characters pertinent to species identification or to illustrate unique specimens, such as holotypes and fossils. To demonstrate this approach, four models were sculpted using Pixologic® ZBrush 4R7 and displayed in a user interface developed using Unity Personal 5.X. Models of the male terminalia of *Araucoderus gloriosus* (Alexander) (Tanyderidae) and *Notofairchildia glyphanos* (Curler) (Psychodidae), were developed with custom animations, including rotation in all directions; expanded view; transparency; colourations and side-by-side comparison of different species. Two other models illustrate larvae of *Edwardsina* Alexander and an undescribed genus of Blephariceridae. 3D Rendering is dependent on an underlying interpretation of morphology. Models can be based on observations, drawings and images captured using light or scanning electron microscopy or detailed reconstructions resulting from studies employing micro-computed tomography (µCT), synchrotron radiation based X-ray and confocal laser scanning microscopy.

A regional collaborative effort in digitising and monitoring African insects

Kudzai Mafuwe[1]*, Brian L. Fisher[2], Balsama Rajemison[3], Andrianjaka Ravelomanana[3], Laban N. Njoroge[4], James J. Odanga[4], Boikhutso L. Rapalai[5], Lucilia Chuquela[6] & Helen Barber-James[7]

[1]Natural History Museum of Zimbabwe, CNR Leopold Takawira and Park Street, Box 240, Bulawayo, Zimbabwe. *kudzimaffy@gmail.com
[2]California Academy of Sciences, San Francisco, U.S.A.
[3]Parc Botanique et Zoologique de Tsimbazaza, Antananarivo, Madagascar.
[4]National Museums of Kenya, Nairobi, Kenya.
[5]Botswana National Museum, Gaborone, Botswana.
[6]Natural History Museum, Maputo, Mozambique.
[7]The Albany Museum, Grahamstown, South Africa.

Keywords: African Insect Atlas, African Pollinator Transect, biodiversity informatics, conservation, digital museum, East Africa, metabarcoding.

The African Insect Atlas (AIA) project was launched in June 2015 and funded under the Global Biodiversity Information Facility (GBIF) Biodiversity Information for Development (BID) projects through the European Union. This project represents a collaboration between East African natural history museums and institutions in Botswana, Kenya, Madagascar, Mozambique, South Africa, Zimbabwe and the California Academy of Sciences (CAS). The aim is to create a digital museum for targeted insect groups. By June 2018, just over 20,000 records had been collated, digitised and shared *via* the GBIF platform using international biodiversity standards and various biodiversity informatics tools. The AIA project greatly improved biodiversity informatics skills for over 50 biodiversity experts in Africa and also expanded entomology training and research in the region. The data mobilised and skills shared through this project will be important tools for African conservation science and policymaking. Through the success of the AIA project, a concept for the African Pollinator Transect (APT) was developed early in 2018, as an extension of the AIA network, to establish local monitoring stations for flying insects, with a specific focus on pollinators, across East Africa. The core of the APT is an international team of leaders in entomology across East Africa, combined with experts in metabarcoding (the Global Malaise Trap team at the Centre for Biodiversity Genomics, Guelph) and CAS. This East African collaboration will strengthen the capacity of individual organisations and help them work in concert to ensure pollinators' data is available for conservation planning.

The female terminalia in lower Diptera as a source for characters in phylogenetic studies

Trude Magnussen* & Geir Søli

Natural History Museum, University of Oslo, P.O. Box 1172, Blindern, NO-0318 Oslo, Norway.
*trude.magnussen@nhm.uio.no

Keywords: Comparative morphology, homology, Ptychopteridae, terminology, Tipulidae, Trichoceridae.

Today there is an extensive and detailed literature on the morphology and functionality of the male terminalia in Diptera, while the terminalia (genitalia) have been afforded less attention. This bias is also reflected in the vague terminology used to describe the terminalia structures in females, where different authors to a large extent use different terminologies, depending on the group in question, with few attempts to homologise the observed structures. This can be explained by a general view among researchers that female terminalia are relatively uniform and of minor significance for separating species. The highly divergent terminal morphology observed in males is in many cases explained by sexual selection, while females exhibit a much slower differentiation of the terminalia structures. A less divergent evolution in the female terminalia, can therefore offer good possibilities to recognise homologies at a higher taxonomic level. The hypothesis is that comparative studies of the female terminalia can produce new insights in their evolution and differentiation, as well as demonstrate structures unique to each family. As a preliminary study the female terminalia were compared in three families: Ptychopteridae, Tipulidae and Trichoceridae. To enable an unambiguous comparison of the observed structures, attempts were made to apply a common terminology, reflecting assumed homologies. The study clearly exposed the complexity in female terminalia, being even higher than expected, but also the feasibility to homologise between structures. These results suggest that structures of both systematic and taxonomic importance can be retrieved through a more thorough examination of female terminalia.

Molecular phylogeny of *Allodia* Winnertz *sensu lato* (Mycetophilidae) constructed using genome skimming

Trude Magnussen[1]*, Geir Søli[1], Jostein Kjærandsen[2], Arild Johnsen[1] & Torsten Struck[1]

[1]Natural History Museum, University of Oslo, P.O. Box 1172, Blindern, NO-0318 Oslo, Norway. *trude.magnussen@nhm.uio.no
[2]Tromsø University Museum, Tromsø, Norway.

Keywords: *Allodia*, *Brachycampta*, Exechiini, mitogenomics, phylogenomics.

This study investigated phylogenomic relationships of the genus *Allodia* Winnertz (subfamily Mycetophilinae, tribe Exechiini), with its two subgenera *A*. (*Brachycampta* Winnertz) and *Allodia sensu stricto*. The general morphology of the two subgenera suggests a close relationship, but the shape and structure of the male terminalia is highly divergent. Therefore, previous studies have suggested the possibility that they represent separate genera. To examine the subgeneric status of the two, low-coverage shotgun sequencing of genomic DNA was applied, commonly referred to as genome skimming. Twenty specimens; representing 16 in-group and four out-group taxa were successfully sequenced. With this approach the aim was to 1) retrieve molecular markers for phylogenetic analyses of the genus; and 2) determine the full mitochondrial genomes of the selected species. In so doing, the aim was to obtain enough data to investigate the potential monophyly of the two subgenera and thereby resolve the systematics of the genus. This is the first reconstruction of mitochondrial genomes from Mycetophilidae, enabling further comparison with the mitochondrial genomes of other Diptera.

Surveying and screening South African entomopathogenic nematodes for the control of the Mediterranean fruit fly, *Ceratitis capitata* (Wiedemann) (Tephritidae)

Antoinette P. Malan, Monique James & Pia Addison*

Department of Conservation Ecology and Entomology, Faculty of AgriSciences, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa.*pia@sun.ac.za

Keywords: Biological control, *Ceratitis*, *Heterorhabditis*, Medfly, nematodes, *Steinernema*.

The polyphagous Mediterranean fruit fly or Medfly, *Ceratitis capitata* (Wiedemann), is an economically important pest species to cultivated fruit globally, including those in South Africa. The third-instar larvae and puparia occur in the soil, where they can be infected by pathogens. Entomopathogenic nematodes (EPNs) are insect-killing parasites that occur naturally in all soil types. The aim of this study was to identify South African EPN species highly pathogenic against Medfly larvae entering the soil to pupariate. Eighty soil samples from fruit orchards in the Western and Northern Cape Provinces of South Africa were baited with susceptible host insects, including the target pest. Both morphological and molecular techniques were applied to identify the EPNs isolated. The pathogenicity of five local EPN species were screened in the laboratory by inoculating single third-instar Medfly larvae with 100 or 50 infective juveniles (IJs) in 50 µl of water. After 48 hours, high Medfly larval mortality was observed. The most virulent EPNs, *Heterorhabditis noenieputensis* Malan, Knoetze & Tiedt and *Steinernema yirgalemense* Nguyen, Tesfamariam, Gozel, Gaugler & Adams were tested further, by inoculating 100 ml of sterilised sand with 2000 IJs. After 24 hours, 10 third-instar Medfly larvae were introduced to the sand. High mortality of Medfly larvae using *H. noenieputensis* indicated promise as a biological control agent, within an integrated pest management system.

Poster

Systematics and phylogenetics of Mesembrinellidae (Calyptratae) – current status, perspectives and implications for studying Oestroidea evolution

Marco Antonio Tonus Marinho

Department of Ecology, Zoology and Genetics, Institute of Biology, Federal University of Pelotas (UFPel), 96010-900 - Pelotas, Rio Grande do Sul, Brazil. marco.marinho@gmail.com

Keywords: Divergence time estimation, molecular phylogeny, Neotropical Region, Oestroidea, taxonomy.

The Mesembrinellidae is a small family of exclusively Neotropical flies, with 38 described extant species and one fossil. It is now widely accepted as a distinct lineage among Oestroidea, with recent phylogenetic studies even suggesting its placement as one of the early branching lineages in the superfamily, which has some important implications for studying the evolution of oestroid flies. In this context, this presentation aims to discuss the current status of Mesembrinellidae taxonomy and systematics, including some new and alternative nomenclatural systems for genera in the family and presents the results of an updated phylogeny of Mesembrinellidae, with additional genes (28S, CAD, ITS2, 16S, COI, COII, Cyt*β*; 5662 sites total) and more taxa (215 terminal units, comprising 210 calyptrates, 185 oestroids and 49 mesembrinellids). Divergence time estimation analyses were also conducted, with five calibration points, including the *Mesembrinella caenozoica* Cerretti *et al*. fossil tested in three different scenarios (reflecting different possible nodes for calibration). For relationships among Mesembrinellidae lineages, results suggest that *Souzalopesiella* Guimarães is sister to a clade composed of (*Laneella* Mello + Mesembrinellinae). Also, results corroborate Mesembrinellidae as sister-group to Ulurumyiidae and suggest this clade as sister to a group composed by Calliphoridae (polyphyletic), Tachinidae, Rhinophoridae and Rhiniidae. The origin of Mesembrinellidae is estimated between 40–30 MYA, depending on the tested scenario and the origin of Oestroidea was dated between 50–45 MYA. Alternative hypothesis for relationships among Mesembrinellidae lineages and the position of the family in the Oestroidea phylogeny are discussed, with their implications for studying Oestroidea evolution.

Taxonomic revision and phylogenetic analysis of *Elmohardyia* Rafael (Pipunculidae), with descriptions of several new species

Dayse Willkenia Almeida Marques[1]*, José Albertino Rafael[2] &
Jeffrey H. Skevington[3]

[1]Instituto Nacional de Pesquisas da Amazônia, Programa de Pós-graduação em Entomologia, 69067–375, Manaus, Amazonas, Brazil. *willkenia@gmail.com
[2]Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil.
[3]Agriculture and Agri-Food Canada, Ottawa, Canada.

Keywords: Distribution, *Elmohardyia*, Eudorylini, phylogeny, Pipunculinae, taxonomy.

Elmohardyia Rafael belongs to the tribe Eudorylini (Pipunculinae) and is restricted to the New World. The genus currently comprises 62 described and a large number of undescribed species. *Elmohardyia* has a very distinctive habitus and bizarrely modified terminalia, being easily distinguishable from other genera. Currently, there is no identification key for species of the genus and phylogenetic relationships among species have not been investigated. This study aims to revise species of *Elmohardyia*, assess the monophyly of the genus and infer relationships among species, based mainly on external morphological characters and male terminalia. More than 600 specimens were examined for the revision and these were compared with all primary types available. Study of material from numerous localities in North, Central and South America allowed an update of geographical records of described species and resulted in the discovery of many new ones. More than 60 new species were confirmed, which indicates that the richness and diversity of the genus is far greater than we previously thought. The genus is recorded for the first time from Belize, Colombia, Ecuador, Guatemala, Guyana and Venezuela. In addition, for some available species DNA (COI–sub-unit I) was extracted, in an attempt to associate males with females and these molecular data are assisting in delimitting species. A phylogeny of the genus based on morphological characters is proposed and preliminary results are presented.

Micropezidae of Madagascar – new collections and new connections

Stephen A. Marshall

School of Environmental Sciences, University of Guelph, Guelph, Ontario N1G 2W1, Canada.
samarsha@uoguelph.ca

Keywords: Collections, Madagascar.

At the time of the last ICD (2014) the Micropezidae of Madagascar were known from around thirty specimens, including eight species organised into four genera of which two were non-African groups. Subsequent opportunities to do some focused micropezid collecting in Madagascar, and to examine Micropezidae recently taken in Malaise traps as part of a larger survey of Malagasy Diptera, have allowed a re-evaluation of the fauna. The Micropezidae of Madagascar now comprise 20 species, but only two genera, one of which is endemic and one of which is shared with continental Africa. This progression illustrates the critical importance of fieldwork and specialist collections to the study of Diptera systematics and biogeography.

3D virtual histology for developmental studies of Diptera – a pilot study of myiasis-causing flies

Daniel Martín-Vega[1, 2], Douglas D. Colwell[3] & Martin J.R. Hall[1]*

[1]Department of Life Sciences, Natural History Museum, Cromwell Road, London, SW7 5BD, United Kingdom. *m.hall@nhm.ac.uk
[2]Universidad de Alcalá, Madrid, Spain.
[3]Agriculture and Agri-Food Canada, Lethbridge, Canada.

Keywords: Calliphoridae, micro-computed tomography, Oestridae.

Myiasis, broadly defined as the infestation of dead or living tissues of live vertebrates with dipterous larvae, has a major negative impact on both animal health and the economics of livestock production and wildlife management. Of special importance are the families Calliphoridae, which includes both obligate and facultative parasitic species and Oestridae, which only includes obligate parasitic species. Oestrid flies do not feed during the adult stage, as they acquire all the necessary nutrients during their parasitic larval stage, so the adult mouthparts and digestive tract are frequently vestigial. The alimentary canal of adult dipterans is, nonetheless, a vital organ system, due to its role as a major regulator of multiple biological and developmental processes. Regrettably, morphological and developmental data on the alimentary canal of adult oestrid flies are scarce and there is a lack of a proper visualisation of this organ system within the pupal and adult bodies. In recent years, the use of X-ray micro-computed tomography (micro-CT) has revitalised and revolutionised morphological and developmental studies, enabling the non-destructive acquisition of high quality data of complex internal structures. The potential value of micro-CT-based 3D virtual histology is explained for morphological and developmental studies of the obligate myiasis-causing species *Oestrus ovis* L. (Oestridae) and the secondary facultative myiasis-causing species *Calliphora vicina* Robineau-Desvoidy (Calliphoridae). It is suggested that micro-CT is a suitable tool for non-destructive comparative studies, which can lead to a better understanding of the morphological changes behind fly metamorphosis, thus providing valuable new insights into several areas of research.

Taxonomic study of rocky shore flies of the genus *Cemocarus* Meuffels & Grootaert (Dolichopodidae) from South Africa

Kazuhiro Masunaga

Lake Biwa Museum, Oroshimo 1091, Kusatsu, Shiga, 525-0001 Japan.
masunaga-kazuhiro@biwahaku.jp

Keywords: *Cemocarus*, new species, South Africa, taxonomy.

The two currently recognised species of the genus *Cemocarus* Meuffels & Grootaert occur exclusively on marine rocky shores of Namibia and South Africa. The type species, *Aphrosylus griseatus* Curran, was described from East London, South Africa. *Cymatopus capensis* Parent, described from Muizenberg, South Africa, was treated as a junior synonym of *A*. *griseatus* in the *Catalogue of the Diptera of the Afrotropical Region* and also by H.J.G. Meuffels and P. Grootaert, when they proposed *Cemocarus* for *A*. *griseatus*. *Cemocarus stuckenbergi* Grichanov was later described from the Eastern Cape Province, South Africa. Suspecting that there may be additional undescribed species in South Africa, dolichopodids were sampled at two localities in South Africa in January and February 2009 and three undescribed species were discovered at Langebaan, Fish Hoek and Muizenberg in the Western Cape Province. Respectively, these can be recognised in having: 1) the greatest body length (5.7 mm), uniseriate acrostichal setae, the apical section of M_4 0.7 times as long as crossvein *dm–m* and the ventral lobe of the hypopygium as long as the cercus, with a broadened tip; 2) a body length of 2.1 mm, biseriate acrostichal setae and the apical section of M_4 as long as crossvein *dm–m*; and 3) the smallest body length (1.8 mm), biseriate acrostichal setae, the apical section of M_4 1.3 times as long as crossvein *dm–m* and a small tubercle bearing one long and two short apical setae in place of the absent ventral lobe of the hypopygium.

Reconnaissance, results and rewards – the balance between dipteran surveys for research, whilst providing education and outreach

Erica McAlister* & Beulah Garner

The Natural History Museum, Cromwell Road, South Kensington, London SW7 5BD, United Kingdom. *e.mcalister@nhm.ac.uk

Keywords: Conservation assessments, Dominica, Operation Wallacea, insects, students, surveys.

The Natural History Museum, London, comprises a world class insect collection of considerable geographical range and historical importance. There is an active collecting policy dating back 250 years that continues to expand upon our scientific and historical legacy, to help us understand and inform upon biodiversity issues. In ever more restrictive financial times, the costs of these expeditions to remote localities can be prohibitive and the necessity of obtaining permits dictates our ability to access biodiverse areas around the planet. Coupled with this, the Museum has an obligation to educate future generations on natural history and its importance in our societies. For the past four years, the Insect Division has partnered with a conservation organisation, *Operation Wallacea*, with the aim of documenting and describing the insect fauna of Dominica (a Neotropical biological hotspot). *Operation Wallacea* combines a network of academics from across the globe, who design and implement biodiversity and conservation management research projects with volunteers who assist them with their research. Coupling scientific outreach with collecting expeditions can benefit collections enhancement, although it is not without its pitfalls (pun intended). A discussion is provided of both the scientific and educational pros and cons of collecting for research using the untrained and more often than not, the uninterested.

Bringing the dead alive – high throughput sequencing of the Natural History Museum, London collection of mosquitoes

Erica McAlister[1]*, Petra Korlevic[2] & Mara Lawniczak[2]

[1]The Natural History Museum, Cromwell Road, South Kensington, London SW7 5BD, United Kingdom. *e.mcalister@nhm.ac.uk
[2]The Wellcome Sanger Institute, Hinxton, United Kingdom.

Keywords: Collections, Culicidae, museums, sequencing, vectors.

Our natural history collections are traditionally used as repositories of species for morphological comparisons and for understanding species distributions and change. The Diptera collection in the Natural History Museum, London (NHM) is no exception. Over the past 30 years, however, molecular analyses of these specimens have also been undertaken, to help understand sibling species relationships and species distributions. Until recently, this has been confined to very recent (or very ancient) material that comprise very little of the current collection. But high throughput sequencing techniques are now being used to explore the collections once more, to better understand taxonomic relationships, population changes over time, the history of insecticide resistance and what parasites are present in these specimens, implicating them in historic transmission. As the DNA of museum collection specimens is often highly degraded, ancient DNA extraction and library preparation methods are being applied on pinned museum specimens of malaria transmitting *Anopheles* mosquitoes. The sample set present in the NHM collection includes individuals that were collected in the same locations across Sub-Saharan Africa, from which present-day individuals are being sampled for population genomic research and includes periods in time where few or no vector control measures were in place, giving the opportunity to see how direct human intervention might have shaped the populations of such an important vector species.

A review of the Oriental-Australian stilt-legged flies (Micropezidae) in the subfamily Eurybatinae

Nur Athiqah Md Yusof* & Stephen A. Marshall

University of Guelph Insect Collection and Insect Systematics Laboratory, School of Environmental Sciences (Bovey), 1216 Edmund C. Bovey Building, University of Guelph, Guelph, ON, N1G 2W1, Canada. *nurathiqah.mdyusof@gmail.com

Keywords: New species, Oriental-Australian region, stilt-legged flies.

The subfamily Eurybatinae (Micropezidae) is a mostly Oriental-Australian group, previously divided into two tribes: Eurybatini and Metopochini. The monophyly of Eurybatinae has long been questioned, especially with regard to the placement of the Metopochini. Data presented here indicate Metopochini to be closely related to Micropezinae, rather than to the Eurybatinae. Thus, Metopochini is here removed from Eurybatinae. With the exclusion of the Metopochini, Eurybatinae currently comprises 10 genera: *Anaeropsis* Bigot, *Cothornobata* Czerny, *Crepidochetus* Enderlein, *Crosa* Steyskal, *Eurybata* Osten Sacken, *Nestima* Osten Sacken, *Notenthes* Marshall, *Papeza* McAlpine and *Trepidarioides* Frey, and an unnamed genus characterised by a unique bulging anterior frontal vitta. The subfamily is divided into two groups characterised by the presence or absence of a developed postmetacoxal bridge. The new genus belongs to the "postmetacoxal bridge group", together with *Crosa*, *Nestima* and *Papeza*. The revised concepts of these genera are here outlined and a summary is provided of their known distribution and biology.

Tackling open-ended taxa – large-scale species discovery and mass phylogenetics of South-east Asian Diptera

Rudolf Meier

Department of Biological Sciences, National University of Singapore, 14 Science Drive 4, Singapore 117543. meier@nus.edu.sg

Keywords: NGS barcodes, phylogenetics, South-east Asia, species discovery.

In 2011, the President of the Royal Society, Robert May, wrote that "... [we] are astonishingly ignorant about how many species are alive on Earth today, and even more ignorant about how many we can lose [and] yet still maintain ecosystem services that humanity ultimately depends upon." (*PLoS Biol* 9: e1001130). He pointed out that it is embarrassing that species estimates for the planet differ by more than one order of magnitude (3–100 million) and calculated that it would take *ca* 500 years to complete species discovery at the current rate (15,000/year). Now is the time to take on this challenge, because DNA sequencing is sufficiently cost-effective that it can be used for pre-sorting specimens into putative species. For this purpose, a non-destructive "NGS barcoding" procedure that is cost-effective (<USD 0.30/specimen) has been developed. Each specimen in a sample is individually barcoded and the barcodes are used to group the specimens into putative species. It is here estimated that the boundaries of 85–90% of these putative species are accurate. For this reason, they can also be used for building species-rich trees based on mitochondrial genomes and 28S rDNA sequence. The new techniques are particularly suitable for open-ended Diptera clades, such as Cecidomyiidae, Phoridae and Sciaridae.

Manual of the South American Diptera – family Pyrgotidae

Ramon Luciano Mello[1]* & Alessandre Pereira-Colavite[2]

[1]Laboratório de Sistemática de Diptera, Instituto de Biociências, Universidade Federal de Mato Grosso do Sul, P.O. Box 549, 79070-900, Campo Grande, MS, Brazil. *ramon.mello@ufms.br
[2]Universidade Federal da Paraíba, João Pessoa, Brazil.

Keywords: Acalyptratae, Neotropical Region, Pyrgotidae, Schizophora, taxonomy, Tephritoidea.

Pyrgotidae are acalyptrate flies of medium to large size (body length: 4–30 mm), with the body colour yellowish brown, with variations of yellow, reddish yellow, brown or black. The wing is hyaline, with distinct patterns of maculae, fasciae or is reticulate. The family can be easily recognised by shape of the head, which is higher than wide, by the absence of ocelli (in most species), the absence of frontal setae and a vibrissa, by the developed mouthparts and by wing venation, with the subcostal vein (*Sc*) reaching the costal vein (*C*) at an acute angle, with vein R_1 setulose and cell *cua* with a pointed projection in the lower corner. Adult flies have nocturnal habits being attracted to light. Larvae are known for their parasitoid behaviour, developing in the abdomens of adult scarabaeid beetles (Coleoptera). The family has a global distribution, with *ca* 365 described species of mainly tropical distribution. The fauna of South America comprises the following genera: *Carrerapyrgota* Aczél (4 species), *Descoleia* Aczél (1), *Idiopyrgota* Aczél (1), *Leptopyrgota* Hendel (33), *Lopadops* Enderlein (1), *Neopyrgota* Hendel (4), *Pyrgota* Wiedemann (3), *Pyrgotosoma* Malloch (1), *Stenopyrgota* Malloch (1), *Teretrura* Bigot (3) and *Tropidothrinax* Enderlein (1). This study is a preview of the chapter on Pyrgotidae that will appear in the forthcoming *Manual of the South American Diptera* and provides information on the South American fauna of Pyrgotidae, including a diagnosis, biology, economic importance, classification, identification, an identification key to genera, synopsis of the fauna and literature cited.

Morphology of male terminalia reveal a new cryptic species of *Senopterina* Macquart (Platystomatidae) from Brazil

Ramon Luciano Mello* & João Paulo Vinicios Rodrigues

Laboratório de Sistemática de Diptera, Instituto de Biociências, Universidade Federal de Mato Grosso do Sul, 79070-900, Campo Grande, MS, Brasil. *ramon.mello@ufms.br

Keywords: Acalyptratae, Neotropical Region, new species, Schizophora, Tephritoidea.

Senopterina Macquart is a genus of Platystomatidae comprising 15 described species confined to the New World. The genus can be recognised as follows: body colour brown to black, with distinct shiny pattern of green to violet, except on head, which is brown to yellowish brown; antennal postpedicel long, reaching face at lower margin; thorax longer than wide; scutellum rounded, with 2–3 apical setae; legs brown to yellowish brown, without setae; and wing hyaline with patterning. *Senopterina brevipes* (F.) and *S. macularis* (F.) are the only species recorded from Brazil. Based on examination of 168 specimens of *Senopterina* from Brazilian material, the occurrence of a new cryptic species was identified, resembling *S. macularis*. The two related species are similar in external morphology, but are distinguishable based on the morphology of the male terminalia. Details are provided of differences in the male terminalia of the two species. The cryptic species is confined to the Brazilian savanna (Cerrado), while *S. macularis* is restricted to tropical forests. Based on this study, it is likely that species richness in the genus is underestimated, with the possibility of other cryptic species in *S. brevipes* and *S. macularis*, over the wide geographical range of the two species in the Neotropical Region.

Poster

Manual of South American Diptera – family Ctenostylidae

Ramon Luciano Mello[1]*, Alessandre Pereira-Colavite[2] & José Albertino Rafael[3]

[1]Laboratório de Sistemática de Diptera, Instituto de Biociências, Universidade Federal de Mato Grosso do Sul, P.O. Box 549, 79070-900, Campo Grande, MS, Brazil. *ramon.mello@ufms.br
[2]Universidade Federal da Paraíba, João Pessoa, Brazil.
[3]Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil.

Keywords: Acalyptratae, Neotropical Region, Schizophora, taxonomy, Tephritoidea.

Ctenostylidae are medium- to large-sized (body length: 3.5–13 mm) acalyptrate flies, with the body reddish, yellow, or yellowish brown. The head and thorax are maculate and the wing is hyaline or hyaline with fasciae of yellow to yellowish brown. The family can be recognised by the slender body, globose head, which equals the size of the thorax, the absent of ocelli and the female antennal arista which is dendritically branched. The proboscis is absent and the legs are long and slender; the wing is generally patterned and vein R_1 is setulose dorsally. Ctenostylids are viviparous or ovoviviparous and larvae are probably parasitoids, although there are no records of host associations. Adults have crepuscular or nocturnal habits being attracted to lights. As the adult's mouthparts are reduced or absent, it is assumed that these flies only feed during the larval stages. The South America fauna is composed by seven species in four genera, namely: *Ctenostylum fuscomaculatum* Rafael, Pimentel & Godoi; *C*. *rufum* Macquart; *Furciseta hyalipennis* Câmara & Rafael; *F*. *plaumanni* (Hennig); *Lochmostylia lopesi* Keiser; *Tauroscypson andina* Aczél; and *T*. *guiana* Curran. This study is a preview of the chapter on Ctenostylidae that will appear in the forthcoming *Manual of the South American Diptera* and provides information on the South American fauna of Ctenostylidae, including diagnosis, biology, economic importance, classification, identification, an identification key to genera, the synopsis of the fauna and literature cited. Drawings illustrating morphological aspects, including wings and terminalia, are presented.

New species and records of *Ataenogera* Kröber (Therevidae: Phycusinae) from Brazil

Luanna L. Mendes[1], Martin Hauser[2], Stephen D. Gaimari[2], José Albertino Rafael[3] & Francisco Limeira-de-Oliveira[1]*

[1]Universidade Estadual do Maranhão (UEMA), Centro de Estudos Superiores de Caxias, CEP: 65604-380, Caxias, Maranhão, Brazil. *limeiraf@gmail.com
[2]California Department of Food and Agriculture, Sacramento, U.S.A.
[3]Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil.

Keywords: Neotropical Region, new species, north-east of Brazil, Phycusinae, taxonomy.

Therevidae is represented by nearly 120 genera with *ca* 1,200 valid species, divided into four subfamilies: Agapophytinae, Phycusinae, Therevinae and Xestomyzinae. In the Neotropical Region, therevids are represented by 137 species in 32 genera, 36 of which occur in Brazil, including *Ataenogera* Kröber, the target group of this work. *Ataenogera* is restricted to the Neotropics with six described species: *A. abdominalis* Kröber, *A. argentifrons* Hauser & Webb, *A. brevicornis* (Bromley), *A. grandis* Lyneborg, *A. irwini* Hauser & Webb and *A. minuta* Lyneborg, three of which are known from Brazil: *A. abdominalis*, *A. brevicornis* and *A. grandis*. The present study aims to examine more recently collected specimens of *Ataenogera* collected in different regions of Brazil. When analysing the specimens, eight species were identified, two previously described, *A. abdominalis* and *A. brevicornis* and six new species. The doubling of the number of species known for the genus is a result of intense collections during 14 uninterrupted months in different regions of Brazil. *Ataenogera* is recorded for the first time in the states of Acre, Ceará, Maranhão, Mato Grosso, Mato Grosso do Sul and Piauí.

Poster

First record of *Pycnopota* Bezzi (Sphaeroceridae: Copromyzinae) for Brazil and description of two new species

Isis Sá Menezes*, Geovânia Freitas, Alexssandro Camargo da Silveira & Rosaly Ale-Rocha

Instituto Nacional de Pesquisas da Amazônia-INPA, Campus II, CEP 69067-375, Av. André Araújo, 2936, Petrópolis, Manaus, Amazonas, Brazil. *isis.sa.menezes@gmail.com

Keywords: Neotropical Region, new species, lesser dung flies, taxonomy, terminalia.

The Neotropical genus *Pycnopota* Bezzi was proposed for the single species *P. manni* Bezzi, described from Bolivia. It is a bizarre fly, uncommon in collections, being characterised mainly by: the long cylindrical heavily sclerotised proboscis which reaches the mid coxa; the clypeus, which is greatly developed with a “horn”; and by the lack of palpi. In these respects the genus differs significantly from other known genera. Moreover, the presence of spines on the costal vein has already raised the question of its placement in the subfamily Copromyzinae, such spines being a characteristic of most representatives of the Heleomyzidae. The specimens studied originate from the collections of Instituto Nacional de Pesquisas da Amazônia and Museu de Zoologia da Universidade de São Paulo, Brazil. The genus is here reported from Brazil for the first time and two new species are described; one from the northern part of Brazil (Roraima State) and one from the south-east (São Paulo State). The described species can be characterised, mainly on the presence of modified differentiated setae on males fore tarsomeres 2–3 and by the flattened mid tarsomeres 2–4, on the number of sclerotised abdominal sclerites and on structures of the terminalia. Images of the specimens and illustrations of the male and female terminalia are provided, plus a distribution map of the species.

Poster

Diptera biodiversity informatics – moving entomological data forward

John M. Midgley

Department of Natural Science, KwaZulu-Natal Museum, 237 Jabu Ndlovu Street, Pietermaritzburg 3201 and Southern African Forensic Entomology Research Group, Department of Zoology and Entomology, Rhodes University, P.O. Box 94, Grahamstown 6139, South Africa. *johnmidge@gmail.com

Keywords: Biodiversity informatics, date usage, entomological collections, review.

Biodiversity informatics is a growing field across many biological disciplines and dipterology is no different. Broadly defined, almost any research can be included in biodiversity informatics, particularly when “next generation” tools are incorporated in analyses. The most common biodiversity informatics in entomology utilises collections data for spatial and temporal analyses, but taxonomic, biological and ecological research can all incorporate biodiversity informatics themes. Museum collections are typically seen as resources for distribution and biogeography analyses, but with thoughtful design and proper application of data models their use can be broadened. Potential biodiversity informatics uses will be discussed further.

Honouring Jason G.H. Londt – Afrotropical Asilidae, the KwaZulu-Natal Museum and a career dedicated to discovering and describing new species

John M. Midgley[1]* & Torsten Dikow[2]

[1]Department of Natural Science, KwaZulu-Natal Museum, 237 Jabu Ndlovu Street, Pietermaritzburg 3201 and Southern African Forensic Entomology Research Group, Department of Zoology and Entomology, Rhodes University, P.O. Box 94, Grahamstown 6139, South Africa. *johnmidge@gmail.com
[2]National Museum of Natural History, Washington D.C., U.S.A.

Keywords: Afrotropical, assassin flies, dedication, Jason Londt, revisionary work, robber flies.

The Afrotropical Asilidae fauna is one of the richest in the world and also one of the most diverse fly families in the region. This knowledge is in large part due to the efforts of Jason G.H. Londt, who has been associated with the KwaZulu-Natal Museum (NMSA), Pietermaritzburg, South Africa, since 1976, first as a serving staff member and later as Emeritus Director. With encouragement from the then Director (Brian R. Stuckenberg), Jason embarked on the study of robber flies, and with the 1974 publication “An introduction to the robber flies of South Africa” by Harold Oldroyd in hand, Jason single-handedly reviewed a significant part of the Afrotropical fauna, with special emphasis on the fauna of Southern Africa. Here, a sketch is provided of his career in robber fly research, his field work in sub-Saharan Africa (particularly South Africa) and his contributions to understanding and identification of Afrotropical Asilidae. Jason Londt has described more than 550 species and 45 genera as new to science, developed identification keys to these taxa and comprehensively re-described numerous other species and genera in 85 publications, which include original illustrations of the male terminalia and other diagnostic features. Although he served as Director of the NMSA, from 1994 to 2003, he nevertheless continued his taxonomic research and published many substantial reviews during this period. It is a great pleasure to convene an Asilidae symposium at ICD9 to honour Jason Londt and his contributions to understanding the extremely diverse Afrotropical robber fly fauna.

Species composition of potential epizootic hemorrhagic disease vector species in North Illinois, U.S.A.

Miguel Ángel Miranda[1]*, Carlos Barceló[1], Chris Anchor[2], Marilyn O'Hara[3] & Lee Cohnstaedt[4]

[1]Applied Zoology and Animal Conservation Research Group, University of the Balearic Islands, Cra. Valldemossa km 7.5. CP: 07122. Palma de Mallorca, Spain. *ma.miranda@uib.es
[2]Cook County Forest Preserve, Illinois, U.S.A.
[3]University of Illinois, Urbana, U.S.A.
[4]Center for Grain and Animal Health Research, USDA, Manhattan, U.S.A.

Keywords: *Culicoides*, epizootic hemorrhagic disease, EHDV, deer, Illinois, U.S.A., vector.

Epizootic hemorrhagic disease (EHD) is an arboviral disease of wild and game reserve populations of White-tail deer in North America. The disease is caused by a virus (EHDV) that belongs to the genus *Orbivirus* (Reoviridae), from which ten serotypes are currently known. Cattle can act as a reservoir of the virus, without showing clinical symptoms. The virus is transmitted by the feeding activity of biting midges of the genus *Culicoides* Latreille (Ceratopogonidae). The species *C*. *sonorensis* Wirth & Jones, also a vector of bluetongue disease, is considered the major vector of EHD in the U.S.A. Several epidemics of EHD have occurred during the past decade in the northern states of the U.S.A, but there is no evidence regarding which species are involved in transmission of EHDV in those states as *C*. *sonorensis* is absent. In 2013 and 2014, surveillance was conducted of potential vector species in several EHD affected counties of the state of Illinois, such as McHenry and Cook counties. For this, ten sampling sites were selected, including three cattle farms and seven natural preserved areas where deer were present and outbreaks of EHD were recorded. Different types of light traps (CDC, USDA and Onderstepoort) were deployed for collecting adult *Culicoides* from dawn to dusk during summer and spring. Details of species composition of the potential *Culicoides* vector species for EHD associated to cattle farms and natural areas are presented.

Twenty-five years of the study of Diptera of economic and health importance in the Balearic Islands, Spain

Miguel Ángel Miranda*, Carlos Barceló, David Borràs, Margalida Miquel, Miriam Monerris, Ricardo Del Rio & Claudia Paredes-Esquivel

Applied Zoology and Animal Conservation Research Group, University of the Balearic Islands, Palma de Mallorca, Spain. *ma.miranda@uib.es

Keywords: *Aedes*, *Bactrocera*, Balearic Islands, *Ceratitis*, *Culicoides*, *Oestrus*, Spain.

Diptera is the most important order of insects, due to the status of some species as pests of crops and as vectors of human and livestock diseases. During the past 25 years, research has been conducted on the bioecology and control of several species of Diptera of economic and health importance in the Balearic Islands, Spain. An overview is presented here of the main results for each species studied, as well as projected research needs. Species, such as *Bactrocera oleae* (Rossi) and *Ceratitis capitata* (Wiedemann) (both Tephritidae) are major pest of olive and fruit crops, respectively. Research on these two species included monitoring using specific female lures as well as electronic traps. Female lures are a cornerstone in the monitoring of *C. capitata*, while electronic traps are promising for use under differing circumstances. In relation to animal health, broad research was conducted on the bioecology and control of biting midges of the genus *Culicoides* Latreille (Ceratopogonidae), that are vectors of livestock diseases, such as African horse sickness and bluetongue. A contribution was made to the better understanding of insecticides for controlling *Culicoides*, as well as to the bionomy of species associated with livestock farms. The prevalence of *Oestrus ovis* (L.) (Oestridae), a nasal botfly of sheep, which is frequently found in the Balearics, was also studied. Finally, as regards human health, studies focused on the bioecology and monitoring of mosquitoes (Culicidae), in particular exotic, invasive species, such as *Aedes albopictus* (Skuse), as well as the taxonomy of indigenous species.

A taxonomic review of Southern African *Stenobasipteron* Lichtwardt (Nemestrinidae)

Musa C. Mlambo[1]*, David Barraclough[2] & Rob Slotow[2]

[1]Department of Freshwater Invertebrates, Albany Museum, affiliated Research Institute of Rhodes University, Somerset Street, Grahamstown 6139, South Africa. *musa.mlambo@gmail.com
[2]University of KwaZulu-Natal, Durban, South Africa.

Keywords: Long-proboscid fly, pollination biology, taxonomy.

Stenobasipteron Lichtwardt is one of three long-proboscid fly genera in the subfamily Nemestrininae (Nemestrinidae), considered important in pollination biology of numerous endemic plant species with elongated corollas. This genus has received virtually no taxonomic attention for the past 80 years, which has resulted in taxonomic confusion, misidentifications and failure to provide correct species names. The genus is endemic to Southern Africa, mainly distributed through the eastern provinces of South Africa and into Swaziland and Zimbabwe. Currently the genus includes three valid species: two from Zimbabwe (*S*. *arnoldi* Bequaert & *S*. *gracile* Lichtwardt) and one from South Africa (*S*. *wiedemanni* Lichtwardt). Extensive morphological examination of more than 250 specimens from South Africa, revealed that this genus has five undescribed species in South Africa, in addition to *S*. *wiedemanni*, which was found to be restricted to forest habitats in the south-eastern provinces of KwaZulu-Natal and the Eastern Cape. The following morphological characters were found to be diagnostic in delimiting species: proboscis length in relation to the body length; frons shape and size; wing venation; and male terminalia. All the new species are distributed in the north-eastern provinces of Mpumulanga and Limpopo and occur in a variety of habitats, *i*.*e*., bushveld and grassland, which is different from closed forest habitat, the preference of *S*. *wiedemanni*. The fauna of neighbouring Southern African countries also requires taxonomic revision.

Poster

Flies on rock pools – survival and emergence of dipterans from dried soil sediments of temporary wetlands

Musa C. Mlambo[1]*, Nonka Mdidimba[2] & Sam Motitsoe[2]

[1]Department of Freshwater Invertebrates, Albany Museum, affiliated Research Institute of Rhodes University, Somerset Street, Grahamstown 6139, South Africa. *musa.mlambo@gmail.com
[2]Rhodes University, Grahamstown, South Africa.

Keywords: Drakensberg, ephemeral pools, resurrection ecology, sleeping chironomids, South Africa.

Organisms adapted to episodic wetlands survive the recurring wet/dry phases by producing desiccation tolerant propagules (*e.g.*, eggs, cysts or other stages in arrested development). Although there are a large number of Diptera that occur in temporary wetlands, there are very few examples of them surviving the dry period through desiccation tolerant propagules. Recent collection of dried soil sediments from various rock pools in the Drakensberg Mountains (KwaZulu-Natal Province, South Africa) and their subsequent hatching assays have yielded a handful of Diptera, suggesting that these taxa survived the dry phase. The taxa involved to date are: an unidentified moth fly (Psychodidae); *Aedes* Meigen sp. (Culicidae); and *Polypedilum* Kieffer sp. (Chironomidae) The last-named taxon is not entirely surprising, as another species in the "sleeping chironomid" group was recently described from Malawi. The larvae of the "sleeping chironomid", *P. vanderplanki* Hinton, represents a well-known example of a chironomid that can undergo complete desiccation for a period of up of to 17 years and when whetted, awakens and resumes normal growth and feeding. The other two taxa, however, were something of a surprise. The floodwater *Aedes* is an interesting find, a known carrier of Rift valley fever virus (Bunyaviridae: Phlebovirus), a severe disease in humans and animals. In the case of the psychodid, there are no records of the family surviving dry periods as eggs in Africa. This presentation highlights various examples of Diptera avoiding desiccation and the DNA barcoding of specimens from rock pools.

General dipterology

Are *Simulium* (*Anasolen* Enderlein), *S.* (*Freemanellum* Enderlein) and *S.* (*Xenosimulium* Crosskey) related to *S.* (*Trichodagmia* Enderlein) (Simuliidae)?

Óscar Sánchez Molina[1]* & Leonardo H. Gil-Azevedo[1]

[1]Departamento de Entomologia, Museu Nacional, Universidade Federal do Rio de Janeiro, CEP 20940-040, Quinta da Boa Vista s/n, São Cristóvão, Rio de Janeiro, RJ, Brazil.
*o.sanchezmolina@gmail.com

Keywords: Afrotropical Region, blackflies, Neotropical Region, phylogeny, Simuliidae.

Simulium (*Trichodagmia* Enderlein) includes 77 species, divided into five species-groups that are distributed in different zoogeographical regions: *S. albellum*-group (Palaearctic), *S. canadense*-group (Nearctic and Neotropical), *S. orbitale*-group (Neotropical), *S. pictipes*-group (Nearctic) and *S. tarsatum*-group (Nearctic and Neotropical). These species-groups correspond to some subgenus of *Simulium* synonymised with *S*. (*Trichodagmia*) based, almost exclusively, on general similarities and without a phylogenetic analysis. The current classification of the group ignores previous proposals according to which some of these subgenera would be close to the Afrotropical subgenera *S*. (*Anasolen* Enderlein), *S*. (*Freemanellum* Enderlein) and *S*. (*Xenosimulium* Crosskey). A phylogenetic analysis was conducted which aimed to test the monophyly of *S*. (*Trichodagmia*) and evaluate its relationship with these Afrotropical subgenera. The internal group comprised 45 terminal taxa, representing the five species-groups of *S*. (*Trichodagmia*), *S*. (*Anasolen*), *S*. (*Freemanellum*) and *S*. (*Xenosimulium*). The out-group consisted of 19 subgenera of *Simulium*. A total of 62 characters of females, males, pupae and last instar larvae were observed. The data matrix was subjected to a parsimony analysis using equal and implied weights. The results obtained indicated that *S*. (*Trichodagmia*) + *S*. (*Anasolen*) + *S*. (*Freemanellum*) + *S*. (*Xenosimulium*) constitute a monophyletic group, besides, these Afrotropical subgenera form a monophyletic group with the Neotropical species-groups *S. orbitale* and *S. tarsatum* of *S*. (*Trichodagmia*). This relation could constitute a hypothetical Gondwanan lineage, due to the fact that all representatives of this clade are found exclusively in Africa and South America.

Composition of the flower flies fauna (Syrphidae) of Andean ecosystems of north-western Colombia

Augusto L. Montoya* & Marta Wolff

Grupo de Entomología, Universidad de Antioquia, Calle 67 No. 53–108, Medellín 1226, Colombia.
*aleon.montoya@udea.edu.co

Keywords: Colombia, conservation, flower flies composition, Neotropical Region, Paramo diversity.

Colombia, located in the north-western corner of South America, is crossed by three cordilleras and two inter-Andean valleys, creating a mosaic of unique microhabitats. The north-west of the country includes the Andean cordilleras, which have generated a diverse dipterofauna; the family Syrphidae, with 312 species (66 genera); mainly distributed in highlands. In this study, Syrphidae composition was studied in the ecosystems of Paramo, forest and grassland in the Central Cordillera. Malaise traps were deployed and hand netting was conducted from 2016–2017. A total of 1,951 specimens, representing 76 species and 53 morphospecies (35 genera) were sampled. Paramo had the highest diversity, with 59 species and 38 morphospecies (32 genera), represented principally by: *Toxomerus* Macquart (28%, 4 spp.), *Argentinomyia* Lynch-Arribálzaga (13%, 7), *Ocyptamus* (*Orphnabaccha* Hull) (11%, 4), *Platycheirus* Lepeletier & Serville (10%, 2); followed by forest, with 38 species and 24 morphospecies (24 genera): *Toxomerus* (23%, 3), *Argentinomyia* (15%, 5), *Allograpta* Osten-Sacken (13%, 5), *Ocyptamus* (*Orphnabaccha)* (10%, 4); and grassland with 33 species and 7 morphospecies (21 genera): *Toxomerus* (42%, 3), *Platycheirus* (8%, 2), *Argentinomyia* (7%, 4), *Fazia* Shannon (6%, 4), *Allograpta* (5%, 3). *Lepidomyia* Loew, *Pseudoscaeva* Vockeroth, *Talahua* Fluke, *Trichopsomyia* Williston and *Tuberculanostoma* Fluke were exclusive to Paramo (> 3,000 m); *Ocyptamus* (*Mimocalla* Hull) and *Ocyptamus* (*Pipunculosyrphus* Hull) to forest (2,850–2,950 m), while *Cacoceria* Hull and *Rhinoprosopa* Hull were exclusive to grassland (2,790–2,840 m). *Ocyptamus* (*Pipunculosyrphus* Hull) is recorded for the first time, together with 11 species, increasing the Colombian fauna to 323 species (68 genera). The ecological functions and habitat preferences of the flies are discussed in a conservation context.

Occupancy models to assess Syrphidae as bioindicators in Colombian Andes ecosystems – an alternative tool

Augusto L. Montoya[1]*, Juan Luis Parra[2] & Marta Wolff[1]

[1]Grupo de Entomología, Universidad de Antioquia, Calle 67 No. 53–108, Medellín 1226, Colombia.
*aleon.montoya@udea.edu.co
[2]Grupo de Ecología y Evolución de Vertebrados, Universidad de Antioquia.

Keywords: Bioindicator, Colombia, flower flies, Neotropical Region, Paramo fauna.

Colombia comprises 34 Paramo complexes, covering 19,330 km^2 of country area. These unique ecosystems include endemic species, with high richness and vulnerability, including flower flies. Syrphidae provide environmental services as pollinators and have functional groups that develop in different resources, with specific environmental requirements. To evaluate the use of syrphids as bioindicators in Andean ecosystems, Malaise traps were deployed and hand netting was conducted from 2016 to 2017. Three ecosystems (Paramo, forest and grassland) were sampled each for two months, over a ten-day period. A total of 1,951 specimens, representing 76 species and 53 morphospecies in 35 genera were sampled. Of these, 19 species in 13 genera were selected to evaluate occupancy related to landscape preferences. The occupancy models considered imperfect detection (the species is present, but not detected or is truly absent) to estimate ψ = psi (probability that a site is occupied), *p* (probability to detect the species given that it is present) and related parameters with less bias. A 300 m radius was selected to measure the area of grassland and forest around each collecting site as occupancy coverables in the software ImageJ-1.52a. Values were standardised with a *Z* transformation and the following models were tested in PRESENCE 2.12.10, using Akaike criterion: psi(.)*p(.), psi(grassland_size)*p(.), psi(grassland_size +grassland_size^2)*p(.), psi(forest_size)*p(.) and psi(forest_size+forest_size^2)*p(.). The detection was low for most species (0.20178–0,5704; mean = 0.35708), meanwhile the occupancy ranges from 0.3333–0.8889 (mean = 0.5545). The best models will be discussed according to local abundance and landscape preference, highlighting the use of occupancy models as alternative tool for recognise habitat marker species in bioindication.

Mimicry in the subtribe Criorhinina (Syrphidae: Eristalinae)

Kevin M. Moran* & Jeffrey H. Skevington

Canadian National Collection of Insects, Arachnids and Nematodes, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada and Carleton University, Ottawa, Canada.
*syrphidae@kevinmoran.com

Keywords: Criorhinina, Eristalinae, mimicry.

Mimicry within the subtribe Criorhinina *sensu stricto* is qualitatively examined. Representatives of the subtribe are among the largest species of Syrphidae and experience tremendous selective pressure to evolve perfect mimicry. The resulting breadth of mimicry is astounding, with species mimicking *Bombus* Latreille (Hymenoptera: Apidae) queens or workers, other types of bees or social wasps. The prevalence of perfect mimicry within the group is examined, with attempts made to link each mimic species to a specific model. Polymorphic mimicry, in its varied forms and the frequency of its occurrence are discussed. Within Criorhinina, single model and multiple model polymorphism, sympatric and parapatric polymorphism and sex-linked polymorphism are all apparent. Additionally, the evolution of mimicry within the group is examined. This is enabled by an eight gene phylogeny: including all of COI, 28S D2–3, CAD1, AATS, PERIOD along with three new loci (for a total of ~ 8kB of data). Unlike previous hypotheses, this phylogenetic analysis reveals that wasp mimicry does not have a single origin and the evolution of these wasp-like characters is examined. It also enables the construction of hypotheses to explain the other myriad forms of mimicry found within the subtribe, with proposed explanations, including range, model availability, emergence times and even the overarching evolution and dispersal of the group.

Systematics of the meniscus midges (Dixidae) – molecular phylogenetics of world taxa and highlights from revisionary studies of Nearctic *Dixa* Meigen

John K. Moulton

Department of Entomology and Plant Pathology, The University of Tennessee, Knoxville, TN 37996-4560, U.S.A. jmoulton@utk.edu

Keywords: Aquatic insect, biodiversity, North America, phylogeny, taxonomy.

Meniscus midges comprise a small family of *ca* 200 described species of aquatic, mosquito-like, culicomorphan Diptera. Larvae move in a characteristic side-winding fashion, ultimately resting in a U-shaped position on emergent substrates at the atmosphere and water interface, hence their vernacular name. There they actively filter fine particulate organic matter from the water column. Pupation occurs on emergent substrates. Adults, which possess denuded wings having a strongly arched vein R_{2+3}, do not feed and typically remain for a short period near the preimaginal habitat, which can be lotic or lentic. Eight extant genera: *Asiodixa* Papp, *Dixa* Meigen, *Dixella* Dyar & Shannon, *Meringodixa* Nowell, *Mesodixa* Belkin, Heinemann & Page, *Metadixa* Peters, *Neodixa* Tonnoir and *Nothodixa* Edwards, are currently recognised. The higher classification of the family remains largely unsettled and no modern phylogenetic analysis has been conducted. This presentation highlights results from: 1) phylogenetic analyses of nucleotides from large portions (*ca* 3 kilobases) of two nuclear loci, Big Zinc Finger and 5intG, acquired from a diverse assemblage of world species; and 2) revisionary studies of Nearctic species of *Dixa* utilising a combined molecular and morphological approach. Implications the resulting trees have upon current supraspecific concepts will be discussed as well as how nuclear DNA fingerprinting has impacted descriptive studies, ranging from simple life stage association to identification and elucidation of cryptic species complexes.

Systematics of Indian species of *Polypedilum* Kieffer (Chironomidae)

Tuhar Mukherjee* & Niladri Hazra

Entomology Research Unit, Department of Zoology, University of Burdwan, Burdwan, West Bengal, India. *tuharmukherjeeofficial@gmail.com

Keywords: Aquatic midges, Chironomini, eurythermic, India, new species.

The genus *Polypedilum* Kieffer is one of the most speciose genera in the chironomid tribe Chironomini of the subfamily Chironominae. The taxon occurs in all zoogeographical regions, except Antarctica and larvae occur in both lentic and lotic habitats. Larvae of the species *Polypedilum* (*Polypedilum*) *nudiceps* Chaudhuri, Guha & Das Gupta are eurythermic and are recorded from both tropical conditions in the foothills and the freezing water temperatures of the Eastern Himalayan alpine zone, contrary to the reports of previous workers. Currently, 44 species belonging to three subgenera (*Polypedilum sensu stricto* (28), *Pentapedilum* Kieffer (5) and *Tripodura* Townes (11)), have been recorded from India. In this study a total of 37 species were examined, including type material, for a morphological cladistic analysis. A new species of the subgenus *Pentapedilum* was also discovered. Some species, including *Polypedilum* (*Po*.) *brumale* Kieffer, *P*. (*Po*.) *fasciatipennis* Kieffer and *P*. (*Pe*.) *macrotrichium* Guha & Chaudhuri, could not be included in the analysis, as they were erected on the basis of female specimens alone and *P*. (*Po*.) *milnei* Kieffer, *P*. (*Po*.) *nigriforceps* (Kieffer) and *P*. (*Po*.) *purimanum* Kieffer were also omitted from the analysis, due to the very poor condition of the type specimens.

Diptera collections as data sources for biodiversity and conservation management planning – a South African case study

Burgert S. Muller

Department of Entomology, National Museum, P.O. Box 266, Bloemfontein 9300, South Africa.
burgert.muller@nasmus.co.za

Keywords: Collections data, South Africa, Chi-squared test, principal component analysis.

Diptera are important contributors in numerous ecosystems, but have traditionally been neglected in favour of other orders, such as Hymenoptera when it comes to understanding their role in ecological services, such as pollination. This view is, however, changing with more and more research highlighting the group's contributions. Natural history collections are often touted as important sources of data in biodiversity and conservation management planning and in many cases, there are decades' worth of temporal and spatial information that could be potentially used and applied to current research needs. It is critical that data quality and fitness for use be evaluated on a per needs basis, or users could run the risk of applying unsuitable datasets to specific biodiversity management plans, ultimately resulting in failed conservation effort. Data was sourced directly from South African institutions, as well as from GBIF datasets. Over 130,000 specimen records from *ca* 15,000 localities, collected over 200 years, were assessed and analysed in terms of geographic, spatial, temporal and environmental coverage across South Africa. Temporal and spatial biases, together with their influence on fitness for use are discussed.

The “*Atherix*” syndrome – an overview of the systematics and taxonomy of Afrotropical Athericidae

Burgert S. Muller* & Ashley H. Kirk-Spriggs

Department of Entomology, National Museum, P.O. Box 266, Bloemfontein 9300, South Africa.
*burgert.muller@nasmus.co.za

Keywords: Afrotropical Region, South Africa, new genus, new species, water snipe flies.

The family Athericidae was erected by B.R. Stuckenberg in 1973 and is considered sister-group to the Tabanidae. Globally, 10 genera, comprising *ca* 100 species (22 Afrotropical) are recognised. These are divided into two subfamilies: Athericinae and Dasyommatinae, of which only the former occurs in the Afrotropics. Five genera of Athericinae are known from this region: *Pachybates* Bezzi and the monotypic *Trichacantha* Stuckenberg (both endemic to South Africa) and *Atrichops* Verrall (Oriental and Palaearctic Regions) and *Suragina* Walker (all regions, except Antarctica). The now unplaced Afrotropical species of the fifth, *Atherix* Meigen (Nearctic and Palaearctic Regions) are no longer considered congeneric with the Northern Hemisphere species of the genus. These “*Atherix*” species, together with other new species, identified by Stuckenberg from the KwaZulu-Natal Museum, from South Africa are potentially classified into four new genera. The adult characters and the biogeography of these new genera are compared to those of existing Afrotropical genera. A rigorous morphological and molecular phylogeny of the Afrotropical representatives of the family will need to be undertaken, with evolutionary relationships and ecology taken into account, all of which will contribute to a systematic and taxonomic revision of Afrotropical Athericidae.

Flies are essential pollinators of Avocado (*Persea americana* Mill.) in Murang’a County, Kenya

Joseph Mulwa[1, 2]*, Ruth Kahuthia-Gathu[2] & Muo Kasina[3]

[1]Kenya Agricultural and Livestock Research Organization (KALRO), Kabete, P.O. Box 14733-00800 Nairobi, Kenya. *josemulwa0009@gmail.com
[2]Kenyatta University, Nairobi, Kenya.
[3]National Sericulture Research Centre, KALRO, Thika, Kenya.

Keywords: Agriculture, Avocado, crop yield, fruit set, Kenya, pollination deficit, pollinator diversity.

Avocado (*Persea americana* Mill.) (Lauraceae) is an important economic crop in Kenya, grown for the domestic and export markets. This study was undertaken to determine its pollination deficit and identify the drivers of pollination in Murang’a County, which has the highest concentration of small scale Avocado (variety Hass) farming in Kenya. Farmers in Kenya are not known to manage pollination and, therefore, the study was essential for developing a strong basis for pollinator protection and use in farming. Data on flower visitors’ activity density were collected over three seasons (August 2015 to October 2016). In addition, with and without pollination trials were undertaken on 95 Avocado trees across the seasons and various fruit set and yield parameters recorded. Over 99% of avocado flower visitors were Diptera and Hymenoptera, while Lepidoptera and Coleoptera were rare visitors. Honeybees (*Apis mellifera* L.) (Hymenoptera: Apidae) had the highest activity density (87%), blowflies (Calliphoridae) (5.3%) and hoverflies (Syrphidae) (3%). Fruit set differed significantly ($P < 0.001$) between terminal branches without (*mean*: 9.38) and with (*mean*: 19.85) externally aided pollination. Additionally, the mean fruit yield differed significantly ($P < 0.002$) per terminal branch between the without (0.165) and with (0.464) externally aided pollination, translating into a 64.5% pollination deficit. While Honeybees were the predominant flower visitors, the presence of Diptera was critical in enhancing pollination and, therefore, require protection. An integrated pollination management of Avocado is suggested for enhanced yield and quality of Avocado to secure farmer incomes and sustain the market.

An overview of some fruit fly (Tephritidae) control activities in Africa over the past decades – success, limitations and future prospects

Maulid W. Mwatawala

Sokoine University of Agriculture, Department of Crop Science and Horticulture, P.O. Box 3005, Chuo Kikuu, Morogoro, Tanzania. mwatawala@sua.ac.tz

Keywords: Africa, pest control.

A limited number of fruit flies (Tephritidae) are pests of economic importance to cultivated fruits and vegetables in Africa. The horticultural industry sector is a source of income, employment, food and nutrition security among African populations. Several native and exotic tephritid pest species occur in Africa. Losses caused by these species are high, especially when effective control measures are not implemented. There have been efforts by various institutions across Africa to manage frugivorous fruit flies. Most recent control activities targeted the invasive species *Bactrocera dorsalis* (Hendel), a key polyphagous species, recorded in most parts of sub-Saharan Africa. There has been a notable shift in the past decade from broadcast chemical application to more bio-rational techniques, falling under biological, physical and cultural control methods. Various integrated pest management (IPM) programmes have been tested and implemented albeit at limited spatial scales. Most programmes are based on monitoring, spot application of baits, attract and kill systems and orchard sanitation. This keynote address discusses the various control methods, their scope of application, advantages, limitations and proposes a way forward. The presentation discusses the prospects of agroecology as a future concept in fruit fly control in Africa and highlights control gaps in the light of synonymisation and the description of new species. Finally, challenges posed by the introduction and spread of invasive species are outlined and discussed.

Simple laboratory method for harvesting fertilised eggs of the Black soldier fly, *Hermetia illucens* (L.) (Stratiomyidae)

Satoshi Nakamura

Japan International Research Center for Agricultural Sciences, Ohwashi 1-1, Tsukuba, 305-8686, Japan. s.nakamura@affrc.go.jp

Keywords: Biology, Black soldier fly, *Hermetia*, low cost maintenance, rearing methods.

The Black soldier fly, *Hermetia illucens* (L.), has been considered as a good candidate for use in organic waste treatment. It can feed on a wide variety of organic matter, can reduce waste accumulation by 60–80% and its larvae and pupae can provide valuable feed for a variety of domesticated animals. There are some reported studies of the rearing of Black soldier fly adults to obtain fertilised eggs. These studies, which were either conducted in a greenhouse or outdoors, used large cages that held 750–1,000 adult flies. Such methods make maintenance at suitable temperatures throughout the year costly and scaling them up could make it inconvenient to conduct precise experiments for collecting biological information about adult flies. To gather the required information, 100 adults were reared (50 males and 50 females) each in small cages (27 × 27 × 27 cm) in the laboratory, provided with either supplementary light-emitting diode (LED) lighting or 2 hours of sunlight exposure per day. Fertilised eggs were obtained from both light treatments, although sunlight enhanced fertilisation increased the proportion of fertilised eggs, patterns of oviposition were similar in both treatments and there were no significant differences in the total numbers of egg clutches, oviposition periods and female longevity. This small-scale rearing method would be helpful in collecting biological information and maintaining cultures of Black soldier fly in the laboratory at low cost throughout the year.

Poster

The microtype tachinid, *Pales pavida* (Meigen) – new findings on larval behavioural avoidance of host's immune response

Satoshi Nakamura[1]* & Toshiharu Tanaka[2]

[1]Japan International Research Center for Agricultural Sciences, Ohwashi 1-1, Tsukuba, 305-8686, Japan. *s.nakamura@affrc.go.jp
[2]Nagoya University, Nagoya, Japan.

Keywords: Host immune system, larval behaviour, *Pales*, parasitoid fly, Tachinidae.

Microtype tachinids deposit eggs containing first-instar larva on food plants of the host, which are then ingested by the host for parasitisation. Reportedly, eggs hatch in the host gut immediately following ingestion and the first-instar larvae move to and remain within certain organs, probably to evade the host's immune responses. These phenomena were described more than 80 years ago, and as far as is known, no further studies have been conducted. This prompted an investigation of larval movements of a microtype tachinid, *Pales pavida* (Meigen) in the last larval stage of the noctuid host *Mythimna separata* Walker (Lepidoptera: Noctuidae). While previous reports noted that larvae of *P*. *pavida* were found in the host's silk glands within one hour of egg ingestion, different results were obtained when at least six eggs were ingested by the host. No larvae were located in the silk glands, but several larvae were located in the testes. Since the host female ovaries at this larval stage are too small to accommodate parasitoid larvae, there is a possibility that the successful parasitisation rate is different between sexes of host larvae; that is that male hosts would be parasitised more frequently than female hosts. In this presentation differences in parasitisation based on the quantity of host resource is discussed.

Investigating the Diptera fauna beneath snow in areas with heavy snowfall in Japan

Takeyuki Nakamura

The Shirakami Research Center for Environmental Sciences, Hirosaki University, Bunkyo-cho 3, Hirosaki, Aomori 036-8561, Japan. craneflyheaven@ybb.ne.jp

Keywords: Flightless insects, subnivean zone, winter craneflies.

The northern part of the Japanese Archipelago along the Sea of Japan is one of the snowiest places on Earth and in some areas snowfalls exceeding 5 m are not uncommon. Although the external climate on snow changes drastically and is often too severe for winter insects, the surface of the ground beneath snow cover (subnivean zone) in Japanese forests is comparatively warm (+0～2°C), moist and stable throughout the winter. In a previous study, it was confirmed that the flightless cranefly, *Chionea* Dalman (Limoniidae) is active in the subnivean zone throughout the winter months in the Shirakami Mountains, Honshu, Japan. In the current study, the subnivean insect fauna of seven localities in Hokkaido and Honshu, Japan were investigated. In order to collect insects exclusively from subnivean environments, pitfall traps were used, comprising square vats (40 x 30 cm), filled with pure propylene-glycol and covered with thick plywood (90 x 90 cm). Seventy such traps were deployed on the ground in the seven localities at the beginning of winter, following the first covering of snow and these were excavated in the spring, before the snow had disappeared and the traps became exposed. Trapping results revealed, that aside from numerous Araneae, Collembola and Coleoptera, Diptera such as Chironomidae, Limoniidae, Phoridae, Sciaridae, Trichoceridae and Sphaeroceridae, were sampled beneath the snow, some being flightless with reduced wings. In this presentation, the diversity of subnivean Diptera is introduced and investigations of this peculiar insect fauna are described.

Poster

Expeditions of Russian zoologists to Central Africa (1912–1914) and resulting Diopsidae collections in the Zoological Institute, St Petersburg, Russia

Emilia P. Nartshuk

Zoological institute of Russian Academy of Sciences, Universitetskaya nab. 1. 199034, St Petersburg, Russia. chlorops@zin.ru

Keywords: Collection, East Africa, F. Eggers, St Petersburg, types.

Two Russian zoologists, V. Dogel and I. Sokolov from St Petersburg University, organised an expedition to British East Africa in 1914. Results were published in a dedicated volume in 1916, with F. Eggers publishing two papers on Diopsidae in the same volume. The first paper was devoted to the Diopsidae fauna, which included a list of species and descriptions of five new species, namely: *Diopsis finitima* Eggers, *Diasemopsis incerta* Eggers, *Dia*. *silvatica* Eggers, *Dia*. *varians* Eggers and *Dia. pulchella* Eggers; and the second paper examined the structure of the compound eyes of Diopsidae. Both papers were written both in Russian and English and Eggers later translated the morphological paper into German (published in 1925). Unfortunately, no material referred to by F. Eggers could be located in St Petersburg University. In 1925, F. Eggers published a further paper on African Diopsidae, based on material collected by M. Tróitzky in German East Africa in 1912. All specimens mentioned in that paper are stored in the collection of the Zoological Institute, St Petersburg. The Diopsidae collection includes type specimens of five new species and two subspecies, *i*.*e*., holotypes of *Diopsis nigricollis* Eggers (without the head) and *D*. *nigriceps* Eggers and syntypes of *D*. *acanthophthalma* Eggers, *D*. *conspicua* Eggers, *D*. *fumipennis* Westwood var. *fascifera* Eggers, *D*. *ichneumonea* L. var. *ichneumonella* Eggers and *D*. *melania* Eggers. Photographs resulting from the 1914 expedition are presented from the archive of S. Fokin (University of Pisa, Italy).

Stalk-eyed flies (Diopsidae) of Vietnam

Emilia P. Nartshuk

Zoological institute of Russian Academy of Sciences, Universitetskaya nab. 1. 199034 St. Petersburg, Russia. chlorops@zin.ru

Keywords: New records, Vietnam.

Stalk-eyed flies (Diopsidae) are mostly distributed in the tropics, with their greatest biodiversity in the Afrotropical and Oriental Regions. Only the single genus *Sphyracephala* Say with a few species occurs in the Holarctic. The Diopsidae fauna of Vietnam have never been studied and no species from Vietnam are listed in the Oriental Catalogue by G.C. Steyskal. Material is now available, collected during different years between 1963 and 2016 by the writer and other Russian entomologists (O.N. Kabakov, B.A. Korotyaev, A.V. Gorokhov, S.A. Belokobylsky and T.V. Galinskaya), in the following provinces: Son La, Ninh Binh, Hoa Binh, Thanh Hoa and Vinh Phuc in northern Vietnam; Gia Lai in central Vietnam and Dong Nai in the south. The following species are represented in the material: two specimens of *Diopsis chinica* Yang & Chen, described from China and collected in Hoa Binh and Ninh Binh Provinces; one specimen of *Diopsis* sp. n. from Dong Nai Province; *Cyrtodiopsis dalmanni* (Wiedemann) or a related species with prominent incrassate constrictions on the apex of the fore femora and low tubercles on the inner bases of the fore tibiae in males, collected in Dong Nai Provinces; *Cyrtodiopsis* aff. *white* (Curran), a new species of *Cyrtodiopsis* with asymmetrical fore legs; and two probable new species of the genus *Teleopsis*: *Teleopsis* sp. n. in the *boettcheri* species-group is the most numerous in Vinh Binh and Hoa Binh Provinces and *Teleopsis* sp. n. in the *motatrix* species-group is only represented by a single specimen from Dong Nai Province.

Current distribution of *Bactrocera latifrons* (Hendel) (Tephritidae) in different agro-ecological zones of Burundi

Liévin Ndayizeye* & (the late) Benoît Nzigidahera

Office Burundais pour la Protection de l'Environnement, Service de Recherche en Biodiversité, P.O. Box. 2757 Bujumbura, Burundi. *ndayizeyelievin@yahoo.com

Keywords: Host-plant, infestation rate, invasive species, rearing, *Solanum*.

The African Eggplant (*Solanum aethiopicum* L.) (Solanaceae) constitutes a basic food crop both in rural and urban areas of Burundi and thus serves as an important source of income for rural farmers. Recently, this crop was infested by *Bactrocera latifrons* (Hendel); an exotic fruit fly species of Asian origin, that was recorded in Africa for the first time in 2006 and was detected for the first time in Kirundo, northern Burundi in 2016. From July 2016 until April 2017, a survey was conducted at 19 sites in the five agro-ecological zones within the country, namely: the Imbo Plain, the western slope of the Congo-Nile Ridge, the Congo-Nile Ridge, the Central Plateaus and the Northeast Depressions. The objective was to map the geographical distribution of *B*. *latifrons* in Burundi and analyse the infestation rate and the level of destruction in African Eggplant production. Fruits of African Eggplant were collected at all sites and fruit flies reared from these samples. A total of 580 individuals of *B*. *latifrons* emerged from 2,156 fruits (total weight: 33.5 kg). Results have indicated that all agro-ecological regions are invaded by this species. The infestation rate varied between 15.13 and 27.33 flies/kg of fruit. There is no significant variation of infestation levels between the agro-ecological regions, but within regions the infestation rate varied significantly between sites. After first detection in 2016, *B*. *latifrons* now occurs throughout the country and poses a threat to neighbouring countries.

Taxonomy and distribution of *Proctacanthus* Macquart (Asilidae) and related genera of robber flies in North America

C. Riley Nelson

Department of Biology and M.L. Bean Museum, Brigham Young University, Provo, Utah 84602, U.S.A. rileynelson@byu.edu

Keywords: Assassin flies, biogeography, morphology, *Proctacanthus*, revision, robber flies, systematics.

The robber fly genus *Proctacanthus* Macquart, has historically been recognised as being composed of three partially overlapping groups: those with straight mouthparts (including the type species *P. philadelphicus* Macquart); those with broad boat-like mouthparts, which curve upward; and those with the terminal cross-section forming a T-shape. The group with T-shaped mouthparts has been given the name *Taurhynchus* Artigas & Papavero and the genus *Eccritosia* Schiner clearly overlaps with those with curved mouthparts. A preliminary analysis indicates that if *Eccritosia* and *Taurhynchus* are recognised as genera, then *Proctacanthus* is rendered paraphyletic. A summary is provided of the phylogenetic relationships among these groups/genera using morphological characters. An identification key is also provided to those species with straight mouthparts, numerous illustrations are provided and a summary is given of the Nearctic distributions of all North American species in the straight mouthparts group.

Bioassessment of fly family diversity using taxon effort relationships on sites with a continuum of grazing and erosion pressures in Mongolia

C. Riley Nelson[1]*, Tristan K. McKnight[2], Paul B. Frandsen[3] &
Rebecca A. Clement[4]

[1]Department of Biology and M.L. Bean Museum, Brigham Young University, Provo, Utah 84602, U.S.A. *rileynelson@byu.edu
[2]St. Lawrence University, Canton, U.S.A.
[3]Brigham Young University, Provo, U.S.A.
[4]The George Washington University, Washington D.C., U.S.A.

Keywords: Biodiversity, conservation, bioassessment, species effort analysis.

Sites near natural water sources were sampled in Mongolia between 2008 and 2011, to assess the diversity of families of flies, using both qualitative hand/net collecting methods and quantitative small yellow pan traps. A total of 49 families of flies were sampled with yellow pans; only three more families were added in thousands of hours of hand collecting. A standardised recording form was used to assess vertebrate grazing pressure and shoreline erosion, classifying each site into one of five grazing categories, ranging from "no grazing evident" to "heavy grazing evident." A total of 2,334 yellow pan traps were deployed at 132 sites and the 17,348 flies sampled were preserved in 70% ethanol. Taxon effort analyses was performed for each of the five grazing categories and the only significant difference found was between the highest grazing intensity and each of the categories with lower grazing. In general, each category contained fly families that peaked in abundance at that grazing intensity. Interestingly, the "no grazing evident" category had the greatest variation in the number of families collected. Carefully documenting changes in a few guilds of fly families at different grazing levels is beneficial for understanding human effects on diversity mediated by grazing domesticated livestock.

Fossil hoverflies (Syrphidae) – possibilities and perspectives

Valentin Nidergas[1], Jiří Hadrava[2]*, Klára Daňková[2], André Nel[1] &
Jakub Prokop[2]

[1]Institut Systématique Evolution Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, 57 rue Cuvier, CP 50, F-75005 Paris, France.
[2]Charles University, Prague, Czech Republic. *hadravajirka@seznam.cz

Keywords: Ecology, evolution, fossils, palaeoentomology.

The description and classification of fossil insects is becoming increasingly important in order to calibrate phylogenetic trees and to understand the palaeoecological consequences of evolutionary history. With only *ca* 100 described fossil species, as opposed to *ca* 7,000 extant species, which is disproportionately low, hoverflies (Syrphidae) are poorly represented in the fossil record, representing a major limitation in interpreting the evolutionary history of the family. Furthermore, many fossil hoverflies in museums and private collections remain undescribed or are unknown to specialists. To contribute to the study of this topic the following areas were explored: 1) evolution of pollination specificities in hoverflies (*e.g.*, a functional morphology approach); 2) evolution of Batesian mimicry with Hymenoptera (analysing the colouration patterns and body shape); and 3) include fossil species in morphological matrices for phylogenetical purposes and calibration of trees. Some preliminary results are presented here and the suitability of the fossil material for evolutionary and ecological purposes is discussed. Due to high diversity of larval strategies in hoverflies, these may also assist in further palaeoenvironmental studies.

Poster

Diptera occurring on pig carcasses in two different habitats within close range in Thuringia, Germany

Senta Niederegger*, Eric Anton & Gita Mall

Department of Forensic Entomology, Institute of Legal Medicine, University Hospital, Am Klinikum 1, 07747 Jena, Germany. *senta.niederegger@med.uni-jena.de

Keywords: Comparative, diversity, forensic entomology, forest, habitat.

Pig carcasses, often used in forensic entomology as a proxy for human bodies, were used to analyse the population of forensically important Diptera and other insects in two distinctly different, but relatively proximate habitats, a deciduous forest near a small village and a former military training ground in an agricultural area near a city. The linear distance between the habitats was 8.5 km. Carcasses were placed within cages during one full year, although at different years in each habitat. Passive (air eclector, pitfall and water) and active (scoop net) collecting techniques were employed to capture carcass-associated and (as a control) non-carcass-associated Diptera. Results indicated similarities in dipteran population in the two habitats, but also considerable and distinct differences. Not surprisingly, dipteran diversity is not primarily based on the substrate presented. Even though total diversity was higher in the forest habitat, a number of species were collected exclusively in the military area, particularly Sarcophagidae. Water traps proved to be the method of choice to verify dipterans. Especially uncommon or otherwise infrequently detected species could be collected regularly using water traps. Multiple species previously not described for Thuringia, *e.g.*, *Chrysomya albiceps* (Wiedemann), could be found with this experimental protocol. These experiments confirm the benefit of long-term monitoring in diverse, preferentially proximate habitats. The use of a variety of collecting techniques and optionally different substrates proved appropriate for establishing detailed and comprehensive regional species lists, not only for forensic applications.

Muscle attachment sites in Diptera larvae – computer-assisted imaging and analysis

Senta Niederegger[1]*, Klaus-Peter Döge[2] & Gita Mall[1]

[1]Department of Forensic Entomology, Institute of Legal Medicine, University Hospital, Am Klinikum 1, 07747 Jena, Germany. *senta.niederegger@med.uni-jena.de
[2]University of Applied Sciences, Jena, Germany.

Keywords: Genus pattern, image processing, larvae, species determination.

Muscle attachment sites (MAS) have proven to be a helpful tool in species determination of dipteran larvae. The MAS form distinctive patterns on the inside of the outer cuticula of maggots. After removing the cuticula from the body and staining with a suitable dye, the patterns can be photographed using a microscope with a camera. The patterns then need to be compared to known patterns in order to determine the species of the maggot analysed. To accelerate species determination and minimise user bias when employing this method, a software tool was developed. The tool extracts the important parts of the patterns and compares them to patterns within a database using statistical methods. Using filters on digital microscope pictures and cross-correlating these within their frequency range allows for calculation of correlation coefficients. Such pattern recognition permits automatic comparison of one larva with a database of MAS reference patterns in order to find the correct or most likely species. Comparison patterns for the database are also generated using the same tool. Biological aspects were further added into the performance for reduction of processing time and effort. This presentation explains the method as well as the computerised approach and introduces the new tool. Contributors of fly species are requested for the expansion of the database and international cooperation is encouraged.

Potential of specimen digitisation in conservation – a case study of Tabanidae in the National Museums of Kenya

Laban N. Njoroge* & Josiah C. Achieng

Section of Invertebrates Zoology, National Museums of Kenya, P.O. Box 40658-00100, Nairobi, Kenya. *Lnjoroge@museums.or.ke

Keywords: Conservation, horse flies, Kenya, specimen digitisation.

Natural history collections in Kenya, including its extensive insect collections, were begun in the late 19th century. Until recently, much of these data have been analogue in specimen labels and therefore inaccessible to researchers. An elaborate process to digitise these collections is underway. The entire horse fly collection is digitised, comprising 1,363 specimens, of which 852 representing 63% originates from Kenya, with the remainder being from other African countries. A checklist of Kenyan species of horse flies, that includes a new country record for *Tabanus sericiventris* Loew, has been developed. Distribution records of horse flies in Kenya have been compiled and mapped, prioritising those species of medical and veterinary importance. This work also identifies past sampling biases for horse flies in Kenya and possibly that of other insect groups. The potential applications of digitised records in conservation efforts and policy development are discussed and recommendations for future dipteran surveys in Kenya are suggested.

Ultraconserved elements in a Diptera-wide phylogeny

Katherine Noble[1]*, Keith Bayless[2], Michael Branstetter[3], Lisa Gonzalez[4],
Brian V. Brown[4] & Donald Feener[1]

[1]Department of Biology, University of Utah, 257 S 1400 E, 84112, Salt Lake City, UT, U.S.A.
*Kgm.noble@gmail.com
[2]CSIRO Australian National Insect Collection, Canberra, Australia.
[3]USDA-ARS, Logan, U.S.A.
[4]Natural History Museum of Los Angeles, Los Angeles, U.S.A.

Keywords: Phylogenomics, sequence capture, target enrichment.

Ultraconserved elements (UCEs) and their variable flanking regions are genomic markers that provide phylogenetic information for shallow and deep evolutionary timescales. A total of 2,834 UCEs were identified by aligning seven Diptera genomes and designed baits for sequencing these loci and their flanking regions. Using both *in silico* and *in vitro* representatives from major lineages of fly evolution, an average of 858 loci across taxa were recovered. This study explores the utility of UCEs for phylogenetic reconstruction within dipteran families and at the order-wide level.

Ultraconserved elements for a phylogeny of the Phoridae

Katherine Noble[1]*, John M. Hash[2], Brian V. Brown[3] & Donald Feener[1]

[1]Department of Biology, University of Utah, 257 S 1400 E, 84112, Salt Lake City, UT, U.S.A.
*Kgm.noble@gmail.com
[2]Smithsonian Institution, Washington D.C., U.S.A.
[3]Natural History Museum of Los Angeles, Los Angeles, U.S.A.

Keywords: Parasitoid, phylogenomics, sequence capture, target enrichment.

Ultraconserved elements (UCEs) and their variable flanking regions are genomic markers that provide phylogenetic information at shallow and deep evolutionary timescales. This study explores the utility of UCEs for estimating phylogenetic relationships in the large and diverse family Phoridae. A Diptera-wide UCE bait set recovered an average of 800 UCE loci across 124 individuals and these data are added to the growing information about evolutionary relationships in this family.

The *Anastrepha* Farm Bill project – development of more rapid and reliable diagnostic tools for all life stages of *Anastrepha* Schiner (Tephritidae)

Allen L. Norrbom[1]*, Raul Ruiz-Arce[2], Gary J. Steck[3], Erick J. Rodriguez[4], Bruce D. Sutton[5], Brian M. Wiegmann[6], Marc Branham[4], Norma Nolazco[7], Alies Muller[8], Aneel Gangadin[9], Clifford Keil[10], Anabel Padilla[10] & Marcoandre Savaris[11]

[1]Systematic Entomology Laboratory, MRC-168, P.O. Box 37012, National Museum of Natural History, Washington D.C. 200137012, U.S.A. *Allen.Norrbom@ars.usda.gov
[2]Mission Laboratory, USDA-APHIS-PPQ, Edinburg, U.S.A.
[3]Florida Department of Agriculture and Consumer Services, Gainesville, U.S.A.
[4]University of Florida, Gainesville, U.S.A.
[5]Smithsonian Institution, Washington D.C., U.S.A.
[6]North Carolina State University, Raleigh, U.S.A.
[7]Servicio Nacional de Sanidad Agraria, Lima, Peru.
[8]Ministry of Agriculture, Paramaribo, Suriname (retired).
[9]National Zoological Collection of Suriname, Paramaribo, Suriname.
[10]Pontificia Universidad Católica del Ecuador, Quito, Ecuador.
[11]Universidade de São Paulo, Piracicaba, Brazil.

Keywords: Diagnostics, fruit flies, phylogeny, taxonomy.

Anastrepha Schiner (Tephritidae) is the largest and most economically important genus in the American tropics and subtropics. It includes major pests of numerous commercial and subsistence fruits, including citrus, mango, guava and peach, as well as numerous species considered minor or potential pests. Through Farm Bill projects in the past few years new morphological and molecular diagnostic tools have been developed, including online adult and larval identification systems and investigating the potential of various DNA regions for diagnostic and phylogenetic analysis. Because the availability of fresh samples has been an impediment to progress in *Anastrepha* taxonomy, emphasis has been placed on the collection of samples from throughout the geographical range of the genus, particularly in previously poorly studied areas (Bolivia, Ecuador, Peru and Suriname). More than 10,000 specimens of more than 100 species have been collected. The project has also resulted in the discovery of new species, host-plant relationships and distribution records.

The state of Nearctic Tachinidae taxonomy as revealed by a single Malaise trap, the Canadian National Collection of Insects and DNA barcoding

James E. O’Hara

Canadian National Collection of Insects, Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, Canada. james.ohara@canada.ca

Keywords: BOLD, DNA barcoding, Malaise trap, Nearctic, survey, Tachinidae.

A survey of Tachinidae was conducted on the edge of Ottawa, Canada, using a single 6-metre, Gressitt and Gressitt-style Malaise trap. The trap was located next to a narrow (200 m) strip of woodland separating urban Ottawa from the agricultural fields of the Ottawa Greenbelt. Approximately 3,000 tachinid specimens were captured, pinned, labelled and databased. Preliminary identifications were performed using the holdings of the Canadian National Collection (CNC). These identifications were refined by two rounds of DNA barcoding of survey and CNC material and further morphological study. The results revealed an unexpectedly high diversity of Tachinidae: over 100 genera (about 30% of all genera known from the Nearctic Region) and over 200 species (about 50% of all species known from the province of Ontario). This is the highest diversity of Tachinidae known from a single Malaise trap placed anywhere in the Nearctic Region. The barcoding of over 600 specimens from the survey and over 2,000 CNC specimens provided much needed data for accurate sorting of specimens to named species, for recognition and resolution of species complexes and for detection of new species. The majority of genera recorded during the survey contain difficult and unresolved species complexes and this generalisation applies equally well to the entire Nearctic tachinid fauna. Taxonomic revisions of these genera may be years away, but in the interim an inventory of DNA barcodes in the Barcode of Life Data System (BOLD) based on reliably determined specimens can provide much needed assistance with the identification of Nearctic Tachinidae.

Bryophytes facilitate outcrossing of *Mitella* (Saxifragaceae) by functioning as larval food for pollinating fungus gnats (Mycetophilidae)

Yudai Okuyama[1], Tomoko Okamoto[2], Jostein Kjærandsen[3]* & Makoto Kato[4]

[1]Tsukuba Botanical Garden, National Museum of Nature and Science, Amakubo 4-1-1, Tsukuba 305-0005 Japan.
[2]Faculty of Applied Biological Sciences, Gifu University, Japan.
[3]Tromsø University Museum, UiT – The Arctic University of Norway, Tromsø, Norway.
*jostein.kjarandsen@uit.no
[4]Kyoto University, Kyoto, Japan.

Keywords: *Boletina*, bryophytes, DNA barcoding, ecology, *Gnoriste*, pollination biology.

Diptera rank among the largest groups of insects acting as pollinators. They have, in some cases, specialised flower-feeding habits, thereby being indispensable as pollinators in a wide range of plant communities, especially where other pollinators are less abundant. Fungus gnats (Mycetophilidae), act as principal pollinators for some plant species in temperate forests. With a few exceptions, they are regarded as obligate fungal feeders as larvae, yet the larval habitats of a large proportion of species remains unknown. This study chronicles a previously unrecognised tripartite interaction, between the plant genus *Mitella* and its allies (Saxifragaceae), their specialised pollinating fungus gnats (*Boletina* Staeger and *Gnoriste* Meigen) and mosses and liverworts (bryophytes) that host the specialised pollinator larvae. Rearing and DNA barcoding confirms some 100 year old observations of the larval habits for these genera, which have been anecdotally repeated in the literature. A novel facilitation mechanism by bryophytes for outcrossing of flowering plants is also proposed, where the pollination success of *Mitella* plants is supported by co-occurring bryophytes, mediated through their pollinators. Such specialised plant/pollinator interactions have evolved multiple times in both Pacific north-western America and East Asia. Since species of *Boletina* and *Gnoriste* represent diverse and abundant fungus gnats in the entire Holarctic Realm, especially in subarctic forest floors and along banks of Arctic and mountain streams with riparian vegetation, these findings raise the possibility that such tripartite interactions of plants, pollinators and their host bryophytes are widespread across temperate to arctic riparian environments.

Poster

X-ray microtomography (micro-CT) of male terminalia sclerites and muscles of *Nothybus kuznetsovorum* Galinskaya & Shatalkin (Nothybidae) and *Cothornobata* Czerny (Micropezidae)

Olga G. Ovtshinnikova[1]*, Dina Gafurova[2] & Tatiana V. Galinskaya[2]

[1]Zoological Institute, Russian Academy of Sciences, Universitetskaya nab. 1, St Petersburg 199034, Russia. *brach@zin.ru
[2]Lomonosov Moscow State University, Moscow, Russia.

Keywords: *Cothornobata*, morphology, musculature, *Neria*, sclerites, terminalia.

Since the results of the study of the male terminalia in *Nothybus kuznetsovorum* Galinskaya & Shatalkin using micro-CT coincides entirely with the results of manual dissection, it is concluded that the method of manual anatomy has not lost its significance. However, micro-CT takes considerably more time than manual anatomy. The undoubted advantage of micro-CT is its higher accuracy and the fact that only one specimen is required for the study, while manual anatomy usually requires 4–5 specimens. A comparative analysis of *Neria commutata* (Czerny) (Neriidae) and *Cothornobata* Czerny (Micropezidae) indicates that an increase in the flexion in the terminalia of males and the displacement of syntergosternite 7 to the ventral side in *Cothornobata* caused the disappearance of the right muscles of tergites 6 and 7. In addition, this increase in flexion apparently led to the fusion of the pregenital hypandrial muscles into a single bundle. One pair of sternite 5 muscles goes on to moving the second segment of the forcipate appendages of sternite 5.

Musculature of the male abdominal segments and terminalia of Phaoniinae and Muscinae (Muscidae)

Olga G. Ovtshinnikova[1]*, Tatiana V. Galinskaya[2] & Vera S. Sorokina[3]

[1]Zoological Institute of Russian Academy of Sciences, Universitetskaya nab. 1, St Petersburg 199034 Russia. *brach@zin.ru
[2]Lomonosov Moscow State University, Moscow, Russia.
[3]Institute of Systematics and Ecology of Animals of Russian Academy of Sciences, Novosibirsk, Russia.

Keywords: *Helina*, *Musca*, muscles, *Phaonia*, *Pyrellia*, sclerites.

Sclerites and musculature of the abdominal and pregenital segments and genitalia of males were studied in *Helina luteisquama* (Zetterstedt), *H*. *bohemani* (Ringdahl), *Phaonia lugubris* (Meigen), *Ph*. *hybrida* (Schnabl) and *Ph*. *meigeni* Pont (Muscidae: Phaoniinae) and in *Musca autumnalis* De Geer and *Pyrellia rapax* (Harris) (Muscidae: Muscinae). Musculature of these species was compared to that in *M*. *domestica* L. (Muscidae) and *Scathophaga stercoraria* (L.) (Scathophagidae), previously investigated by O.G. Ovtshinnikova. The homology of abdominal and pregenital sclerites were traced within the subfamilies Muscinae and Phaoniinae, based on the points of muscle attachment. This revealed reduction processes in the pregenital complex of sclerites and muscles in Muscinae as compared to Phaoniinae and further revealed reduction processes in the hypandrial complex of sclerites and muscles in *Musca* as compared with *Py*. *rapax*; in Muscinae as compared with Phaoniinae; and in Muscidae as compared with *Scathophaga stercoraria* (Scathophagidae).

Diptera diversity in deciduous forests of Canton Ticino, southern Switzerland

Lucia Pollini Paltrinieri

Museo cantonale di storia naturale, Viale C. Cattaneo 4, 6900 Lugano, Switzerland.
lucia.pollini@ti.ch

Keywords: Biodiversity survey, forest, sampling techniques, Switzerland.

Forests cover over 50% of the surface of the Canton of Ticino, located in the south of the Swiss Alps. Despite this, very little is known about their biodiversity, particularly in respect to Diptera. The Cantonal Museum of Natural History was commissioned to undertake a broad study of forests near Locarno. Six entomological sampling methods were employed to assess and compare time and costs during a full year (July 2015 to July 2016). Three stations were surveyed in a *Querco-castagnetum* forest using Malaise traps, Aerial Malaise traps (SLAM trap) and three slightly different attractant traps (transparent with wine, transparent with beer and yellow with wine). Eighteen taxonomic groups were sorted from the samples and sent to specialists for identification; Hymenoptera and Diptera were identified to the family level. Over 103,000 Diptera individuals were processed, representing 64 families, 25 of which (54% of total), are identified to date, representing 119 species. Thus far, the faunistic results include: one yet undescribed species of Periscelididae, seven species new to Switzerland and seven rare species or species recorded for the first time from Ticino. The sampling efficiency of the different methods employed has also been compared. Although the attractant traps were the most efficient (80% of specimens), both methods (interception and attractant) are complementary and quantitatively equally efficient in terms of the sampled species diversity. Data analysis allowed better calibration of catch effort and provided a more effective sampling plan for the surveys carried out in 2018.

The bacterium *Wolbachia* and the Mediterranean fruit fly (Tephritidae) – a multidimensional symbiosis

Nikos T. Papadopoulos & George Kyritsis

Laboratory of Entomology and Agricultural Zoology, Department of Agriculture, Crop Production and Rural Environment, University of Thessaly, Fytokou Street, 38446 Volos, Greece. nikopap@uth.gr

Keywords: Area wide IPM, *Bactrocera*, *Ceratitis*, fruit flies, incompatible insect technique, Medfly, sterile insect technique.

The endosymbiont bacterium *Wolbachia pipientis* besides inducing cytoplasmic incompatibility, feminisation and parthenogenesis, may elicit an array of additional effects on the physiology and behaviour of its arthropod hosts that may dramatically affect fitness. Although widespread in arthropods, it has not been found in wild populations of important insect pests, such as the Medfly, *Ceratitis capitata* (Wiedemann) and the Olive fly, *Bactrocera oleae* (Rossi). Trans-infection of laboratory adapted populations of both Medfly and the Olive fly has been considered as an important step towards establishing incompatible insect technique (IIT) programmes against these devastating pests. Trans-infected lines may serve as an important model system to address a list of questions regarding the effects of *Wolbachia pipientis* on its hosts. Focusing on Medfly, this presentation provides an overview of results obtained in the laboratory of Entomology and Agricultural Zoology at the University of Thessaly, Greece, regarding effects of *Wolbachia symbiosis* on the life history and behavioral traits. In a nutshell, these results demonstrate that effects of *Wolbachia* depend on both the Medfly genetic background and the strains of the bacterium considered. *Wolbachia* infection generates a list of phenotypes as far as the mating behaviour of both male and female flies is concerned. Considering all acquired results and recent efforts to establish a small-scale mass rearing of the *Wolbachia* infected Genetic Sexing Strain Vienna 8 Medfly strain the possible application of IIT against the Medfly is discussed.

A new species of *Apenthecia* Tsacas and new records of Drosophilidae from Kenya

Mehrdad Parchami-Araghi

Insect Taxonomy Research Department, Iranian Research Institute of Plant Protection (IRIPP), Agricultural Research, Education and Extension Organization (AREEO), Tehran 19395–1454, Iran. maraghi20@yahoo.ca

Keywords: Afrotropical Region, *Apenthecia*, Kenya, *Leucophenga*, Steganinae, taxonomy, *Zaprionus*.

In the course of examining the Drosophilidae collection of the Canadian National Collection of Insects (CNCI), Ottawa, Canada, a single male specimen of the genus *Apenthecia* Tsacas (subfamily Steganinae), was discovered and was recognised as an undescribed species. The specimen originates from "Kenya, Nyanza Province, Nyamarandi Village, 20.vi–4.vii.2006 (CNC333873)" and further represents the first record for the genus *Apenthecia* for Kenya. The entirely Old World genus *Apenthecia*, comprises 15 described species and was erected by L. Tsacas in 1983, to include three representatives of the genera *Amiota* Loew (2 species) and *Erima* Kertész (1), together with five newly described species. As a result, *Erima* was re-defined as a monotypic Australasian genus. *Apenthecia* is divided into two subgenera, of which the endemic Afrotropical subgenus *Apenthecia sensu stricto* (with 10 species) is distinguished from the primarily Oriental subgenus *A*. (*Parapenthecia* Toda & Peng) (5 species) in having a single scale-like posterior fronto-orbital seta, as opposed to two in *A*. (*Parapenthecia*). The new species superficially resembles the South African species *A*. *argentata* Tsacas, but clearly differs from it in the shape of the surstylus and distiphallus. The steganines *Leucophenga goodi* Kahl and *L*. *cuthbertsoni* Malloch, as well as the drosophilines *Zaprionus neglectus* Collart and *Z*. *arduus* Collart are newly recorded from Kenya.

Poster

Further contribution to the vinegar fly (Drosophilidae) fauna of the New World

Mehrdad Parchami-Araghi

Insect Taxonomy Research Department, Iranian Research Institute of Plant Protection (IRIPP), Agricultural Research, Education and Extension Organization (AREEO), Tehran 19395–1454, Iran. maraghi20@yahoo.ca

Keywords: Drosophilinae, *Lordiphosa*, Nearctic Region, New World, North America, *Stegana*, Steganinae.

A new species of the subfamily Steganinae is recognised from the U.S.A. (New Mexico) and found to be the second representative of the subgenus *Stegana* Meigen *sensu stricto*, besides *S*. *vittata* (Coquillett), in the New World. The new species is defined by the black palpus, pale yellow postpedicel and the spectacularly sclerotised distiphallus. The species *Stegana* (*Steganina*) *wheeleri* Lštovka & Mácais newly reported from Canada (British Columbia); it was previously known only from Tennessee in the U.S.A. The species *Lordiphosa hexasticha* (Papp), in the subfamily Drosophilinae, is recorded here for the first time from the New World. The species is otherwise distributed in Finland, Germany, Hungary, Romania and Russia (Siberia) and was collected in the Alberta Province of Canada. The genus *Lordiphosa* Basden comprises 61 species, of which only *L*. *basdeni* (Wheeler) is known from the New World, reportedly in Canada and the U.S.A. (Michigan and Ohio). *Lordiphosa hexasticha* is distinguished from the rest of the species in the genus, in having six rows of acrostichal setae (usually four rows occur in other species) and by the highly reduced cerci, as well as the characteristically parallel margins of the epandrium and the shape of the surstyli. The biology of the *Lordiphosa* species is poorly known, although their larvae are believed to develop in decaying plant material. All the specimens used in this study are housed in the Canadian National Collection of Insects (CNCI), Ottawa, Canada.

Poster

Recent findings in the Iranian Drosophilidae fauna, with discovery of two new species of *Gitona* Meigen

Mehrdad Parchami-Araghi[1]*, Ebrahim Gilasian[1], Farzaneh Basavand[2],
Hosnieh Mousavi[3], Ali-Akbar Keyhanian[4] & Abbas Mohammadi-Khorramabadi[5]

[1]Insect Taxonomy Research Department, Iranian Research Institute of Plant Protection (IRIPP), Agricultural Research, Education and Extension Organization (AREEO), Tehran 19395–1454, Iran.
*maraghi20@yahoo.ca
[2]Agricultural Research and Natural Resources Research Center, Bampour, Iran.
[3]Agricultural Research Station, Chabahar, Iran.
[4]Iranian Research Institute of Plant Protection, Tehran, Iran.
[5]Shiraz University, Shiraz, Iran.

Keywords: Drosophilinae, *Gitona*, Iran, Middle East, Palaearctic Region, *Paracacoxenus*, Steganinae.

Over the past decade, an extensive collection of Iranian Diptera has been developed, by deploying Malaise traps throughout the seasons in the wetlands and other natural habitats of Iran. In addition, hand-made traps, baited with rotting fruit and vinegar were also deployed, which led to the capture of a large number of saprophagous flies of various families. This sampling resulted in the discovery of the invasive alien pests: African fig fly, *Zaprionus indianus* Gupta and Spotted wing Drosophila, *Drosophila suzukii* (Matsumura) (Drosophilidae), both of which are recorded from Iran for the first time. Unlike most steganines, representatives of the subfamily Drosophilinae were found to be the most abundant visitors to baited traps. At relatively low elevations throughout the south-eastern border region of Baluchestan, two steganine species were sampled, one of which represented an undescribed species of *Gitona* Meigen, sampled in the environs of Bampour (27°11'56"N, 60°29'52"E; 525 m), while the other species, *Paracacoxenus perspicax* (Knab) was sampled in the Bahu-kalat Region, located farther eastwards, towards Pakistan's border (25°42'04.8"N, 61°25'25.5"E; 23 m). A second undescribed species of *Gitona* was sampled at Haftad-Gholleh Protected Area, farther north and at a higher elevation (34°07'05.3"N, 50°16'25.3"E; 2219 m). External morphology and characters of the male terminalia indicate both *Gitona* species to be new to science.

Is this the end of Syrphoidea? – Flower flies (Syrphidae) and big-headed flies (Pipunculidae) are not sister-groups

Thomas Pauli[1, 2], Trevor O. Burt[2]*, Keith M. Bayless[3, 4], Karen Meusemann[1, 2, 4], Brian M. Wiegmann[3], Alexander Donath[2], Lars Podsiadlowski[5], Christoph Mayer[2], Alexey Kozlov[6], Alexandros Vasilikopoulos[2], David K. Yeates[4], Shanlin Liu[7, 8, 9], Xin Zhou[10, 11], Bernhard Misof[2], Ralph S. Peters[2] & Ximo Mengual[2]

[1]University of Freiburg, Freiburg, Germany.
[2]Zoologisches Forschungsmuseum Alexander Koenig, Leibniz Institut für Biodiversität der Tiere, Adenauerallee 160, D-53113 Bonn, Germany. *trevburt@gmail.com
[3]North Carolina State University, Raleigh, U.S.A.
[4]Australian National Insect Collection, Canberra, Australia.
[5]University of Bonn, Bonn, Germany.
[6]Heidelberg Institute for Theoretical Studies, Heidelberg, Germany.
[7]China National GeneBank-Shenzhen, Shenzhen, China.
[8]BGI-Shenzhen, Shenzhen China.
[9]University of Copenhagen, Copenhagen, Denmark.
[10]Beijing Advanced Innovation Center for Food Nutrition and Human Health, Beijing, China.
[11]China Agricultural University, Beijing, China.

Keywords: Hoverflies, lower Cyclorrhapha, “Aschiza”, molecular phylogeny, transcriptome, 1KITE, new-generation sequencing.

Syrphoidea has long been suggested to be a superfamily based on morphological characters, containing the families Pipunculidae and Syrphidae. Recent molecular phylogenies and new interpretation of some morphological characters raised some questions about the validity of this clade. Using transcriptomic data from the 1KITE Project, the phylogenetic relationships between the lower Cyclorrhapha and Schizophora were explored. Nineteen taxa were included representing the families Lauxaniidae, Lonchopteridae, Phoridae, Pipunculidae, Platypezidae, Platystomatidae, Sepsidae, Syrphidae and Ulidiidae, with Dolichopodidae as out-group. A completely resolved tree with maximal support for all nodes was produced from 678,763 amino acid positions using maximum likelihood as optimality criterion. Eumuscomorpha was recovered as monophyletic and resolved as the sister-group of Platypezoidea. Syrphoidea was not recovered and Pipunculidae was resolved as the sister-group of Schizophora. Within Syrphidae, Pipizinae and Syrphinae were resolved as sister-groups, while Eristalinae were recovered as paraphyletic. Within the Syrphinae the tribe Bacchini was not supported as monophyletic. These results indicate that Pipunculidae and Syrphidae are not sister-groups, thus the superfamily Syrphoidea as currently defined is not supported by the molecular dataset.

Seasonality of Diptera families throughout the year in the Campos de Palmas wildlife refuge, Paraná, Brazil

Adriana C. Pereira[1]*, Diaine Cortese[1], Laércio Peixoto Amaral-Neto[1] & Luciane Marinoni[2]

[1]Instituto Federal do Paraná, PRT 280, Trevo CODAPAR, Palmas, PR, Brazil CEP 85555-000. *adriana.couto@ifpr.edu.br
[2]Universidade Federal do Paraná, Curitiba, Brazil.

Keywords: Abundance, conservation, diversity, seasonality.

Faunal surveys are essential, especially in the Neotropical Region, where only a small percentage of the diversity of insects is known. This study aimed to list the families of Diptera present in the Conservation Unit Campos de Palmas wildlife refuge, evaluating diversity, abundance and niche overlap, thus offering support for future taxonomic studies. Seasonal sampling was undertaken between December 2013 and September 2014, using Malaise traps in three different vegetation fragments (open field, border, and forest). These fragments are located in a Conservation Unit situated in one of the last remaining grassland areas in the Southern Region of the state of Paraná, Brazil. All traps were exposed in pairs in each fragment for the period of a week. Sampling resulted in 6,485 specimens representing 52 families of Diptera. The most abundant families were Sciaridae (n = 1874; 28.9%), Phoridae (n =565; 8,7%), Cecidomyiidae (n = 420; 6.5%) and Chironomidae (n = 411; 6.3%). There was variation in the distribution of Diptera specimens in different seasons and areas. Greatest abundance was recorded in the spring months (September–December), while species richness peaked in the summer months (December–March). For Simpson's index, winter (June–September) was the most diverse season, while for Shannon's index it was summer. In respect to sampling localities, the open field site was more diverse for both indices. In this survey, Diptera exhibited extensive niche overlap. The Conservation Unit is home to a diversity of Diptera and it is necessary to strengthen conservation measures in such environments.

Families of Diptera in Palmas highland grasslands of Brazil and the importance of comprehensive studies

Adriana C. Pereira[1]*, Diaine Cortese[1] & Luciane Marinoni[2]

[1]Instituto Federal do Paraná, PRT 280, Trevo CODAPAR, Palmas, PR, Brazil. *adriana.couto@ifpr.edu.br
[2]Universidade Federal do Paraná, Curitiba, Brazil.

Keywords: Brazil, highland grasslands, Neotropical Region, Palmas, survey.

A comprehensive monitoring survey was conducted using Malaise traps in a Conservation Unit located in the Palmas Highland Grasslands, southern Brazil. The region is considered in the literature to be a key area for the conservation of Brazil's southern highland grasslands. Two weekly collections were undertaken in four sites with a different floristic composition: a fragment of indigenous forest (area A); a forest margin (area B); a native grassland field (area C); and a forest site with *Pinus taeda* L. removed (area P). The total Diptera yield during the study comprised 92,864 specimens, sampled in 400 traps, which were identified to family level. To date, specimens resulting from 94 traps have been processed and identified (23.5%), comprising 62 families. Considering there are currently 96 Diptera families recorded for Brazil, sampling to date represents 64.5% of these. The most abundant families sampled were Cecidomyiidae, Phoridae and Sciaridae, with over 1,000 individuals each. The high number of families collected reflects the importance of comprehensive studies of this kind. Sixteen families were represented by less than 10 specimens each, including the Acroceridae, Heleomyzidae and Tanypezidae. Because of the low frequency of these families in the general population, a less comprehensive study focusing exclusively on these would be impaired. Thus, the importance of carrying out family-centred studies is emphasised because, although they are not appropriate for some ecological inferences, they are the best means to obtain records for infrequent or less abundant groups.

Is it a match? What are the evolutionary relationships between ant-decapitating flies (Phoridae) and their hosts?

Thalles Platiny Lavinscky Pereira[1]*, Silvio Shigueo Nihei[1] & Brian V. Brown[2]

[1]Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, Rua do Matão, Travessa 14, No. 101, 05508-900, São Paulo, SP, Brazil. *thallesplp@gmail.com
[2]Entomology Section, Natural History Museum of Los Angeles County, 900 Exposition Boulevard, Los Angeles, CA 90007, U.S.A.

Keywords: *Cremersia*, *Eibesfeldtphora*, Formicidae, *Neodohrniphora*.

The first phylogenetic hypothesis proposed indicated that *Cremersia* Schmitz and *Neodohrniphora* Malloch as sister genera. *Neodohrniphora* was classified in three subgenera: *N*. (*Eibesfeldtphora* Disney), *N*. (*Neodohrniphora* Malloch) and *N*. (*Wallerphora* Disney). More recently, following a morphological analysis, further studies raised the subgenus *Eibesfeldtphora* to genus rank and synonymised the genera *Cremersia* and *Neodohrniphora*, justifying the separation by differences in the ovipositor of *Cremersia* and *Eibesfeldtphora*. The aim of this study was to revise the genera *Cremersia* and *Neodohrniphora* and reconstruct the phylogenetic relationships among *Cremersia*, *Eibesfeldtphora* and *Neodohrniphora*, based on morphological data. The intention was also to infer evolutionary associations between Phoridae and their ant hosts, using a historical perspective by means of a reconciliation analysis. As a result, four names of *Neodohrniphora* are considered as valid names and seven new species are described; for *Cremersia*, 17 names are considered as valid and nine new species are described. The ovipositor structures provided the diagnostic characters for the separation of species and genera. The morphological analyses recovered *Cremersia*, *Eibesfeldtphora* and *Neodohrniphora* as monophyletic and separate lineages that are here recognise as genera. Considering their hosts, each phorid genus is restricted to an ant genus, demonstrating “a match”. *Neodohrniphora* are parasitoids of *Acromyrmex* Mayr, *Eibesfeldtphora* parasitoids of *Atta* F. and *Cremersia* parasitoids of army ants: *Labidus* Jurine, *Neivamyrmex* Borgmeier and *Nomamyrmex* Borgmeier (Formicidae). These results indicate similarities between the evolutionary histories of the studied genera and their ant hosts. Despite this, further studies with all Phoridae parasitoids are important to better elucidate coevolution.

The KwaZulu-Natal Museum's contributions to the PINDIP project

Tricia Pillay[1]*, John M. Midgley[1, 2] & Kurt Jordeans[3]

[1]KwaZulu-Natal Museum, Private Bag 9070, Pietermaritzburg 3200, South Africa. *tpillay@nmsa.org.za
[2]Department of Zoology and Entomology, Rhodes University, Grahamstown, South Africa.
[3]Royal Museum for Central Africa, Tervuren, Belgium.

Keywords: Afrotropics, biodiversity, museum collections, plant-pollinator networks, South Africa.

The KwaZulu-Natal Museum (KZN Museum) is a partner in the "Pollinator Information Network for Two-Winged Insects" (PINDIP). One of the aims of the PINDIP project is to increase the numbers of identified specimens that can be easily accessed for use in research. This presentation showcases the contributions of the KZN Museum to the PINDIP project. The KZN Museum has over 220,000 identified Diptera specimens with representatives in each of the seven most important Diptera families involved in pollination. These are the Bombyliidae, Calliphoridae, Mythicomyiidae, Nemestrinidae, Rhiniidae, Syrphidae and pangonine Tabanidae. The relevant information from the specimens in each family has been captured electronically in a database. This information has been used to produce distribution maps for each family that show genera and species diversity. The digitised information will enable the KZN Museum to share specimen data electronically which will minimise the need to physically handle specimens, thereby preserving them. The distribution maps can be used to establish patterns in pollinator diversity. This will emphasise the important role that Diptera families play in pollination processes. The contributions of the KZN Museum to the PINDIP project will also highlight the need for greater interest in the Diptera diversity of the Afrotropical Region.

Identity and distribution of the enigmatic genus *Pyrgometopa* Kertész (Drosophilidae)

Gabriela Pirani[1]* & David Grimaldi[2]

[1]Department of Biology, University of Sao Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *gabi.pirani3107@gmail.com
[2]American Museum of Natural History, New York, U.S.A.

Keywords: Morphology, Neotropical Region, *Stegana*, Steganinae, vinegar fly.

The genus *Pyrgometopa* Kertész was described in 1901 to include a striking drosophilid species from Peru, *P*. *penicillate* Kertész, with an ocellar tubercle bearing a thick tuft of long, spine-like setae. Known only from the unique female holotype, the genus has been virtually uncited in the literature for a century. In 1989, T. Okada ascribed the genus to the subfamily Steganinae (tribe Steganini), close to the extinct *Electrophortica* Hennig, described from Baltic amber inclusions and the extant genus *Soedorbomia* Hendel, from Mongolia. The first detailed morphological study of *Pyrgometopa* is here presented, based on new material from Brazil, French Guiana and Peru, including descriptions of the egg and the male and female terminalia. Results confirm that Okada was correct in placing the genus in the tribe Steganini, but the new material clearly indicates that *Pyrgometopa* is a synonym of the virtually cosmopolitan genus *Stegana* Meigen. Despite its bizarre features, *Pyrgometopa* possesses all the defining features of *Stegana*: wings folded against the sides of the body; wing veins R_{4+5} and M_1 converging towards the pointed wing tip; presence of crossvein *bm–m*; with dorsobasal setae on the mid tibia; scale-like microtrichia on the frons; and structure of the spermathecal capsule and cibarial sensilla. It also exhibits distinctive features that include the loss of both pairs of dorsocentral setae and partial fusion of the male surstylus and epandrium, allowing some inference as to its relationships within *Stegana*.

Poster

Is the tribe Cladochaetini the largest New World radiation of Drosophilidae?

Gabriela Pirani[1]*, Dalton de Souza Amorim[1] & David Grimaldi[2]

[1]Department of Biology, University of Sao Paulo, Av. Bandeirantes 3900, 14.040-901, Ribeirão Preto, SP, Brazil. *gabi.pirani3107@gmail.com
[2]American Museum of Natural History, New York, U.S.A.

Keywords: *Cladochaeta*, *Diathoneura*, *Myiomia*, open-ended taxon.

The essentially Neotropical tribe Cladochaetini is a particularly interesting clade of Drosophilidae, which currently includes the two recent genera *Cladochaeta* Coquillett (with 137 described species) and *Diathoneura* Duda (39 species) and the extinct genus *Myiomia* Grimaldi (1 species). It can be considered an “open-ended” taxon, with almost 200 described and numerous undescribed species. Both extant genera have complex male terminalia and several species exhibit elaborate male dimorphisms. The two genera are, however, contrasts: *Cladochaeta* adults are externally uniform, rarely collected and their larvae are parasites, parasitoids and possibly predators (open discussion) of other immature arthropods; *Diathoneura* are externally diverse, abundant and their larvae develop in flowers. There has been significant advances in the knowledge of *Cladochaeta* in recent years, with the description of several new Brazilian species, the genus has been more extensively sampled to increase distribution records and new host records are now known that have expanded the range of hosts from only Cercopidae (Hemiptera) to other surprising hosts, such as Araneae and aculeate Hymenoptera. Data have been gathered on rarity, abundance and diversity, based on a year-long sampling project at Zurquí, Costa Rica (ZADBI), during which 25 species of *Cladochaeta* and 40 species of *Diathoneura* were sampled using Malaise, pan and light traps. As another example, in Orellana, Ecuador, more than 40 species of *Cladochaeta* were sampled using canopy fogging methods alone. With these elevated numbers of undescribed species and considering the extent of under sampling, it is possible that Cladochaetini is the largest radiation of Drosophilidae in the New World. A taxonomic revision of *Diathoneura* and a morphology-based phylogenetic hypothesis of the tribe are in progress.

A first phylogeny of world Thaumaleidae

Robert J. Pivar[1]*, John K. Moulton[1] & Bradley J. Sinclair[2]

[1]The University of Tennessee, Department of Entomology and Plant Pathology, 2505 E.J. Chapman Drive, 370 Plant Biotechnology Building, Knoxville, Tennessee, 37996, U.S.A. *rpivar@vols.utk.edu
[2]Canadian National Collection of Insects and Canadian Food Inspection Agency, Ottawa, Canada.

Keywords: Madicolous, midge, molecular, phylogeny, seepage.

Thaumaleidae (seepage or madicolous midges), are a small family of aquatic Diptera. The vernacular name refers to the larval habitat, which are always a thin film of vertical flowing water (*i.e.*, madicolous). These habitats include waterfalls, rock-face seepages, splash zones around waterfalls and along cascading mountain streams. Thaumaleids are poorly known and rarely collected as a result of their habitat specificity. There are currently eight recognised genera found worldwide, except in Antarctica. The monophyly of the family is well supported, but generic concepts and relationships have never been rigorously tested, no phylogenies have been published and the validity of several genera is questionable. The goal of this research is to produce the first comprehensive phylogeny for Thaumaleidae to ascertain generic relationships and test current generic concepts. Nucleotide sequences from three nuclear genes (Big Zinc Finger, Molybdenum Cofactor Sulfurase and Elongation Complex Protein 1) were acquired from at least one representative of each genus and several outgroup taxa and were then analysed phylogenetically, using maximum parsimony, maximum likelihood and Bayesian methods. Results support the recognition of six genera within two clades: a Northern Hemisphere clade and a Southern Hemisphere clade. Within the Northern clade, *Trichothaumalea* Edwards is sister to *Thaumalea* Ruthe (including *Androprosopa* Mik and *Protothaumalea* Vaillant). The Southern clade includes *Afrothaumalea* Stuckenberg as sister to *Austrothaumalea* Tonnoir (including *Oterere* McLellan) + [*Neothaumalea* Pivar, Moulton & Sinclair + *Niphta* Theischinger]. This first comprehensive phylogeny for Thaumaleidae establishes a predictive framework with which to erect a stable classification and test myriad evolutionary hypotheses.

Phylogeny of Miltogramminae (Schizophora: Sarcophagidae) revisited – new evidence from anchored hybrid enrichment (AHE) method

Marcin Piwczyński[1]*, Brian M. Wiegmann[2], Brian K. Cassel[2], Thomas Pape[3] & Krzysztof Szpila[1]

[1]Department of Ecology and Biogeography, Nicolaus Copernicus University in Toruń, Lwowska 1, PL-87-100 Toruń, Poland. *piwczyn@umk.pl
[2]North Carolina State University, Raleigh, U.S.A.
[3]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Flesh flies, maximum likelihood method, molecular phylogeny, NGS.

Miltogramminae is one of the three subfamilies recognised in Sarcophagidae. Recently, the phylogeny of Miltogramminae was studied using four molecular (three mitochondrial and one nuclear genes). The resulting tree suggests that: 1) Miltogramminae can be divided into the ‘‘lower miltogrammines” containing two clades of mainly saprophages and a clade of ‘‘higher miltogrammines” with mainly kleptoparasitic species; 2) only three genera turn out to be non-monophyletic: *Miltogramma* Meigen, *Senotainia* Macquart and *Pterella* Robineau-Desvoidy; and 3) the genus *Sarcotachina* Portschinsky, which has traditionally been considered as belonging to the subfamily Paramacronychiinae, is placed in one of the clades of ‘‘lower miltogrammines”. However, the majority of nodes in the tree are poorly supported, making any taxonomic changes premature. An updated phylogenetic hypothesis is presented, based on phylogenomic data obtained using the anchored hybrid enrichment (AHE) method of probe-based exon capture. A total of 195 loci for 92 taxa of Miltogramminae and 7 out-groups were obtained. The reconstructed tree is fully resolved with high support values for almost all nodes. The topology corroborates results from earlier studies, with the only exception being that the species-rich genus *Miltogramma* is now found to be monophyletic. Moreover, representatives of the genera *Eremasiomyia* Rohdendorf and *Hoplacephala* Macquart, not included in earlier studies, are added to the tree. It is argued that these results provide a good basis for a new classification of the subfamily. The utility of AHE for phylogenetic inference is also discussed.

Living at the end of the world – remarkable fungus gnats (Mycetophilidae) of Chukotka

Alexei Polevoi

Forest Research Institute of Karelian Research Centre of the Russian Academy of Sciences, Pushkinskaya 11, 185910, Petrozavodsk, Russia. alexei.polevoi@krc.karelia.ru

Keywords: New genera, new species, Russia.

The Chukotka Autonomous District is located in the extreme north-east of Russia. Most of the territory of the district is located beyond the Arctic Circle, which determines the subarctic climate, with long winters and cool summers. Being barely accessible, the territory of Chukotka is a real “white spot”, with regard to the insect fauna, and until recently, no information was available on the fungus gnats of the region. Faunistic studies in the Anadyr River valley, undertaken from 2013–2014, revealed 170 species of Diadocidiidae, Keroplatidae and Mycetophilidae, indicating a potentially rich and peculiar fauna of Sciaroidea. Twenty-eight species of Mycetophilidae could not be reliably identified, which includes a range of undescribed taxa. The most exciting findings are two species belonging to unknown genera of the subfamily Gnoristinae. One of these species resembles *Coelosia* Winertz and *Synapha* Meigen morphologically, the other is similar to *Aglaomyia* Vockeroth and *Hemisphaeronotus* Saigusa. Two unknown species of the relatively small genus *Neuratelia* Rondani, are also worthy of note. Further unidentified species include representatives of the 11 genera of the subfamilies Gnoristinae, Mycetophilinae and Sciophilinae. One of the peculiar features of the fauna of Chukotka is the significant ratio of species (over 9%) otherwise known only from Fennoscandia. New taxa from Anadyr River valley also include seven species recently discovered in northern Norway, Finland and Russian Karelia. Considering the practical absence of data from northern Russia (east of Murmansk Province and Karelia) we may expect the future discovery of such species in the intermediate territories.

Does citizen science contribute to the study of lesser-known species-groups? – the case of volunteers and dolichopodid flies in Flanders (Belgium) (Dolichopodidae)

Marc Pollet[1, 2, 3]* & Dirk Maes[1]

[1]Research Institute for Nature and Forest, Herman Teirlinckgebouw, Havenlaan 88 bus 73, B-1000 Brussels, Belgium. *mpollet.doli@gmail.com
[2]Ghent University, Ghent, Belgium.
[3]Royal Belgian Institute for Natural Sciences, Brussels, Belgium.

Keywords: Citizen science, Flanders, identification, observations, rarity estimates, red list, volunteers.

Since 1981, Dolichopodidae have been rather intensively surveyed in Belgium and Flanders, the northern part of Belgium, in particular, producing the first Red List of Dolichopodidae of Flanders in 2000. Subsequently, over 633,000 specimens of 271 species have been collected and identified. The sampling sites cover 41% of the UTM 5 km grid cells in Flanders, making it one of the best studied regions for Dolichopodidae in the world. At a resolution of 1 km, however, they account for only 3.7% of the Flemish territory, which rendered an updated version of the Red List non-IUCN compliant. During nearly three decades, most of the dolichopodid data collection has been undertaken by professionals, but times are changing. Thanks to the data portal “waarnemingen.be” and the mobile application “ObsMap” since 2008 citizens can easily upload observations and images of species and add an identification. These identifications are subsequently validated by taxonomic specialists. A total of 1,005 observations in the data portal, collected by 185 citizen scientists since 2008 and covering 193 UTM 5 km grid cells (30% of all 5 km grid cells in Flanders) were analysed. About 43% of the identifications proved correct and a species name could finally be assigned to three-quarters of the observations. Eighty-two of the 271 species were observed by volunteers, also including six very to extremely rare species. In general, however, proportionally more common species were better represented than rarer species. The role of citizen science in dolichopodid research in Flanders is further elaborated upon.

How hot is the Mitaraka biodiversity spot in south-western French Guiana for Diptera?

Marc Pollet[1]*, Diego Aguilar Fachin[2], Rosaly Ale-Rocha[3], Dayse Willkenia Almeida Marques[3], Claudio José Barros de Carvalho[4], Vladimir Blagoderov[5], Stéphanie Boucher[6], Scott E. Brooks[7], Jeffrey M. Cumming[7], Gregory R. Curler[8], Carlos José Einicker Lamas[9], Woody Fitzgerald[10], Jean-Paul Haenni[11], Tiago Kütter Krolow[12], Augusto Loureiro Henriques[3], Rodrigo Marques Vieira[3], Jorge L. Mederos López[13], Jonas Mortelmans[14], Steven Paiero[15], Lucas Roberto Pereira Gomes[4], Gabriela Pirani[2], José Albertino Rafael[3], Menno Reemer[16], Paula Ricardi[17], Justin Runyon[18] & Vera Cristina Silva[2]

[1]Research Institute for Nature and Forest (INBO), Herman Teirlinckgebouw, Havenlaan 88 bus 73, B-1000 Brussels, Belgium; Research Group Terrestrial Ecology (TEREC), Ghent University, K.L.Ledeganckstraat 35, B-9000 Ghent, Belgium; and Entomology Unit, Royal Belgian Institute for Natural Sciences (RBINS), Vautierstraat 29, B-1000 Brussels, Belgium. *mpollet.doli@gmail.com [2]Universidade de São Paulo, Ribeirão Preto, Brazil; [3]Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil; [4]Universidade Federal do Paraná, Curitiba, Brazil; [5]National Museums Scotland, Edinburgh, United Kingdom; [6]McGill University, Sainte-Anne-de-Bellevue, Canada; [7]Agriculture and Agri-Food Canada, Ottawa, Canada; [8]Indianapolis, U.S.A.; [9]Museu de Zoologia, São Paulo, Brazil; [10]Pacific NW Diptera Research Lab, Corvallis, U.S.A.; [11]Muséum d'histoire naturelle Neuchâtel, Neuchâtel, Switzerland; [12]Universidade Federal do Tocantins, Porto Nacional, Brazil; [13]Museu de Ciències Naturals de Barcelona, Barcelona, Spain; [14]Ghent, Belgium; [15]University of Guelph, Guelph, Canada; [16]Naturalis Biodiversity Center, Leiden, The Netherlands; [17]Federal University of Rio de Janeiro, Rio de Janeiro, Brazil; [18]Montana State University, Bozeman, U.S.A.

Keywords: Biodiversity, first records, French Guiana, Mitaraka, new species, surveys, taxonomy.

All Taxa Biodiversity Inventories or ATBI's face considerable challenges, related to sample processing, specimen identification and research outputs. In this respect "Our Planet Reviewed French Guiana" 2014–2015 Expedition can be considered a real success. This survey was conducted in the Mitaraka Mountains (south-western French Guiana) in February–March and August 2015 and involved 50 researchers, including 28 entomologists. During the first fieldwork period, over 31 different collecting techniques were applied and 401 traps were operational in a perimeter of *ca* 1 km^2 around the base camp. A total of 223 invertebrate samples were gathered, split up into *ca* 30 dipteran fractions and ultimately disseminated among 32 taxonomic specialists. Results on the Diptera fauna of Mitaraka are presented, with some families considerably exceeding the species richness recorded during the ZADBI survey at Zurquí (Costa Rica).

Diversity and bionomics of Diptera occurring in moving sand on river bottoms in northern European Russia

Andrey Przhiboro

Zoological Institute of the Russian Academy of Sciences, Universitetskaya nab. 1, St. Petersburg 199034, Russia. Dipteran@mail.ru

Keywords: Adaptations, Chironomidae, larvae, life history, Limoniidae, psammorheophiles.

Moving sand on river bottoms in sites with high current velocity is an extreme habitat, widely distributed in running waters of the Palaearctic Region. Taxa in a few insect groups have managed to colonise this habitat and these are specifically adapted to these peculiar conditions. Larvae of Diptera usually predominate among psammorheophilous macroinvertebrates, but their systematics, bionomics and adaptations are poorly known, as compared to micropsammon (Ciliata and Rotifera). Psammorheophilous Diptera are chiefly represented by Chironomidae (mostly the *Harnischia*-group and Orthocladiinae), Ceratopogonidae (Palpomyiinae) and Limoniidae. This presentation briefly reviews psammorheophilous Diptera in running waters of northern European Russia, which are divided here into three ecological groups. Ecological features, life history, adaptations and geographical distribution are considered in more detail for “Orthocladiinae acuticauda”, a unique representative of Chironomidae, as compared with other chironomids and psammorheophiles in other families of Diptera.

Diptera in high latitude Arctic rivers of the polar desert zone

Andrey Przhiboro

Zoological Institute of the Russian Academy of Sciences, Universitetskaya nab. 1, St Petersburg 199034, Russia and Northern Arctic Federal University, Severnaya Dvina Emb. 17, Arkhangelsk 163002, Russia. Dipteran@mail.ru

Keywords: Arctic, *Arctotipula*, benthos, biomass, Chironomidae, larvae, polar desert, *Tipula*.

Immatures of Diptera are the main component of invertebrate communities in high latitude freshwater and semi-aquatic habitats. As distinct from water bodies in the boreal and tundra zones, the freshwater and semi-aquatic communities of Diptera in the high latitude Arctic, *i.e.*, in the polar desert zone, in freshwater bodies situated in extreme Arctic conditions, remain virtually unstudied. During two expeditions of the Arctic Floating University (2016 and 2018), a study was conducted of benthic and semi-aquatic shoreline communities of macroinvertebrates in three rivers of the northern part of Novaya Zemlya Archipelago, European Russia (76–77°N), with special attention to Diptera. In these rivers, Diptera are represented by three families, Chironomidae, Limoniidae and Tipulidae. Chironomidae and *Tipula* (*Arctotipula* Alexander) (Tipulidae) were predominant, in terms of abundance and biomass. *Tipula* (*Arctotipula*) larvae are apparently the largest non-marine free-living invertebrates of the polar desert zone. The taxonomic composition, structure and some other features of dipteran communities and fauna are compared with those in the Arctic running waters situated to the south and in the temperate zone.

Immature Diptera and other macroinvertebrates in the habitats of bipolar-distributed *Sphagnum* species – a comparison of bogs in north-western Russia and southern Chile

Andrey Przhiboro

Zoological Institute of the Russian Academy of Sciences, Universitetskaya nab. 1, St Petersburg 199034, Russia. Dipteran@mail.ru

Keywords: Bipolar-distributed species, bog, community, larvae, Patagonia, rearing, Russia, *Sphagnum*.

Sphagnum mosses form strongly different species-specific bog habitats. Many *Sphagnum* species have "bipolar" distributions, with part of their range in temperate zones of the Holarctic and Antarctic areas, as distinct from all bog-inhabiting arthropods. Invertebrate communities in sphagnum habitats may serve as a model to evaluate the relationships of historical and ecological factors in community evolution. No comprehensive studies of macroinvertebrate communities have been conducted in sphagnum habitats of distant regions. Five small bogs were examined, situated in temperate zones of the boreal and Patagonian regions, with well-developed habitats dominated by one of two bipolar-distributed species, *Sphagnum magellanicum* Brid. (typical of drier sites) and *S*. *cuspidatum* Ehrh. ex Hoffm. (strongly hygrophilous). Two of the bogs are located in north-western Russia (Karelia near the North Polar Circle and near St Petersburg) and three bogs in southern Chile (in Tierra del Fuego and near Punta Arenas). Two seasonal series of quantitative samples were taken in each bog. Additionally, laboratory rearings of Diptera larvae from *Sphagnum* substrata and from individual immatures were used. The structure of macroinvertebrate communities in the *Sphagnum* layer was assessed, including abundance and biomass. Communities in the same habitats types of the boreal and Patagonian bogs are formed by quite different faunal elements, but have striking resemblance in many features and are characterised by similar abundance and biomass. Taxonomic richness is similar at the level of order and family, but in many families the number of genera and species is higher in boreal bogs than in Patagonian bogs.

The effect of fat and protein in larval diet on adult size of *Chrysomya megacephala* (F.) (Calliphoridae)

William Rawson[1]*, Rozane Badenhorst[2] & Martin H. Villet[1]

[1]Department of Zoology and Entomology, Rhodes University, African Street, Grahamstown 6139, South Africa. *wrawson@gmail.com
[2]AgriProtein Holdings Ltd., Cape Town, South Africa.

Keywords: Allometry, blowflies, diet, forensic entomology, industrial entomology.

Chrysomya megacephala (F.) is a globally distributed, synanthropic blowfly of forensic importance that is being studied for its potential industrial and commercial use, as both an organic waste reducer and an organic waste to protein converter. The effects that various fat and protein ratios in the larval diet had on adult *C. megacephala* were assessed. Diet was found to effect the size and weight of puparia and adult flies. Direct correlations were found between morphometric aspects, such as wing length, tibial length and dry body weight. The presence of fat in the early stages of the larval foraging phase had a significant impact on puparial weight, adult dry weight and adult wing and tibial lengths. For both forensic and industrial applications, the presence of fat in the larval diet should be considered as a significant influencer of the size of the adult flies.

Poster

Potential agents for biological control in Tunisian crops – the hoverflies (Syrphidae)

Antonio Ricarte[1]*, Meriem Ayadi[2], Ben Halima Kamel Monia[3] & Mª Ángeles Marcos García[1]

[1]CIBIO Research Institute (Centro Iberoamericano de la Biodiversidad), Universidad de Alicante, Carretera San Vicente del Raspeig s/n, 03690 San Vicente del Raspeig, Alicante, Spain.
*ricarte24@gmail.com
[2]Institut des Régions Arides Médenine, Faculté des Sciences de Gabès, Tunisie.
[3]Institut Supérieur Agronomique (ISA), Université de Sousse, Tunisie.

Keywords: Biological control, greenhouse, horticultural crops, oasis, predatory hoverflies, species checklist, Tunisia.

Hoverfly larvae have a wide trophic diversity, including species predatory on other insects that cause damage to crops, such as aphids (Hemiptera: Aphididae). These predatory species belong to the subfamily Syrphinae and play a critical role in ecosystems as natural enemies of sucking insects on plants. Some syrphines, such as *Sphaerophoria rueppellii* (Wiedemann), are already reared on mass and are used commercially for biological control of aphids in greenhouses. Prior to using a pest control agent, however, its taxonomy, requirements and distribution must firstly be known in detail. For a biological control strategy to be successful, selected control agents should ideally be of native origin, in order to avoid ecosystem imbalances. As a basic step towards the use of hoverflies as control agents an updated checklist of the syrphine species recorded from Tunisia is presented. New data on syrphines from oases and greenhouses in the Kebili Region are also presented.

Poster

Recent advances in the taxonomy of western Palaearctic hoverflies of the genus *Chrysotoxum* Meigen (Syrphidae)

Antonio Ricarte[1]*, Zorica Nedeljković[2], Ljiljana Šašić Zorić[2], Ante Vujić[2],
Rüstem Hayat[3] & Mª Ángeles Marcos García[1]

[1]CIBIO Research Institute (Centro Iberoamericano de la Biodiversidad), Universidad de Alicante, Carretera San Vicente del Raspeig s/n, 03690 San Vicente del Raspeig, Alicante, Spain.
*ricarte24@gmail.com
[2]University of Novi Sad, Novi Sad, Serbia.
[4]Isparta, Turkey.

Keywords: *Chrysotoxum* intermedium, DNA analysis, Europe, morphological evidence, Spain.

In the Palaearctic Region, the genus *Chrysotoxum* Meigen consists of over 70 species of wasp-mimicking hoverflies, with yellow and black body colouration, very long antennae and a strongly convex and margined abdomen. Species level taxonomy is sometimes difficult, due to subtle morphological differences and high levels of intra-specific variability. The taxonomy of *Chrysotoxum festivum* (L.) and *C. vernale* Loew was studied recently and new taxa have been erected in the western Palaearctic. The taxonomy of other widespread species, however, such as *C. intermedium* Meigen has been neglected. Recent advances in ongoing research on the genus *Chrysotoxum* are here presented, based on material from Greece to Spain, to provide a morphological hypothesis for the *C. intermedium* species complex. The first morphological and molecular evidence is provided for the Iberian and Anatolian *C. vernale* hoverflies to be regarded as a separate species.

Poster

Towards a revision of the New World *genus Meromacrus* Rondani (Syrphidae)

Antonio Ricarte[1]*, Jeffrey H. Skevington[2], Gabriel J. Souba-Dols[1] &
Mª Ángeles Marcos García[1]

[1]CIBIO Research Institute (Centro Iberoamericano de la Biodiversidad), Universidad de Alicante, Carretera San Vicente del Raspeig s/n, 03690 San Vicente del Raspeig, Alicante, Spain.
*ricarte24@gmail.com
[2]Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa, Canada.

Keywords: Breeding sites, DNA analysis, *Meromacrus*, male terminalia, Neotropical Region, new species, puparia, SEM imaging.

Hoverflies of the genus *Meromacrus* Rondani are large-sized flies, with tomentose maculae, which together with their bare eyes distinguish them from the other eristalinae genera. The larvae are saprophagous in rot holes and decaying plant stems. The 43 species of the genus range from the southern United States to northern Argentina and Chile in the Neotropics. As a first step towards a revision of the genus, *Meromacrus* material collected in Costa Rica, Cuba, Mexico and Peru from 1990–2014 was examined and compared with type material of *M. canusium* (Walker), *M. gloriosus* Hull, *M*. *laconicus* (Walker) and *M*. *melmoth* Hull. Two species were recognised as new to science, based on adults reared from larvae collected in novel breeding sites and the puparia of these new species were studied with scanning electron microscopy. The name *M*. *gloriosus* is proposed as a junior synonym of *M*. *draco* Hull and the species *M*. *canusium* is retained as a valid species. The male terminalia of *M*. *ruficrus* (Wiedemann) is figured and compared with those of other *Meromacrus* species. These species concepts were supported by DNA data from COI.

Phylogenetic relationships of the subfamily Chloropinae (Chloropidae) worldwide

Paula Raile Riccardi[1]* & Dalton de Souza Amorim[2]

[1]Department of Entomology, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil.
*paularriccardi@gmail.com
[2]University of São Paulo, Ribeirão Preto, Brazil.

Keywords: Chloropinae, classification, phylogeny, shoot flies, Chloropidae.

The family Chloropidae currently comprises 202 genera divided into four subfamilies. The most diverse subfamily is the Oscinellinae with 124 genera globally. This study, however, focuses on the subfamily Chloropinae, which comprises 995 described species in 76 genera. Most chloropine larvae are associated with monocotyledons as shoot flies, but there is great variation in feeding habits, *e.g.*, predation and fungal associations have been reported. A suprageneric classification of the subfamily has been proposed in the literature, based on informal phylogenetic studies, with tribes or groups of genera delineated. The Chloropinae are known to be monophyletic, but the relationships among constituent genera are still poorly understood and several genera are clearly paraphyletic. This study applied a cladistic analysis of the subfamily, including representatives of 74 genera and 124 characters. Some of the major clades recovered support some of the traditional tribes proposed in the literature, *i.e.*, Chloropini, Diplotoxini and Meromyzini, but in some cases with slightly different generic compositions, with some tribes better corresponding to grades. A phylogenetic classification is proposed for the subfamily, with a total of ten tribes, two of which are newly proposed. The genus *Chloropella* Malloch is clearly recovered as sister to the remainder of the subfamily and requires a tribe of its own. Some few genera are rogue taxa in the phylogeny and were regarded as *incertae sedis*.

Comparative morphology of male terminalia of *Lepidodexia* Brauer & Bergenstamm (Sarcophagidae)

Paula Raile Riccardi* & Cátia Antunes de Mello-Patiu

Department of Entomology, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil. *paularriccardi@gmail.com

Keywords: Comparative morphology, flesh flies, male terminalia, taxonomy.

Males of the subfamily Sarcophaginae exhibit rather complex male terminalia, being highly significant in the differentiation of species. The genus *Lepidodexia* Brauer & Bergenstamm *sensu* Pape belongs to this subfamily, with 187 species assigned to 32 subgenera, 11 of which are monotypic. The genus is confined to the New World and occurs mainly in the Neotropics, with some Nearctic species. *Lepidodexia* was characterised by Pape as having the postalar wall bare, the phallus with the juxta forming an angle with the distiphallus and a spinose lobe adjacent to the vesica. Not all taxa share this combination of characters, however, and there is no cladistic analysis to support the monophyly of the group. Other character proposed to support monophyly of the genus include the paraphallic apical expansions, the juxta dislocated anteriorly and the undulate distal margin. The aim of this study was to provide information regarding structures of the male terminalia as a framework to understand relationships among *Lepidodexia* subgenera using morphology. To this end, abdominal sternite 5, the gonites and phallus of *L*. (*Chilopodomyia*) *lenti* (Lopes), *L*. (*Gymnocamptops*) *grisescens* (Townsend), *L*. (*Hallina*) *elaborata* (Hall), *L*. (*Johnsonia*) *teutonia* (Lopes), *L*. (*Lepidodexia*) *apolinari* Lopes and *L*. (*Travassossisca*) korytkowskii (Lopes) were studied and interpreted.

Poster

Three new Cretaceous fossil discoveries and an overview on the fossil Diptera fauna from Chapada do Araripe, Ceará, Brazil

Leonardo Silvestre G. Rocha[1]*, Antonio Álamo Feitosa Saraiva[1], Allysson Pontes Pinheiro[1] & Rafaela Lopes Falaschi[2]

[1]Departamento de Ciências Biológicas, Universidade Regional do Cariri, Crato, CE, Brazil. *leonardo.rocha@urca.br
[2]Museu de Zoologia, São Paulo, Brazil.

Keywords: Cretaceous, fossils, palaeoenvironments, SEM.

Most publications employing molecular clocks, date the origin of the Diptera from the Permian Period, with a rapid radiation in the Triassic. There are few fossils from that period, however, especially in South America and Brazil specifically. Papers on Brazilian fossil Diptera recognise Brazilian Diptera fossils from just three formations: Santana (Lower Cretaceous, north-eastern Brazil); Tremembé Formation and Entre-Rios Formation (both Oligocene, south-eastern Brazil). The oldest Brazilian fossils are thus Lower Cretaceous and six taxa are recorded from that formation: Asilidae, Bibionomorpha, Chironomoidea, Simuliidae, Tabanidae and Tipulidae. The fossils from Santana Formation are famous for their preservation, including soft tissues and most authors consider that palaeoenvironment as a freshwater lake, rich in invertebrates, especially insects. Three specimens from that formation were identified as three of the clades occurring at Santana Formation: one chironomid with long legs and a small head, one well-preserved tipulid, with an elongated head and a tabanid with apparently extended wings. All specimens were illustrated with SEM. The Santana Formation palaeoenvironment probably housed an assemblage of aquatic/moist environment Diptera, as well as at least two bloodsucking families, probably associated to the rich pterosaur fauna. The presence of angiosperms gives hope of finding more advanced taxa, especially nectarivorous/parasitoid species.

Poster

Comparative morphology of the terminalia of Conopidae

Leonardo Silvestre G. Rocha[1]*, Allyene Paúra B. Santos[2],
Cátia Antunes de Mello-Patiu[3] & Carlos A. Marques[4]

[1]Departamento de Ciências Biológicas, Universidade Regional do Cariri, Crato, CE, Brazil. *leonardo.rocha@urca.br
[2]Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil.
[3]Museu Nacional, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil.
[4]Instituto Federal de Educação, Ciência e Tecnologia do Rio de Janeiro, Nilópolis, Brazil.

Keywords: Morphology, SEM, terminalia, transformation series.

The family Conopidae is a peculiar taxon of Hymenoptera-mimicking flies that are parasitoids as larvae and nectarivorous as adults. The morphology of the terminalia is of great importance in their taxonomy. Specimens of *Myopa* F., *Physocephala* Schiner, *Stylogaster* Macquart and *Zodion* Latreille, were examined. Specimens of Lauxaniidae, considered as sister-group to Conopidae in most analyses, and Syrphidae were used as out-groups. Literature-based data were also used. All specimens were illustrated using SEM. A matrix comprising 62 characters and six terminal taxa was submitted to a heuristic search and the resultant topology was used to plot the transformation series. *Stylogaster* has a male terminalia morphology more similar to the groundplan of Diptera, with many moving parts used to grasp the female. By constrast. The female terminalia in *Stylogaster* is rather immobile and highly modified, compared to other Diptera. Non-stylogastrines are a monophyletic group, including the fossil species *Palaeomyopa tertiaria* Meulnier. Sternite 5 in both sexes is enlarged, ventrally projecting and covered with sculptured and spiculate microtrichia. Male cerci and surstyli are greatly reduced and partially fused to the epandrium and the phallus is flattened. In females, the terminalia is shortened and modified for the oviposition of sticky eggs and to make a wound in the host’s cuticle, using hook-shaped lateral lobes. A simplification of the terminalia is observed in both sexes in the non-stylogastrine clade, probably related to the morphological, host preference and oviposition behaviour changes of the females.

Seasonal and elevational diversity gradient of Dixidae, Limoniidae, Tipulidae and Simuliidae along streams of the Parque Nacional do Itatiaia, Brazil

Durval S. Santos*, Jéssica Gouvêa Ferreira, Carine S. Pedrosa,
Ivyn Karla L. Souza, Caio Cézar D. Corrêa, Óscar Sánchez Molina,
Tatiana N. Docile & Leonardo H. Gil-Azevedo

Department of Entomology, National Museum - UFRJ, zipcode20940-040, Quinta da Boa Vista s/n, São Cristóvão, Rio de Janeiro, RJ, Brazil. *durvaluerj@gmail.com

Keywords: Culicomorpha, high elevation, Neotropical Region, species diversity, Tipulomorpha.

Itatiaia National Park (PNI) is in Atlantic Forest; a tropical mountain rainforest with high biodiversity in Brazil. The families Dixidae, Limoniidae, Simuliidae and Tipulidae are abundant in this ecosystem, although few investigations have explored the ecology of these flies. The aim of this study was to describe and compare seasonal and elevational gradient diversity of dipteran communities in PNI. Specimens were sampled with Malaise traps placed in a transversal position to streams at three elevations (low: 830 m, intermediate: 1,200 m and high: 2,100 m) and during two seasons (dry season: July–August, wet season: October–November). Diversity comparison was made at species/morphospecies level. A total of 3,210 specimens, representing 130 species were examined: Dixidae (58 specimens; 4 species), Limoniidae (2,529; 101), Tipulidae (54; 15) and Simuliidae (569; 10). A total of 1,411 specimens and 65 species were sampled at low elevation, 906 and 78 in intermediate and 897 and 56 in high. The dry (1,433; 63) and wet (1,777; 105) seasons vary too, with exclusive species more frequent in high elevation (32) and wet-season (67). Shannon index indicates that points in high elevation (3.32) and wet-season (3.33) were the most diverse. Pielow index indicates that the intermediate elevation (0.76) and wet (0.7) samples are more uniform, with low samples most exclusive area (0.44). An NMDS ordination analysis revealed that most of the variation could be explained by elevation and seasonality ($p < 0.01$). These results indicate that seasonality is more influential on the composition of this community than elevation, but that elevation influences the exclusion of species.

Poster

An old pest with a New World twist – identity issues in the seedcorn maggot complex of *Delia* Robineau-Desvoidy (Anthomyiidae)

Jade Savage

Bishop's University, 2600 College Street, Sherbrooke, Quebec J1M 1Z7, Canada. jsavage@ubishops.ca

Keywords: Agricultural pests, cryptic species, *Delia*, identification, seedcorn maggots.

In Canada and other New World countries, growers are increasingly concerned with damage to a variety of vegetable and field crops caused by polyphagous representatives of the seedcorn maggot complex (*Delia florilega* (Zetterstedt) and *Delia platura* (Meigen)). *Delia platura* was first reported from the New World in the 1800s and has generally been assumed to have been introduced from Europe along with many other invasive species. The recent discovery of two distinct genetic lines with unique distribution patterns (one Holarctic and one New World), suggests the presence of a new cryptic species for the group that could be native to the New World. The implications of this finding for the management of *D*. *platura* in the New World is discussed and plans to characterise reproductive isolation, host preferences and development in the two genetic lines of *D*. *platura* are outlined. The use of real-time PCR assay, coupled with high-resolution melting analysis (HRM) to discriminate between *D*. *florilega* and both genetic lines of *D*. *platura* (all of which are apparently identical in the immature stages) will also be presented.

The mystery of "*Eurigaster*" *clathrata* Nowicki (Tachinidae) exposed

Franz-Rudolf Schnitzler

c/o Landcare Research, Private Bag 92170, Auckland Mail Centre, Auckland 1142, New Zealand.
schnitzlerr@landcareresearc.co.nz

Keywords: New Zealand, *Proscissio*, synonymy, taxonomy.

This presentation outlines the rediscovery of the presumed missing type specimen of the New Zealand "*Eurigaster*" *clathrata* (Tachinidae), described and privately published by M. Nowicki. This species was erroneously placed in the genus *Pales* Robineau-Desvoidy (Tachinidae) by previous workers and also proposed as a synonym of *P*. *usitata* (Hutton). A later proposal suggested that *clathrata* should be removed from *Pales*. The questionable placement of *clathrata* prevented this species being included in any taxonomic research on New Zealand Tachinidae. Nevertheless, numerous workers still identified tachinids, especially *Pales* specimens generated through surveys as *clathrata*. Comparison of the male external and terminalia characters of *clathrata* and comparison of these to those of *Proscissio lateralis* Malloch support the placement of *clathrata* in the genus *Proscissio* and the synonymy of *P*. *lateralis* with *P*. *clathrate* is here proposed.

The hidden Neriidae morphology – a new ultrastructural approach on the study of the male terminalia

Tatiana Alejandra Sepúlveda[1], João Manuel Fogaça[1], Diego de Santana Souza[2], Lucas Roberto Pereira Gomes[1]*

[1]Universidade Federal do Paraná, Department of Zoology, Rua Francisco H. dos Santos, Jardim das Américas, 81531-980, Curitiba, PR, Brazil. *lucaspergos@gmail.com
[2]Museu Nacional, Rio de Janeiro, Brazil.

Keywords: Cactus flies, morphology, Nerioidea, New World.

The terminalia of Neotropical Neriidae have been recurrently declared as uniform in several taxonomic works. Most studies, however, are limited to the general description of external structures of terminalia, such as the epandrium, surstylus and cercus. Scanning Electron Microscopy (SEM) technology was used in this study to examine and compare the morphology of the male terminalia of six of the eight valid genera of Neotropical Neriidae, in order to test the assumptions of uniformity by previous authors and to verify whether terminalia characters can be used for systematic purposes. Results revealed that although the male terminalia of Neotropical Neriidae have rather conservative external morphology, their internal structures can be taxonomically informative, both at specific and suprageneric levels. All genera examined have one line of minute setulae along the paramere dorsally, one conspicuous setula ventrally on the postogonite and the cercus is rather uniform; characters that are possibly synapomorphic for Neotropical Neriidae. Main differences were found in the distal distiphallus, which has a membranous spike dividing it from the basal distiphallus. This spike exhibits different shapes and textures that can be useful to infer relationships at generic level. Also, the inner margin of cercus and the shape and texture of epandrium and distal distiphallus bear important phylogenetic information at suprageneric level. Likewise, the postgonite has rows of thick and short spines, varying among different genera, while the surstylus appears to carry a phylogenetic signal only for specific determination.

Poster

Time after time – phylogeny of Tanypodinae (Chironomidae) suggests multiple independent loss and reacquisitions of the mandibles by non-biting midges

Fabio Laurindo da Silva[1]* & Viktor Baranov[2]

[1]Department of Zoology, Institute of Biosciences, University of São Paulo, São Paulo, Brazil.
*fabiologia@gmail.com
[2]University of Munich, Munich, Germany.

Keywords: Fossil, mandibles, mouthparts development, phylogenetics.

The subfamily Tanypodinae was established first on adults with support provided from immature stages. The larva differs from other Chironomidae in the strong development of the prementum and mentum, even though the premental elements of the ligula and paraligulae exhibit homologous development in some species of the subfamily Podonominae. In this study morphological characters were sampled across all life stages and tribes, involving 62 genera and 123 species and including evidence from modern and fossil chironomids. The monophyly of the Tanypodinae finds support from all trees resulting from an equal weighted analysis, or from a character matrix under implied weights. Internal relationships within the subfamily support all proposed tribes, namely: Anatopyniini, Clinotanypodini, Coelopyniini, Fittkauimyiini, Macropelopiini, Natarsiini, Pentaneurini, Procladiini and Tanypodini. Moreover, Tanypodinae is divided into two distinct well-supported groups: Pentaneurini + Natarsiini and non-Pentaneurini and these as sister to a clade formed by the fossil genera. In the last-named group, which appears to be composed of highly derived Tanypodinae midges, as may be confirmed by the geological records and dated phylogeny, functional mandibles we found. The presence of this feature suggests multiple independent loss and reacquisitions of the mandibles by non-biting midges, which violates Dollo's law, *via* re-evolution of complex, once lost character, in addition to be of a wider evolutionary relevance.

Revision of the Southern African endemic genus *Stuckenbergomyia* Smith (Empidoidea: Hybotidae)

Bradley J. Sinclair

Canadian National Collection of Insects and Canadian Food Inspection Agency, OPL-Entomology,
K.W. Neatby Bldg., C.E.F., 960 Carling Ave., Ottawa, ON, Canada K1A 0C6.
bradley.sinclair@canada.ca

Keywords: Brandberg, Mozambique, Namibia, new species, South Africa.

The Afrotropical Hybotidae primarily comprise genera in the subfamilies Hybotinae and Tachydromiinae, with a single genus in the Ocydromiinae. There are three endemic genera in Hybotinae, whereas the Tachydromiinae include two apparently endemic undescribed genera. The genus *Stuckenbergomyia* Smith is an odd genus, characterised by a short spur vein arising from wing cell *cua*. The genus is endemic to Southern Africa, recorded from Mozambique, South Africa, Zimbabwe and now from the Brandberg in Namibia. Originally assigned to the Ocydromiinae, the genus is currrently *incertae sedis* in the Hybotidae. Its phylogenetic assignment will be discussed. Species of *Stuckenbergomyia* are believed to occur in dry montane grasslands and pollen grains found in dissected abdomens indicate that species are flower visitors.

Study of the impact of natural ecosystems degradation on the abundance and diversity of hoverflies (Syrphidae) in Burundi

Eugène Sinzinkayo[1]*, Kurt Jordaens[2] & Wouter Dekoninck[3]

[1]Office Burundais pour la Protection de l'Environnement, 2757 Bujumbura, Burundi.
*Sineuge60@gmail.com
[2]Royal Museum for Central Africa, Tervuren, Belgium.
[3]Royal Belgian Institute of Natural Sciences, Brussel, Belgium.

Keywords: Agriculture, biodiversity, Burundi, checklist, flower flies, hoverflies, pollination.

In the framework of the conservation of biodiversity and the reinforcement of taxonomic capacity in Burundi, a research project has been launched entitled "Study of the impact of natural ecosystems degradation on the abundance and diversity of pollinating Syrphidae in Burundi".The overall objective of the project is to compile a checklist of the Syrphidae of Burundi and to increase taxonomic knowledge of the family in Central Africa. Specifically, the aim is to inventory and identify flower visiting Syrphidae species and the plants visited, in both natural and agricultural ecosystems and to establish a reference collection of the Syrphidae of Burundi. This will result in a detailed description of their distribution, relative abundance and occurrence frequency on flowering plants. In addition, the study will investigate the effects of degradation of natural ecosystems on the diversity and abundance of pollinating Syrphidae. This project is a continuation of recent research, where 26 species of Syrphidae in 16 genera were identified from Burundi.

An unexplored treasure – a revision of Australian *Tomosvaryella* Aczél (Pipunculidae)

Jeffrey H. Skevington[1]* & Mihaly Földvári[2]

[1]Canadian National Collection of Insects, Arachnids and Nematodes, Agriculture and Agri-Food Canada, K.W. Neatby Building, 960 Carling Avenue, Ottawa, Ontario, Canada, K1A 0C6. *jhskevington@gmail.com
[2]Natural History Museum, University of Oslo, Norway.

Keywords: Australia, revision, taxonomy, *Tomosvaryella*.

Australia remains one of the last frontiers of undiscovered entomological diversity. Like many families of insects, the big-headed fly (Pipunculidae) fauna of Australia has been only partly explored. Twelve genera and 79 species are currently documented for the continental fauna and over half of these have been described in the past 20 years. *Tomosvaryella* Aczél is currently known from five species, but recent collecting efforts have greatly increased the amount of material available for study. A total of 2,124 specimens have now been assembled and from these over 70 species of *Tomosvaryella* have been identified (over 65 new species). This confirms *Tomosvaryella* to be the most diverse Australian pipunculid lineage. In fact, once this work is completed, it is expected that *Tomosvaryella* will be seen to comprise over half of the described continental diversity of big-headed flies. Given that *Tomosvaryella* is most diverse in xeric regions, it does not come as a huge surprise that Australia holds such a treasure trove of undescribed diversity. This presentation will focus on *Tomosvaryella*, but will also explore pipunculid diversity in general. Patterns of distribution will be examined and hilltopping behaviour and sampling protocols will be discussed. Predictions will also be made of what the fauna will look like once completely studied.

Palaeoglaesum Wagner (Psychodidae: Bruchomyiinae) – an extinct genus from “Burmese amber”

Kornelia Skibińska*, Wiesław Krzemiński & Katarzyna Kopeć

Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland. *yukisiak@gmail.com

Keywords: “Burmese amber”, Cretaceous, male hypopygium, new species.

The family Psychodidae consist of more than 3,000 extant species, divided into seven subfamilies (Bruchomyiinae, Datzine, Horaiellinae, Phlebotominae, Psychodinae, Sycoracinae and Trichomyiinae), of which the subfamily Bruchomyiinae is regarded as one of the most “primitive”. Psychodidae are considered as one of the oldest lineages of Diptera, known from the Early Jurassic and probably from the Late Triassic. The genus *Palaeoglaesum* Wagner, described from Cretaceous “Burmese amber” (earliest Cenomanian, *ca* 99 MYA) inclusions, belongs to this subfamily. The genus comprises five fossil species: *P. bisulcum* Wagner; *P. mulleri* Wagner; *P. notandum* Wagner, *P. quadrispiculatus* Stebner, Solórzano Kraemer, Ibáñez-Bernal & Wagner; and *P. velteni* Wagner. The genus is characterised by the highly specific and complicated composition of the male hypopygium. A revision of the genus is currently underway, which will help to develop a more complete knowledge of the morphology of this group and to facilitate description of new species.

Hydrellia Robineau-Desvoidy (Ephydridae) – the good, the bad and the unknown

Rosali Smith*, Julie Coetzee & Martin P. Hill

Centre for Biological Control, Zoology and Entomology Department, Rhodes University, Grahamstown, 6140, South Africa. *rosalismith2@gmail.com

Keywords: Biological control, *Egeria*, *Hydrellia*, plant-insect interactions, aquatic weeds.

Hydrellia Robineau-Desvoidy (Ephydridae) is a large genus of leaf-mining flies associated with aquatic and semi-aquatic plants. Some species have become infamous agricultural pests, for example the rice pests *H*. *griseola* Fallén, *H*. *philippina* Ferino and *H*. *sasakii* Yuasa & Isitani. Herbivory in aquatic ecosystems has only recently been accepted as a driver of community structure and thus ecosystem functioning. Despite some infamous *Hydrellia* species, others have been found to fulfil crucial roles as aquatic plant pollinators and to exert top-down pressure for weedy plants. This is seen in the growing use of *Hydrellia* species as biological control agents (the use of natural, host-specific enemies to manage invasive alien species). For example, *H*. *balciunasi* Bock and *H*. *pakistanae* Deonier have been used extensively in the biological control of the world's worst submerged aquatic weed, *Hydrilla verticillata* (L.f.) Royle (Hydrocharitaceae). South Africa has a long history of freshwater aquatic plant invasions and, with the successful management of floating aquatic weeds, has undergone a regime shift, from floating aquatic plant dominance to submerged aquatic plant dominance. In 2018, South African researchers released their first submerged aquatic weed biocontrol agent, *H*. *egeriae* Rodrigues for the management of *Egeria densa* Planchon (Hydrocharitaceae), more commonly known as Brazilian waterweed. During pre-release surveys, however, biological control researchers have frequently encountered indigenous *Hydrellia* species and with little information available on these flies considerable additional work is still required to determine their biology and ecological importance.

Filth fly (Muscidae) research in southern New Mexico – past, present and future contributions

Brandon G. Smythe

Center for Animal Health and Food Safety, Veterinary Entomology Research Laboratory, New Mexico State University, MSC 3BF, P.O. Box 30003, Las Cruces, NM 88003, U.S.A. *bsmythe@nmsu.edu

Keywords: Filth flies, New Mexico.

The Veterinary Entomology Research Laboratory of New Mexico State University has a vast history of contributions to the field to veterinary entomology. Academic contributions and long-lasting collaborations with private industry partners have provided the framework for this laboratory to play a key role in advancing integrated pest management approaches to filth fly control. We will take a look at the efforts from former leaders in the laboratory, provide a synopsis of current projects and collaborations and evaluate future goals and objectives specific to filth fly management options.

The "*Lutzia* conundrum" is only skin deep – a framework for resolving Culicini (Culicidae) classification

Louwrens P. Snyman[1]*, Luis Neves[1] & A. Paulo G. Almeida[2, 3]

[1]Vector and Vector-Borne Diseases Research Programme, Department of Veterinary Tropical Diseases, Faculty of Veterinary Sciences, University of Pretoria, South Africa. *lokisnyman@gmail.com
[2]Universidade Nova de Lisboa, Lisbon, Portugal.
[3]University of Pretoria, Pretoria, South Africa.

Keywords: *Culex*, Culicidae, Culicini, *Lutzia*, mosquitoes, phylogeny.

Despite the medical, veterinary and economic importance of the tribe Culicini (Culicidae), the classification of the group is unstable, as mosquito taxonomists do not have a framework for working together. Various and changing methods by different groups have until now been applied to try and resolve aspects thereof; most notably, single-gene trees (barcodes) and morphology alone. These methods may lead to possible unwarranted problems highlighted in the classification system. The so called "*Lutzia* conundrum" is such an example and the subject of this study. Four concatenated datasets were constructed from Genbank, one from rDNA, one from mitochondrial genes, one from rDNA and mitochondrial genes and one from molecular and morphological data, to analyse the phylogeny of *Culex* L. All datasets were analysed using data-display networks, maximum likelihood and Bayesian inference statistics. *Lutzia* Theobald consistently renders *Culex* paraphyletic and is not a self-standing genus, but a subgenus within *Culex*. The current morphological data available are also shown to be inadequate for phylogenetic inference at the genus level. It is proposed that *Lutzia* be reinstated as a subgenus within *Culex* and that the subgenera *Metalutzia* Tanaka and *Lutzia* be reduced to sections. A framework for broad-spectrum collaboration using an integrative evolutionary approach to yield a robust classification for Culicini at the genus level is proposed.

An overview of the horse flies (Tabanidae) of South Africa – centralising and assessment of major collections for spatiotemporal analysis

Louwrens P. Snyman[1]*, Luis Neves[1], Laetitia Lempereur[2] & Albe C. Bosman[3]

[1]Vectors and Vector-borne Diseases Research Programme, Department of Veterinary Tropical Diseases, Faculty of Veterinary Sciences, University of Pretoria, South Africa. *lokisnyman@gmail.com
[2]University of Liège, Liège, Belgium.
[3]Iziko Museums of Cape Town, Cape Town, South Africa.

Keywords: Digitisation, museum collections, *Specify*, spatiotemporal analysis, South Africa.

Tabanidae, commonly known as “horse flies”, are a large cosmopolitan family, with *ca* 4,400 described species globally. Both sexes are important pollinators and females usually requiring a blood meal for maturation of ova, making them efficient vectors of disease causing pathogens. Despite their importance, they have been largely neglected by researchers, especially in the Afrotropics. The aim of this study is to elucidate some fundamental aspects of horse fly biology in South Africa, by centralising digitised data from the major natural history museums in the region. Approximately 6,000 records have been digitised and collated into a *Specify* database from an approximate 17,000 specimens housed in 10 museums in the region. The collections from the 10 institutions, including six collections in neighbouring countries, are briefly discussed. Spatiotemporal analysis according to biomes (Albany thicket, Desert, Forests, Fynbos, Grassland, Indian ocean belt, Kalahari savanna sub-biome, Central Bushveld sub-biome, Lowveld savanna sub-biome, Nama karoo and Succulent karoo), revealed baseline information regarding their biology within these biomes. The database is represented by a total of 230 species of which 96 species are unique to only one biome, calculated from over 3,500 records. The grassland biome is home to approximately 40% of the unique records. The majority of the records are from north eastern KwaZulu-Natal, followed by Kruger National Park and areas surrounding Cape Town (all South Africa). Future studies should aim to digitise the remaining specimens to create species pages with brief descriptions, high resolution photographs, distribution maps and spatiotemporal patterns available online.

Why on the snow? Diversity and life strategies of snow active Diptera in central Europe

Agnieszka Soszynska-Maj

Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Banacha 12/16, 90-237 Lodz, Poland. agnieszka.soszynska@biol.uni.lodz.pl

Keywords: Chironomidae, Heleomyzidae, life strategies, Limoniidae, Phoridae, snow activity, Sphaeroceridae, Trichoceridae.

In central Europe, where the annual snow cover may last for three months or longer, winter-active insects are an important part of the fauna. Diptera in general are well adapted to life in extreme conditions and dominate the fauna of sites at high latitudes and/or altitudes, sites with a continental climatic regime and of caves. The snow surface is used by them for courtship and copulation, dispersal and foraging. At the same time, winter-active insects are a source of food for spiders, non-hibernating insectivorous shrews or even for bats. There are 28 families of Diptera for which representatives were found on the snow. However, most flies that are well adapted for activity at low temperatures and that have been recorded on snow belong to six dipteran families: Heleomyzidae, Limoniidae, Phoridae, Sphaeroceridae and Trichoceridae, and the most abundant within this community: the aquatic winter-emerging midges (Chironomidae). These flies are active on snow surfaces quite regularly at temperatures down to -4°C, but exceptionally even below -16°C thanks to behavioural, morphological and physiological adaptations. This presentation gives an overall insight into the results of a long-term study on snow-active insects in lowlands and mountainous areas in Poland. Recent studies revealed that the most significant effects of climate change are observed in winter, which are becoming milder in central Europe, causing a decreasing number of days with permanent snow. The winter emergence and mate strategies of the above fly families are discussed in a light of global warming.

General dipterology

Why not look like a fly? – a case of convergence between the Mecoptera and Diptera

Agnieszka Soszynska-Maj[1]*, Katarzyna Kopec[2] & Wiesław Krzeminski[2]

[1]Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Banacha 12/16, 90-237 Lodz, Poland. *agnieszka.soszynska@biol.uni.lodz.pl
[2]ISEA PAS, Krakow, Poland.

Keywords: “Burmese amber”, convergence, Mecoptera, Pseudopolycentropodidae, wings reduction.

Two very peculiar species of scorpionflies from Myanmar amber inclusions (“Burmese amber”), dated to the Mid-Cretaceous ~99 MYA, were described in the genus *Parapolycentropus* Grimaldi & Rasnitsyn. They belong to the family Pseudopolycentropodidae, to which 12 fossil species in four genera have been assigned thus far. The oldest known representatives of this family are known from the beginning of the Middle Triassic (Ladinian) of France. Species of the genus *Parapolycentropus* are small-sized, gracile, mosquito-like Mecoptera (body length: 3 mm), with strongly narrowed and lengthened fore wings, while the vestigial hind wings are reduced to minute lobes. Characters unique among the Mecoptera include: the aristate antennae, mouthparts with a long, fine and stylate proboscis, a short *Sc* vein, one point connection between veins *Mb* and *Rb* (similar to arculus in Diptera), a partial reduction of second cubital vein and only one anal vein. The reduction of wings is a typical adaptation of insects that lead parasitic, social, or a ground-dwelling mode of life, or in alpine habitats. However, the reduction of one pair of the wings is typical only in Diptera and is very rare in other insects (*e.g*., males of Strepsiptera and some Ephemeroptera). The lack of hind wings, large eyes and aristate antennae enabled *Parapolycentropus* to have agile flight. Their mouthparts are similar to the extant blood/flower-feeding flies. However, the Mid-Cretaceous age of the inclusions would rather suggest the predatory strategy of these scorpionflies. These unique characters obviously suggest convergence of the genus *Parapolycentropus* to mosquito-like habits and behaviour.

Insect decline in Germany and elsewhere in Europe – a major loss in pollination with case-studies on hoverflies (Syrphidae)

Axel Ssymank

Research Associate of the Zoologisches Forschungsmuseum Alexander Koenig, Falkenweg 6, 53343 Wachtberg, Germany. Ssymanka@t-online.de

Keywords: Biodiversity conservation, Europe, flower flies, Germany, hoverflies, pollination.

Dramatic losses of insect biomass have been proven by studies of the Entomological Association Krefeld (EVKr), resulting in the statistically elaborated paper “More than 75 percent decline over 27 years in total flying insect biomass in protected areas” by Hallmann *et al*., published in 2017. This research indicated an alarming average decline in insect biomass over the past 27 years, even in well protected sites for nature conservation. While general declines over Germany were already known from the Red Data Lists of species, losses obviously do not stop on the border of nature conservation areas or in EU Natura 2000 sites, at least in the German lowlands. Meanwhile, further data at species level are available and case studies on hoverflies (Syrphidae) will be provided. Studies in other parts of Europe with different insect groups are confirming that this is not a regional phenomenon, although exceptions do exist. A short overview of major reasons for such decline will be given and the first steps towards an action plan to stop insect decline and establishing insect monitoring schemes will be discussed. A Federal Research Project of the German Agency for Nature Conservation (BfN) by the EVKr investigates a broad set of different insect groups and will continue to look into the details of insect decline and its reasons.

Biogeographical histories and evolutionary relationships among Australian Dacini fruit flies (Tephritidae)

Melissa Starkie

Queensland University of Technology, GPO Box 2434, Brisbane, 4001, QLD, Australia. Melissa.Starkie@hdr.qut.edu.au

Keywords: Australia, biogeography, Dacini, phylogenetics, taxonomy, total evidence.

Australia is home to three of the four major genera within the tephritid tribe Dacini: *Bactrocera* Macquart, *Dacus* F. and *Zeugodacus* Hendel. With 111 described species within the Australian Dacini, their diversity and affinity in the Western Pacific raises questions surrounding their origin, diversification and systematic relationships to each other. With minimal sequence data and conflicting morphological evidence, taxonomic and phylogenetic relationships are difficult to resolve. Only through a combination of both morphological and molecular data can conclusions be reached about: the relationships among Australian endemic and off-shore species; the usefulness of species groupings (complexes, subgenera *etc*.); the utility of morphological characters in phylogenetic analyses; and biogeographical influences on species distributions and diversification. This research seeks to comprehensively sample the entire Australian Dacini, along with adequate representation of the larger regional fauna, to develop a robust molecular phylogeny for the continental fauna as a basis for addressing some of these issues. A prime example of how morphological and molecular characters can be in disagreement is evident within the *Bactrocera recurrens* Hering species complex. Intraspecific variation within this complex, such as wing and abdomen patterning, blurs the lines of species boundaries. A multi-gene analysis has revealed polyphyly and little genetic variation among taxonomically distinct species. The steps taken to resolve this complex are presented, together with details of how such methods could be applied to similarly problematic groups within the Australian dacine fauna.

Improving the current state of fruit fly (Tephritidae) larval taxonomy

Gary J. Steck[1]*, Allen L. Norrbom[2], Bruce D. Sutton[3], Erick J. Rodriguez[4], Louis A. Somma[1], Marc Branham[4], Matthew R. Moore[1, 4], Norman B. Barr[5], Raul Ruiz-Arce[5], Terrance Todd[5], Alies van Sauers-Muller[6], Norma Nolazco[7], Brian M. Wiegmann[8] & Brian K. Cassel[8]

[1]Florida Department of Agriculture and Consumer Services, Division of Plant Industry, 1911 SW 34th Street, Gainesville, Florida 32605, U.S.A. *Gary.Steck@FreshFromFlorida.com; [2]USDA ARS Systematic Entomology Laboratory, Washington D.C., U.S.A.; [3]Smithsonian Institution, Washington, D.C., U.S.A.; [4]University of Florida, Gainesville, U.S.A.; [5]USDA APHIS Science and Technology, Edinburg, U.S.A.; [6]Ministry of Agriculture, Paramaribo, Suriname; [7]SENASA, La Molina, Peru; [8]North Carolina State University, Raleigh, U.S.A.

Keywords: *Anastrepha*, *Bactrocera*, *Ceratitis*, *Dacus*, *Zeugodacus*, COI gene, identification, SEM.

Larvae in infested fruits and other commodities are regularly transported across regional and national borders, these being the main invasive stage of pest fruit flies. Our ability to accurately identify larvae, even the economically important species, using morphology is generally poor. The goals of this study were to: 1) acquire immature stages of numerous fruit fly species for which larval stages have not been described; 2) obtain COI and other DNA sequence data to corroborate species identity of larvae and expand the library of known fruit fly genetic variation; 3) prepare morphological descriptions and identification keys to larvae; and 4) incorporate larval morphology data into the current framework of tephritid classification. Fieldwork was conducted in Bolivia, Brazil, Colombia, Ecuador, Peru and Suriname. A large collection was amassed of research material, comprising over 40,000 adults representing at least 125 species and *ca* 9,000 larvae, representing at least 60 species of *Anastrepha* Schiner. The larvae include representatives of 17 of the 23 species-groups of *Anastrepha*. A corresponding library of COI sequence data allowed successful matching of unidentified larvae to adults of known and/or undescribed species in most cases. For the first time, there is sufficient representation of several *Anastrepha* species-groups to determine the presence/absence of larval synapomorphies with useful taxonomic value. Data from the *A. mucronota* Stone species-group is provided as an example. Similar patterns in larval morphology are emerging among other groups of pest fruit flies, including the major pest genera *Bactrocera* Macquart, *Ceratitis* MacLeay, *Dacus* F. and *Zeugodacus* Hendel.

Molecular phylogeny and evolution of world Tachinidae

John O. Stireman III[1]*, Pierfilippo Cerretti[2], James E. O'Hara[3], Jeremy D. Blaschke[4] & John K. Moulton[5]

[1]Department of Biological Sciences, Wright State University, Dayton, OH 45435, U.S.A.
*john.stireman@wright.edu
[2]'Sapienza' Università di Roma, Rome, Italy.
[3]Canadian National Collection of Insects, Ottawa, Canada.
[4]Union University, Jackson, U.S.A.
[5]University of Tennessee, Knoxville, U.S.A.

Keywords: Ancestral state reconstruction, diversification, host use, Oestroidea, parasitoid, tachinid fly.

Phylogenetic relationships were reconstructed within the diverse parasitoid fly family Tachinidae, using four nuclear loci (7800 bp) and an exceptionally large sample of more than 500 taxa from all major zoogeographical regions. The position of the earthworm-parasitising subfamily Polleniinae (Calliphoridae *sensu lato*) as sister to Tachinidae is strongly supported. The analyses recovered each of the four traditional tachinid subfamilies and most recognised tribes, with some important exceptions in the Dexiinae and Tachininae. Most notably, the tribes Macquartiini and Myiophasiini form a clade sister to all other Tachinidae and several genera of Palpostomatini form a lineage sister to Dexiinae + Phasiinae. Although most nodes are well supported, relationships within several lineages that appear to have undergone rapid episodes of diversification (early branching Dexiinae and Tachininae, Blondeliini) were poorly resolved. Reconstruction of host use evolution generally supports the hypothesis that the ancestral host of tachinids was likely a beetle with repeated host shifts to caterpillars and extensive radiation of tachinids on these hosts. Reconstructions of reproductive strategy based an alternate methods were discordant, however it appears most likely that ancestral tachinids possessed unincubated, thick shelled eggs from which incubated eggs evolved repeatedly, potentially expanding available host niches. These results provide an extensive foundation for understanding the phylogeny and evolution of this important and diverse family of parasitoid insects.

Afrotropical Conopidae – 200 years of research on a beautiful group of Afrotropical flies

Jens-Hermann Stuke

Roter Weg 22, 26789 Leer, Germany. jstuke@zfn.uni-bremen.de

Keywords: Afrotropical Region, Conopidae, historical overview.

The first part of this presentation summarises historical research regarding Conopidae in the Afrotropical Region. Since the first Afrotropical *Conops* was described from South Africa by C.R.W. Wiedemann in 1819, only just over 100 papers have been published on the subject. To date, some 188 Conopidae species are reported from the region, but our knowledge of distribution and biology remains dispersed and fragmentary. The second part of the talk provides an overview of recent research by the writer to supplement this knowledge. The discussion covers the extent to which Afrotropical Conopidae can be identified reliably at present, the regions for which records are underrepresented and the themes on which research should focus in the future.

Molecular phylogeny of the subfamily Platypezinae (Platypezidae)

Gunilla Ståhls

Finnish Museum of Natural History, Zoology Unit, P.O. Box 17, 00014 University of Helsinki, Finland. gunilla.stahls@helsinki.fi.

Keywords: Molecular, phylogeny, Platypezinae.

A molecular phylogeny of the subfamily Platypezinae (Platypezidae) is inferred from analysis of DNA sequence data of standard genes (mtDNA COI and nuclear ribosomal 28S and 18S markers) and discussed with a recent molecular phylogeny of the Platypezidae, where relationships of Platypezinae remained largely unresolved. Focal questions were phylogenetic placement of *Metaclythia currani* Kessel and monophyly of the genus *Lindneromyia* Kessel & Maggioncalda. This study is especially focused on applying an extended taxon sampling, particularly from the Afrotropical Region, in addition to including an additional gene. Representatives of all Platypezinae taxa were included and analysed under maximum likelihood and Microsaniinae was used as out-group. Results are presented and discussed.

A new species of the wormlion genus *Alhajarmyia* Stuckenberg (Vermileonidae) – the second wormlion fly described from Kenya

Vaughn R. Swart[1]* & Robert S. Copeland[2]

[1]Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa. *SwartVR@ufs.ac.za
[2]International Centre of Insect Physiology and Ecology, Nairobi, Kenya.

Keywords: Afrotropical, *Alhajarmyia*, biogeography, *Isalomyia*, new species.

In 1999, *Lampromyia umbraticola* Stuckenberg & Fisher was described from the Al Hajar Mountains of northern Oman, being the first recorded species of the family Vermileonidae from the Arabian Peninsula and in 2003, B.R. Stuckenberg erected the new monotypic genus *Alhajarmyia* to contain it. He further suggested that dispersal from an East African ancestor may have produced the *Alhajarmyia* lineage in the Arabian Peninsula. A second species, *A. stuckenbergi* Swart, Kirk-Spriggs & Copeland, was described in 2015 from the Taita and Kasigau Hills in Kenya, being the first recorded species of the family Vermileonidae from East Africa. In this presentation the collection of an additional new Kenyan species of *Alhajarmyia* is reported. The discovery of a new species of *Alhajarmyia* from a locality 220 kms north of Kasigau and Taita Hills stands as further evidence in support of Stuckenberg's prediction of the occurrence of related species in East Africa. The new species differs from its congeners in characters of the male and female terminalia and in wing venation. It was collected at an elevation of 551 m in indigenous secondary dry forest at the base of Endau Mountain. The type locality, an isolated inselberg in arid eastern Kenya has been tentatively dated to the late Mesozoic.

Pathogen detection in bat flies (Hippoboscidae: Nycteribiinae) and their potential utilisation in host conservation

Tamara Szentiványi[1, 2]*, Laura Clément[2], Laurie Ançay[2], Loïc Brun[2],
Wanda Markotter[3], Teresa Kearney[4], Ernest Seamark[5], Muriel Dietrich[6],
Philippe Christe[2] & Olivier Glaizot[1, 2]

[1]Museum of Zoology, Palais de Rumine, Place de la Riponne 6, CH-1014 Lausanne, Switzerland.
*tamara.szentivanyi@unil.ch
[2]University of Lausanne, Lausanne, Switzerland.
[3]University of Pretoria, South Africa
[4]Ditsong National Museum of Natural History, Pretoria, South Africa.
[5]African Bats, Pretoria, South Africa.
[6]UMR Processus Infectieux en Milieu Insulaire Tropical, Sainte-Clotilde, La Réunion.

Keywords: Bat fly, conservation, Nycteribiinae, pathogen.

Bats are known as “keystone species” as they perform important ecosystems services. Nevertheless, their importance is also significant as reservoir species for zoonotic diseases. During this work, an evaluation was made of dipteran hematophagous ectoparasites in pathogen detection and their potential importance in future bat conservation projects is discussed (*e.g.*, voucher specimen collection and/or highly invasive blood sampling avoidance). Bat blood and ectoparasites were analysed to detect three distantly related pathogenic groups, using molecular methods (*i.e.*, the bacteria *Bartonella* Strong *et al*., the alveolate *Polychromophilus* Dionisi and the trypanosome *Trypanosoma* Gruby) and the detection rate was compared between hosts and ectoparasites. Two bat species were sampled and tested, *Miniopterus natalensis* Smith (South Africa) and *M. schreibersii* (Kuhl) (Hungary, Italy and Spain) and their highly specific ectoparasites, *Nycteribia schmidlii scotti* Falcoz and *N. schmidlii* Schiner, respectively. Results revealed that depending on the pathogen, the detection rate was different, but can be useful in determining pathogen presence and diversity. Future perspectives on host conservation and zoonosis monitoring are discussed.

Host associations and distribution of South African bat flies (Hippoboscidae: Nycteribiinae)

Tamara Szentiványi[1, 2]*, Wanda Markotter[3], Muriel Dietrich[3], Teresa Kearney[3], Ernest Seamark[4], Philippe Christe[2] & Olivier Glaizot[1, 2]

[1]Museum of Zoology, Palais de Rumine, Place de la Riponne 6, CH-1014, Lausanne, Switzerland.
*tamara.szentivanyi@unil.ch
[2]University of Lausanne, Biophore, CH-1015 Lausanne, Switzerland.
[3]University of Pretoria, South Africa.
[4]Ditsong National Museum of Natural History, Pretoria, South Africa and University of the Witwatersrand, Johannesburg, South Africa.

Keywords: Bat fly, Chiroptera, distribution, Nycteribiinae, South Africa.

Bat flies (Hippoboscidae: Nycteribiinae) are represented by 72 described species (or subspecies) in the Afrotropical Region, nine of which occur in South Africa (including only wingless bat flies, previously known as the family Nycteribiidae). Despite recent studies, little is known regarding the diversity and host associations in the Afrotropical nycteribiine fauna. Parasite sampling was undertaken from 2010–2017 at five collecting sites in South Africa, from both frugivorous and insectivorous bat species. Bat flies were collected from 469 individual bats of 11 species. A total of 808 nycteribiine flies were sampled representing seven species: *Basilia* sp., *Eucampsipoda africana* Theodor, *Nycteribia schmidlii scotti* Falcoz, *Penicillidia fulvida* Bigot, *Phthiridium ovalis* (Theodor), *P*. *scissa scissa* (Speiser) and *P*. *tecta* (Theodor). Recorded host associations and distribution data were collated from the literature, resulting from research conducted in 18 countries in the Afrotropics. This study revealed previously unknown host associations, including: *N*. *schdmilii scotti* associated with *Myotis tricolor* (Temminck); *Penicillidia fulvida* with *Cloeotis percivali* Thomas, *Rhinolophus smithersi* Bayliss & Cotterill and *Rousettus aegyptiacus* (Geoffroy); *Ph*. *ovalis* with *Rh*. *blasii* Peters and *Rh*. *simulator* K. Andersen; *Ph*. *scissa scissa* with *Rh*. *simulator* and *Rh*. *smithersi*; and *Ph*. *tecta* with *Rh*. *smithersi*. New associations for South Africa species are: *Nycteribia schmidlii scotti* and *Pe*. *fulvida*, both associated with *Nycteris thebaica* E. Geoffroy Saint-Hilaire. Bat fly host specificity, which was interpreted from the published literature and this research, appeared to be monoxenous (associated with a single host species), stenoxenous (associated with phylogenetically closely related hosts), or polyxenous (multiple, phylogenetically distantly related host species).

Toward morphological identification of third-instar larvae of forensically important blowflies (Calliphoridae) of Africa

Krzysztof Szpila[1]*, Kirstin A. Williams[2], Mfon Ekanem[3], Marise Heyns[4] & Martin Villet[5]

[1]Department of Ecology and Biogeography, Faculty of Biology and Environmental Protection, Nicolaus Copernicus University, Lwowska 1, 87-100 Toruń, Poland. *szpila@umk.pl
[2]KwaZulu-Natal Museum, Pietermaritzburg, South Africa.
[3]University of Uyo, Uyo, Nigeria.
[4]University of Cape Town, Cape Town, South Africa.
[5]Rhodes University, Grahamstown, South Africa.

Keywords: Africa, forensic entomology, identification key, larvae, species identification.

The lack of reliable, accessible identification tools is a serious obstacle to the practice of forensic entomology in most African countries. This situation affects common and ubiquitous groups, such as necrophagous Calliphoridae (blowflies). At least 16 species of African calliphorids have confirmed or potential forensic significance. The third-instar larvae of ten of these have been described, but the preimaginal morphology of the other six species remains unknown. Additionally, available morphological data are of varying quality and most species' descriptions are in need of revision using modern protocols. Using new larval material for the twelve most common species, the usefulness of traditional, commonly applied and newly discovered taxonomic characteristics are critically reviewed. For third-instar larvae, the most promising characters resulted from an analysis of the shape and distribution of larval spines. From analysis of this material using the new protocol, a preliminary identification key to third-instar larvae of African blowflies of forensic importance is presented, based on features that are easily observable, even in poorly equipped laboratories. This identification key will be expanded in the future to include species for which the larvae are not currently described.

Comparative morphology of the piercing-type ovipositor in the tribe Blondeliini (Tachinidae) and its phylogenetic implications

Takuji Tachi[1]*, Yu-Zen Huang[1] & Hiroshi Shima[2]

[1]Biosystematics Laboratory, Kyushu University, 744 Motooka, Fukuoka 819-0395, Japan.
*tachi@scs.kyushu-u.ac.jp
[2]Kyushu University Museum, Fukuoka, Japan.

Keywords: Apomorphy, female postabdomen, homology, modification, parallel evolution.

A piercing-type female ovipositor occurs in some genera of the tachinid tribe Blondellini, *e.g.*, *Blondelia* Robineau-Desvoidy, *Celatoria* Coquillett and *Medinodexia* Townsend. In D.M. Wood's (1985) "A taxonomic conspectus of the Blondeliini of North and Central America and the West Indies", he used this feature in couplet 1 of the generic identification key to the Blondeliini, to include the genera: *Blondelia*, *Celatoria*, *Compsilura* Bouché, *Eucelatoria* Townsend, *Proroglutea* Townsend and *Vibrissina* Rondani. According to Herting's (1956) paper "Das weibliche Postabdomen der Calyptraten Fliegen (Diptera) und sein Merkmalswert für die Systematik der Gruppe", the piercer is a modification of female abdominal sternite 7. In the paper "Molecular phylogeny of the subfamily Exoristinae (Diptera, Tachinidae), with discussions on the evolutionary history of female oviposition strategy", published in 2010, T. Tachi and H. Shima indicated that the piercing ovipositor evolved independently in the *Blondelia*-group and in *Medinodexia*. In this study, morphological features of the piercing ovipositor of the Blondeliini, were examined, particularly the invagination of the abdominal segments and the phylogenetic implications of this structure in Blondeliini phylogeny are evaluated and discussed.

Species diversity of Dolichopodidae unravels the partition of Oriental and Palaearctic Regions in Tibet

Chufei Tang* & Ding Yang

Department of Entomology, College of Plant Protection, China Agricultural University, Beijing, China. *tcf0816@126.com

Keywords: Dolichopodidae, long-legged flies, new species, new records, Tibet, zoogeography.

The Himalayan region of Tibet is traditionally regarded as the border of the Oriental and Palaearctic Regions, but its own regional affiliation remains disputed. Dolichopodidae is well known for its high species diversity. A five-year survey of Dolichopodidae was conducted in 21 sites of Tibet around 30 degrees of north latitude. Previously, only 39 species in 21 genera were recorded in the fauna of Tibet. As a result of this study, however, the number has risen to 114 species in 25 genera, of which 62 species in 16 genera are new to science and 13 species of 7 genera represent first records for Tibet. Notably, the genera *Alishania* Bickel, *Argyra* Macquart, *Chrysotus* Meigen, *Plagiozopelma* Enderlein, *Sciapus* Zeller and *Xanthochlorus* Haliday are reported from Tibet for the first time, with *Alishania*, *Sciapus* and *Xanthochlorus* being first records for the Himalayan region as a whole. *Hercostomus* Loew showed high species diversity in all sampled sites and species diversity in Nyingchi is distinctly higher than in the other areas sampled. Species from Lhasa and Qamdo exhibit a strong affinity to the Palaearctic Region, while species from Shannan and Nyingchi indicate affinities to the Oriental Region. By contrast, species from Xigaze exhibit mixed affinities with both the Oriental and Palaearctic. The pattern of species diversity is not, therefore, in accordance with latitudes.

Elevated atmospheric CO_2 promoted speciation in mosquitoes (Culicidae)

Chufei Tang[1]*, Katie E. Davis[2], Cyrille Delmer[3], Ding Yang[1] & Matthew A. Wills[3]

[1]Department of Entomology, College of Plant Protection, China Agricultural University, Beijing, China.
*tcf0816@126.com
[2]University of York, York, United Kingdom.
[3]University of Bath, Bath, United Kingdom.

Keywords: Elevated atmospheric CO_2, global warming, mosquitoes, MRP supertree, speciation rate.

Mosquitoes are of great medical significance as vectors of deadly diseases. Despite this, little is known about their evolutionary history or how their present day diversity has been shaped. Within a phylogenetic framework, a strong correlation is shown between climate change (temperature and atmospheric CO_2) and mosquito speciation rates: the first time such an effect has been demonstrated for insects. Information theory reveals that although climate change is correlated with mosquito evolution, there are other important factors at play. One such driver identified is the rise of mammals, which are significant hosts of Culicidae. Additional, unspecified, processes must be implicated in order to fully explain the association between climate change and biotic evolution. Regardless of the precise mechanism, a strong historical association is demonstrated in this presentation. This finding, taken in combination with projected rises in atmospheric CO_2 from anthropogenic activity, has important implications for culicid vector distributions and abundance and consequently for human health.

Diversity underestimated? Identifying lineages in the hypervariable keystone pollinator species *Prosoeca peringueyi* (Lichtwardt) (Nemestrinidae) from the Succulent Karoo biodiversity hotspot

Genevieve L. Theron[1]*, Allan G. Ellis[2], Bruce C. Anderson[2], Steve D. Johnson[1], Florent Grenier[2] & Timotheüs van der Niet[1]

[1]School of Life Sciences, University of KwaZulu-Natal, Private Bag X01, 3209 Scottsville, South Africa. *genevieveltheron@gmail.com
[2]Stellenbosch University, Stellenbosch, South Africa.

Keywords: DNA barcoding, morphological variation, niche partitioning, pollination, tangle-vein flies, taxonomy.

Global biodiversity hotspots represent ideal natural laboratories for studying the factors which drive the evolution and maintenance of both functional diversity and species richness. Poor species-level taxonomy, however, may result in hampered understanding of ecological and evolutionary processes. This study focuses on the morphologically variable long-tongued nemestrinid fly species *Prosoeca peringueyi* (Lichtwardt), from the Succulent Karoo biodiversity hotspot in Southern Africa – a keystone pollinator of dozens of plant species. Variation, both within and among populations often exhibit discrete rather than continuous patterns. In particular, extended proboscis length of *P*. *peringueyi* varies across its geographical range and also within single populations. The aim of this study is to identify operational taxonomic and morphological units to assess whether these coexist in communities by potentially partitioning local feeding resources and whether rapid evolution of traits determining feeding niches has occurred. DNA sequences for barcoding and phylogenetic techniques were applied, combined with proboscis length measurements of *P*. *peringueyi*, sampled from multiple different localities throughout the Succulent Karoo Biome. Comparison of proboscis lengths of flies with distinct genotypes within sites will reveal whether niche differentiation may explain coexistence of multiple lineages. Using these results, in combination with mapping of proboscis lengths and floral tube lengths onto a phylogenetic tree, can further distinguish between rapid, local evolution of proboscis length, or by ecological sorting. The results of this study will reveal whether mutualistic networks are as asymmetrical as previously thought. This study therefore has the potential to provide insights into the origin and maintenance of biodiversity.

Preliminary results of a morphological and molecular identification of Afrotropical Rhiniidae (Calyptratae)

Arianna Thomas-Cabianca[1]*, Eliana Buenaventura[2], Anabel Martínez-Sánchez[1] & Santos Rojo[1]

[1]Departamento de Ciencias Ambientales y Recursos Naturales. Universidad de Alicante, Aptdo 99 E-03080 Alicante, Spain. *athomasbio@gmail.com
[2]National Museum of Natural History, Washington D.C., U.S.A.

Keywords: COI barcode, diversity, nose flies, taxonomy.

Rhiniidae was recently accorded family rank on phylogenetic grounds. The family includes 376 described species, with ~150 species in 16 genera recorded from the Afrotropical Region. The taxonomic identification of many rhiniid species is highly challenging, there are many phenotypic similarities, females are not properly linked to conspecific males, larvae are largely unknown and their identification relies heavily on male terminalia characters. Accurate identification of males and females is relevant to conservation and pollination studies. In this study, COI barcode fragments of rhiniid specimens sampled in Kenya and South Africa were used in order to: test morphology-based identifications; link female morphotypes with conspecific males; and explore the phylogenetic relationships between genera and species. Intraspecific and interspecific genetic distances were calculated and reconstructed using neighbour-joining, maximum likelihood and Bayesian inference phylogenetic trees, to infer putative species limits and monophyly. Also provided for each species is a critical discussion, a morphological diagnosis and illustrations of the habitus and male and female terminalia. All thirteen morphology-based identified species were recovered as monophyletic and 100% identification success was obtained. Thus, the COI barcodes showed efficiency as an alternative means for rhiniid identification in the Afrotropical Region.

Spatial and temporal dynamics of Calliphoridae (Calyptratae) in an urban perturbation gradient in a locality of northern Venezuela

Arianna Thomas-Cabianca[1, 2]*, Jose Rafael Ferrer-París[3] & Ángel Viloria[1]

[1]Laboratorio de Biología de Organismos, Centro de Ecología, Instituto Venezolano de Investigaciones Científicas (IVIC), Carretera Panamericana, km 11 Altos de Pipe, Apartado postal 20632, Caracas 1020-A, Estado Miranda, Venezuela. *athomasbio@gmail.com
[2]Universidad de Alicante, Alicante, Spain.
[3]Instituto Venezolano de Investigaciones Científicas, Maracaibo, Venezuela.

Keywords: Blowflies, ecology, forensic entomology, synanthropy.

Little is known about the diversity and biology of Calliphoridae in northern South America, especially in Venezuela. In particular, the effects of deforestation/urbanisation (and their associated synanthropic processes) on Calliphoridae species remains poorly known. In this context, the goal was to evaluate the relationship between Calliphoridae and different anthropic perturbation and climatic conditions and determine the synanthropic degree of each species. Between November 2012 and June 2013 monthly collections were conducted in urban, semi-urban and wild environments. Environmental variables and Calliphoridae abundance and richness were recorded monthly. Rényi diversity profiles were used for evaluating diversity patterns. The synanthropic degree for each species was determined using an innovative statistical approach (species indicator index-IV) and Nourteva Synanthropic Index-SI. A total of 5,169 specimens were collected (14 species, four genera). Abundance was highest in wild areas and lowest in urban areas. *Lucilia cuprina* (Wiedemann) (IS = +88.26; IVu = 0.978) had the strongest association with urban environments; *Hemilucilia semidiaphana* (Rondani) (IS = -65.90; IVsu = 0.1751) and *Chrysomya megacephala* (F.) (IS = +50.65; IVsu = 0.5007) with semi-urban; and *H. semidiaphana* (IS = -65.90; IVw = 0.7188) and *H. segmentaria* (F.) (IS = -99.08; IVw = 0.6783) with wild. Temperature, relative humidity, month and type of environment were the most important variables for understanding the community dynamics. Species diversity did not show clear temporal or spatial patterns, while abundance and richness increased at higher temperatures and lower humidity. This study provides important information about the response of Calliphoridae to urbanisation and deforestation, relevant for forensic entomology and ecological applications.

Discovering the diversity and biology of South African nose flies (Rhiniidae) through entomological collections

Arianna Thomas-Cabianca[1]*, Anabel Martínez-Sánchez[1], Martin H. Villet[2] & Santos Rojo[1]

[1]Departamento de Ciencias Ambientales y Recursos Naturales. Universidad de Alicante, Aptdo 99 E-03080 Alicante, Spain. *athomasbio@gmail.com
[2]Rhodes University, Grahamstown, South Africa.

Keywords: Afrotropical, checklist, distribution, maps, taxonomy.

Rhiniidae, a taxon of ~376 known species, was recently accorded family rank on phylogenetic grounds. Around 150 recorded species in 16 genera are Afrotropical, 60 of which occur in South Africa. Taxonomic knowledge of this group is mostly outdated, as most taxonomic studies in South Africa were conducted from the 1950s to 1980s (mostly by Salvador Peris and Fritz Zumpt) and there is little information available on biology and ecology. To update this knowledge, an annotated checklist of species for South Africa was developed, based on the holdings of fifteen entomological collections in Africa, Europe and North America. Identification tools and distribution/occurrence maps were also developed. Over 3,800 rhiniids were examined, resulting in five new records for South Africa (*Cosmina undulata* Malloch, *Isomyia cuthbertsoni* (Curran), *Stomorhina apta* Curran, *S*. *chapini* Curran and *Thoracites kirkspriggsi* Kurahashi) and seven new species awaiting description. The annotated checklist includes comments on important novel biological information, seasonality, historical occurrence maps, identification keys to each genus and high-definition photographs for each species, including lateral, dorsal and frontal views and male terminalia. This research demonstrates the importance of reviewing entomological collections to improve knowledge of diversity and of using specimens' labels as an invaluable data resource for interpreting temporal and spatial occurrence, environmental preferences and plants associations, *inter alia*, relevant to conservation, pollination, pest management and historical biogeography.

Diversity of Diptera families on wild and cultivated plants in Cameroon

Sidonie Fameni Topé[1]*, Fernand-Nestor Tchuenguem Fohouo[2] & Dorothea Brückner[3]

[1]Department of Biological Sciences, Faculty of Sciences, University of Maroua, P.O. Box 814, Maroua, Cameroon. *sidofameni@gmail.com
[2]University of Ngaoundéré, Adamaoua, Cameroon.
[3]Forschungsstelle für Bienenkunde, Bremen, Germany.

Keywords: Agriculture, Cameroon, crops, Diptera, insects, pollinator diversity.

In Cameroon, as in many other countries, Diptera pollination has attracted less attention than pollination by bees (Hymenoptera), where published data mostly concern representatives of the family Apidae. The current study is a synthesis of published works (2008–2018) on the relationship between wild and cultivated plants and several fly families, undertaken in four regions of Cameroon. The results revealed that on 12 plant species the entomofauna included eight Diptera families (in order of prevalence): Calliphoridae, Muscidae, Syrphidae, Tephritidae, Stratiomyidae, Drosophilidae, Bombyliidae and Asilidae. Some flower visiting species were pollinators and nectarivorous, among these, some are known to collect nectar (*e.g.*, *Chrysomia pachymera* (Séguy) (Calliphoridae), *Musca domestica* L. (Muscidae) and *Paragus borbonicus* Macquart (Syrphidae)), whereas others collect pollen only (*e.g.*, *Episyrphus* sp. (Syrphidae), *Drosophila* sp. (Drosophilidae) and *Anastoechus* sp. (Bombyliidae)). One flower visitor, *Dacus bivittatus* (Bigot) (Tephritidae), is known to damage fruits. Some dipteran species exhibited high flower visit frequency. For example, the flower visit frequency of *M. domestica* on *Ricinus communis* L. (Euphorbiaceae) was 38.8%. It is important, therefore, to assess the impact of pollinating Diptera on fruit and seed yields of crop species, in order to manage their populations in Cameroon.

An update of diversity of soldier flies (Stratiomyidae) from Colombia and notes on distribution in Colombian biogeographical provinces

Juliana Torres Toro[1]*, Diego Aguilar Fachin[2], Diana Grisales[3] & Marta Wolff[1]

[1]Grupo de Entomología, Universidad de Antioquia, Cll. 67 #53–108, Medellín, Colombia.
*julianaerobia@gmail.com
[2]Universidade de São Paulo, Ribeirão Preto, Brazil.
[3]Instituto Superior de Formación Docente Salomé Ureña, Santo Domingo, Dominican Republic.

Keywords: Colombia, distribution, lower Brachycera, Neotropical Region, new records.

Stratiomyidae comprises 12 subfamilies, 367 genera and more than 2,800 species globally, that are mainly associated with decaying vegetable matter (larvae) and flowers (adults). Currently, ten subfamilies, 32 genera and 86 species of soldier flies have been recorded for Colombia. The main objectives of this study were to update the biodiversity of Stratiomyidae and to explore some common patterns of distribution of genera in Colombia. Based on more than 4,600 specimens of stratiomyids examined from Colombian collections, 48 genera, 21 of which are recorded for the first time in the country were identified. These genera occur in the Colombian biogeographical provinces of Cauca, Choco-Darien, Guajira, Imeri, Magdalena, Napo, Paramo and Sabana. The Neotropical genera *Diaphorostylus* Kertész, *Leucoptilum* James and *Panacris* Gerstaecker exhibited a tropical moist forest and transition zones of Andean forest distribution. Most *Oplachantha* Rondani species occurred in the high Andean forest, along with the three Andean cordilleras (Central, Occidental and Oriental), although a few species occur in tropical forest. *Chalcidomorphina* Enderlein appears to be restricted to tropical forest, contrasting with *Himantigera* James, which was only found in a very specific high Andean ecosystem. By contrast, global genera, such as *Hermetia* Latreille, *Ptecticus* Loew, *Sargus* F. and genera occurring in other zoogeographical regions (*Cyphomyia* Wiedemann and *Merosargus* Loew), have a broad distribution, occupying several ecosystems and provinces in the country. This study raises the number of stratiomyid genera occurring in Colombia from 32 to 53 and adds new points of distribution of these genera and species.

Insect pollinators of Cocoa, *Theobroma cacao* (L.) (Malvaceae) in Cameroon

Nadia Karelle Toukem[1]*, Rachid Hanna[1], Sevilor Kekeunou[2] & Apollin Fotso[1]

[1]International Institute of Tropical Agriculture (IITA), P.O. Box 2008, Yaoundé, Cameroon. *n.toukem@cgiar.org
[2]University of Yaoundé, Yaoundé, Cameroon.

Keywords: Cocoa, Cecidomyiidae, Ceratopogonidae, Diptera, trapping techniques.

Cocoa agroforestry systems (CAS) promote biodiversity conservation, climate regulation and economic growth in tropical zones. There has been very little attention, however, to determine the role of pollinators, despite the fact that the Cocoa tree is known as a self-incompatible tree and largely requires insects for successful pollination. A study was conducted to determine the diversity of potential insect pollinators of Cocoa flowers. Various traps were deployed in a 7-year old Cocoa orchard at weekly intervals, from July 2016 to January 2017. Per plot flower-visiting insects were sampled with an aspirator for 10 minutes (08h00–11h00) from three Cocoa trees. Insects were identified to order, but Diptera were identified to family level. In total 10,134 insects were collected. Common orders were Diptera (34%), Hymenoptera (30%), Hemiptera (13%), Coleoptera (9%), Thysanoptera (5%) and Psocoptera (8%). Diptera comprised mostly (in order of prevalence): Drosophilidae, Tephritidae, Cecidomyiidae, Sciaridae, Dolichopodidae and Phoridae and Ceratopogonidae, Diopsidae, Culicidae, Psychodidae, Tipulidae and Chironomidae to a lesser extent. Complementary field observations indicated that among Diptera only drosophilids, cecidomyiids and ceratopogonids visited Cocoa flowers, while aphids, thrips, ants and small parasitic wasps were observed on flowers. Surprisingly, ceratopogonids, which are widely recognised as the main Cocoa pollinators, were extremely rare (1% of flowers visitors) in the study area. Given the high abundance of cecidomyiids on Cocoa flowers (37%), it is here suggested that this family may also represent important pollinators of Cocoa in Cameroon. Further exclusion investigations will shed light of the role of Cecidomyiidae on Cocoa flower pollination.

Resolving the fly tree of life

Michelle D. Trautwein

California Academy of Sciences, 55 Music Concourse Dr, San Francisco, CA 94118, U.S.A.
mtrautwein@calacademy.org

Keywords: Phylogenomics, transcriptomes.

The resolution of the fly tree of life is increasingly well known, in part due to analyses based on large scale genomic data. Using transcriptome data from over 3,000 genes, the higher-level relationships of flies is estimated. In particular, it is aimed to elucidate relationships within phylogenetically ambiguous radiations of lower Diptera, lower Brachycera and Schizophora. The variation between topological results is explored, based on concatenation and species tree methods. The analyses recovered traditional groupings, as well as novel placements in need of further testing. Within lower Brachycera, the effectiveness of taxon sampling (>1,000 taxa) was compared to gene sampling. Thorough genomic sampling advances the resolution of the fly tree of life, but some key regions of ancient, rapid radiation remain tangled.

Towards a taxonomic revision and phylogeny of Natalimyzidae (Schizophora: ? Sciomyzoidea)

Pfarelo Grace Tshivhandekano[1]*, Ashley H. Kirk-Spriggs[2] &
Lelethu U.P. Heshula[1]

[1]Department of Zoology and Entomology, Fort Hare University, Alice 5700, South Africa.
*ptshivhandekano@ufh.ac.za
[2]National Museum, Bloemfontein, South Africa.

Keywords: Afrotropical Region, new taxa, phylogeny, revision, taxonomy.

The Natalimyzidae is one of only four families endemic to the Afrotropical Region in the extant fauna, although amber inclusions are known from Baltic amber, indicating a much wider geographical distribution in the geological past. Although recognised for some 40 years, the family was only formally described in 2006 and is currently only known from a single described genus and species, making it the most poorly studied families of flies in the Afrotropical Region. Despite this, numerous new species await descriptions, especially from South Africa. *Natalimyza* Barraclough & McAlpine, possesses a character state combination which is more readily reconcilable with the Sciomyzoidea than with any other schizophoran superfamily, but the placement is unresolved, pending the outcome of a detailed morphological and molecular phylogeny. Currently the family is regarded as sister-group to the non-Afrotropical Heterocheilidae. Larvae appear to be microflora grazers on decaying grass, probably during the dry winter months, but the immature stages remain unknown and undescribed. Grassland species sometimes occur sympatrically and at a particular habitat there may be a succession of species through the seasons. This ongoing projects aims to revise the family, describe the new taxa, obtain and describe the immature stages and undertake a molecular and morphological phylogeny to determine true relationships with sister-groups.

Poster

Taxonomic revision of the Neotropical genus *Rhabdotylus* Lutz (Tabanidae)

Mauren Turcatel

Smithsonian Institution, National Museum of Natural History, 10th and Constitution NW, Washington D.C., 20560-0169, U.S.A. TurcatelM@si.edu

Keywords: Horse fly, identification key, *Rhabdotylus*, taxonomy.

The Neotropical genus *Rhabdotylus* Lutz (Tabanidae) was described by A. Lutz in 1913, based on *Tabanus planiventre* Wiedemann. Later, G. Enderlein considered *Rhabdotylus* and *Dicladocera* Lutz as synonymous and designated *T*. *planiventre* as the type-species of his new genus *Gymnochela* (Enderlein). Subsequently, O. Kröber affirmed that both were synonymous with *Amphichlorops* Lutz, and G.B. Fairchild, noting the similarities in the head morphology of *Rhabdotylus* and *Stibasoma* Schiner, proposed *Rhabdotylus* as a subgenus of *Stibasoma*. More recently, P. Trojan revalidated *Rhabdotylus* as a genus, based on the differences in body pilosity and leg structure. Because of this continued discussion, a review is provided of the genus *Rhabdotylus* and the four species of the genus are re-described, namely: *R*. *planiventre* (Wiedemann), *R*. *ruber* (Thunberg), *R*. *venenata* (Osten Sacken) and *R*. *viridiventre* (Macquart). A dichotomous identification key based on external morphological characters is presented, along with high-resolution images of the type specimens.

Positioning the displacement of major mango and citrus fruit flies (Tephritidae) by *Bactrocera dorsalis* (Hendel) since its introduction in Nigeria

Vincent Umeh[1]*, Hygenus Ibekwe[2] & Lloyd Garcia[3]

[1]National Horticultural Research Institute, PMB 5432, Idi-Ishin, Jericho Reservation Area, Ibadan, Nigeria. *vumeha@yahoo.com
[2]National Horticultural Research Institute, Mbato, Nigeria.
[3]USDA, APHIS, Raleigh, U.S.A.

Keywords: *Bactrocera*, *Ceratitis*, fruit flies, displacement, Nigeria, pests.

Currently, major fruit flies pests of mango and citrus in Nigeria are representatives of the genera *Bactrocera* Macquart and *Ceratitis* Macleay. Prior to 2003, *Bactrocera* spp. were not recorded from Nigeria. Major Afrotropical species of economic importance included: *C. capitata* (Wiedemann), *C. cosyra* (Walker) and *C. fasciventris* (Bezzi) on mango and *C. capitata* and *C. ditissima* (Munro) on citrus. A continuous decrease of these pest species was recorded from the period of the introduction of *Bactrocera dorsalis* (Hendel) in Nigeria to the present. From initial *C. capitata* and *C. ditissima* populations of on average of 4 flies/trap/day on sweet oranges in 2004, the population reduced to 0–1 flies/trap/day in 2016 in dry and wet season catches. Incubated sweet orange fruits, which recorded an average of 2–2.5 flies/fruit of *C. capitata* and *C. ditissima* before the advent *B. dorsalis* reduced to 0.5–0 flies/fruit from 2005–2016. On mango, the study revealed 96% and 90% reduction of *C. cosyra* populations in trap catches and incubated fruits respectively, between 2005 and 2016. Similarly, on citrus *Ceratitis* spp. population reduction of more than 98% compared to *B. dorsalis* was recorded. These studies confirmed active displacement of *Ceratitis* spp. by *B. dorsalis*. This study also updates the checklist of fruit flies associated with mango and citrus at present in various agro-ecological zones of Nigeria and the climatic factors affecting the major species of economic importance on these crops.

New species of *Bruggmannia* Tavares (Cecidomyiidae) from the Neotropical Region, with comments on host-plant association

Maria Virginia Urso-Guimarães[1, 2]* & Carolina de Almeida Garcia[2]

[1]Laboratório de Sistemática de Diptera, DBio, CCHB, Universidade Federal de São Carlos – Campus Sorocaba, Rodovia João Leme dos Santos, Km 110 – SP-264, Bairro do Itinga, Sorocaba, SP, Brazil, 18052-780. *mvirginiaurso@gmail.com
[2]Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil.

Keywords: Gall maker, phylogenetic analysis, host-plant association, Neotropical Region, taxonomy.

Bruggmannia Tavares is a genus of the tribe Asphondyliini (Cecidomyiidae), endemic to the Neotropical Region, with 19 known species, mostly from Brazil. The known species of *Bruggmannia* induce simple or complex galls in species of the host-plant families Myrsinaceae, Nyctaginaceae and Rubiaceae. A new species from Parque Nacional da Chapada dos Guimarães, Mato Grosso State, Brazil is described based on adults, pupa, morphotype of gall and associations with the host-plant, *Anacardium humile* A. St.-Hil. (Anacardiaceae). This is the first record of an association of *Buggmannia* and a host-plant of the family Anacardiaceae. The phylogenetic position of the *Bruggmannia* sp nov. among the other species of the genus was performed using parsimony analysis. The analysis resulted in one most parsimonious tree, including 12 species of *Bruggmannia* in three main branches, one of them including *Bruggmannia* sp. nov. as sister-group of *B*. *pustulans* Möhn and *B*. *randiae* Möhn. A strong association with host-plants of the Nyctaginaceae family also discussed in this study.

Poster

A review of the genus *Sepedoninus* Verbeke (Sciomyzidae) with the description of *S. madagascariensis* sp. n. from Madagascar

Jean-Claude Vala

LBLGC-INRA, Université d'Orléans, USC 1328, 45067, Orléans, France. Université d'Orléans.
UFR Sciences and Laboratoire Biologie LBLGC, BP 6759 – 45067 Orléans cedex 2, France.
*jean-claude.vala@wanadoo.fr

Keywords: Acalyptrata, Afrotropical Region, identification key, morphology, new species, snail-killing flies.

The Afrotropical Sciomyzidae fauna comprises 68 extant species in 12 genera. The genus *Sepedoninus* Verbeke currently comprises two described species: *S*. *curvisetis* Verbeke (synonym: *S*. *straeleni* Verbeke, *nec* Knutson), recorded from Cameroon, Democratic Republic of Congo and Nigeria and *S*. *planifrons* Verbeke, recorded from Democratic Republic of Congo and Uganda. The genus was formerly regarded as being endemic to the Afrotropics, but an undescribed species is now known from Borneo in the Oriental Region. Examination of the collections of Muséum national d'Histoire naturelle, Paris, France, revealed a female specimen collected in Madagascar in 1930, which clearly belongs to the genus *Sepedoninus*, but differs significantly from the two described species. The new species is described as *S*. *madagascariensis* sp. n. and an identification key to the four species of *Sepedoninus* is presented, including the two undescribed species from Borneo and Madagascar.

Taxonomy and feeding behaviour of Afrotropical snail-killing flies (Sciomyzidae)

Jean-Claude Vala[1]*, William L. Murphy[2] & Jay Abercrombie[3]

[1]LBLGC-INRA, Université d'Orléans, USC 1328, 45067, Orléans, France. Université d'Orléans. UFR Sciences and Laboratoire Biologie LBLGC, BP 6759 – 45067 Orléans cedex 2, France.
*jean-claude.vala@wanadoo.fr
[2]7835 Tufton Street, Fishers, U.S.A
[3]2321 Bixler Drive, Suffield, U.S.A.

Keywords: Acalyptratae, distribution, identification key, malacophagy, Schizophora, taxonomy.

Sciomyzidae, or snail-killing flies, numbers 542 valid extant species and three subspecies in 61 genera globally. The Afrotropical fauna comprises 68 species in 12 genera, including four that are endemic: *Ethiolimnia* Verbeke, *Sepedonella* Verbeke, *Tetanoptera* Verbeke and *Verbekaria* Knutson (*Sepedoninus* Verbeke, formally regarded as endemic is here excluded; an undescribed species is known from the orient). Included in this total are two recently described species from Nigeria by Knutson & Deeming and one from Madagascar by Vala. J. Verbeke published the most important research on Afrotropical Sciomyzidae during the 1950s and early 1960s and as part of this project published literature on Afrotropical Sciomyzidae was reviewed and specimens were examined in various collections, including the two major collections housing Verbeke's type material and other specimens of Afrotropical origin, *i.e.*, Institut royal des Sciences naturelles de Belgique, Brussels and Musée royal de l'Afrique centrale, Tervuren (both Belgium). A new illustrated identification key to genera of Afrotropical Sciomyzidae is presented, including taxonomic changes as well as additions to recognised genera and species within each genus. Larval development of only 12 Afrotropical Sciomyzidae species are known and the vast majority of Sciomyzidae are malacophagous. Larval feeding behaviour of some Afrotropical species that are not malacophagous are outlined and unusual larval morphological characters for two species are described, that allow rapid and correct species identifications. This presentation is dedicated to the memory of Lloyd Knutson and expands on the chapter on Sciomyzidae which will appear in Volume 3 of the *Manual of Afrotropical Diptera*.

Matching tubes and tongues – local coevolution or ancient species sorting?

Timotheüs van der Niet[1, 2]*, Gustavo Cisneros[1], Harro de Moor[1], Amanda Hoogenboom[1], Ruth Cozien[1], Ethan Newman[3] & Bruce C. Anderson[3]

[1]Naturalis Biodiversity Centre, P.O. Box 9517, 2300 RA Leiden, The Netherlands. *vdniet@gmail.com
[2]University of KwaZulu-Natal, Pietermaritzburg, South Africa.
[3]Stellenbosch University, Stellenbosch, South Africa.

Keywords: Coevolution, Drakensberg, geographical mosaic, Nemestrinidae, pollination, tongue, tube.

Geographical covariation of functional plant and pollinator traits has been thought to originate from locally operating coevolution. In particular, the absence of a correlation between geographical distance and trait differences suggests that coevolutionary dynamics may differ, even across short gradients. Population level sampling of nuclear and mitochondrial DNA sequences of the charismatic nemestrinid long-tongued fly species *Prosoeca ganglbaueri* Lichtwardt (Nemestrinidae) are used to investigate genetic signatures of evolutionary processes in a geographical context. Along two altitude gradients in the northern and southern Drakensberg of South Africa, long-tongued populations were found at low elevations, whereas short-tongued populations occurred at high elevations. A phylogenetic analysis revealed that in both cases long- and short-tongued populations are not sister, but rather belonged to different clades. Ancestral character state reconstructions further suggested that tongue length at these highly divergent sites did not necessarily evolved *in situ*. Finally, no evidence was found for a correlation between genetic and geographical distance, suggesting that ranges of preexisting lineages have recently shifted. It is concluded that the current paradigm of a geographical mosaic of coevolution may not apply to South African long-tongued and long-tubed mutualistic partners. Instead, recent climatic perturbations may have resulted in large-scale range shifts, accompanied by species sorting, resulting in current patterns of trait covariation.

Photographs as a means of revealing the adaptive function of morphological characters

Nikita E. Vikhrev

Department of Entomology, Zoological Museum of Moscow University, Bolshaya Nikitskaya 2, Moscow 125009, Russia. nikita6510@ya.ru

Keywords: Dolichopodidae, ecology, *Hydrophorus praecox*, photographic registration.

Hydrophorus praecox (Lehmann) (Dolichopodidae) is a common and widespread species, with males having a characteristic ventral spine at the apex of the fore tibia. In general, it is assumed that modifications of the male legs in Diptera are usually adaptations for courtship or copulation, but the true function of these adaptations is virtually never known. In Senegal, numerous pairs of *H. praecox* were observed for extended periods moving together in the copulating position, but without true copulation. Unpaired males attempted to dislodge coupled males, but these attempts were unsuccessful. Thus, males of *H. praecox* act in a similar fashion to dragonflies, which also spend long periods in tandem to avoid the concession of females to other males. *Hydrophorus* feed on lower Diptera larvae that occur in silt and females continue to hunt and feed while in tandem, while males can neither hunt nor afford to leave the female. It was observed, that in order to feed, the male fly moved its body far forwards and took larvae directly from the female's mouthparts. Examination of photographic images recording this behaviour, revealed that although the male's body moves forward, the apex of the fore tibia remains in the same position, with the ventral spine of the fore tibia is inserted into the female's posterior spiracle. The adaptive function of the apical spine is, therefore, clarified by photographic examination. Use of the tibial spine serves to allow males to firmly grip females in tandem and thus resist attacks by other males, and at the same time, permits males to move forwards to feed.

Poster

Geographic variation of acoustic preferences and host specificity in frog-biting midges (Corethrellidae)

Jonas Virgo[1]*, Kathrin P. Lampert[1, 2], T. Ulmar Grafe[3] & Thomas Eltz[1]

[1]Department of Animal Ecology, Evolution and Biodiversity; Ruhr-University Bochum, Universitätsstrasse 150, 44801 Bochum, Germany. *jonas.virgo@rub.de
[2]University of Cologne, Cologne, Germany.
[3]University Brunei Darussalam, Brunei Darussalam.

Keywords: *Corethrella*, “eavesdroppers”, hematophagy, phonotaxis.

Phonotactically oriented female frog-biting midges (*Corethrella* Coquillet) obtain blood meals from calling male frogs, locating them by “eavesdropping” on their advertisement calls. Observed variations in acoustic preferences are likely to be a result of adaptation to regional frog-host communities, transmission properties of the environment, variation in noise levels and/or phylogenetic constraints. This study investigated how acoustic preferences of frog-biting midges differ between various locations (Pacific and Atlantic slopes) and habitats (lentic and lotic) in Costa Rica and between Costa Rica and Borneo. The influence of frog host communities and potential key host species on the divergence of midge acoustic preferences are discussed, as well as potential effects arising from habitat filters, local soundscapes and phylogeny.

Poster

Host choice and acoustic preferences of frog-biting midges (Corethrellidae) in lowland Pacific Costa Rica

Jonas Virgo[1]*, Kathrin P. Lampert[1, 2], T. Ulmar Grafe[3] & Thomas Eltz[1]

[1]Department of Animal Ecology, Evolution and Biodiversity; Ruhr-University Bochum, Universitätsstrasse 150, 44801 Bochum, Germany. *jonas.virgo@rub.de
[2]University of Cologne, Cologne, Germany
[3]University Brunei Darussalam, Brunei Darussalam.

Keywords: *Corethrella*, “eavesdroppers”, hematophagy, phonotaxis.

Ectoparasitic frog-biting midges of the genus *Corethrella* (Coquilllet) detect their blood hosts, male frogs, by “eavesdropping” on their advertisement calls. Variable attraction rates to different calls have been observed, suggesting a selective perception or preference for certain call characteristics. During field studies in lowland Pacific Costa Rica, midge attraction to both recorded natural frog calls and synthetic call models displayed with acoustic traps were investigated and results were compared to midge samples collected directly from frogs. Midges were attracted to a broad range of sounds, but showed pronounced attraction to those with low peak frequencies (< 1 kHz) and short pulse durations (~300 ms), most closely resembling the calls of their most preferred blood hosts. Although it was found that calls of syntopic frog species attracted different *Corethrella* species in significantly different proportions, acoustic niche differentiation among midge species appeared to be moderate. In comparison, midges collected directly from frog hosts showed more pronounced host preferences, indicating different levels of specificity within the midge community. It is suggested that additional close-range, non-acoustic (*i.e.*, chemical) host recognition cues could explain this pattern.

The relevance of short-proboscid pollinators associated with flowers with nectar spur

Anna Vlašánková[1, 2], Eliška Padyšáková[1, 3], Michael Bartoš[3, 4], Ximo Mengual[5]*, Petra Janečková[2, 4] & Štěpán Janeček[3, 4]

[1]Institute of Entomology, The Czech Academy of Sciences, České Budějovice, Czech Republic.
[2]University of South Bohemia, České Budějovice, Czech Republic.
[3]Charles University, Prague, Czech Republic.
[4]Institute of Botany, The Czech Academy of Sciences, Třeboň, Czech Republic.
[5]Zoologisches Forschungsmuseum Alexander Koenig, Leibniz Institut für Biodiversität der Tiere, Adenauerallee 160, D-53113 Bonn, Germany. *x.mengual@leibniz-zfmk.de

Keywords: Coevolutionary race, exploitation barrier, insect visitors, pollinator shift, tubular flowers.

Since the time of Charles Darwin, biologists have considered the floral nectar spur to be an adaptation representing a high degree of plant specialisation. Nevertheless, some researchers suggest that plant-pollinator communities are more complex and that even morphologically specialised plants attract a wide spectrum of visitors. The flower visitors of *Impatiens burtonii* Hook.f. (Balsaminaceae) were surveyed in Cameroon, West Africa. In this study, the depth of the proboscis insertion into the spur, the distance of the nectar surface from the spur entrance and the visitor's effectiveness were measured. Three insect species frequently contacted the stigmas of *I. burtonii* flowers and can, therefore, be considered potential pollinators. The hoverfly *Melanostoma* sp. n., with the shortest proboscis, was most active early in the morning and fed on pollen and nectar near the spur entrance. The honeybee *Apis mellifera* L. and the hoverfly *Rhingia mecyana* Speiser were the most frequent visitors before and after noon, respectively. Although *R. mecyana* (the only visitor able to reach the end of the spur) was the most frequent and effective flower visitor, it did not deposit the largest number of pollen grains per visit. Nectar spurs may function as complex structures allowing pollination by both short- and long-proboscid visitors and separating their spatial and temporal niches. Spurred plants should be considered as more generalised than previously thought and they are exposed to more diverse selection pressures than previously believed.

Is dirty work useful in taxonomy and systematics?

Emma Wahlberg

Department of Zoology, Swedish Museum of Natural History, P.O. Box 50007, SE-104 05 Stockholm, Sweden. emma.wahlberg@nrm.se

Keywords: eDNA, Empidoidea, NGS.

With vast number of species, open ended and orphan taxa, there are Diptera groups that are overlooked in both ecological and evolutionary research. In contrast to these flies, the active human experts studying these constitute a very small number. Many species are notoriously difficult to identify, even for well-trained experts. How can these people contribute to ecological and natural history research in taxonomically immense groups? Molecular tools for larger scaled surveys and environmental sampling are incessantly being developed, giving new opportunities to study large taxon groups in a wide context. With over 10,000 known species globally, the superfamily Empidoidea is no exception. In ecological studies, surveys and general collections, individuals are seldom identified further than to family level. To further complicate the situation, several species are difficult to collect with common traps and demand time consuming manual labour to collect. In an effort to demonstrate novel approaches in taxonomic and systematic research, as well as bringing taxonomy closer to ecology, new methods of sampling and sequencing are explored. Molecular barcodes from soil, sediment and water are used to discover both known and new taxa. Environmental DNA could be used not only to survey specific localities, but also map and study species and higher taxonomic groups in a biogeographical context.

Progress in the systematics of Empidoidea and why it matters

Emma Wahlberg

Department of Zoology, Swedish Museum of Natural History, P.O. Box 50007, SE-104 05 Stockholm, Sweden. emma.wahlberg@nrm.se

Keywords: Phylogeny, molecular methods.

The large and morphologically diverse Empidoidea occupy a vast array of habitats and different species-groups express a great variation in life histories and morphology. The group has been subject to multiple revisions and for the past decades the internal relationships are considered unknown. Although several studies regarding, for example, biological indicators, pollination and land use include records of Empidoidea, they mostly do not identify taxa to species or even to genus level. Unstable classifications, unplaced genera and difficult taxonomic problems may discourage non-specialists. Here, a phylogeny based on the mitochondrial genes COI and Cyt*β* and the nuclear genes CAD, EF-1*α* and IDH in a Bayesian analysis is presented. Several groups withstand testing, but novel relationships were also found in the evolutionary context and can present more thorough and stable phylogenetic hypothesis than presented previously. These results illustrate that the higher systematics of Empidoidea are more similar to previous tentative molecular studies than those based on morphological data, but several subfamilies and tribes based on morphology are corroborated. A synthesis of old and new methods and collaboration within the specialist community may prove vital in the move towards both a stable classification and accessibility of Empidoidea taxonomy.

Soil, sediment and water – hands down in fly surveys?

Emma Wahlberg

Department of Zoology, Swedish Museum of Natural History, P. O. Box 50007, SE-104 05 Stockholm, Sweden. emma.wahlberg@nrm.se

Keywords: Empidoidea, eDNA, environmental study.

The Empidoidea is a large superfamily within the Diptera, comprising over 10,000 known species globally. The group has been subject to multiple revisions and for the past decades internal relationships have been debated. Studies involving biological indicators, pollination and land use often include records of Empidoidea. However, in many cases taxa are not identified to species or even genus level. Ecological data associated with the correct taxa is vital in research, especially in a group that exhibits a vast array of life histories, behaviour, feeding habits and habitat choice, as does Empidoidea. Environmental DNA, molecular fragments in environmental samples, is a method developed and refined contemporary with next generation sequencing practices. Recently, these methods have proved successful in studies involving microbial, botanical and mammalian diversity and ecological communities. Here a pilot study is presented, using eDNA to explore the possibilities in finding Diptera in general and Empidoidea specifically, through sequencing of DNA fragments from water, sediment and soil samples. This method promises less work hours in the field, fewer determination errors and less invasiveness than traps. Protocols previously published and developed using mock samples are tested, developed and refined to produce field protocols for ecology and biodiversity studies within Diptera.

Poster

Evolutionary relationships among Australian snail parasite blowflies (Calliphoridae: Ameniinae)

James F. Wallman*, Nathan J. Butterworth & Nikolas P. Johnston

Centre for Sustainable Ecosystem Solutions, School of Biological Sciences, University of Wollongong, NSW 2522, Australia. *jwallman@uow.edu.au

Keywords: Ameniinae, blowflies, molecular systematics, parasites.

Blowflies of the subfamily Ameniinae (Calliphoridae) are among the most impressive representatives of the Australian fly fauna, notable for their metallic colouration, often combined with white spots or bands. They comprise seven genera, of which six occur in Australia and two, *Amenia* Robineau-Desvoidy and *Paraplatytropesa* Crosskey, are endemic to that continent. Other genera are also variously found in Indonesia, New Guinea and throughout the Oriental Region. *Amenia* is the most speciose genus of Australian ameniines, with ten known species. The biology of the subfamily is poorly known, but all species are probably macrolarviparous and larval parasites in land snails. Despite their striking appearance and widespread distributions, the Australian species have received little attention in recent years. Here an overview is provided of the state of knowledge of the group and an analysis, based on mitochondrial and nuclear DNA, of species relationships and their placement within the Calliphoridae.

An identification system using DNA sequences and image methods for fruit flies of economic importance (Tephritidae)

Jiang-ning Wang, Xiao-lin Chen*, Xin-wen Hou & Ying-ying Chen

Chinese Academy of Sciences, Beijing 100101, China. *xlchen@ioz.ac.cn

Keywords: Deep learning, DNA sequence identification, fruit fly pests, image identification.

Many species of Tephritidae are damaging to fruit, which have negative impacts on the international fruit trade. This requires rapid and accurate species identifications where expertise is often lacking. Automatic or semi-automatic identification of fruit flies are greatly needed for diagnosing causes of damage and quarantine protocols for economically relevant insects. A fruit fly identification system, named AFIS2.0, has been developed which can combine DNA sequences and image recognition methods in combination. Currently, the methods based on images and DNA sequence are two independent identification methods which have been developed along their own directions and each has its own advantages and disadvantages. What is being done is to integrate these two methods under one software frame to try to enable the quarantine officers to identify fruit flies more easily, quickly and accurately. This work is based on the existing full- / semi-automatic fruit fly image identification methods developed by deep learning and the molecular identification tools based on Blast+. The basic frame of AFIS2.0 has been completed, but more DNA sequences and image data need to be integrated and the dual images and DNA sequence tests will be carried out soon.

Taxonomy of Fanniidae (Muscoidea) in China

Ming-fu Wang[1]* & Dong Zhang[2]

[1]Institute of Entomology, Shenyang Normal University, Shenyang, 110034, China.
*wangmingfu403@163.com
[2]School of Nature Conservation, Beijing Forestry University, Beijing, China.

Keywords: Identification, morphology-based phylogeny.

Fanniidae (Cyclorrhapha: Calyptratae: Muscoidea) are cosmopolitan flies currently known for over 400 species globally. In China, 160 species are recorded, including one species in *Euryomma* Stein, two species in *Piezura* Rondani and 157 species in *Fannia* Robineau-Desvoidy, which account for 40% of species of the family; moreover, 61% (*i.e*., 98 species) are endemic in China. According to a morphology-based phylogenetic analyses, all 160 species were divided into 12 groups, including 21 species in the *Fannia scalaris*-group, 3 in the *F*. *lepida*-group, 6 in *F. hirticeps*-group, 23 in *F*. *carbonaria*-group, 16 in *F*. *postica*-group, 4 in *F*. *jezoensis*-group, 5 in *F*. *metallipennis*-group, 13 in *F*. *fuscinata*-group, 6 in *F*. *posticata*-group, 25 in *F*. *serena*-group, 20 in *F*. *mollissima*-group and 18 species in *F*. *canicularis*-group. Identification keys for species-group and species were developed. This study suggests that, with 98 endemic species, which make up 61.25% of Chinese fanniid diversity, the abundant and diverse Chinese fanniids comprise 40% of its worldwide diversity.

A forensic entomological analysis can yield an estimate of post-mortem interval and not just minimum post-mortem interval – many practitioners have done it

Jeffrey D. Wells

Department of Biological Sciences, Florida International University, 11200 SW 8th Street, Miami, FL 33199, U.S.A. jedwell@fiu.edu

Keywords: Carrion insect succession, death investigation, pre-appearance interval.

The forensic entomology literature contains many variations on the claim that forensic entomologists cannot estimate the post-mortem interval (PMI). Common supporting reasoning was that estimating PMI must involve: 1) predicting specimen age; and 2) assuming that the oldest insect collected was deposited on or near the corpse very soon after death. The main criticism targeted that assumption of immediate oviposition/larviposition, but sometimes the argument went further and included the claim that the time period from death until initial insect colonisation (sometimes called the pre-appearance interval) is unknowable. As a result, according to this logic, one can never estimate maximum PMI (dead not more than X amount of time) using entomological knowledge, only minimum PMI (dead not less than X amount of time). Apparently, such critics never acknowledged the numerous publications proposing a method of PMI estimation using a succession rather than a development analysis. A succession experiment includes measurement of the pre-appearance interval and a succession analysis yields an estimate of how long the corpse was at the site of discovery. If death occurred at that site then the estimate equals PMI. The logic of this approach is perhaps most clear in a “no-insect” case, in which an analyst reaches a conclusion concerning how long the corpse, obviously killed where found, could have been at that location and not yet been colonised by carrion insects (maximum PMI). I will illustrate this using a murder trial during which several North American forensic entomologists estimated maximum PMI or PMI.

The potential role of post-mortem interval prediction performance in forensic entomological research design and interpretation

Jeffrey D. Wells[1]* & Lynn R. LaMotte[2]

[1]Department of Biological Sciences, Florida International University, 11200 SW 8th Street, Miami, FL 33199, U.S.A. *jedwell@fiu.edu
[2]Louisiana State University Health Sciences Center, New Orleans, U.S.A.

Keywords: Coverage proportion, error rate, forensic entomology, predictive model, statistical methods, validation.

The most common forensic entomological application is inferring some portion of the post-mortem interval (PMI). Usually a prediction of PMI (or insect age, *etc*.) should be a range, rather than a point estimate, and it is now possible to calculate a confidence set for an estimate of carrion insect age or succession interval, using multivariate data with both continuous and categorical responses. In turn, prediction performance can be objectively measured as the coverage proportion; a standard statistical method for describing the error rate, in terms of both correct and incorrect estimates. PMI prediction method performance should be the most important measure of the scientific validity and maturity of forensic entomology as a discipline. It can also be a useful guide to experimental design and the interpretation of experimental results. This presentation illustrates how this approach can be used to: 1) choose a better sampling scheme; 2) calculate the amount of replication required; 3) focus on the most important variables to record; and 4) determine if an effect of a treatment on growth or succession rate is of practical importance rather than statistically significant.

Poster

Phylogenetic analysis of South African *Aedes* Meigen, *Anopheles* Meigen and *Culex* L. (Culicidae) based on COI, ITS2 and ND4 sequences

Liezl Whitehead[1]*, Vaughn R. Swart[1], Marieka Gryzenhout[2] &
Lizette L. Koekemoer[3]

[1]Department of Zoology and Entomology, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa. *whiteheadl@ufs.ac.za
[2]University of the Free State, Bloemfontein, South Africa.
[3]National Institute for Communicable Diseases, Johannesburg, South Africa.

Keywords: *Aedes*, *Anopheles*, *Culex*, DNA, molecular phylogeny, vector.

Investigations into mosquito phylogeny can help illuminate relationships between species, giving insight into potentially shared characteristics, such as susceptibility to insecticide resistance and vector competence. The current research aims to investigate the molecular phylogeny and diversity of *Aedes* (Meigen), *Anopheles* (Meigen) and *Culex* (L.) species sampled in the Free State and Eastern Cape Provinces, South Africa. Sampling methods will include the use of a CO_2 baited nets, sweep netting and hand collection. Sampling will be conducted in a variety of bioregions, in both natural and urban habitats, to ensure that a representative sample of species is collected. The study will utilise three gene regions, namely cytochrome oxidase subunit 1 (COI), NADH dehydrogenase subunit 4 (ND4) and internal transcribed spacer 2 (ITS2) for the molecular phylogeny. Phylogenetic relationships will then be inferred using the DNA sequences, which will be compared with current phylogenetic hypotheses. Little molecular research has been conducted on South African *Aedes* and *Culex*, thus research may identify potential species complexes and undescribed species. It would also provide the opportunity to gather up-to-date data on community composition, distribution and habitat association of vectors in the Free State and Eastern Cape Provinces, creating a foundation for future research and vector control efforts. The field data could also aid epidemiological studies in assessing risk and probability of infection and disease occurrences.

Italy's most common flesh fly re-identified – with insights on relationships within *Sarcophaga* Meigen *sensu stricto* (Sarcophagidae)

Daniel Whitmore[1, 2]*, Giorgia Giordani[3], Steen Thorleif Dupont[2] & Stefano Vanin[3]

[1]Department of Entomology, Staatliches Museum für Naturkunde, Rosenstein 1, 70191 Stuttgart, Germany. *whitmore.daniel@gmail.com
[2]Natural History Museum, London, United Kingdom.
[3]University of Huddersfield, Huddersfield, United Kingdom.

Keywords: COI barcodes, Croatia, distribution, Europe, morphology, Oestroidea, Palaearctic.

The west Palaearctic subgenus *Sarcophaga* Meigen *sensu stricto* currently comprises just under 35 valid species and is most diverse in the eastern part of its range, although it is understudied in southern Europe and North Africa. Despite including some of the most common and widespread sarcophagids in Europe, the group has a history of misidentifications, including that of the type species of the family, due to the great morphological similarity of its species. The recent study of a large series of specimens collected with Malaise traps in Italy uncovered a long-standing misidentification of two species under the name *Sarcophaga variegata* (Scopoli). The second species was preliminarily identified morphologically as *S. croatica* Baranov, a species previously only known from the type locality. This identification was confirmed by a broader molecular analysis, using DNA barcodes, which provided new insights into relationships within the *S. variegata* species-group and the distribution of these species in continental Italy. Specimens used in the analysis were collected from numerous sites along the Adriatic and Tyrrhenian coasts of Italy from Trentino-Alto Adige to Sicily, as well as from Croatia, the type locality of Baranov's species. This analysis indicates a clear distinction between the two species at the molecular level and confirms that knowledge of this subgenus is far from complete, even in western Europe.

Phylogenomic strategies to resolve major fly radiations – characters, complexity and the new data-rich paradigm

Brian M. Wiegmann

North Carolina State University, Department of Entomology and Plant Pathology, Raleigh, NC 27695, U.S.A. bwiegman@ncsu.edu

Keywords: Anchored hybrid enrichment, phylogenomics, phylogeny.

Large phylogenomic data sets have greatly improved the resolving power of fly molecular systematics analyses. Complex species radiations, adequate sampling of characters and taxa and challenging analytical issues, all remain critically important for reconstructing fly phylogeny. Working together with an international team of dipterists, large datasets have been compiled from genomes, transcriptomes and hybrid enrichment, to investigate fly relationships at multiple levels of the hierarchy. These new data analyses demonstrate the potential of these datasets to reveal relationships within the major fly radiations. New results are presented from phylogenetic analyses using all publically available fly genomes, from large transcriptome harvests and from anchored hybrid enrichment (AHE), to help resolve relationships in key areas of the fly tree of life. New k-mer based methods that provide character data from thousands of non-targeted loci are demonstrated and evaluated, against approaches where gene orthology is established *a priori*. Insights into the origin and evolution of the earliest fly lineages, the relationships among lower brachyceran families, the phylogeny of acalyptrate Schizophora and the diversification of mosquitoes are presented as examples of the challenges and resolving power of these data. The on-going search for new data strategies is key to successfully implementing phylogenomics research. With this new paradigm inspiring dipterological collaborations, biologically plausible phylogenetic hypotheses are sought that will provide reliable context for evolutionary investigations in flies.

Seasonal and spatial distribution of forensically important blowflies in Makhanda, Eastern Cape, South Africa

Kirstin A. Williams[1]* & Martin H. Villet[2]

[1]Department of Natural Science, KwaZulu-Natal Museum, Private Bag 9070, Pietermaritzburg, 3200, South Africa. *kwilliams@nmsa.org.za
[2]Rhodes University, Grahamstown, South Africa.

Keywords: Blowfly, Calliphoridae, seasonal distribution, spatial distribution, South Africa.

The seasonal activity of adults of eight forensically important blowfly species: *Calliphora croceipalpis*, Jaennicke, *Chrysomya albiceps* (Weidemann), *C. chloropyga* (Weidemann), *C. marginalis* (Weidemann), *C. megacephala* (F.), *C. putoria* (Weidemann), *Lucilia sericata* (Meigen) and *L. cuprina* (Weidemann), was quantified in Makhanda (Grahamstown), South Africa, using modified Red-Top fly traps baited with chicken liver and placed in the field at eight locations for four consecutive days each fortnight for 14 months. The seasonal distribution of each species compared well to published seasonal distributions of these blowflies elsewhere in South Africa. These showed favourable comparisons to the seasonal trapping of this study. This information is important for determining when and where certain species are likely to occur for use in forensic cases.

Composition of Diptera communities associated with macrofungi in Colombia

Marta Wolff* & Carolina Henao Sepúlveda

Grupo de Entomología, Universidad de Antioquia, Cll. 67 #53–108, Medellín, Colombia.
*marta.entomologia@gmail.com

Keywords: Colombia, fungus, high Andean ecosystems, interactions.

Studies of Diptera/fungus interactions provide important information regarding the ecology and biology of species, but such associations have been poorly studied in Neotropical ecosystems. The purpose of this study was to ascertain the possible ecological associations between Diptera and macrofungi in high elevation Andean ecosystems in Colombia. A total of 2,601 specimens, representing 26 families of Diptera, were reared from 24 families of fungi in Colombia. Diptera were reared from fruiting bodies of large fungi sampled between developmental stages III and IV, in various forests, ranging from 1,500–3,000 masl. from September to December 2016–2017. The majority of reared specimens belonged to the family Sciaridae (29.1%), reared from 18 fungus families; followed by Drosophilidae (21.2%) reared from 18, Mycetophilidae (16.1%) from 13, Phoridae (11.7%) from 14, Psychodidae (9.4%) from 11, Limoniidae (6.2%) from six, Ceratopogonidae (1.9%) from one and Muscidae (1.1%) from four fungus families. The families Anisopodidae, Anthomyiidae, Cecidomyiidae, Chironomidae, Chloropidae, Dolichopodidae, Empididae, Ephydridae, Keroplatidae, Milichiidae, Muscidae, Richardiidae, Scatopsidae, Sphaeroceridae, Stratiomyidae, Syrphidae, Tachinidae and Ulidiidae were all represented by less than ten individuals. Most of the Diptera recorded can be classified as polymycophagous, only Ceratopogonidae and Limoniidae exhibited preference for fungi of the family Polyporaceae. Such interactions constitute important knowledge in the understanding of forests dynamics and the organisms that inhabit them.

Application of delimitation methods to determine intra-specific molecular diversity in Miltogramminae (Sarcophagidae)

Dominika Wyborska[1]*, Marcin Piwczyński[1], Kamran Akbarzadeh[2] & Krzysztof Szpila[1]

[1]Department of Ecology and Biogeography, Faculty of Biology and Environmental Protection, Nicolaus Copernicus University in Toruń, Poland. *dominika.wyborska@wp.pl
[2]Tehran University of Medical Sciences, Tehran, Iran.

Keywords: COI gene, Iran, species delimitation.

Miltogramminae flies (Sarcophagidae) are mostly kleptoparasites of solitary bees and wasps, most frequently observed in the desert and semi-desert regions of Asia and Africa. The majority of species are described based on hard to grasp characters, such as differences in the abdominal colour pattern, specialised chaetotaxy of the first pair of male legs or head proportions. It was, therefore, decided to test whether morphological diversity corresponds to genetic diversity, using molecular variation in COI gene (1,530 bp) in species of the genera *Apodacra* Macquart, *Miltogramma* Meigen and *Sphecapatodes* Villeneuve, occurring in Iran (collectively over 380 specimens representing 15 species). A haplotype network analysis of COI revealed a few groups within each studied morpho-species, which differ from 40 to even 80 mutations. This intra-specific diversity may suggest the sympatric occurrence of cryptic species. In order to verify these preliminary observations, a delimitation analysis was conducted by ABGD and GMYC models. The ABGD model, on the one hand, was in line with morphological variation, except three individuals tentatively determined as *A*. *plumipes* Villeneuve. The GMYC model, on the other hand, recognised for some combination of parameters more species than expected from the morphological analysis. Hence, results were unstable and depended mainly on the chosen substitution model. It is concluded that morphological characters used to recognise species of Miltogramminae are in the majority of cases in accordance with the analysis of COI barcode marker, although high local intraspecific genetic variation exists and requires further investigation.

First descriptions of the female terminalia of Afrotropical *Phthiria* Meigen (Bombyliidae: Phthiriinae)

Carolina Yamaguchi[1]* & Carlos José Einicker Lamas[2]

[1]Institute of Bioscience, University of São Paulo (USP), R. do Matão, 14 Butantã, São Paulo, SP, 05508-090, Brazil. *c.yamaguchi@usp.br
[2]Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil.

Keywords: Afrotropical Region, bee flies, female terminalia, taxonomy.

The Phthiriinae is a subfamily of small bee flies that includes two tribes (Phthiriini and Poecilognathini), 134 described species and 12 genera, characterised by an evident sexual dimorphism. The genus *Phthiria* Meigen is distributed in the Afrotropical, Neotropical, Oriental and Palaearctic Regions, with 62 valid species, of which 22 are recorded from the Afrotropics, six from the Neotropics, 33 from the Palaearctic and one from the Oriental Region. *Phthiria* species are superficially very similar externally and identification is mainly based on characters of the male terminalia. In the first half of the 20th century, Albert John Hesse published one of the most significant works on Afrotropical Bombyliidae, being the first author to recognise the importance of the male terminalia in the taxonomy of the group. Since Hesse, no revisionary work has been undertaken on Afrotropical *Phthiria* and the female terminalia and spermathecae have remained unknown. In this study a detailed description, illustrations and images of the female terminalia of 12 Afrotropical *Phthiria* species are provided for the first time and these characters will be applied in an identification key under construction. The female terminalia of Afrotropical *Phthiria* can also assist with the segregation of *Phthiria* from other Phthiriini genera, as a tubular spermathecal bulb is present in all studied Afrotropical species and the lack of a thin membrane on the apical ducts and the presence of basal and apical sclerotised collars, also proved important to segregate Afrotropical species from those occurring in other regions.

Poster

Cladistic analysis of Phthiriinae Becker (Bombyliidae) using morphological characters

Carolina Yamaguchi[1]*, Neal L. Evenhuis[2] & Carlos José Einicker Lamas[3]

[1]Institute of Bioscience, University of São Paulo (USP), R. do Matão, 14 Butantã, São Paulo, SP, 05508-090, Brazil. *c.yamaguchi@usp.br
[2]Bernice Pauahi Bishop Museum, Honolulu, U.S.A.
[3]Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil.

Keywords: Bee flies, phylogeny, subfamily, systematics, taxonomy.

The Phthiriinae are small bee flies, comprising two tribes, 12 genera and 134 species, characterised by an evident sexual dimorphism. Currently, the Phthiriini encompasses seven genera: *Acreophthiria* Evenhuis, *Acreotrichus* Macquart, *Australiphthiria* Evenhuis, *Elektrophthiria* Nel, *Neacreotrichus* Cockerell, *Phthiria* Meigen, *Pygocona* Hull and Poecilognathini five genera: *Euryphthiria* Evenhuis, *Hirsutophallus* Yamaguchi, Lamas & Evenhuis, *Poecilognathus* Jaennicke, *Relictiphthiria* Evenhuis and *Tmemophlebia* Evenhuis. The main objective of this project was to undertake a phylogenetic analysis of the Phthiriinae and specifically to test the monophyly of the subfamily, tribes and genera in order to propose a new classification for the subfamily. The cladistic analysis included species of all genera, represented in a matrix with 74 terminal taxa and 216 morphological characters. Results indicate four MPTs in the equal weight analysis and one single tree in the implied weight analysis, which was chosen for discussion. The monophyly of Phthiriinae is recovered. A new subfamily is proposed for *Elektrophthiria*, once it is positioned outside the group. The tribes Phthiriini and Poecilognathini are also monophyletic. Genera are recovered as monophyletic for the most part, although *Phthiria*, *Poecilognathus*, *Relictiphthiria* and *Tmemophlebia* were recovered as paraphyletic. To enable the monophyly of *Phthiria*, a new genus will be erected to gather the Afrotropical species and *Poecilognathus* will be rendered monophyletic following the withdrawal of *Po*. *philippianus* Rondani and *Po*. *xanthogaster* Hall, which will be placed in two new monotypic genera, belonging to Phthiriini and Poecilognathini, respectively. Therefore, *Tmemophlebia* will be considered a junior synonym of *Relictiphthiria*.

Poster

Shedding the first light on the evolution of the stomach botflies (Oestridae: Gasterophilinae)

Liping Yan[1]*, Dong Zhang[1] & Thomas Pape[2]

[1]School of Nature Conservation, Beijing Forestry University, Beijing 100083, China.
*yanlp523@qq.com
[2]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Gasterophilinae, mitochondrial genome, phylogeny, stomach botfly.

The stomach botflies consist of three genera, *Cobboldia* Brauer, *Gyrostigma* Hope, and *Gasterophilus* Leach, larvae of which are obligate parasites of elephants, rhinoceroses and equids respectively, living a mysterious life in the digestive tract of their hosts. Stomach botflies have thus received great attention. Their evolutionary history has rarely been studied however. To trace the evolution of stomach botflies, the mitogenomes we sequenced for six out of currently eight known species of *Gasterophilus*, one *Gyrostigma* species and one *Cobboldia* species. The phylogeny of stomach botflies was reconstructed on the broadest taxon sampling hitherto and for the first time based on molecular data. Maximum likelihood analysis and Bayesian inference were employed to reconstruct the phylogeny, using all thirteen protein-coding genes and two rRNA genes, with two oestrid species as out-groups. The relationship is estimated to be (*Cobboldia*, (*Gyrostigma*, (*Gasterophilus pecorum* (F.), (*Ga*. *intestinalis* (De Geer), (*Ga*. *haemorrhoidalis* (L.), *Ga*. *inermis* (Brauer))), (*Ga*. *nasalis* (L.), *Ga*. *nigricornis* (Loew))))). Based on the resultant phylogenetic framework of stomach botflies, the first insights into the evolutionary history of the stomach botflies is presented, including the host shift and evolution of oviposition and third-instar larval attachment locations.

Pseudopomyza (Pseudopomyzidae) *versus* the Limosininae (Sphaeroceridae) – parallel systematics studies and insights into acalyptrate diversity

Tiffany Yau* & Stephen A. Marshall

University of Guelph Insect Collection and Systematics Laboratory, School of Environmental Sciences, Edmund C. Bovey Building, University of Guelph, Guelph, ON, Canada, N1G 2W1. *tyau@alumni.uoguelph.ca

Keywords: Comparative morphology, Neotropical Region, new species, Pseudopomyzidae, Sphaeroceridae.

Two very distant clades of small to minute flies from the New World have offered contrasting taxonomic challenges and rewards. One is a group of brightly and distinctively marked shiny yellow and brown species, the other group presents a uniform and dull appearance. Looks can be deceiving however. The seemingly dull flies in the genus *Bromeloecia* Spuler (Sphaeroceridae: Limosininae) have character-rich wings and wing interference patterns and informatively elaborate terminalia. The attractive species of *Pseudopomyza* (*Rhinopomyzella* Hennig) (Pseudopomyzidae), alternatively, offer a limited and highly homoplastic character set. Current revisions of these two contrasting groups are compared and contrasted, concluding that the only thing they have in common is a remarkably high proportion of new species awaiting description and naming.

Mecoptera, molecules and morphology – phylogenomic perspective on the origin of Diptera

David K. Yeates[1]*, Karen Meusemann[2], Frank Friedrich[3], Michelle D. Trautwein[4], Bernhard Misof[5] & Rolf G. Beutel[6]

[1]Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, Australia. *david.yeates@csiro.au
[2]University of Freiburg, Freiburg, Germany.
[3]Universität Hamburg, Hamburg, Germany.
[4]California Academy of Sciences, San Francisco, U.S.A.
[5]Zoological Research Museum A. Koenig, Bonn, Germany.
[6]Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Jena, Germany.

Keywords: Antliophora, Mecoptera, morphology, phylogenomics, Siphonaptera, transcriptome.

The Mecoptera (scorpionflies) play a crucial role in the evolutionary cradle of insect lineages that gave rise to the Diptera in the Permian. No consensus has been achieved regarding the monophyly of Mecoptera and their relationship to Diptera (true flies) and Siphonaptera (fleas), using morphology and Sanger-era molecular datasets. In order to apply as much data as possible to the problem, these relationships were addressed using transcriptome-derived phylogenomic datasets using the 1KITE data analysis pipeline. Results are here presented of analysing “relaxed” and “strict” phylogenomic datasets spanning between 0.5 million and 1.4 million amino acid sites. Partitioned analyses based on protein domains indicated strong signal for a paraphyletic Mecoptera, with the enigmatic Nannochoristidae placed as sister-group to fleas. Also identified was a weak signal for a monophyletic Mecoptera, with Boreidae sister to (Nannochoristidae + remaining families). Quartet mapping showed that these data are not biased by uneven data-distribution or model violation, due to heterogeneity. Although the strongest signal supports a paraphyletic Mecoptera, its monophyly based on Four-Cluster Likelihood Mapping and AU tests cannot be rejected. The recent increase in knowledge of the morphology of larval and adult scorpionflies has not had decisive impact on our knowledge of Antliophora phylogeny. An unusual configuration of the male postabdomen supports the monophyly of Mecoptera. Other features of adults and larvae suggest either Nannochoristidae or Boreidae are sister to the remaining families. Nannochoristidae share derived features of the adult mouthparts and pharynx with fleas, however, these also occur in Diptera and probably evolved independently in the three groups.

NGS barcoding accelerates species discovery of "open-ended" taxa in a largely neglected and highly threatened tropical habitat

Darren Yeo[1]*, Amrita Srivathsan[1], Jayanthi Puniamoorthy[1], Foo Maosheng[2] & Rudolf Meier[1]

[1]Department of Biological Sciences, National University of Singapore, Science Drive 4, S1A 05-20, Singapore 117543. *darrrn.yeo@gmail.com
[2]Lee Kong Chian Natural History Museum, Singapore.

Keywords: Barcoding, community ecology, habitat assessment, Mycetophiliformia, Phoridae, sequencing, tropical rainforest.

Taxa such as the Phoridae and Mycetophiliformia are both hyper-diverse and poorly understood, with many species in the tropics yet to be discovered. With a fast and cost-effective specimen-based NGS barcoding pipeline, totals of *ca* 500 species of phorids (4,031 specimens) and 300 species of mycetophiliformids (4,658 specimens) were discovered from various habitat types across Singapore: mangroves, tropical rainforest, freshwater swamp forest and disturbed secondary forest. This was part of a mangrove insect study, involving 30,810 Diptera specimens from 2,597 Malaise trap samples representing 485 trapping months. The specimens are sequenced non-destructively, pre-sorted *via* NGS barcodes and are available for downstream morphological verification and further taxonomic work. Ecological analyses on these samples reveal mangroves to have highly distinct and unexpectedly species-rich dipteran communities, even when compared to neighbouring tropical rainforest. This has significant conservation implications as a globally imperilled habitat is host to a substantial yet largely unknown proportion of the global insect diversity. This study demonstrates the importance of developing new techniques to greatly accelerate the rate of insect species discovery and community-level habitat assessment, especially in hyper-diverse, "open-ended" taxa in threatened ecosystems.

Phylogenetics of lower Cyclorrhapha using next-gen sequencing and morphological data

Andrew D. Young[1, 2]*, Jeffrey H. Skevington[2], Bradley J. Sinclair[2], Jeffrey Cumming[2], Keith M. Bayless[3], Scott Kelso[2], Bernhard Misof[4], Brian M. Wiegmann[5], Emily M. Lemmon[6] & Alan. R. Lemmon[6]

[1]California Department of Food and Agriculture, 3288 Meadowview Road, Sacramento, CA, 95832, U.S.A. *adyoung@gmail.com
[2]Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa, Canada.
[3]Australian National Insect Collection, Canberra, Australia.
[4]Zoological Research Museum Alexander Koenig, Bonn, Germany.
[5]North Carolina State University, Raleigh, U.S.A.
[6]Florida State University, Tallahassee, U.S.A.

Keywords: Bayesian inference, hybrid enrichment, maximum likelihood, phylogenetics, transcriptomics.

Phylogenetic hypotheses for lower Cyclorrhapha (Brachycera) were constructed using existing transcriptome and hybrid enrichment sequence data, as well as an extensive morphological matrix. Each data matrix was analysed separately. Analyses were performed using 43 in-group taxa and a variety of analytical parameters and programs. Final molecular results are largely concordant with previously published molecular phylogenetic studies and demonstrate the utility of combined transcriptomic and hybrid enrichment data. Major phylogenetic relationships recovered include: Apystomyiidae sister to Cyclorrhapha, Lonchopteridae as sister to either the remainder of Cyclorrhapha (in nucleotide analyses), or sister to the remainder of Platypezoidea (in amino acid analyses), Opetiidae sister to *Microsania* Zetterstedt, either as part of Platypezidae or separate from it and Pipunculidae sister to Schizophora. Some of these results conflicted with the analysis of the morphological data. The failure to unambiguously recover a sister family to the remainder of Cyclorrhapha demonstrate that the phylogenetics of this group will remain a contentious issue for the foreseeable future.

Revision of Australian *Psilota* Meigen (Syrphidae)

Andrew D. Young[1, 2]*, Jeffrey H. Skevington[2], Wouter van Steenis[3] &
F. Christian Thompson[4]

[1]California Department of Food and Agriculture, 3288 Meadowview Road, Sacramento, CA, 95832, U.S.A. *adyoung@gmail.com
[2]Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa, Canada.
[3]Breukelen, the Netherlands
[4]Ponte Vedra, U.S.A

Keywords: Australia, COI, Eristalinae, new species, species complex, taxonomy.

The 34 species of Australian *Psilota* Meigen are revised, with 26 new species described. Currently recognised, but previously described species are re-described, with the males of *P. auricauda* Curran and *P. basalis* Walker, described for the first time. Six previously described species (*P. erythrogaster* Curran, *P. hirta* Klocker, *P. queenslandica* Klocker, *P. rubra* Klocker, *P. rubriventris* Bigot and *P. shannoni* Goot), cannot be recognised; these belong to the currently intractable *P. cuprea* and *P. tristis* species-groups, that will be addressed in a future publication. The genus is rarely collected and species poor in the Nearctic (3 species), Palaearctic (8 species) and Oriental (4 species) Regions, but is abundantly found in the Australasian Region, which is the centre of diversity. Unlike other *Psilota*, many Australian species are strongly iridescent or otherwise brightly coloured. What is known of *Psilota* natural history is based on studies and accounts of a few species, including two relatively common Australian species. It is hoped that by revising the Australian fauna and providing an identification key to species, together with full colour plates in an open-access format, that the profile of this intriguing genus can be elevated in Australia. This in turn may lead to new observations of their natural history, increasing our knowledge of the genus further.

Is the term surstylus a meme?

Tadeusz Zatwarnicki

Institute of Biology, University of Opole, ul. Oleska 22, 45-052 Opole, Poland. zatwar@uni.opole.pl

Keywords: Eremoneura, homology, male terminalia.

As compared to the rest of the Diptera, the male terminalia of Eremoneura are highly modified. It is widely accepted that the gonostylus is lost and replaced by a new structure, separated from the epandrium, termed the surstylus (pleural: surstyli). The term was first proposed by G.C. Crampton in 1923 for the epandrial projection and was later applied, again by Crampton in 1936, for the secondary clasping lobes in higher Diptera. There are several indicators of the homology of clasping lobes in Eremoneura with the gonostylus such as musculature, ontogeny and transformation series. Several theories on the origin of surstyli (*e.g.*, that this is derived from sternite 10, or that the gonostylus is attached to the hypandrium) have already been rejected and the reduction of the gonostylus and presence of the surstylus in Eremoneura is largely supported by empty words. The male terminalia of *Apystomyia* Melander (Apystomyiidae), with the ventral elongation of the epandrium, are cited to support the surstylar concept. Nonetheless, *Apystomyia* also bears a developed gonostylus, attached to the hypandrium, which indicates its position in Brachycera: “Orthorrhapha” (close to Apioceridae, Apsilocephalidae and Hilarmorphidae), not in Eremoneura; its subepandrial sclerotisation may have developed independently. It is argued that the term surstylus is “ballast”, functioning like a meme in the dipterological literature. Ontogenetic comparative studies in major lineages of Diptera, which are already available for *Drosophila* Fallén (Drosophilidae), could easily determine the true origin of clasping lobes in Eremoneura.

Phylogeny of the tribe Atissini (Ephydridae)

Tadeusz Zatwarnicki

Institute of Biology, University of Opole, ul. Oleska 22, 45-052 Opole, Poland. zatwar@uni.opole.pl

Keywords: Atissini, phylogeny, proboscis.

The tribe Atissini was proposed by E.T. Cresson, Jr. in 1942, for a group of shore flies with densely microtomentose, curved aristal branches and the posterior notopleural seta distinctly removed dorsad from the notopleural sutural margin and the current limits of the genus were established by T. Zatwarnicki in 1992. Atissini represent the smallest shore flies and these rarely exceed 2 mm in length. Seven genera are known: *Asmeringa* Becker, *Atissa* Haliday *in* Curtis, *Cerobothrium* Frey, *Isgamera* Giordani Soika, *Ptilomyia* Coquillett, *Schema* Becker and *Subpelignus* Papp. Relationships among Atissini genera are based on characters of the proboscis, especially the shape of the pseudotracheae, the structure of the cibarial sensillae and also the shape of the ventral receptacle. Results of a phylogeny of the Atissini are presented, which indicate two recognised branches, with the most derived group (*Asmeringa* + *Cerobothrium* + *Isgamera*) characterised by the lack of ventral cibarial sensillae and the hypopygium with a genital plate.

Poster

Tachinidae of the Hengduan Mountains of south-western China

Chuntian Zhang[1]*, Qiang Wang[2], Jiayu Liu[3], Zhiyuan Yao[1], Zhe Zhao[4], Peng Hou[5], Houcan Liang[1] & Xinyi Li[1]

[1]Liaoning Key Laboratory of Biological Evolution and Biodiversity, College of Life Science, Shenyang Normal University, Shenyang 110034, Liaoning, China. *chuntianzhang@aliyun.com
[2]Shanghai entry exit inspection and Quarantine Bureau, China Customs, Shanghai, China.
[3]Guizhou Medical University, Guiyang, China.
[4]Chinese Academy of Sciences, Beijing, China.
[5]Department of Entomology, China Agricultural University, Beijing.

Keywords: Biodiversity, biogeography, China, Hengduan Mountains, tachinid flies, taxonomy.

The Hengduan Mountains (350,000–500,000 km^2, including north Yunnan, a sliver of east Myanmar, east Tibet and west Sichuan) in south-western China are recognised as one of the world's 36 biodiversity hotspots. These mountains are contiguous with the south-eastern edge of the Qinghai-Tibet Plateau, which began forming *ca* 65 MYA, as the Indian tectonic plate drifted northward and collided with the Eurasian plate. The uplift of the Hengduan Mountains region created a spectacular series of seven parallel high mountain ranges separated by six deep valleys with fast-flowing rivers. The combination of high mountains, deep valleys, climatic variation and rapid evolution has resulted in the Hengduan Mountains becoming one of the most biologically diverse temperate forest ecosystems in the world. The Hengduan Mountains hotspot is exceptionally rich in Tachinidae, as reflected in the high number of species and endemics recorded from Sichuan (418 species in 126 genera, 134 endemic) and Yunnan (428 species in 121 genera, 148 endemic), compared to all of China (1,253 species in 280 genera, 40 tribes of 4 subfamilies; 438 endemic). A large number of tachinid specimens were collected from two provinces during expeditions organised by Shenyang Normal University (SYNU), the National Zoological Museum of China, Institute of Zoology, Chinese Academy of Sciences (IZCAS) and China Agricultural University (CAU) and Shanghai Entomological Museum (SEMCAS) since 1981. A checklist (660 species, 147 genera, 29 tribes of 4 subfamilies, 166 endemic) of the Tachinidae collected from Yunnan and Sichuan is provided.

Transcriptomic perspective of Sarcophagidae (Oestroidea) phylogeny

Dong Zhang[1]*, Liping Yan[1] & Thomas Pape[2]

[1]School of Nature Conservation, Beijing Forestry University, Beijing 100083, China.
*ernest8445@163.com
[2]Natural History Museum of Denmark, Copenhagen, Denmark.

Keywords: Flesh flies, kleptoparasitism, phylogenomics, transcriptome.

With almost 3,000 known species, Sarcophagidae (flesh flies) are one of the most diverse groups of Calyptratae, but the phylogenetic position and relationships are still debatable. Transcriptomes were obtained from 25 sarcophagid species and combined with transcriptomic data of another 12 calyptrate species, from which the first transcriptomic phylogeny of Sarcophagidae was inferred from different datasets (3,723, 2,320 and 603 genes respectively). Following a modified 1KITE pipeline, the phylogenomic analyses of amino acid and nucleotide sequences yielded robust and congruent results. The monophyly of Sarcophagidae is strongly supported, with Sarcophagidae being sister-group of (Oestridae [as represented by *Cuterebra* Clark] + Mystacinobiidae) and subfamily level relationships are inferred as (Sarcophaginae, (Paramacronychiinae, Miltogramminae)). With a supertree approach, sarcophagid phylogeny is reconstructed at genus level, with the broadest taxon coverage ever, based on which the geographical origin and ancestral larval life habit of Sarcophagidae were traced.

Brachyceran flies in Mid-Cretaceous “Burmese amber” – diversity and ecological significance

Qingqing Zhang[1, 2]* & Bo Wang[1]

[1]State Key Laboratory of Palaeobiology and Stratigraphy, Nanjing Institute of Geology and Palaeontology and Center for Excellence in Life and Paleoenvironment, Chinese Academy of Sciences, 39 East Beijing Road, Nanjing 210008, China. *qqzhang@nigpas.ac.cn
[2]University of Science and Technology of China, Hefei, China.

Keywords: Brachycera, “Burmese amber”, Diptera, fossil, Mesozoic, Mid-Cretaceous.

The lower Brachycera is among one of the most dominant groups of Diptera and also one of the most ecologically ubiquitous and significant. All of the major brachyceran lineages above the family level originated before the earliest age estimates for the appearance of flowering plants and the fossil record is quite abundant in the Mesozoic, especially in the Late Jurassic and Early Cretaceous. “Burmese amber” from Kukawng Valley, northern Myanmar, yields abundant insect inclusions, with a geological age of *ca* 99 MYA (Mid-Cretaceous), consistent with the radiation of angiosperms. Diptera are quite diverse in “Burmese amber” and the three-dimensionally preserved insects provide excellent material to compare fossils with extant groups and provide further evidence of their phylogeny, biogeography and coevolution with plants. Extant groups (including Asiloidea, Nemestrinoidea, Stratiomyomorpha, Tabanomorpha and Xylophagomorpha) and the extinct superfamily Archisargoidea in the lower Brachycera all occur as fossil inclusions in “Burmese amber”. To date, at least 16 families of early branching brachyceran flies have been found in “Burmese amber”, among them the extinct flower-visiting Zhangsolvidae, endoparasitoid Eremochaetidae, the relict family Apsilocephalidae and the extant, predominant flower-visiting Bombyliidae. These brachyceran groups recorded in “Burmese amber” played a significant role in the origin of coevolutionary relationships with basal angiosperms. The rise of angiosperms not only resulted in increasing diversity of flower-visiting flies, but also facilitated turnover and evolution of other specialised flies.

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