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ABSTRACTS

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10 – 15 August 2014

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8th International Congress of Dipterology

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Preface

This volume contains the abstracts of 410 oral and poster presentations submitted to the organizing committee of the 8th International Congress of Dipterology in Potsdam, Germany, from 10th–15th August, 2014. This hefty booklet attests to a record Congress attendance, covering a broad range of dipterological topics and representing the activity and success of the dipterological community worldwide.

The table of contents is sorted by the 22 symposia to facilitate search for particular topics. Indices at the back of the volume list the names of all authors and key words. Abstracts are arranged in alphabetical order by first author, and names of presenting authors are marked with an asterisk. The header for each abstract indicates the relevant symposium and presentation format (oral or poster); the footer provides the correct citation of this volume.

Most abstracts were edited to a certain extent by the respective symposium organizers as well as the editors, in consultation with the authors. The content of abstracts remains the sole responsibility of the authors. Layout and indexing were done by Sara Werner (pcma). We thank Harald Fuchs for the cover photo and are glad that he chooses to incorporate dipterans in his artistic work.

We extend our thanks to all ICD8 participants and to all those who helped organize the Congress or generously supported it in different ways.

Netta Dorchin, Marion Kotrba, Ximo Mengual, Frank Menzel
July 2014

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Table of contents

Abstracts sorted by symposia and first author:

Acalyptratae

Advances in Neotropical Dipterology

Applied Dipterology

Behavioral ecology

Bibionomorpha

Biodiversity surveys

Calyptratae

Culicomorpha

Diptera anatomy and morphology

Diptera biogeography – patterns and processes

Empidoidea

Evolution and ecology of parasitoid Diptera

Forensic Dipterology

Fossil Diptera

Global Dipterology

Higher-level phylogeny of Diptera

Molecular identification of Diptera

Plenary talk

Psychodomorpha

Sciomyzidae

Stalk-eyed flies

Syrphoidea

Taxonomy and Phylogeny of Orthorrhapha

Tephritoidea

Tipulomorpha

Traps, attractants and collection techniques for dipterans

8th International Congress of Dipterology

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Abstracts

Blowfly phenology and trap catches in cold climate areas

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Keywords: *C. vicina*, blowfly, phenology, community, cold climate, seasonality

Standardised field trapping of blowflies may provide knowledge of species-specificity in seasonality and reproductive phenology. During a 6-year mass trapping project, undertaken to suppress the population of the blowfly *Calliphora vicina*, a three-component lure was developed. The attractive properties of this attractant is closely linked to egg development and egg laying behaviour in both wind tunnel and field studies. Used in traps, this lure may thus provide a greater understanding of the dynamics of the entire blowfly community and the blowflies' spatio-temporal distribution in different habitats. The long term and large-scale trapping project describes the seasonality of several forensically important species in cold climate areas. The trapping area is located in a coastal region north of the polar circle where central life history events such as hatching, adult prolonged existence and egg laying are strongly dependent on the temperature. The focus species is *C. vicina* and its phenological plasticity, but catches of *C. uralensis*, *C. vomitoria*, *Protophormia terraenovae*, and *Cynomya mortuorum* are also described and discussed according to the seasonal coexistence and separation from *C. vicina*.

A review of the genus *Tabanus* Linnaeus, 1758 (Diptera: Tabanidae) from Egypt

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Keywords: Horse flies, new record, *Atylotus*, distribution

The Egyptian fauna of the genus *Tabanus* Linnaeus is reviewed. Only seventeen species are recognized instead of the previous 21. This is because six species have been removed as doubtful records, and an additional two species have been added (*T. leucostomus* Loew, 1858 (new record) and *T. arenivagus* Austen, 1920). A key to Egyptian species of *Tabanus* is included together with illustrations. Specimens examined and distributions are given for each species. The status of the six species doubtful to occur in Egypt is discussed.

Psychodomorpha [poster]

The Psychodidae collections at the Natural History Museum, London

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Keywords: Psychodidae, reference specimen collection, NHM

The entomology collections held at the Natural History Museum (NHM) in London, are among the most important and impressive in the world. The museum no longer has a dedicated medical diptera section and now looks to the wider research community to work, in collaborate with the diptera curatorial team at the NHM, to mine the wealth of data held in its Psychodidae collection. We hope that this overview of the collection, with details of coverage, types, and historical specimens, will renew interest in using this importance collection to facilitate current research. Indeed compilation of the data for this poster has highlighted to us the importance of the non-medical Psychodidae holdings at the NHM, which though they do not rival the medical in terms of overall numbers, contain an equivalent number of type specimens, as well as significant holdings of dry specimens which could prove amenable to modern DNA methods.

All approaches will be considered; however an important plank of the museum’s current science strategy is to digitize its collections, so projects which incorporate specimen digitization will be viewed favorably. The research community can gain access to the collection through our system of research loans. Potential visitors to the collection should bear in mind that the NHM is part of the EC-funded Synthesys program (http://www.synthesys.info/), and possesses state of the art facilities for specimen imaging using a wealth of techniques.

A new on-line key to the third instar larvae of European blowfly species of forensic importance

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Keywords: European blowflies, forensic entomology, Calliphoridae, Lucid key

The Biodiversity Information Standards (TDWG) body has been working towards developing standards for the exchange of biological and biodiversity data. Standards such as that for Structured Descriptive Data (SDD) have aided advances in the way identification keys are built and deployed. It is now common to offer both standard single-path dichotomous keys as well as multi-access electronic keys, and to publish SDD compatible source data. Key builders now have a choice of software ranging from user friendly commercial tools like Lucid (www.lucidcentral.org) to open access tools such as the mx software (mx.phenomix.org/index.php/main_page) which, though free, does require the user to have access to some programming knowledge.

The second author has published a traditional dichotomous key to the third instar larvae of European blowfly species of forensic importance. This has been used as the basis for a new electronic multi-access key which will be hosted on the Natural History Museum's website (www.nhm.ac.uk). The on-line key has been built using the Lucid 3.4 software. Such multi-access or interactive keys allow the user to enter the key at any point and use only those characters relevant to the specimen they are attempting to identify. This may be of particular advantage in the forensic field where the freshness and quality of preservation of the material being examined can vary widely. However creating the full character-taxon matrix required for a polytomous key is not without challenges.

A selection of useful review papers will be highlighted which discuss, the advantages and disadvantages of different key forms, and approaches to publishing such multi-format keys which will maintain the concepts of authorship and citation.

Distribution of *Tabanus* (Insecta: Diptera) in Turkey

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Keywords: Fauna of Turkey, *Tabanus*, Tabanidae, horse fly

Horse flies are commonly known as biological and mechanic vector of some diseases like anthrax and brucellosis. According to this, this family has economically great importance in veterinary. *Tabanus* specimens have been collected in 67 provinces and plenty of counties with mallasia traps, nzi traps and water traps as a purpose of determinate seasonal activation and distribution of tabanids which the vectors for bacteries, protozoons and viruses during 1999–2014. In total, 56 *Tabanus* species and 10 sub-species identified with keys and literatures. Among these species *Tabanus hauseri* Olsufjev, 1967, *Tabanus hissaricus* Baratov, 1962, *Tabanus holtzianus* Enderlein, 1927, *Tabanus tenuicornis* Enderlein, 1932 and subspecies *Tabanus laetitinctus sordes* Bogatchev & Samedov, 1949 have been reported for the first time in Turkey. Distribution of this species and their zoogeographical situations briefly discussed.

From read to write access to legacy taxonomic treatments

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Keywords: Digital library, data conversion, scientific communication, taxonomic treatments

Taxonomic publications are the way we taxonomist communicate our results. The main subject are treatments of taxa. With other words, each taxonomic name usage is accompanied by a bit of text that either provides for the first time a treatment of this taxon, or in later cases a reference to the first usage and bits of additional information. Traditionally, they are embedded in printed publications, and dependent on data and results provided outside the treatment proper. The advent of digital publications did not change so far this concept. However, this format makes it impossible to find, extract and reuse these treatments that are considered the basic building blocks for biological sciences. This is even more frustrating since the content is highly structured and rich in data that can be re-used for different purposes, could be linked from external sites and links could be embedded to provide access to the underlying data, such as specimen records, images, etc.

The Plazi workflow is a tool to convert legacy taxonomic publications into semantically enhanced, linked treatments and make them available for re-use in third party applications such as species-ID, Encyclopedia of Life or the Global Biodiversity Information Facility. Tools like the GoldenGate parser provide semiautomatic support to convert entire documents or parts of, like bibliographic references or materials citations, in semantically enhanced linked data. That means that terms relevant to taxonomy are tagged with elements that are defined in reference vocabularies such as the Darwin Core. Links can be embedded to digital objects such as specimens using persistent identifiers or bibliographic references using among persistent Digital Object Identifiers (DOI). The converted documents can be uploaded and made accessible through the Plazi repository.

Access to treatments is an objective of the proposed Open Biodiversity Knowledge Management System within the EU-Funded Pro-iBiosphere project.

Applied Dipterology [poster]

Traumatic myiasis agents in Iran with a record of a new dominant species, *Wohlfahrtia magnifica* (Diptera: Sarcophagidae)

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Keywords: Traumatic myiasis, *Wohlfahrtia magnifica*, Iran

CANCELED

First record of *Muscina prolapsa* (Harris, 1780) (Diptera: Muscidae) in Iran

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Keywords: *Muscina prolapsa*, fly traps, Fars province, Iran

CANCELED

Taxonomy and Cladistics of the genus *Noctiliostrebla* Wenzel, 1966 (Diptera: Streblidae)

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Keywords: Noctilionoidea, bat flies, host-parasite specificity, phylogeny

Noctiliostrebla Wenzel, 1966 belongs to Streblidae, a family of highly specialized ectoparasites of bats, currently comprising four species divided into two groups: group A, *N. dubia* (Rudow, 1871) and *N. traubi* Wenzel, 1966, and group B, *N. aitkeni* Wenzel, 1966 and *N. maai* Wenzel, 1966. The genus is included within the subfamily Trichobiinae, along with *Paradyschiria* S peiser, 1900 considered as its hypothesized sister-group. With a complicated systematic classification and few taxonomic studies, *Noctiliostrebla* constitutes a very homogeneous group with difficult separation among its species. Restricted to the American continent, its species exhibit a high specificity with regard to the two host species of the genus *Noctilio* Linnaeus, 1766, *N. albiventris* Desmarest, 1818 and *N. leporinus* (Linnaeus, 1758). There are no phylogenetic studies dealing with *Noctiliostrebla*and most of the studies on Streblidae were performed to reconstruct higher-level relationships among families of Hippoboscoidea. The present project aims to revise the genus *Noctilostrebla* and to reconstruct the phylogenetic r elationships among its species using morphological and molecular data set, including three mitochondrial genes and one nuclear gene. As a result, the four species were considered valid and are here redescribed, while six new species are described. Of eleven total species, five are restricted parasites of *N. albiventris* and six of *N. leporinus*. The abdominal structures provided the only diagnostic characters found for the species separation. Both the morphological and molecular analyses recovered *Noctiliostrebla* as monophyletic and supported the division of the genus into two morphologically distinct clades. The analyses with mitochondrial and nuclear genes diverged among a few clades, which may be a reflection of a recent and rapid diversification inside the genus. The results showed similarities between the evolutionary histories of *Noctiliostrebla* and their hosts and further studies, preferably relying on both groups, are important to elucidate the problems encountered.

Efficacy of entomopathogenic fungi isolated from the nest of the samsum ant, *Pachycondyla sennaarensis*, against larvae of the mosquitoes *Aedes caspius* and *Culex pipiens*

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Keywords: Entomopathogenic fungi, *Pachycondyla sennaarensis*, *Aedes caspius*, *Culex pipiens,* biocontrol

The use of entomopathogenic fungi is a promising alternative to chemical control against mosquitoes. In February 2013, two fungi were isolated from the Samsum ant, *Pachycondyla sennaarensis* (Mayr) (Hymenoptera: Formicidae) collected in Riyadh, KSA. One of these fungi, identified as *Fusarium solani,* was highly pathogenic against larvae of the mosquito *Aedes caspius* (Diptera: Culicidae). *F. solani* killed 100% of *Ae. caspius* within 5 days of exposure to the concentration of $5x10^7$ cfu/ml. Also, results indicated that *F. solani* was more virulent to the mosquito larvae than *F. chlamydosporum* at the concentration of 8×10^7 cfu/ml. The histopathological examination indicated that spores of *F. solani* can invade the wall of *Ae. caspius* larvae. Both *F. solani* and *F. chlamydosporum* were not effective against *Ae. caspius* and *Culex pipiens*. These results suggest that *F. solani* could be an effective tool for managing *Ae. caspius* proliferation and hence diseases transmission.

Biological activity of *Xanthium strumarium* seeds extracts against *Aedes caspius* and *Culex pipiens* (Diptera: Culicidae) and different cancer cell lines

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Keywords: *Aedes*, cancer, insecticide

Effects of ethanol extracts of *Xanthium strumarium* on the mortality of *Aedes caspius* and *Culex pipiens* (Diptera: Culicidae) and different cancer cell lines were investigated. The results showed that ethanol extracts of plant seeds caused 100% mortality of larvae at a concentration of 1000 µg/ml after 24 hr of treatment. The LC_{50} and LC_{90} values of *X. strumarium* were found to be 531.07 and 905.95 µg/ml against *Ae. caspius* and 502.32 and 867.63 µg/ml against *Cx. pipiens*.

Among the cell lines tested, the Jurkat cell line was the most sensitive to the methanol extract and ethyl acetate fraction with LC_{50} value of 50.18µg/ml and 48.73µg/ml respectively. Conversely, methanol extracts were not that toxic to the A549 cell line though the toxicity increased on further. The percentage of growth inhibition was dose dependent for the methanol extract and ethyl acetate fraction. However, the ethyl acetate fraction showed higher toxicity to all cell lines tested when compared to methanol extract.

The ethyl acetate fraction investigated in this study appears to have a weak larvicidal activity but a promising cytotoxic activity. Future studies will include purification and investigation in further detail of the action of *X. strumarium* phytochemicals and synthesis of new active derivatives for their biological application.

Forensic Dipterology [poster]

Developmental rates of *Chrysomya megacephala* (F.) (Calliphoridae) reared in substrate containing fluoxetine hydrochloride under different temperatures

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Keywords: Blowfly, growth curves, entomotoxicology, forensic entomology

Studies demonstrated that temperature and drugs, among other factors, may affect the development of insects reared on carcasses, which can lead to errors in the post-mortem interval (PMI) estimative when it is based on larval development. This study presents the developmental rates of *Chrysomya megacephala* (Fabricius) (Calliphoridae) reared in substrate containing fluoxetine hydrochloride (FH) (Daforin™, 20 mg/ml oral solution) under different temperatures. Fluoxetine hydrochloride, a selective serotonin reuptake inhibitor prescribed for depression, can lead to abstinence syndrome when its use is abruptly interrupted. Rabbits (*Oryctolagus cuniculus*) were used as experimental models. The animals of the FH groups received 3xFH therapeutic dose (=1mg/Kg per day) and of the control groups received physiological saline solution, both during four days by oral gavage. After, the rabbits were euthanized, had the liver removed and placed on plastic vials. Newly hatched larvae were placed to fed on the liver in a proportion of 1.5 larvae/1g of tissue, and kept on growth chambers with controlled temperatures (20, 25, 30 and 35°C). Five larvae were weighted individually every 12 h until the pupal stage. One-way ANOVA was performed to compare the effect of the treatments and temperatures on the larval development, using age (h) and weight gain (mg) as dependent variables and Duncan's multiple comparisons test to compare the means. Chi-square was used to compare the total time of development (eggs to adults) among treatments. The weight gain was not influenced by FH ($F=0.27$; $p=0.6066$), but it was affected by temperatures ($F=6.39$; $p=0.0003$) – the groups reared at 20°C were significantly different from the others. The total time of development was influenced by FH and temperature ($X^2=5.2848$; $p=0.0215$) and presented a negative correlation ($\rho=-0.05$). Thus, studies comprising associated variables are important to enhance the accuracy on PMI estimative models based on biological insect data.

Taxonomy and Phylogeny of Orthorrhapha [poster]

New record for the Turkish Tabanidae fauna (Insecta: Diptera)

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Keywords: New records, horse fly, Tabanidae, Turkey

New records are presented for a number of species collected from East Black Sea region of Turkey. Four species represent new records for Turkey: *Hybomitra arpadi* (Szilady, 1923), *Hybomitra aterrima* (Meigen, 1820), *Hybomitra montana* (Meigen, 1820) and *Hybomitra morgana* (Surcouf, 1912). Notes on distribution of the species are provided and briefly discussed. Materials of this study were collected from East Black Sea region of Turkey with Malaise and Nzi traps, which baited with 1-octen-3-ol in 2009, 2010 and 2011 years. Captured specimens identified according to proper literature. The Anatolia has an extremely important position in terms of biological diversity due of geographic and climatic features.

Because three major elements of Palearctic region; Mediterranean, Asian and European parts can be found together in Anatolia. In addition, both species belong to ancient Mediterranean and species lately migrated from Northern sides are hosted by Black Sea region. Furthermore the high mountains range from the region border to Samsun leads a jam formation in Amasya, Samsun and Çarsamba triangle for many species belonging Siberian and Boreal elements. On the other hand the Caucasus forms show a continuous spread towards to middle of Black Sea region. Nevertheless in Turkey quantitative or qualitative data concerning the Tabanidae family are completely not known. In this study, four species were added to Turkish horsefly fauna. With the results of this last report, Tabanidae is representing with 171 species and 14 subspecies in Turkey.

Two new species of horse flies (Diptera: Tabanidae) from Turkey

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Keywords: New species, horse fly, Tabanidae, Diptera

The Anatolia has an extremely important position in terms of biological diversity due of geographic and climatic features. Because three major elements of Palearctic region; Mediterranean, Asian and European parts can be found together in Anatolia. Although many species have been recorded in the checklists of horse flies of Turkey (Kılıç 1999; 2006), numerous new records for fauna of Turkey and new species have still to be described and much work must yet be done before a satisfactory classification is achieved. Two new species described part of the results obtained by the author during research projects of the Anadolu University in Eskişehir in Turkey.

Tabanus labranda sp. n. and *Tabanus ela* sp. n. are described from Turkey. Diagnoses of the mentioned species based on the females are given, identification key for these species, charts of diagnostic characters of closely related species as well as illustrations of important characters of these species are presented. Distributions and variability of species are briefly discussed.

Diversity of blowflies in Colombia

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Keywords: Calliphoridae, Mesembrinellidae, Colombia, sampling, diversity

The family Calliphoridae comprises 1524 species, 150 are Neotropical, of which 50 approximately are known from Colombia, included Mesembrinellids. Most of the blowfly studies in Colombia are conducted due to their forensic and medical relevance, but little is known about diversity patterns neither in different environments nor along altitude gradients. Modified Van Someren Rydon traps baited with 250 gr. of rotten fish heads and chicken viscera were used for sampling, each operated during 48 hours. We sampled eighteen localities (72 traps) in all natural regions of Colombia (Amazon, Pacific, Andean, Caribbean, Orinoquia), from 0 to 3260 m a.s.l., and from synanthropic to pristine areas including Páramo. A richness of 24 species were found, more than 20,000 specimens were collected, identified and preserved, including a new species of Mesembrinellidae. Diversity and rarefaction curves for each locality were calculated and compared. Species distribution and diversity trends by locality, natural region and along an altitude gradient are discussed. Finally recommendations regarding sampling efforts for future diversity studies are given.

Phylogenetic analysis of Phoridae (Diptera: Cyclorrapha), with emphasis on relationships between non-Metopininae genera

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Keywords: Phylogeny, morphology, subfamilies delimitation

Phoridae is a family of small flies (0.4–4.0 mm body length), which includes about 4,000 described species with great morphological and ecological diversity. Although the considerable improvement in the knowledge of the phorids during the XX century, the diversity of the family is still considered poorly known as well as its systematics. The first main subfamilial delimitation of the Phoridae was made by Schmitz, dividing it into three subfamilies, holding a separate family for the Termitoxeniidae. Brown, based on a phylogenetic study of the family, divided Schmitz's "Phorinae" into three distinct subfamilies. The contrasting classifications are still in dispute in the literature (Schmitz with some modifications) and little consensus has been achieved.

This study investigated the generic relationships within Phoridae, with emphasis on the non-Metopininae genera. A phylogenetic analysis based on morphological data of 93 taxa was performed, representing 70 of the 90 genera of the non-Metopininae Phoridae. Characters often downweighted in phylogenetic discussions due to supposed plasticity, as the legs chaetotaxy and hypopygium morphology, were included in the analysis and have their importance justified. According to the results, the exclusion of some genera renders a monophyletic Hypocerinae; Phorinae sensu Brown was recovered polyphyletic in respect to many different groups; Conicerinae was recovered paraphyletic; Aenigmatiinae correspond to a pair of independent clades with similar changes towards a limuloid condition. The synapomorphies of the main clades and the evolution of peculiar characteristics of the family are discussed, as well as characters from the literature and codification strategies.

Crampton, thorax sclerites and basal Diptera phylogeny

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Keywords: Diptera, phylogeny, morphology, thorax sclerites, evolution

Guy Chester Crampton publishes along this prolific career an important number of papers studying in considerable detail the morphology of thorax sclerites in various dipteran families and also in some other groups of insects. Moreover, he made some considerably sound inferences of relationships between the dipterans based on his careful in a pre-Hennigian times of dipterology. Thorax morphology was further used by Snodgrass, Shaw and Matsuda, without a cladistic approach, to infer relationships. Nevertheless, thoracic sclerite morphology has been neglected at large as a source of information for Diptera phylogeny reconstruction. This study shows considerable differences in the thorax pleural sclerites in various basal Diptera families. Moreover, there is considerable within-family stability of the thorax morphology patterns, indicating low plasticity. The characters are largely congruent with some other kinds of data – as immature morphology, wings, sequences – and adds up as a consistent additional source of information for the reconstruction of the basal phylogeny of the Diptera. Some of the characters sustaining clades in the analysis are uniquely derived among the holometabolans. A Tipulomorpha including Trichoceridae, Pediciidae, Limoniidae, Tipulidae and Cylindrotomidae is monophyletic and sister to most other families of the order. The Bibionomorpha is monophyletic with the inclusion of Anisopodidae and with the exclusion of the Scatopsoidea. A large monophyletic group includes the families gathered within the Psychodomorpha and Brachycera. This includes the Axymyiidae, Perisommatidae, the Scatopsoidea, Psychodidae, Tanyderidae, Blephariceridae, and Ptychopteridae.

Dipterans spreading in time and space – from the Jurassic to the Cretaceous, from temperate to tropical

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Keywords: Biogeography, Diptera evolution, Mesozoic, temperate environments, tropical environments

The evolution of the dipteran taxa ranked as families mostly developed between the Late Permian to the Early/Mid Cenozoic. The globe, and its terrestrial environment, has change considerably along this time span of about 180 million years. A deeper understanding of the evolution of the Diptera, therefore, demands information, not only of the phylogeny of the order, but also biogeographical, paleontological and ecological information. In this paper we associate information on phylogeny of different groups of Diptera – Trichoceridae, Limoniidae/Tipulidae, Anisopodidae, Keroplatidae, Mycetophilidae, Chironomidae, and Canthyloscelidae/ Scatopsidae – with its distribution to show that basal offshoots of each of these groups have consistently temperate distributions; the “higher” clades being mostly tropical. We further associate the phylogeny of the Diptera with paleontological data to show that some of these geographical shifts optimized over the trees seem to be associated with the Jurassic/Cretaceous borderline. Probably concur at this stage of the Mesozoic changes in paleoclimate and change in forest dominance from gymnosperms to angiosperms. It is fairly well known that basal stems of these families apparently hold to a considerable degree some plesiomorphic traits of the biology of immatures and adults. Some more complex biologies, especially associated to angiosperms, are more derived traits in the evolution of the families.

Infestation predisposition and relative susceptibility of certain edible fruit crops to the native and invading fruit flies (Diptera: Tephritidae) in the New Valley Oases, Egypt

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Keywords: Infestation predisposition, relative susceptibility, edible fruits, *Ceratitis capitata, Bactrocera zonata*

Infestation predisposition and relative susceptibility of the most common edible fruits cultivated in the New Valley Oases against *Ceratitis capitata* (Wiedemann) and *Bactrocera zonata* (Saunders) have been determined. Because high percentage of pupae was unable to produce adults, the percentage of the emerged adult flies was used to express the real ability of infestation. At Kharga province Naring ranked the first in terms of the infestation predisposition by 57.04% real infestation. The rest host fruits exhibited variable infestation predisposition lasted by Apple (11.25%). Quitely difference in the infestation predisposition appeared in Dakhla Oases. In Moot province, Guava ranked the first by 45.00%. However, in Bodkholo province Apricot ranked the first by 62.22%. Variations among the rest of the tested host plants were determined and discussed. In general, data showed that *B. zonata* ranked the first in respect to the number and the percentage of the emerged adults than *C. capitata*. Classification of the tested host plants to their susceptibility degrees to fruit flies indicated that Naring ranked the first in terms of susceptibility to *C. capitata* and *B. zonata* complex and appeared as highly susceptible (HS) host plant. It followed by Guava and Orange which appeared as susceptible (S) host plants. Inversely, Mandarin and Apple showed some sort of resistance and appeared as relatively resistant (RR) host plants. However, Mango appeared as moderately resistant (MR), because it harbored the lowest numbers of emerged adult flies. On the other hand, Fig could be considered as a resistant (R) host plant, because no adult flies emerged from pupae collected from its fruits. Host plants free from infestation were hoped but not found.

Sepsidnet as a model for digital reference collections

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Keywords: Cybertaxonomy, virtual collection, Sepsidae

Reference collections are important tools used by many entomologists for confirming identifications by comparing undetermined specimens with those identified by taxonomic experts. However, such collections have serious limitations: users have to travel in order to access the specimens, or vice versa where specimens are mailed. Here I describe how high-quality imaging can be used to create virtual reference collections that have the advantages of being (1) accessible to all entomologists with internet access, (2) cover more species than most physical collections, and (3) are easier to maintain and update. By using high-resolution imaging, such collections can also remain diagnostically relevant because it makes it likely that character systems are captured that may become important for species identification in the future. I demonstrate the value of such digital reference collections by demonstrating "Sepsidnet", an online collection for Sepsidae (Schizophora) that includes high-quality images for ca. 40% of the species and 80% of the generic diversity. Sepsidnet also includes a species comparator tool that allows the user to compare up to six 'virtual' specimens simultaneously.

3D Design in morphological research: modeling of fly anatomy using CG technology

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Keywords: Computer graphics, blender, morphology, shape analysis, data visualization

Readily available 3D Computer Graphics (CG) software allows for the creation and animation of 3D shapes. Although designed for industry (e.g., video games, special effects in movies), these new technologies are becoming widely used by scientists from different fields, including anthropology, astronomy, and structural biology. But CG technology has also much to offer for systematists and evolutionary biologists. CG software can be used to design, manipulate, and animate morphological models based on conventional images (e.g. macrophotography or scanning electron microscopy). Here we demonstrate how Blender, a free CG software package, can be used for studying the morphology of sepsid flies with their strongly modified forelegs and sternites. We demonstrate how to create and animate 3D models for the entire body of sepsids, including fine details such as the microscopic shape of the genitalia and surface textures such as microtrichosity and hairs. We furthermore argue that creating and animating 3D models can be fast and be used for shape analysis (e.g. shape similarity and complexity). We also show how to make use of Blender animation tools for producing intuitive simulations for testing functional hypotheses. We illustrate this point by showing how the muscle movements powering the sternite brushes of sepsids can be simulated and how male forelegs interact with female wings during mating.

Taxonomy and phylogenetic insights for the *Trichomyia* Haliday in Curtis (Diptera: Psychodidae: Trichomyiinae) from the Neotropical region

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Keywords: Moth flies, new records, new species, psychodid

The genus *Trichomyia* Haliday in Curtis is found worldwide (except Antarctica) with the greatest species richness in the Neotropical region. With 76 species, the neotropics comprises more species than all those found elsewhere combined (five Nearctic, nine Palearctic, five Afrotropical, six Oriental region, and 46 Australia and New Guinea). Three main morphological groups are recognized in the genus: group A, comprising species with four well-separated palpus segments and group B, species with three palpus segments, and another group with four palpus segments, of which the first two palpi are separated by a small articular area. To improve classification of *Trichomyia* seven subgenera were proposed mainly for tropical *Trichomyia* of group B: *Apotrichomyia* Duckhouse, *Dactylotrichomyia* Duckhouse, and *Dicrotrichomyia* Duckhouse (from Australia and New Guinea); *Gondwanotrichomyia* Duckhouse (from southern Africa and New Zealand); and *Septemtrichomyia* Bravo, *Opisthotrichomyia* Bravo, *Syntrichomyia* Araújo & Bravo, and *Brachitrichomyia* Bravo & Araújo (from the Neotropical region). We examined 1,330 specimens of *Trichomyia* that were mostly Brazilian (from the states of Amazonas, Pará, Bahia, Roraima, Rondônia, and Minas Gerais), in which we describe 44 new species. This is an increase of 37% for the Neotropical region, a greater number of species than the combined total elsewhere. Distributions of five species of *Trichomyia* were expanded. The wide morphological diversity in *Trichomyia* we noted in this study make it difficult to establish groups of species, and so a generic revision is urgently needed using modern methodologies, including cladistics to generate hypotheses about these taxa and their interrelationships. A phylogenetic analysis is necessary to test monophyly of *Trichomyia* and of its subgenera, as well as for a general classification.

Life table and efficacy of the syrphid fly *Allograpta exotica* (Diptera: Syrphidae), a control agent of the cowpea aphid *Aphis craccivora* (Hemiptera: Aphididae)

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Keywords: *Allograpta exotica, Aphis craccivora*, biological control, functional response

Immature stages of *Allograpta exotica* (Wiedemann, 1830) are important natural enemies of common agricultural pests such as aphids (Hemiptera: Aphididae). Life history, life table and functional response of *Allograpta exotica* were determined using the cowpea aphid *Aphis craccivora* Koch, 1854 as prey under controlled conditions of temperature, humidity and light.

The recorded development duration of *A. exotica* was 2.0, 6.3 and 5.8 days for eggs, larvae and pupae respectively, with an average of 14.1 days from egg to adult emergence. The adult longevity was not significantly sex dependent, but imagoes lived longer than in previous studies. The offspring sex ratio was favourable to males.

The mortality and survival rates were recorded on a daily basis for all immature stages and adults. The age specific survival rate was also calculated. The highest mortality occurred in eggs followed by mortality in 1st and 2nd instar larvae.

Functional response is one of the most important behavioural characteristics that reveal different aspects of prey-predator interactions. In the present study, different levels of aphid densities (30, 40, 50, 60, 70, 80 and 100) were used. Logistic regression was used to distinguish the shape of the functional response (type II or III). The optimum predator-prey ratio was 1:80. Potential use of *A. exotica* in augmentative biological control is discussed.

Acalyptratae [poster]

Genetic diversity of prophenol oxidase in the invading species *Drosophila albomicans*

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Keywords: *Drosophila albomicans*, invasion, prophenol oxidase

Drosophila albomicans Duda, 1924 (2n=6) belongs to the Family Drosophilidae, Subfamily Drosophilinae, Genus *Drosophila*, Subgenus *Drosophila*, *nasuta* subgroup, and *immigrans* species-group. *D. albomicans* has a Pan-Pacific distibution, as well as in the Indian Ocean Islands, and has been reported in Amami-ohshima in Japan, which belongs to the Ryukyu Islands, 28°N and 129°E, a population that is regarded as the northernmost for this species. In 1984, *D. albomicans* was collected along the coast of the Inland Sea area, 34–35°N and 133–135°E, by Japanese scientists, and one of us (N.A.) has also collected many specimens using bate trap in the Kono-shima area, Okayama Prefecture, western part of Japan since 1985. This species has become invasive and is the dominant species in Japan. Phenol oxidase is a multifunctional enzyme the genetic diversity of which has been reported in relation to phylogenetic analyses among several *Drosophila* species. Local populations of *D. albomicans* can be estimated using the Wright' Island-model and the stage of incipient/criptic speciation and the molecular evolution just after the invasion event.

Cataloguing the World's Chironomidae (Diptera) – a progress report

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Keywords: Diptera, Chironomidae, World Catalogue

A project to create a World Catalogue of Chironomidae was envisaged in the spring of 2006. Part 1, dealing with all the smaller subfamilies from Buchonomyiinae to Telmatogetoninae, was published in 2009. In 2012, Part 2, on the subfamily Orthocladiinae was published. Part 4, dealing with all fossil taxa is expected in 2015 and Part 3 on the subfamily Chironominae is likely to be published two years later in 2017. Worldwide there are currently 6,220 valid species. The final stage will involve updating the entire catalogue, with any additions and corrections, and combining all parts into a single work that will be freely available online.

Review of the subfamily Stratiomyinae Latreille (Diptera: Stratiomyidae) from Egypt

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Keywords: *Odontomyia, Oplodontha, Stratiomys*, type specimen, distribution

The Egyptian fauna of the subfamily Stratiomyinae was revised. The study recorded seven species in three genera [*Odontomyia* (two species), *Oplodontha* (one species), *Stratiomys* (four species)]. *Stratiomys anubis* Wiedemann, 1830 is removed from synonymy of *S. longicornis* (Scopoli, 1763) and considered as a valid species. *Stratiomys segnis* Becker, 1906 and *S. efflatouni* Lindner, 1925 are newly synonymized with *S. anubis* based on examining the male type specimen of the first and comparing the original description of the second with material of *anubis* which was recorded and examined by Lindner 1925. Also, *Odontomyia megacephala* Olivier, 1811 is newly synonymized with *O. angulata* Panzer, 1798 based on examining the Egyptian material of the former which was recorded and examined by Lindner 1925 and comparing it with German and Tunisian material of *O. hydroleon* and *O. angulata*. *Oplodontha oasina* (Lindner, 1925) is newly synonymized with *Op. pulchriceps* (Loew, 1858) based on examining the Egyptian material of the former which was recorded and examined by Lindner 1930 and comparing it with UAE material of the latter species. *Stratiomys anubis* is recorded in Morocco, Tunisia and Turkey for the first time, while *Op. pulchriceps* is recorded in Egypt for the first time. Key to the Egyptian stratiomyine genera and species is included. Illustrations, specimens examined, and distributions for the species are included.

Novel gene origination in stalk-eyed flies

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Keywords: Transcriptome, sexual dimorphism, testes, sex chromosome, gene duplication

The emergence of new genes is an essential component of biodiversity. Throughout their evolutionary history, genomes acquire new genetic material that facilitates phenotypic innovation and diversification. Recently, there has been considerable interest in the occurrence of lineage-specific genes and the functional impact of these new genes on organismal fitness. Developmental processes associated with reproduction function and sexual dimorphism appear particularly likely to involve recently evolved genes but the study of this diversity has been limited to model organisms with well-annotated genomes. Comparative transcriptomics, however, is beginning to provide an alternative means for investigating the evolutionary dynamics of new genes in non-model organisms. In this study, we examine the transcriptional diversity across several stalk-eyed fly species to identify novel, lineage-specific genes that function in the reproductive system of these flies. Stalk-eyed flies have become a model system for studying sexual selection as they possess highly exaggerated, sexually dimorphic eyestalks as well as postcopulatory sperm competition that is driving rapid sperm evolution. Annotated proteins from several species have been assembled into gene family clusters with sequences from several other insect species, producing one of the most comprehensive comparative transcriptome datasets for any non-model organism. Our transcriptome analysis has identified over 1500 duplication events in the genus *Teleopsis* relative to *Drosophila* as well as over 1000 new genes with large open ready frames (>250 aa) but no homology to other insects. Functional analysis of these new genes reveals a number of interesting evolutionary patterns including 1) they are preferentially associated with the neo-X chromosome and testes-specific expression, 2) they appear to resolve sexual conflict as they are significantly more likely to exhibit sex-biased gene expression in somatic tissues and 3) they have produced a novel, testes-specific, basal transcription apparatus.

Culicomorpha [poster]

Fauna and diversity of chironomids (Diptera: Chironomidae) from the Crimean Peninsula (Ukraine)

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Keywords: Chironomidae, the Crimean Peninsula, biodiversity

The fauna of Chironomidae of the Crimean Peninsula (Ukraine) is nearly unstudied (Baranov 2011). The Chironomids from the Crimea were also hardly unstudied until recently, but new records raised the number of Crimean Chironomidae from 49 spp. (Tseeb, 1948) to 135 (Baranov 2013, Baranov & Ferrington, 2013).

At least one species of the Crimean Chironomidae, *Parotrthocladius* korneyevi Baranov 2011, is endemic to the peninsula. Several records of the notably rare specimens were made in Crimea; for example, *Chaetocladius insolitus* Caspers, 1987 was previously recorded only from Austria, Germany and Ireland (Ashe & O'Connor, 2012). Distribution of the Chironomidae biodiversity in the Crimea is very patchy, mostly due to water sources scarcity in the region. Some halophilic species, such as *Chironomus salinarius* and *Halliella taurica* could be extremely numerous and cause local nuisance in some recreation sites (i.e. the Sakske saline lake). In general, chironomids, as many other aquatic insects in Crimea, are facing threat of local extinction due to droughts and habitats destruction caused by overtake of water from rivers for agricultural and household needs. Further research on midge fauna and diversity will helps to improve water quality monitoring and protection policy in the region.

First record of the *Corethrella* (Diptera: Corethrellidae) from the Rovno amber (Eocen)

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Keywords: *Corethrella*, new species, amber

Frog-biting midges (Diptera: Culicomorpha: Corethrellidae) are a family of small midges feeding as adults on frogs and toads, with larvae inhabiting small stagnant water bodies. 105 extant and 7 fossil species have been described, assigned to the single genus *Corethrella* Coquillett, 1902. Corethrellids are most abundant and diverse in tropical regions. Females of this unique family possess features which neither Borkent (2008) nor us could interpret otherwise than striking adaptations to frog blood feeding. *Corethrella* and two culicid genera are the only groups of blood-feeding dipterans in which preying females can locate their hosts through frog calls. Corethrellidae Edwards, 1932 have a well-documented geological history, with records from the Lower Cretaceous Lebanese and Upper Cretaceous Burmese ambers, and from various Cenozoic ambers including Baltic, Bitterfeldian and Dominican ones. Until now there were no records of the family from the Rovno amber (Ukraine).

Late Eocene (35 mya) Rovno amber is a southern coeval analogue of the famous Baltic amber collected in northwestern of Ukraine. Rich fauna with more than 300 arthropod families has been found in the Rovno amber. During our collaboration with the Department of the Invertebrate zoology, University of Gdańsk (Poland) one male of Corethrellidae was found by Dr. Elżbieta Sontag and Prof. Ryszard Szadziewski. Another specimen (female) was found while checking the set of the Rovno amber mothflies (Diptera; Psychodidae). Two new species are under description and their phylogenetic position within *Corethrella* is discussed.

The fauna of hover flies (Diptera: Syrphidae) of Russia

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Keywords: Syrphidae, fauna, Russia

The hover fly fauna of Russia currently numbers 843 species. Of them, 472 species belong to the subfamily Eristalinae, 307 to the Syrphinae, 52 to the Pipizinae and 12 to the Microdontinae. The generic composition shows similar shares: 64 Eristalinae genera, 31Syrphinae genera, 5 Pipizinae genera and 1 Microdontinae genus. Such ratios of genera and species are likely to be characteristic of the entire Palaearctic region, except for the north of the Arctic where the highest number of taxa goes to the subfamily Syrphinae. The subfamily Microdontinae is completely absent from northern Arctic, and the Pipizinae is represented by a single species. Overall, the nucleus of the Russian fauna, as well as of the entire Palaearctic region except for its arid areas, consists of the widespread species occurring from Britain to Kamchatka. The highest species diversity is recorded for the genus *Cheilosia* containing 119 species, followed by *Platycheirus* with 74 species and *Chrysotoxum* with 36 species. It should be noted that large genera such as *Merodon* and *Eumerus* which show the maximum of their species diversity in the southern areas of the Palaearctic region, are represented in Russia only by 5 and 21 species respectively. There are three centres of species richness in the territory of Russia: the North Caucasus, the Altai-Sayan Mountains system and the south of the Russian Far East.

Platypalpus (*pallidiventris*) – variability or complex of siblings?

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Keywords: Empidoidea, Hybotidae, *Platypalpus pallidiventris* complex, Europe, morphological variability

Collin, in his famous book on British Empididae noticed that he rarely saw females of *P. longiseta* (PL) with “male” legs (fore tarsi yellow with only last segment contrastingly black). If females with “male” legs exist, why do males with “female” legs not exist? Such PL male would lead to *P. pallidiventris* (PP) in keys (color of base of third antennal segment is sometimes difficult to observe because it looks differently in ventral and dorsal views). This inspired us to re-examine *Platypalpus* specimens from the collections of the CULSP in detail. Preliminary results showed that: (1) the color of male legs may be of the PP type, also in PL specimens; (2) PP is a relatively constant species in both in terms of somatic characters and genitalia; (3) PL is extremely variable in the following characters: color, length and shape of third antennal segment, color of palpus (pale yellow to dark), front coxa, front femur (clear yellow to brown), and fore tarsi (both PP type and PL type present, sometimes also intermediates); and (4) genitalia of PL type (left cercus strongly bent in lateral view ending in sharp tip) seems to be very different between specimens, especially: shape of left epandrial lamella (triangle, oblong to trapezoid) and left cercus (with or without ventral projection, different length of apical process). In addition, we identified at least three different types of genitalia within PL specimens. We try to resolve if this phenomenon represents intraspecific variability or a multispecies assemblage within the current PL species concept.

The use of X-ray micro CT for nondestructive analysis of a peculiar schizophoran fly in Baltic amber

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Keywords: X-ray microCT, Baltic amber, Sphaeroceroidea

A fly specimen (No 1374-1), from the Hoffeins Collection (CCHH), was subject to 3D micro CT scan and subsequent computer reconstruction. The scanning of the fly was performed on the microtomographic station GE v|tome|x L 240 of the CEITEC in Brno. High geometric magnification 64.4 was used and the resolution about 3 µm was achieved. We utilized the nannofocus x-ray tube with the accelerating voltage 80 kV and tube current 150 µA. Both, the data acquisition and the volume processing (the tomography reconstruction), were done by GE phoenix datos|x 2 software. The data was then processed with Volume Graphic VG Studio Max 2.2 software. Results of tomography reconstruction: (1) the interior of the fly contained surprisingly large number of skeletal fragments not at all visible under binocular observation, (2) small irregular pits were artefacts caused by occasional merging of a skeletal fragment with surrounding body surface by computer reconstruction, (3) small setae were not visualized from an unknown reason. The fly studied represents probably still undescribed family allied to superfamily Sphaeroceroidea (sensu F. McAlpine) characterised by the following apomorphies: (1) lunula greatly enlarged and bare, (2) male eyes dichoptic, (3) male abdominal segments 6–8 fused, (4) legs strongly setose with two preapical setae dorsally, (5) subscutellum strongly convex. Computed microtomography proved to be a powerful tool for observing structures otherwise invisible on (and inside) amber inclusions. The microtomography scanning followed by computer reconstruction and visualization of objects may really represent a revolution in taxonomy, and it may in near future replace classical descriptions.

Addressing an ‘open-ended’ taxon: a combination of broad taxon sampling and high-throughput sequencing increases resolution in the *Tabanus* radiation

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Keywords: Diversification, hematophagy, high throughput sequencing

The 1340 described species currently placed in *Tabanus* make it the most species rich genus in the Orthorrhapha. This radiation fits the idea of an ‘open-ended’ genus due to the species richness, worldwide distribution, lack of comprehensive taxonomic work, and scale of undescribed diversity. A study focusing on the phylogeny of worldwide *Tabanus* is needed to understand the drivers and patterns of the evolution of this lineage and to make future taxonomic work more manageable. We extracted five genes totaling 6 kb of nucleotide data from one hundred species in the *Tabanus* group, including nearly all genera of Tabanini and at least one species from every biogeographic region. Molecular phylogenetic investigation of this data shows that *Tabanus* includes at least fourteen other genera containing over 900 species, including *Haematopota*. Neotropical species are the successive sister groups to the rest of *Tabanus*. The rest of the species of Tabanini s.l. fall into about 8 major groups, some of which correspond to previously established genera. Relationships among these major groups have no resolution or support. New methods are needed to address this complex problem. In order to provide a useful and illuminating framework phylogeny, we need to determine which groups we can separate from *Tabanus* to preserve genera such as *Haematopota*. We sought a new data source from a next generation sequencing approach – anchored hybridization exome capture, for representatives of each major group of Tabanini. This subset will then support the ‘6kb 100 terminal’ data set. We will investigate whether this method of supplementing a subset of taxa with large gene harvests can lead to highly supported nodes among the major lineages of Tabanini and shows promise in understanding the phylogeny of hyperdiverse genera.

Seeking support in Schizophora

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Keywords: Schizophora, Acalyptratae, ancient rapid radiation, transcriptome based phylogeny

The schizophoran radiation is a period in the evolutionary history of flies characterized by conflict and uncertainty that has persisted in spite of studies that include robust sampling of genes and taxa. Studies with broad taxon sampling have low support and studies with taxon sampling focused on Schizophora subgroups conflict with one another. For instance, the three taxon statement of *Ceratitis*, *Drosophila*, and *Musca* has had every possible topology in published phylogenies, and few with high support values. The monophyly of half of the superfamilies have not been recovered, and the placement of Conopidae and the Calyptratae are not clear. Statistical support values are low among most family level relationships in the Schizophora. This study seeks to provide a framework for some headway into an evidence-based, robustly supported phylogeny of the Schizophora. Transcriptomes of forty target species will be the data source for this investigation into increasing our confidence of the phylogeny of this fly lineage. As a first pass at a useful categorization, we will group families of Acalyptratae in three main areas; sister to the rest of Schizophora, closely related to Calyptratae, and within the main Acalyptratae. By synthesizing previous phylogenetic hypotheses and offering a new one with unprecedented gene coverage from transcriptome data, this study will provide a well supported and compelling phylogeny of the Schizophora.

Arthropods on mummies in the Catacombe dei Cappuccini in Palermo, Italy

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Keywords: Forensic entomology, mummies, Catacombe dei Cappuccini

In July 2012, over several days and nights, our team examinded 622 mummies in the basement of the Capuchin monestary in Palermo, with corpses dating back mostly between the 17th to 20th century. The mummies passed through different, mixed stages of decay, even though their decompositional end state is mummification.

Except mummy PriNb27 which did not have a head, we found that most heads were skeletonized, i.e., not mummified. There were no statistical differences in the type of decay between mummies of males, females, monks, regular priests nor between the mummies of persons with other occupations (lawyers etc.).

We found insect remains on 260 mummies, yet no evidence of blowfly remains (Calliphoridae) which are usually very common in early decomposition. Instead, we found others arthropods typical for corpses, e.g., *Hydrotaea ignava* (Harris, 1780) (Diptera: Muscidae), *Fannia scalaris* (Fabricius, 1794) (Diptera: Fanniidae), *Conicera tibialis* Schmitz, 1925 (Diptera: Phoridae), *Leptocera* sp. (Diptera: Sphaeroceridae), *Necrobia rufipes* (De Geer, 1775) (Coleoptera: Cleridae), *Gibbium psylloides* (Czenpinski, 1778) (Coleoptera: Ptinidae), *Oryzaephilus surinamensis* (Linnaeus, 1758) (Coleoptera: Silvanidae), Alysiinae (Hymenoptera: Braconidae), *Tinea pellionella* (Linnaeus, 1758) (Lepidoptera: Tineidae) and some pseudoscorpions (Pseudoscorpionida, Arachnida).

Only 260 of the 622 mummies showed signs (skin lesions) that may, from our experience with decomposing bodies, have been caused by insect activity.

Comparing males, females, virgins, monks, priests, and the members of other professions, only priests and virgins showed a significant difference in insect colonization patterns (Wilkoxon). This may be due to very different methods of mummification.

Genetic structure and positive selection detection in populations of *Cochliomyia hominivorax* (Diptera: Calliphoridae)

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Keywords: *Cochliomyia hominivorax*, insecticide resistance, genetic structure, myiasis, positive selection

Livestock production is an important economic activity in Brazil, but has been suffering significant losses due to the impact of parasites. The New World screw-worm fly (NWS), *Cochliomyia hominivorax*, is an important ectoparasite and myiasis causing fly endemic from the Americas, which stands out in this scenario. The geographic distribution of NWS has been reduced after the implementation of the sterile insect technique (SIT), being considered eradicated in North and part of Central America. In South America, NWS is controlled by chemical insecticides, which indiscriminate use can cause the selection of resistant individuals. Previous studies associated the Gly137Asp and Trp251Leu mutations in the active site of carboxylesterase E3 to resistance of diethyl and dimethyl organophosphates, respectively. The selective pressures that have shaped E3 gene evolution from the point of view of non-synonymous mutations were investigated considering populational data. Samples of *C. hominivorax* from 21 sites in South America were sequenced for a fragment of E3 gene that comprise part of intron I2, exon E3, intron I3 and part of exon E4. The results of AMOVA and pairwise FST indicate that there is genetic structure between sites when considering sequences of E3 gene and CR, COI and COII mitochondrial genes. However, SAMOVA results showed a low correlation between genetic and geographic data, indicating that this specie has a complex population structure. Three genetic groups were distinguished between the sites by DAPC. Linkage disequilibrium tests were significant between the two mutations related to organophosphate insecticides resistance, indicating a negative association between them.

Baltic amber Dolichopodidae: a rich and abundant fauna

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Keywords: Baltic amber, Dolichopodidae, collections, taphonomy, species richness

Although there are no Cretaceous records of Dolichopodidae *s.s.*, the family underwent explosive radiation in the early Tertiary and is one of the commonest and richest insect families in Baltic amber. This diversity in amber is due to the life habit of many dolichopodids, that of resting and living on tree trunks, thereby increasing the likelihood of their entrapment in sticky resin. Based on some 4000 inclusions from both institutional holdings and private collections, the fauna comprises some 160 species in 32 genera (some 125 species and 22 genera to be newly described). Although many recent subfamilies and genera are present, there are many new and often enigmatic taxa. The Baltic amber fauna is reviewed and briefly compared with those of other Tertiary ambers, notably the Eocene Cambay amber from India, and the Miocene Chiapas fauna from Mexico. Of note is the early Baltic amber radiation of the distinctive recent Australian/ New Caledonian medeterine genus *Atlatlia*. The various collections of Baltic amber inclusions are discussed, and the private collections of selected pieces are shown to be markedly richer than the usually unselected holdings of institutions. This talk is illustrated by many striking photos from amber.

Diptera diversity on Mt Wilhelm, Papua New Guinea: faunal change with elevation

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Keywords: New Guinea Diptera, biodiversity survey, faunas and elevation, Drosophilidae, Dolichopodidae

The terrestrial component of the IBISCA sponsored “Expedition Papua New Guinea 2012–2013” (http://laplaneterevisitee.org/) comprised a biodiversity survey of terrestrial arthropods on a transect of Mt Wilhelm (el. 4509 m). The Malaise trapping program ran for 16 consecutive days, producing daily samples from each of four Malaise traps at eight 500 m intervals between 200 m and 3700 m, giving a total of 512 samples. Sorting took place at Wanang 3, a remote field station in Madang Province, a 6–7 hours walk from the nearest road. Diptera usually comprise the most abundant order in Malaise samples, and the large volume of material required a “triage”, and only those families that were abundant *and* that had active and willing workers were extracted from the residue soup. Sampling results on Diptera are presented here and two of the most abundant families, Drosophilidae (some 1300 specimens) and Dolichopodidae (some 1550 specimens) are discussed in more detail. Species richness and change with elevation, biogeography and other aspects of the Mt Wilhelm fauna are reviewed. Attention is also drawn to the practical aspects of Malaise sampling, especially trap placement and intra-site variation, supplemented by the video “Green Tree Ants at the Malaise Trap Café”.

Fungus gnats online: seven years of progress

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Keywords: Online resource, scratchpads, Sciaroidea, collaboration

Since its beginning in 2007, Fungus Gnats Online (FGO, www.sciaroidea.info) has become the largest authoritative digital resource on Sciaroidea. This presentation will demonstrate the outcome of the previous seven years' worth of data accrual. I will also show the recent functionality additions to the site, and show how the site can be used for efficient taxonomic work and communication. Other possible future uses for FGO will be discussed based on how other Scratchpads sites are being used.

Mating behavior of three *Platystoma* species in Israel (Diptera: Platystomatidae)

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Keywords: Mating trophallaxis, copulatory courtship, *Platystoma*

Mating trophallaxis in Diptera, involving a liquid secretion, has so far been studied only sporadically and not comparatively, and has hitherto been reported briefly from only a few platystomatid species. The mating behavior, and in particular the copulatory courtship, of three species of *Platystoma* (*P. arcuatum* and two undescribed species) is reported both qualitatively and quantitatively and described comparatively and in detail for the first time, using a behavioral coding and analysis software (*The Observer*). This copulatory courtship presents in the form of trophallaxis, taking place during mating. Additional behavioral elements comprising the mating rituals were recorded, sequenced and analyzed.

The MycetoPhylo Project: a collaborative approach to describing the biological variation and phylogeny of Mycetophilidae

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Keywords: Phylogeny, systematics, Sciaroidea, morphology, immatures

The key to understanding any group of organisms lies in as complete an understanding of their biology and evolution as possible. In systematics the starting point to this understanding involves examining the organisms' morphology and/or molecules for shared derived characters. This requires a common vocabulary for structures, which reflects the homology of those structures across the group. If these structures are homologized correctly then the various character states that are present can be used to construct a robust phylogeny of the relationships in the group. Here we present the framework for a collaborative venture that will undertake this task for the Mycetophilidae, The MycetoPhylo Project. The intent is to produce richly illustrated comparative papers, on different sources of characters (head – genitalia, immatures, biology, molecules), across all the genera and subgenera/species-groups in the family. An organizing committee for the general project has been established (the authors of the current talk) to address pending questions and issues, and to encourage the projects to adhere to the time-schedule. After production of the comparative papers, a general paper on Mycetophilidae phylogeny would then be authored by any interested contributors, integrating all of the available data. This will be the first comprehensive treatment of a dipteran family in this manner, providing a stable morphological vocabulary, and well supported phylogeny, to work from in future Mycetophilidae systematics work.

Jeweled tarantula killers of the Nearctic: systematics, phylogeny and natural history of *Eulonchus* Gerstaecker (Diptera: Acroceridae)

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Keywords: Acroceridae, parasitoid, systematics, spiders, phylogeny

Species in the Diptera family Acroceridae (spider or small-headed flies) have complex and interesting life histories, and have often proven difficult to study due to their rarity. All species with known larvae are parasitoids of spiders (Araneae) in their immature stages, killing and completely consuming the host's soft tissues in the final larval stage before pupation. The family currently contains approximately 525 species in 55 genera classified into three extant subfamilies (Panopinae, Acrocerinae, and Philopotinae), though phylogenetic analyses using DNA sequence data disagree with this subfamilial arrangement. The panopine genus *Eulonchus* Gerstaecker, is endemic to the Nearctic. The larvae are endoparasitoids of tarantulas (Mygalomorphae) and are relatively common, at least in western North America. All species have long proboscises for nectar feeding, and can often be collected while visiting flowers, where they can be important pollinators. The genus currently contains six species, though some previous workers have suggested that a number of new species may exist and suggested that a revision of the genus was necessary. Here we report the results of a revision of this genus, along with the first phylogeny of the species relationships, based on DNA sequence data. More than 1000 specimens from the entire generic distribution were examined for the revision, and compared with all types. We found no new species based on morphology, though some species did show a range of variation in several characters, most notably in proboscis length and body color. It is possible that future molecular work may be able to show distinct populations that could be considered separate species, if these differences can be tied to different host use, phenology or other characteristics. We also discuss the natural history of the genus, especially with respect to host and parasitoid distribution and potential evidence of coevolution.

Copulatory dialogue: female tsetse fly signal during copulation to influence male genitalic movements

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Keywords: Tsetse flies, copulatory dialogue, stimulatory behavior

Females have traditionally been considered to be passive participants in the act of copulation. Female behaviour during copulation that could function as communication with the male is probably more common than previously appreciated, but its functional significance remains little studied. Recent discoveries suggest however that females sometimes signal to males during copulation in order to elicit male responses. Two female behavior patterns that might function as signals to the male during copulation were studied in the tsetse fly *Glossina pallidipes*. Both were associated with male squeezes with his powerful genitalic cerci on the female's abdomen. One female behavior (wing vibration) apparently induced the male to shorten his squeezes. The other, body shaking, is a more forceful, apparently negative behavior associated with wing vibration. Possible functions of male and female signals are discussed

Crane flies (Tipuloidea) of Churchill, Manitoba, Canada

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Keywords: Tipuloidea, Churchill MB, Canada, DNA barcodes

Churchill, situated on Hudson Bay, lies at treeline, between the Northern Boreal and Tundra Zones.
Intensive collections of insects made here in 1947–1957, 1978–1979 and 1989 were compared with recent collections from 2006–2010. Currently 84 species are known from Churchill, 59 from the 20th Century and 68 from the 21st Century, but only 44 species are in common (52%). This suggests a noticeable shift in species populations, probably attributable to climate change.

The more recent specimens were barcoded using a small section of DNA: COI-5P with the hope that each species would be uniquely identified, but only 59 out of 68 species received unique barcodes. Several errors in identification were easily spotted and some females and immatures were confidently assigned to species, however, the congruence between the bar codes and the morphologically determined species is only about 85%. This small segment of DNA is insufficient for confidently distinguishing each species in this study. Contamination and small sample size influenced these results.

ZADBI: the Zurqui All-Diptera Biodiversity Inventory

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Keywords: Costa Rica, survey, inventory, specimen processing, parataxonomists

The Zurqui All Diptera Biodiversity Inventory (ZADBI) is the first modern effort to compile a complete list of species of Diptera at a mainland tropical site. It is probably the largest Diptera inventory ever attempted, with over 50 collaborating experts worldwide identifying all species (some as unnamed morphotypes) at a 1600 m elevation cloud forest site in Costa Rica. The site at Zurquí de Moravia, is limited to a 150 x 266 meter sampling area, including a variety of terrestrial and aquatic habitats. Stringent controls of collecting effort and full curatorial preparation of specimens by a team of five parataxonomists prevents the pitfalls usually associated with large surveys from overwhelming the collaborating taxonomists with far too many unprepared specimens. Halfway through the project in March, 2014, early results indicate a spectacular diversity of species, especially of small flies in Cecidomyiidae, Phoridae, and other commonly encountered families.

Homology and congruence in the most comprehensive phylogeny of the subfamily Sarcophaginae (Diptera: Sarcophagidae)

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Keywords: Morphological phylogeny, male terminalia, homology, Sarcophaginae, flesh flies

The most comprehensive genus-level phylogenetic study of the subfamily Sarcophaginae is presented. A morphology-based phylogenetic analysis is performed with 140 terminal taxa and including all genera of Sarcophaginae, using both parsimony and Bayesian inference. No fewer than 130 of the morphological characters used in this study come from the male terminalia. The homology of some of the male genitalic characters is assessed for the first time. Parsimony analysis with equal weights resulted in 18 most parsimonious trees. This cladistic study found 37 genera to be monophyletic and 2 genera (*Retrocitomyia* and *Titanogrypa*) to be polyphyletic. The remaining 12 genera are monotypic, but none emerged inside any of the non-monotypic genera. A large clade of mainly dung decomposers was recovered, which included the genera *Dexosarcophaga*, *Nephochaetopteryx*, *Oxysarcodexia*, *Oxyvinia* and *Ravinia*. Support was obtained for treating *Sarcodexia* as a subgenus of *Peckia*, but not for *Helicobia* and *Lipoptilocnema* as subgenera of *Sarcophaga*. Morphological synapomorphies are discussed for the major genera, including a review of the character interpretations of previous authors. New genitalic structures were discovered in little studied genera like *Carinoclypeus*, *Comasarcophaga*, *Halliosca*, *Lipoptilocnema*, *Spirobolomyia* and *Udamopyga*. The present phylogeny shows which genera are most in need of a systematic revision, and it also provides a morphological circumscription for all the genera of Sarcophaginae.

Flesh flies, rogues and molecules – the diversification of *Sarcophaga* (sensu lato) (Diptera: Sarcophagidae)

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Keywords: *Sarcophaga* phylogeny, rogue taxa, 28S secondary structure, molecular systematics, Sarcophagidae

The mega-diverse genus *Sarcophaga* Meigen, which includes more than 900 named species arranged into 133 subgenera, makes up for almost half of the diversity of the subfamily Sarcophaginae. Current knowledge of evolutionary relationships is based on morphological and molecular analyses with poorly supported hypotheses or small taxon sets, or both. The results presented in this study provide the most comprehensively sampled phylogenetic analysis of *Sarcophaga* subgenera, and it is the first to include representatives from all regional faunas. The monophyly and phylogenetic relationships of selected subgenera were examined, and the placement of a recently discovered new species from Turkey was given special attention. Sequence data from two gene regions were used: the mitochondrial protein-coding gene cytochrome c oxidase subunit I (COI) and the nuclear 28S ribosomal RNA gene. The secondary structure of three expansion segments (D1, D2, D3) of 28S is presented for the family Sarcophagidae and used for the first time in a multiple sequence alignment. Molecular data were analyzed using maximum likelihood and Bayesian inference. A study of rogue species resulted in a long list of potentially removable taxa, from which less than 50% caused a remarkable increase in posterior probabilities and bootstrap supports. The backbone of the phylogeny was not consistently supported, but more distal nodes were better supported. All New World subgenera emerged as monophyletic. The monophyly of few of the subgenera from the Afrotropical, Oriental/Australasian and Palaearctic regions was consistently supported. Although with low support, Afrotropical taxa were found to be the earliest diverging lineages, which is in conflict with currently available evidence favouring a New World origin and early diversification of *Sarcophaga*. A better sampling of Nearctic taxa and more (nuclear) gene sequences should be considered for future studies.

‘Anomalous diversity’? A case for high tropical parasitoid richness in tachinid flies

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Keywords: Tachinidae, inverse diversity gradient, New World, Nasty Host Hypothesis, rarefaction

The vast majority of insect groups show increasing species richness towards the tropics. However, certain groups of ichneumonid wasps have been claimed to have an inverse diversity relationship; their diversity declines towards the tropics. Several workers have proposed that this pattern of ‘anomalous diversity’ applies to other parasitoid groups. Several explanatory hypotheses have been proposed to explain this pattern. Here we examine whether this pattern extends to tachinid flies. We compare species accumulation curves of five tachinid sampling projects across New World latitudes from Ohio to Ecuador. Our analysis suggests New World tropical tachinid diversity is at least as high as temperate diversity, if not more so. We evaluate differences which may allow tachinid flies to circumvent ecological constraints felt by parasitoid wasps. Future analyses will include rearing-based datasets.

Empidoidea [poster]

Revision of the Neotropical genus *Opeatocerata* Melander, 1928 (Diptera: Empididae: Empidinae)

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Keywords: Neotropical distribution, taxonomy, Empidini

Opeatocerata was proposed by Melander (1928) based on the type species *Empis rubida* Wheeler & Melander, 1901, from Mexico. The genus has a Neotropical distribution, with six previously known species: *O. rubida* (Wheeler & Melander, 1901), *O. stubbsi* Smith, 1989, *O. cooperi* Smith, 1989, *O. lopesi* Smith, 1989, *O. melanderi* Câmara & Rafael, 2011 and *O. trilobata* Câmara & Rafael, 2011. The genus is a monophyletic group based on the upper ommatidia being larger than the lower ones, an aristiform stylus, about 2–3 x longer than the short-ovate postpedicel, the 8th tergite and sternite divided in two plates (except in one undescribed species), a membranous or partly membranous hypandrium, a tetralamellar ejaculatory apodeme and the epandrium with a membranous anterior margin and fused with the cercus. Here *Opeatocerata* is revised based on primary types and including 15 new species. We believe that the actual number of species in the Neotropical region is much higher than previously reported.

New species of *Hemerodromia* (Diptera: Empididae) from Brazilian Amazon basin

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Keywords: Taxonomy, Hemerodromiini, Neotropical distribution

The empidid genus *Hemerodromia* Meigen includes about 140 described species distributed across the Palaearctic, Nearctic, Neotropical, Afrotropical and Indomalayan Realms. *Hemerodromia* is readily distinguished from other members of the tribe by Hemerodromiini by wing characters (fork R4+5 and M1+2 present, cells bm+dm fused, cell cup absent, vein Sc fused with C basally, becoming more or less separated about level with radiocubital node, vein h absent), and the strongly dorsoventrally flattened head. In the Neotropical Realm there are 11 known species, one of them from Brazil, there is no record of the genus from the Brazilian Amazon basin. The Brazilian Amazon basin is an ecoregion that lies between the Tapajós and Xingu rivers that flow within the Amazon Basin of central-eastern Brazil. Characterized by a high density of lianas (woody vines), which create a low, open understory, this region hosts impressive levels of biodiversity. *Hemerodromia* specimens deposited in Coleção de Invertebrados do Instituto de Pesquisas da Amazônia (INPA) were examined. There are 10 new species to describe from the Brazilian Amazon Basin. Most Amazon species are similar to typical *Hemerodromia*, but some species present modifications: 2 species have a modified wing vein (R2+3 very short), 3 species have a long gonocoxal apodeme and ejaculator apodeme, 1 species has the cercus greatly enlarged. The Amazon basin is the biggest drainage system in the world and undoubtedly has a rich fauna and *Hemerodromia* and is likely to be very diverse, so we believe that the actual number of species in this region is much higher than reported to date.

Phylogenetic analysis of *Hemerodromia* Meigen (Diptera: Empididae)

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Keywords: Empidoidea, Hemerodromiini, Neotropical region, phylogeny

Hemerodromia Meigen is a large Empididae genus, that seems to be very diverse in the Neotropical region from where, eventually, many new species will be described. *Hemerodromia* has a global distribution and includes about 140 described species. The genus is readily distinguished from other members of the tribe Hemerodromiini by wing characters (fork R4+5 and M1+2 present, cells bm+dm fused, cell cup absent, vein Sc fused with C basally, becoming more or less separated about level with radiocubital node, vein h absent), and the strongly dorsoventrally flattened head. A preliminary phylogenetic analysis was carried out to determine the relationships among the species and to test the monophyly of the genus. Here, we present the results of this analysis using the 58 morphological characters of 42 ingroup species from all biogeographic regions and 1 *Chelipoda,* 1 *Phyllodromia,* 1 *Neoplasta,* 1 *Metachela,* and 1 *Chelifera* species as outgroup; trees were rooted with *Opeatocerata* (Empidinae). In addition, fractions of two genes (12S and mtCOI) were sequenced in 27 *Hemerodromia* species from all over the world, with emphasis on the Neotropical region. Both morphological and molecular data show that *Hemerodromia* is monophyletic. The morphological data show a basal species from South Africa and some distinct Neotropical lineages, but the relationship among another species remains unclear. The clade of *Chelifera + Hemerodromia* has a good branch support and *Neoplasta + Metachela* appears to be its sister clade.

Life table analysis of survival and reproduction of the syrphid fly *Eristalinus aeneus* (Diptera: Syrphidae) under artificial breeding

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Keywords: *Eristalinus aeneus*, two-sex life table, reproduction, artificial breading

Many hover flies that belong to the subfamily Eristalinae play an important ecological role, mainly due to their contribution in the pollination process. Moreover, some Eristalini species have been reared in captivity (including mass-rearing) in order to use them as pollinators under controlled conditions, such as in isolation cages or in greenhouses, to improve seed setting for diverse crops. *Eristalinus aeneus* is our target species, which is being developed on massive rearing to use as pollinators.

A life table describes the development, survival, and fecundity of a cohort and provides basic data on population growth parameters. The raw data analysis of a two-sex life table is used here to calculate the life table parameters for *E. aeneus*. The life tables has been constructed using laboratory data collected under controlled conditions (40 ± 10% RH, 25 ± 5 ˚C and a 12L:12D photoperiod) in order to revealing the maximal growth potential of the population.

The main purpose of this research is to obtain the intrinsic rate of increase (r), the net reproduction rate (Ro), the mean generation time (T) and the finite rate of increase (λ) by the age-stage, two-sex life table, in order to take both sexes and the variable developmental rate among individuals and between sexes into consideration.

Cladistic analysis of the Diaphorinae (Diptera: Dolichopodidae)

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Keywords: Dolichopodidae, Diaphorinae, morphology, phylogeny

Diaphorinae is one of the largest subfamilies of Dolichopodidae, with more than 800 described species, representing appr. 12% of the family. Nevertheless the group seems a rather heterogeneous assemblage of genera and demands a broad examination to properly delimit its boundaries. A comprehensive cladistic analysis of Diaphorinae was carried out for the first time, including all genera currently assigned to the subfamily. A data matrix with 83 taxa and 77 characters was analysed under the parsimony criterium, using implied weighting. Two uniquely derived features (the lateral groove on the female tergite 10; the loss of the distal part of the male sternite 9) were considered synapomorphies for a herein restricted subfamily concept, which is similar to that of Ulrich (1981). A supra-generic arrangement for the subfamily is proposed with three lineages: (1) *Aphasmaphleps* Grichanov, *Asyndetus* Loew, *Cryptophleps* Lichtwardt and *Shamshevia* Grichanov; (2) *Achradocera* Becker, *Chrysotus* Meigen, *Dubius* Wei, *Falbouria* Dyte and *Lyroneurus* Loew; and (3) *Diaphorus* Meigen, *Melanostolus* Kowarz, *Ostenia* Hutton and *Trigonocera* Becker. The paraphyly of *Asyndetus*, *Chrysotus* and *Diaphorus* is discussed as a result of the maintenance of other genera in their respective groups. Moreover, the following genera should be excluded from the Diaphorinae: *Keirosoma* Van Duzee, *Phasmaphleps* Bickel and *Terpsimyia* Dyte, *Nurteria* Dyte & Smith (nested within the Sympycninae), and *Argyra* Macquart, *Dactylonotus* Parent, *Somillus* Brèthes (including *Pseudargyra* Van Duzee) and *Symbolia* Becker (composing the Argyrini Negrobov along with *Anepsiomyia* Bezzi, and left *incertae sedis* within Dolichopodidae). A better resolution within the Diaphorinae still depends on the recovery of its sister-group and certainly will shed light to the relationships among the other subfamilies of Dolichopodidae.

Sciomyzidae: their potential role as bioindicators of lowland wet grasslands

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Keywords: Bioindicators, Sciomyzidae, biodiversity

High Nature Value (HNV) farmland represents a new approach to the identification and monitoring of areas of conservation importance in farming landscapes throughout Europe. In the West of Ireland, many of these areas are contained within Wet-Grassland habitats which are subjected to pastoral farming. Lowland wet grassland in particular can support a rich mosaic of plant and animal communities within agricultural landscapes. The conservation of invertebrate biodiversity in such areas often requires attention to small scale habitat features which may be overlooked in conventional conservation planning. There is a pressing need to identify appropriate invertebrate bioindicators that can be monitored on the basis of their potential as biodiversity surrogates and/or use in detecting changes in environmental or ecological conditions.

Sciomyzidae appear to satisfy the considerations proposed by a number of reviews with cost effectiveness, ease of collection and identification, and ubiquity within the habitat of interest forming the main criteria. As well as these pragmatic attributes, sciomyzids also meet the suitability criteria for use as environmental, ecological and novel biodiversity indicators. Their ubiquitous association with damp habitats and ecological differentiation driven by hydrology and vegetation structure signify them as indicators of wetland features in agricultural systems. In agricultural landscapes, particularly wet grassland, such features could prove strategic in the conservation of invertebrate biodiversity. Sciomyzidae are hereby explored as potential invertebrate diversity surrogates as well and indicators of environmental and ecological change

What do the Muscidae tell us about evolution in the Andes?

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Keywords: Biogeography, diversity, house flies, phylogeny, taxonomy

The Andes Mountain range is among the most poorly known areas in South America regarding diversity in the Muscidae. Of the nearly 900 species in 80 genera of Muscidae in the Neotropics, about 30% of the known species are found in the Andes. Of the 27 genera in the Andes, only species in the six genera *Apsil* Malloch, *Brachygasterina* Macquart, *Drepanocnemis* Stein, *Palpibracus* Rondani, *Philornis* Meinert and *Reynoldsia* Malloch have proposed phylogenies. Recently increased efforts to sample Diptera in Chile, Ecuador and Colombia have found that the Muscidae are surprisingly diverse in the Andes. The number of new species is amazing, including traditionally orphan genera *Coenosia* Meigen, *Helina* Robineau-Desvoidy, *Limnophora* Robineau-Desvoidy, *Mydaea* Robineau-Desvoidy and *Reinwardtia* Brauer & Bergenstamm and well-known genera (with full or partial revisions in the last 15–20 years) such as *Agenamyia* Albuquerque, *Apsil* Malloch, *Brachygasterina*, *Neodexiopsis* Malloch, *Neomuscina* Townsend, *Pilispina* Albuquerque, *Phaonia* Robineau-Desvoidy, *Philornis* and *Polietina* Schnabl & Dziedzicki. New species of *Drymeia* Meigen were surprisingly found in the highlands of Colombia when previously it was an Holarctic genus with only one species occurring in Central America (Mexico) and unknown from South America. Also, a new genus with two species was found in Ecuador, one very abundant at 3000 meters of altitude. This new genus is a sister-group of *Philornis*, which is essentially Neotropical comprising more than 50 species, few of which reach North America. The detailed study of these new findings will greatly contribute to the understanding of the evolution of Muscidae in the Andes.

Gall midges (Diptera: Cecidomyiidae) associated with coastal shrub vegetation in Rio de Janeiro, Brazil

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Keywords: Galling species, insect-plant interaction, restinga

Cecidomyiidae is a worldwide family with 6000 species in 736 genera. In the State of Rio de Janeiro (Southeast region) 95 species in 47 genera are recorded, most associated with galls. Surveys in the coastal shrub vegetation (restinga) of Rio de Janeiro and São Paulo states have shown a great richness of galls. We investigated the gall midges from five municipalities of Rio de Janeiro: Saquarema, Arraial do Cabo, Araruama, Cabo Frio and São João da Barra. The collections were done each two months, from June 2011 to May 2012. 38 points were investigated during 45 minutes in each collect. Galls were taken to laboratory and acconditioned in pots for rearing the insects. Some samples of each gall morphotype were dissected for obtaining immatures. The pots were checked daily for adults emergence. The Cecidomyiidae specimens were mounted in slides following Gagné (1994), and identified using taxonomic keys and compared with original descriptions. All specimens were deposited in the collection of Museu Nacional, Rio de Janeiro. 90 Cecidomyiidae species were found on 27 genera. Most of them were galling species (n=88), but one predator and one free-living species in flowers were also recorded. The galling species (n=88) were associated with 59 plant species in 26 families. Most of the galls occurred on leaves and the plant families with the highest richness of galls were Myrtaceae and Fabaceae. *Dasineura*, *Lopesia* and *Neolasioptera* were the richest genera. The only predator and the only free-living species were represented respectively by *Lestodiplosis* and *Contarinia*, found in flowers of Fabaceae (*Stylosanthes guianensis* and *Chamaecrista ramosa,* respectively). Most of the genera were represented only by one species. Hymenoptera and Thysanoptera were found as parasitoids and inquilines in some galls. The richness of galls in the surveyed areas reveals the importance of restinga for the Cecidomyiidae fauna.

Great diversity in a small family: the Rhinophoridae as a paradigm

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Keywords: Phylogeny, morphology, first instars, male terminalia, reproductive strategies

Rhinophoridae are a small oestroid fly family that contains about 150 valid species worldwide, currently arranged in approximately 30 genera. The monophyly of the family is considered somewhat tentative as unique autapomorphies are found exclusively in the first instar larva, which is known for a small subset of genera only. Also, the phylogenetic position of the family within the Oestroidea is still largely unresolved. All rhinophorid species for which breeding records exist are endoparasitoids of woodlice, representing the only insect parasitoids to have exploited Crustacea as hosts. Moreover, the first instar larva of these flies is highly adapted for an endoparasitoid life. Rhinophoridae appear to have their peak of species diversity around the Mediterranean, which can partly be ascribed to the longer and more thorough taxonomic exploration of this area, but it may partly reflect the high diversity and population density of their hosts. However, rhinophorids are by no means restricted to the West Palaearctic subregion, being present, although scattered, on nearly all the continents with several endemic taxa, and they are often simply overlooked or neglected by taxonomists.

A solid phylogenetic reconstruction of these enigmatic flies may shed new light on the origin and diversification of oestroid calyptrates. To achieve this would ideally include obtaining a large amount of molecular data as well as biological and morphological information on pre-imaginal instars. This talk presents the results of a cladistic analysis of a large morphological data set drawn from both adults and first instars and with taxa from all continents. Morphology has still much to offer for a better understanding of phylogenetic relationships within the Rhinophoridae, and the rhinophorid fauna of the world is still surprisingly poorly known.

A morphological phylogeny of Tachinidae

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Keywords: Tachinidae, phylogeny, reproductive strategies, host associations

We present the main results of a quantitative phylogenetic analysis of the family Tachinidae conducted using 135 morphological characters from 492 species belonging to 180 tachinid genera, including the four currently recognized subfamilies (Dexiinae, Exoristinae, Phasiinae, Tachininae) and all major and widespread tribes. Our analyses generally support the subfamily groupings Dexiinae + Phasiinae and Tachininae + Exoristinae, though reconstructing the Coleoptera-parasitizing Myiophasiini, Palpostomatini and Macquartiini (Tachininae) as sister to all other tachinids. Only the Exoristinae and the Phasiinae were recovered as monophyletic assemblages under a wide range of weighting schemes. The Dexiinae, which were previously considered a well-established monophyletic group based on two autapomorphic character states, are here reconstructed as being paraphyletic with respect to the Phasiinae. The subfamily Tachininae which is composed of numerous morphologically heterogeneous taxa, is reconstructed as a paraphyletic grade from which the monophyletic Exoristinae arose. The latter, although weakly supported, are reconstructed as a monophyletic lineage but phylogenetic relationships within Exoristinae are largely unresolved. Also, in attempting to reconstruct the evolution of oviposition strategies we found that the laying of non-embryonated eggs (ovipary) may have evolved several times independently from ovolarviparous ancestors, thus suggesting that ovolarvipary could have characterized an early tachinid ancestor. Finally, we performed a parsimony-based ancestral reconstruction of host associations and found that despite the fact that the great majority of tachinids attack Lepidoptera larvae, these are unlikely to be the ancestral hosts for the family. Interestingly, in our analysis we found a general agreement between host use and monophyly of most of the lineages.

Phylogeny of the Atomosiini (Asilidae)

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Keywords: Robber flies, Laphriinae, cladistic analysis

The Atomosiini are a group of small robber flies that comprise 34 genera and over 200 species around the globe. Although they seem to be the most species-rich group of Asilidae in Neotropical forests, they are easily overlooked in the field due to their small size and usual preference for shadowy environments. Their monophyly is historically well supported and they are characterized by the presence of a heavily sclerotised postmetacoxal bridge. The goal of this research is to present an evolutionary hypothesis for the tribe based on different phylogenetic estimation methods, using morphological data. The discussion will focus on the evolution of traits relevant to the systematics of the group, and its taxonomy implications.

An on-going systematic study of the stalk-eyed fruit flies (Diptera: Tephritidae: Trypetinae)

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Keywords: Stalk-eyed fruit flies, *Pelmatops* Enderlein, *Pseudopelmatops* Shiraki

The stalk-eyed fruit flies include two genera, *Pelmatops* Enderlein and *Pseudopelmatops* Shiraki. They have close relationship with *Ichneumonosoma* Meijere and *Soita* Walker in Adramini. New findings on morphology, biology and geography of *Pelmatops* and *Pseudopelmatops* during recent 4 years are reviewed. The phylogeny of *Ichneumonosoma*, *Pelmatops*, *Pseudopelmatops* and *Soita* based on morphological and molecular data is conducted. The cladistic result based on morphological characters show that the monophyly of *Ichneumonosoma*, *Pelmatops*, *Pseudopelmatops* and *Soita* is well supported, and the stalk-eyed fruit flies have more close relationship with *Ichneumonosoma* than with *Soita*. Except that, the female aculeus images are mapped onto cladogram, their evolution possibility and morphology-function implication between female aculeus and host plants are tentatively discussed.

An automated image identification system for fruit flies of economic importance (Diptera: Tephritidae)

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Keywords: Fruit fly, automatic identification, computer version

There is an urgent need for an automated or semi-automated identification of fruit flies of economic importance, especially for quarantine or agriculture departments in many countries. A fruit fly identification system (AFFIS) that focuses on species of economic importance has been developed. It combines an automatic image identification method and manual interference in order to keep a balance between operability and accuracy. AFFIS utilizes pattern recognition, information retrieval, relational database, and ontology technology to combine the pattern recognition framework with digital keys. The system currently covers 5 genera and 60 species. The average recognition rate of the automatic method is about 80%, and of the semi-automatic method about 90% for the species included in the system. These results show that the system is effective in fruit fly identification both for expert and laypersons with little knowledge about the morphology of Tephritidae.

Drosophila suzukii (Diptera: Drosophilidae) in Korea: research history and seasonal occurrence pattern

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Keywords: *Drosophila suzukii*, seasonal occurrence, population fluctuation, Korea

CANCELED

Molecular identification of Diptera [poster]

Mitochondrial DNA Sequence Variation of the Spotted-wing *Drosophila*, *Drosophila suzukii* (Diptera: Drosophilidae)

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Keywords: *Drosophila suzukii*, mitochodrial COI, genetic relationship, haplotype

CANCELED

Applied Dipterology [poster]

Maggot debridement therapy using *Lucilia sericata* eggs

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Keywords: Larval therapy, wound healing, blow fly eggs

Maggot debridement therapy has become an effective treatment of chronic non-healing wounds. During the treatment, sterile live fly larvae (usually *Lucilia sericata* maggots) are introduced into the wound in a bagged or free form within special dressings. Maggots feed on necrotic tissue and secrete a wide array of antibacterial and growth-promoting substances which aid in wound healing. Larvae are left to develop in the wound for 48–72 hours and are then removed and discarded. To produce sterile medicinal-grade larvae, blowfly eggs are surface-sterilized and left to hatch on nutritious media overnight, while a parallel sample of eggs is taken for sterility tests. If sterility is confirmed, the newly-hatched maggots are sent by courier to the healthcare center for use in the treatment of wounds. However, application and containment of free maggots in the wounds may be laborous. The larvae are very mobile and must be applied by specially trained personnel. Moreover, maggots do not respond well to prolonged transport and storage conditions, which may cause problems in cases of delayed delivery and/or application. Our observations indicate that, rather than the maggots, sterile blowfly eggs may be applied to the wounds during maggot debridement therapy. *L. sericata* eggs, if sterilized and packed within 4.5 hours after oviposition and delivered 24 hours later, hatch within the next few hours under simulated wound conditions. Handling of the eggs is very easy and newly-hatched larvae grow comparably fast to maggots which had been applied as live larvae. Additionally, the eggs tolerate transport and storage for longer periods of time without negative effects on larval survival. However, development of rapid sterility tests is necessary if eggs are to be used in wound treatment.

Integrative taxonomy and the resolution of cryptic species complexes

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Keywords: *Bactrocera dorsalis*, species complexes, integrative taxonomy

Cryptic species complexes are groups of two or more biological species which have few or no consistent morphological differences between them. Cryptic species complexes can be found in any group of organisms, yet there are some lineages where complexes are particularly prevalent: within the Diptera this includes the mosquitoes and the tephritids. While the species within some complexes can be easily distinguished from each other by relatively straightforward molecular techniques, e.g., use of the COI barcode region, this is not the case for many tephritids. In such instances alternative strategies need to be applied. Using the *Bactrocera dorsalis* species complex as a case study, this talk explains the value in using an integrative taxonomic approach to resolve species boundaries within economically important tephritid species complexes. Integrative taxonomy uses multiple, independent lines of evidence to delimit species boundaries, and has a strong theoretical underpinning within the speciation literature. The strength of the integrative approach lies in the explicit testing of hypotheses and the use of multiple, independent species delimitation tools. In the case of pest members in the *B. dorsalis* complex, these tools have been applied by independent labs around the world, leading to very strong, multi-national consensus outcomes. As part of discussing the integrative approach, emphasis will be placed on the subtle but important differences between integrative and iterative taxonomy, and how the latter approach applied to the *B. dorsalis* complex led to incorrect conclusions which had major implications for quarantine, trade, and horticultural pest management. Finally, a case is made for a core set of species delimitation tools (pre- and post-zygotic compatibility tests, multi-locus phylogenetic analysis, chemoecological studies, and morphometric and geometric morphometric analyses) to be adopted as standards by tephritologists aiming to resolve economically important species complexes.

Plenary talk

Mosquitoes and the prospects for malaria elimination

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Keywords: *Anopheles funestus*, insecticide resistance, South-eastern Africa

Malaria parasites are transmitted to humans by anopheline mosquitoes. The parasite undergoes an obligatory sexual stage within the mosquito midgut that takes up to 14 days to complete. This presents a window of opportunity for us to control the mosquito populations before they have sufficient time to become infective. Unfortunately, both mosquitoes and parasites have been around a lot longer than humans and so far have managed to find ways of getting around all the drugs and insecticides that we throw at them.

In Africa today there are approximately 140 recognised species of *Anopheles* mosquitoes. Only 4 of these are really good vectors of malaria parasites and are widespread over the continent. Three of them are highly adapted to humans and human habitations and should, therefore, be easy to control using current technology. The fourth is more cosmopolitan and is equally happy to feed on cattle as well as humans and rest both indoors and outdoors, making it a much more difficult vector to control. All four species have developed high levels of resistance to the insecticides we use for vector control and given the limited number of chemicals that are approved by the World Health Organization for this purpose, there is an urgent need for new and innovative methods for controlling malaria vector mosquitoes.

Phylogeny of *Psychoda* sensu lato (Psychodidae: Psychodinae) inferred from morphological data: one more step towards a consensus classification?

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Keywords: Psychodini, cladistic analysis, morphology, new genus

The genus *Psychoda* Latreille is the oldest grouping in the family Psychodidae, and has already gone through several changes concerning its delimitation. In the past 60 years, there was an extensive discussion among specialists about the limits of this genus, as well as the limits of the tribe Psychodini, to which it belongs, but no agreement has been reached. Nowadays, the main proposals for this group of dipterans can lead to more than 400 species being classified into 1–13 different genera. In this study we aimed to present a hypothesis of phylogenetic relationship in *Psychoda* sensu lato and recover its position among related genera. Slide mounted specimens (mostly types) from several museums were studied, and 110 morphological characters were proposed based on 99 species. Phylogenetic trees were generated through the parsimony algorithm, using implied weighting in the program TNT. According to the consensus tree, *Psychoda* sensu lato is a polyphyletic group, and we suggest that It should be divided into at least three genera: *Psychoda* Latreille, *Psychodocha* Ježek and a new monotypic genus. Inside the genus *Psychodocha*, the clades corresponded to the geographical distribution of species, while in *Psychoda* no such pattern was recovered. The tree also suggests further subdivisions of the genus *Psychoda*, with the subgenus *Tinearia* being corroborated, and a new delimitation of the subgenus *Logima*. Other generic and subgeneric propositions for *Psychoda* sensu lato are discussed in light of the phylogenetic hypothesis and a broad definition of the tribe Psychodini is corroborated, in which the genera with flattened labellum, *Neomaruina* Vaillant, *Epacretron* Quate, and *Rhipidopsychoda* Vaillant, were recovered as the closest relatives of *Psychoda*, *Psychodocha* and the new genus herein proposed.

Male eyespan size is associated with meiotic drive in wild stalk-eyed flies (*Teleopsis dalmanni*)

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Keywords: Meiotic drive, sex ratio, sexual selection

This study provides the first direct evidence from wild populations of stalk-eyed flies to support the hypothesis that male eyespan is a signal of meiotic drive. Several stalk-eyed fly species are known to exhibit X-linked meiotic drive. A recent QTL analysis in *Teleopsis dalmanni*, found a potential link between variation in male eyespan, a sexually selected ornamental trait, and the presence of meiotic drive. This was based on laboratory populations subject to artificial selection for male eyespan. In this study we examined the association between microsatellite markers and levels of sex ratio bias (meiotic drive) in 12 wild *T. dalmanni* populations. We collected two data sets: a) brood sex ratios of wild-caught males mated to standard laboratory females, and b) variation in a range of phenotypic traits associated with reproductive success of wild-caught males and females. In each case, we typed individuals for 8 X-linked microsatellite markers, including several that previously were shown to be associated with male eyespan and meiotic drive. We found that one microsatellite marker was very strongly associated with meiotic drive whilst a second showed a weaker association. We also found that, using both independent datasets, meiotic drive was strongly associated with male eyespan, with smaller eyespan males being associated with more female-biased broods. These results suggest that mate preference for exaggerated male eyespan allows females to avoid mating with males carrying the meiotic drive gene and is thus a potential mechanism for the maintenance and evolution of female mate preference.

What's the next Diptera Manual?

Marcia Couri

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Keywords: Diptera fauna, biodiversity, manual, South America

Large projects focusing on the faunal survey and research in biodiversity occurred in Brazil, mainly in the 80s (e.g. Polonoroeste (Rondonia and Mato Grosso) and Profaupar (Paraná)) were of utmost importance for the knowledge of the dipteran fauna, also increasing its representation in the scientific collections. More recent projects developed in the last 10–15 years in Brazil with similar purposes to characterize and map the diversity of the dipterans of unexplored areas, focused mainly the Atlantic Forest, “Cerrado” (Brazilian Savanah), Pantanal, Chaco and Caatinga and Amazonian and Semi-arid regions. Also in Colombia, collections have been made in the central Mountain Range at altitudes from 400 to about 3800m and also in the Atlantic coast. These projects brought many new data to science, which are fundamental for the conservation and comprehension of the distribution of the species and also resulted in a strong engagement among the teams. Inside this atmosphere arose the decision to launch the project of the “Manual of South American Diptera”. Another crucial point was the amount of qualified and trained students in many dipteran families during the last years. In addition, the closer partnership relations with specialists of other countries reinforced the pleasant and stimulating ambience for such a joint proposal. Similarly to other previously published Manuals, it will represent an advance in access to the knowledge of the Diptera of South America, becoming a reference for students and researchers of Diptera. MSAD has six editors, more than 70 authors/co-authors and is organized in two volumes with 11 introductory and 114 systematic chapters. This is a three-years project and will include temperate and high-altitude fauna and high-resolution illustrations. MSAD is dedicated to all scientists who started the dipterology in South America, especially to our professors to whom we have all our gratitude and admiration.

Male terminalia: seminal discoveries in Diptera phylogeny

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Keywords: Tipulomorpha, Axymyiidae, Neodiptera, Apystomyiidae, Eremoneura

Male terminalia are a major source of phylogenetic information within Diptera at all taxonomic levels, because of tremendous morphological diversity associated with sexual selection resulting from female choice, as well as suites of characters correlated with adaptive shifts in mating position and evolutionary changes linked to the process of sperm transfer. The character system is reviewed in Diptera by overlaying apomorphic changes on published cladograms. New synapomorphies include: anteroventral parameral apodeme for the Tipulomorpha; parameral sheath encompassing desclerotized aedeagus for Neodiptera (exclusive of Axymyiidae); endoaedeagus for Xylophagomorpha + Tabanomorpha. Apystomyiidae are classified as the sister group to Eremoneura based on four synapomorphies (i.e., lateral ejaculatory processes absent, subepandrial sclerite extending from base of hypoproct to phallus, bacilliform sclerites extending to tips of the epandrium and surstyli functionally developed, but not articulated) and lack of eremoneuran synapomorphies (i.e., loss of gonostyli, presence of postgonites and phallic plate). The Diptera sperm pump with a functional ejaculatory apodeme is a possible autapomorphy of Diptera, exclusive of Nymphomyiidae and Deuterophlebiidae.

Psychodomorpha [poster]

Redescription of *Aposycorax chilensis* (Tonnoir) (Diptera: Psychodidae: Sycoracinae) with the first identification of a blood meal host for the species

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Keywords: *Sycorax*, moth fly, hematophagy, morphology, molecular

Adults of *Aposycorax chilensis* were collected from several sites during fieldwork in Chilean Patagonia, December 2013. Specimens were swept or aspirated from roadside seeps and found in greatest numbers during the morning hours. DNA was extracted from a recently blood-fed female and was subjected to the polymerase chain reaction using vertebrate-specific 16S primers. An amplicon was obtained and the resulting sequence was found to have 97% identity with two frogs in the genus *Batrachyla,* thus establishing this species' preference for amphibian hosts. The male and female *A. chilensis* are redescribed and illustrated in detail. Rotation of the male genitalia and implications for mating positions are discussed.

Morphology of the male terminalia in Psychodidae and Tanyderidae (Diptera)

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Keywords: Morphology, genitalia, moth fly, sand fly, homology

The male terminalia of Psychodidae and Tanyderidae are examined and compared. In Psychodidae, terminalia morphology is extremely variable among and within subfamilies while in Tanyderidae it is more uniform. Homologization of characters including parameres, epandrial claspers and cerci is attempted and illustrated using color-coding. The phylogenetic significance of these and other characters and the difficulty of sampling representative taxa are discussed. Male terminalia of some Horaiellinae and Sycoracinae exhibit morphological evidence for a close relationship between Psychodidae and Tanyderidae while others do not. Species of Trichomyiinae, Bruchomyiinae, Phlebotominae and Psychodinae have greatly modified male terminalia making it challenging to determine homology and identify synapomorphies. Clarifying the phylogenetic placement of Psychodidae and Tanyderidae within Diptera and resolving relationships among the six psychodid subfamilies will require a total evidence approach coupled with careful sampling of representative taxa.

Behavioral and ecological drivers of host associated differentiation in gall midges (Cecidomyiidae) on desert shrubs in Israel

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Keywords: Speciation, mate choice, host plant, natural enemies

Host associated differentiation (HAD) is the process by which an adaptation to a new host leads to the formation of new species. When two hosts are sympatric or parapatric, reproductive isolation between the original and newly formed populations depends on behavioral, phenological and genetic factors. In the current study we tested behavioral, ecological and genetic evidence for HAD in the gall midge *Dasyneuriola* sp. that induces bud galls on *Suaeda asphaltica* and *Suaeda fruticosa* (Chenopodiaceae) in Israel. We used mate-choice experiments to test for assortative mating, and host-choice experiments to test if mated females show oviposition preference on their natal host. Analysis of mtCOI sequences failed to differentiate between the host-associated populations, but an AFLP analysis resulted in a clear division between them, indicating that they constitute partially isolated host races. The gall midges did not exhibit assortative mating in no-choice tests, and only partial host preference, whereby females from *S. asphaltica* were more selective than those from *S. fruticosa*. The population on *S. asphaltica* has a much shorter activity period than that on *S. fruticosa*, suggesting that phenological differences play a major role in maintaining reproductive isolation between them. We also documented attack levels by several species of parasitic wasps in the galls to explore the potential role of natural enemies in this system.

The biodiversity survey of Diptera of South-West Saudi Arabia

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Keywords: Saudi Arabia, biodiversity, surveys

Despite the medical and economic importance of Diptera in general they are poorly known and studied in the Middle East including
Saudi Arabia. The 520 species of Diptera, including all new recent records for the entire country of Saudi Arabia is probably far short of the actual species richness.

In an attempt to estimate its real dipteran species diversity, a survey specifically focused on Diptera was set up at 16 different localities in Southwest Saudi Arabia (which show major affinity to the Afrotropical region), using Malaise traps, sweeping, yellow pan trap, rearing, and probably also light-trapping. The main aims of this project are: (a) to identify the species of Diptera of Southwest Saudi Arabia (Jazan, Aseer & Najran Provinces), (b) to develop a reliably identified Diptera collection, (c) to establish a data base by compiling all available data on Diptera of Saudi Arabia from the literature, and (d) to examine the affinities of dipterous faunas of the Arabian Peninsula with those of the three adjacent zoogeographic regions (Afrotropical, Palaearctic and Oriental). Collections have been made from sea level to 2200m and material is preserved in alcohol.

Preliminary results revealed the occurrence of unexpected species from all three zoogeographic regions especially at high altitudes. Diptera taxonomic specialists are kindly invited to collaborate in the identification process. It is hoped to establish a better appreciation of the differences in dipterous fauna according to altitude within the sampling area.

When did the Tipulidae lift off?

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Keywords: Fossils, Tipulomorpha, Tipulidae, phylogeny

In order to date the origin of the family Tipulidae, the phylogeny of the Tipulomorpha is examined using data from Triassic, Jurassic and Early Cretaceous fossil species. Character states that enable the reconstruction of the phylogeny are discussed. Among the examined species a lineage is recognized comprising Late Jurassic and Early Cretaceous members of extinct and extant genera of Tipulidae. These fossils represent the earliest known taxa of the family, and the Late Jurassic species are the oldest known Tipulidae to date.

Lower Diptera and Southern Hemisphere biogeographical patterns

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Keywords: Biogeography, Phlebotominae, Psychodidae, Southern Hemisphere, vicariance

Studies on various groups of the Lower Diptera suggest that their oldest lineages evolved in the Southern Hemisphere. Resulting distribution patterns are usually attributed to the breakup of the supercontinent of Gondwana since the Late Jurassic. An overview is given of previously published studies on Lower Diptera vicariance biogeography in the Southern Hemisphere. The first results of an ongoing study of the phylogeny and biogeography of the Psychodidae with a current focus on the subfamily Phlebotominae are used to illustrate general biogeographic patterns. The study is also presented to accentuate the hybrid origin of the fauna of South America, which can be separated in a distinct northern tropical and a southern temperate component that reflect divergent biogeographic histories.

Tephritoidea [poster]

Enriched ginger root oil (EGO)lure as an alternative for both trimedlure and terpinyl acetate in detecting and monitoring of target *Ceratitis* pest species (Diptera: Tephritidae)

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Keywords: *Ceratitis capitata, Ceratitis cosyra, Ceratitis rosa*

The males of some *Ceratitis* fruit flies are known to be attracted to specific parapheromones. These substances are routinely used for detecting and monitoring the presence and relative population abundance of particular pest species such as *Ceratitis rosa*, *C. capitata* and *C. cosyra*. Two standard parapheromones, trimedlure (routinely used for *C. rosa* and *C. capitata*) and terpinyl acetate (routinely used for *C. cosyra*), were compared with enriched ginger root oil (EGO)lure using standard yellow fruit fly traps. The comparison was conducted at 10 sites along an altitudinal transect in Morogoro region (Central Tanzania) from 540 to 1650 masl for a period of nine weeks. The captures reflect that all three target species were collected at higher numbers in the EGOlure charged fruit fly traps, compared to the conventional trimedlure and terpinyl acetate charged traps. It is argued that EGOlure can act as a suitable and more efficient alternative for trimedlure and terpinyl acetate parapheromones. In addition, EGOlure has the added advantage that it combines the taxon spectrum for the two latter substances, thus requiring the use of only a single attractant.

Deadwood and Diptera: Determining threshold values for sustainable biomass harvesting with a focus on the Sciaroidea (Diptera)

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Keywords: Biomass-harvesting, thresholds, Sciaridae, emergence-trapping, Sciaroidea

In managed boreal forests, residual deadwood such as branches, stumps and logs are key deadwood microhabitats for Diptera. This residual deadwood is being targeted for biofuels as a mitigation measure for climate change. Losses of residual deadwood from biomass harvesting threaten saproxylic Diptera, particularly those taxa within the Sciaroidea. These impacts may persist over long periods and result in an extinction debt. We identified deadwood habitat preferences of Sciaroidea across a range of diameter and decomposition classes. We then determined how much deadwood must be retained to maintain assemblages of Sciaroidea.

We used 40 eclector traps on fallen jack pine (*Pinus banksiana*) deadwood to rear adult flies *in-situ*. We collected specimens in 2012 in Ontario, Canada. We compared assemblages derived from logs spanning 7–25 cm diameter and across early and advanced decomposition classes. All Sciaroidea were identified to species where possible. We compared abundance, diversity and composition using non-metric multidimensional scaling and generalized linear modelling. We also reared Sciaroidea in 48 *ex-situ* cages to estimate intra-log variability. We hypothesized that logs in advanced decay stages will harbor more species of fungi and thus greater diversity of Sciaroidea. We also expected abundance and diversity of the Sciaroidea to increase with increasing log diameter.

Approx. 500 Sciaridae specimens have been identified to date of 43 species, several of which are new to Canada, North America and one *Bradysia* sp. that is potentially new to science. Preliminary ordinations and GLMs show a slight though significant demarcation between advanced decay assemblages versus early decay assemblages, which may be more apparent with more sampling. Diameter appears to be an important variable despite using provisional data.

We are using this information to quantify thresholds of deadwood retention under biomass harvesting and integrate Sciaroid biology into applied forest management.

The role of the Carpathians as cumulative refugia: a case study of the relic-endemic cranefly, *Pedicia staryi* Savchenko, 1986 group (Diptera: Pediciidae)

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Keywords: Carpathian, crane fly, phylogeny, COI, morphology

The Carpathians had an important role as speciation center and refugia for aquatic and semiaquatic insects in Europe. Despite this fact, studies regarding population genetic structure and evolution of these species are scarce, mostly in the case of narrow endemic taxa. In this study we focused on the phylogenetic relationships of three range-restricted crane flies in the Carpathians in relation to their sibling species using sequences of a mitochondrial (COI) marker. The Maximum Likelihood and Bayesian Inference phylogenetic trees show the *Pedicia staryi* complex (sensu Savchenko, 1986) to be monophyletic. The three Carpathian endemics (*Pedicia apusenica, Pedicia lobifera, P. staryi*) form a well-defined clade that diverged about 8.56 million years ago from its most widespread sister species, *Pedicia straminea*. *Pedicia staryi* and *P*. *apusenica* form a clade including *P*. *apusenica* and four well defined *P*. *staryi* lineages that have an insular-like distribution through the Carpathians. Morphological divergences are highly congruent with the molecular data in the case of some micro-morphological structures of the male genitalia, supporting the differentiation of these five cryptic groups, which is likely the result of an allopatric speciation process. The molecular clock show that these processes occurred during the Miocene-Pliocene period and are most probably connected to the different arridification cycles of the area. These results demonstrate the importance of the Carpathians as “cumulative refugia” in the case of aquatic and semiaquatic organisms.

Phylogeny of Apioceridae and Mydidae based on morphological characters of imagines

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Keywords: Orthorrhapha, phylogeny, morphology

A phylogenetic hypothesis of Apioceridae (flower-loving flies) and Mydidae (mydas flies) is presented based on 231 characters of the imagines. Apioceridae are known only from 138 described species distributed in Argentina/Chile, Australia, South Africa, and western North America while mydids occur more-or-less world-wide, but are most diverse in arid and semi-arid environments with some 472 species known to date. This study is based on a comprehensive, world-wide taxon sampling of 30 Apioceridae species (22% of current species diversity) and 137 Mydidae species (111 described species =24%, plus 26 undescribed species), respectively, from all over the world with an additional 30 species as outgroup taxa. While the monophyly and adelphotaxon relationship of the two family taxa was never questioned and is supported in the present study, the phylogenetic relationships within Mydidae have never been postulated with cladistic methods. Therefore, the monophyly of the most speciose subfamily taxa of Mydidae, i.e., Leptomydinae, Mydinae, and Syllegomydinae, and the southern Hemisphere endemics, i.e., Apiophorinae, Diochlistinae, and Megascelinae, is tested. The character evolution of several interesting features such as the reduced proboscis for feeding and the different ovipositor morphologies for egg laying are discussed. The oldest fossil Mydidae, *Cretomydas santanensis*, from the Crato Formation of Brazil (approximately 112 myo) is included in this study and placed phylogenetically as the adelphotaxon to the Australian genus *Diochlistus*.

Open access, unique identifiers, and cybertaxonomic tools for sharing Diptera research data

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Keywords: Open access, globally unique identifiers, data sharing

The importance of globally unique identifiers is explored and illustrated for modern approaches to taxonomy, phylogeny, and biodiversity research in general. The goal is to highlight several cybertaxonomic workflows in order to provide access to Diptera research data in public, online, open-access depositories to the benefit of the entire biological research community. Globally unique identifiers (Life Science Identifiers (LSIDs)), digital object identifiers (DOIs), or persistent URLs need to be employed in all aspects of research that includes Diptera specimens, taxon names and nomenclatorial acts, authors and articles, digital illustrations and images, distribution maps, specimen occurrence records, museum collections, or other data pertaining to a particular study. Only through the use of such identifiers and open-access availability will future generations benefit from our research directly and will be able to re-use and re-purpose the data we have gathered today. Adding novel data based on new observations, specimens, or techniques can then accelerate the research output and adoption of standards, allow for the test of hypotheses, and make taxonomic and phylogenetic research more transparent for the benefit of society at large. The hope is that such tools will also help to overcome the taxonomic impediment and accelerate the rate at which we describe biodiversity. While several journals, in particular those of Pensoft Publisher, provide many of these tools to authors, these tools can easily be incorporated into research projects submitted to more traditional journals. In summary, only through the adoption of an open-access policy to all data and the use of unique identifiers to connect data through computer networks will we succeed to truly make our Diptera research data available to our present and future colleagues.

Revision of the Neotropical species of *Trichopoda* Berthold, 1827 and *Ectophasiopsis* Townsend, 1915

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Keywords: Tachinidae, Phasiinae, *Trichopoda*, taxonomy

Trichopoda Berthold, 1827, is a Tachinidae genus belonging to the subfamily Phasiinae, originally distributed in the Americas. The Phasiinae species are Hemiptera parasitoids, especially Heteroptera, and have great importance in biological control. The genus is included in the "*Trichopoda typica*" group *sensu* Sabrosky (1950), together with the genus *Eutrichopoda* Townsend, 1908. The genus *Trichopoda* includes several nominal species many of which have been synonymized, while some were transferred to different genera. Even though the group is morphologically remarkable and also very important from an agricultural point of view, there is no revisionary work dealing with its species. Prior to the present study, 22 Neotropical valid species were included in *Trichopoda*, divided in two subgenera. In this study, we propose new synonyms, new combinations, and new revalidations, and describe new species. *Ectophasiopsis* Townsend, 1915, a monotypic genus, is also revised and being placed in the "*Trichopoda typica*" group, and one *Trichopoda* species is being transferred to it, and also a new specie is described. This genus-group is being redefined here, with new characters and a new composition. We provide identification keys for the three genera of the "Trichopoda typica" group, as well as identification keys to species of *Trichopoda* and *Ectophasiopsis*. We present photographs of males and females of all studied species, as well as illustrations of almost all male and female terminalia.

A Real Challenge – The Barcoding Fauna Bavarica Diptera Campaign

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Keywords: Barcoding, COI, Diptera, Bavaria

The Barcoding Fauna Bavarica (BFB) campaign started in 2009. Its aim is to create a DNA barcode library focusing on species occurring in Bavaria. Bavaria represents the biggest of all German states with a landmass of 70,000 km². It also harbors the highest biodiversity of all German states (with high altitude biomes, foothill areas and forested lowlands), with at least 35,000 animal species reported, representing a significant portion of the central European fauna.

As the existing collections turned out to be insufficient for the BFB, fresh material had to be collected. In order to get a high proportion of the Bavarian Diptera fauna within a short time we used 100 Malaise traps distributed over a wide variety of habitat across southern Germany. Sorting this material and the identification of as many species as possible are the most challenging part of the project. So far 1,215 species from 70 families have been identified (estimated number of Diptera species in Bavaria >8,000).

We were able to create 2,051 COI barcode sequences using 3,152 specimens (success rate 65%) covering 725 species of Bavarian Diptera (7.5% of all species reported from Germany). The current DNA barcode library contains 27 families and COI barcoding permits an identification of 77.5% of the species analyzed (725/936).

In a side project conducted in the "Bayerischer Wald" national park, we were able to create additional COI barcodes of 20,180 unidentified specimens, which were collected in two Malaise traps over 4 months in the summer of 2013, containing more than 1,000 species (the majority not yet present in the dataset, and which will be determined via "reverse-taxonomy").

Over 250 years of taxonomic and faunistic studies on European biting midges (Diptera: Ceratopogonidae)

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Keywords: Ceratopogonidae, Europe, taxonomy, faunistics, history

The Ceratopogonidae is one of the most diverse families of Diptera, with 6,190 extant species known worldwide and placed in 111 genera. Fossils are represented by 274 species in 49 genera (30 extant, 19 extinct), and abundant in amber deposits ranging from the Lower Cretaceous to the Miocene. Within this extant fauna, 590 species in 27 genera are reported from Europe, and 476 of these have their type localities here. The highest number of species are known from Germany (256), France (247), Poland (219) and Estonia (184).

The first validly named Ceratopogonidae was proposed by Carolus Linnaeus in 1758 for *Culicoides pulicaris* (as *Culex*), and up to 1900, 110 further new species were described. Most species (363) were discovered during the 20th century. Jean-Jacques Kieffer (1857–1925) was the most prolific author of specific names within the family. He introduced 260 names, of which 90 remain valid and 170 became synonyms. Other noteworthy taxonomists were Hans Remm, who described 43 valid European species, Johann Meigen (38), Maurice Goetghebuer (37), Jean Clastrier (33), Johannes Winnertz (29) and Frederick Wallace Edwards (16).

The most species rich genera in Europe are: *Culicoides* (120 species), *Forcipomyia* (89), *Dasyhelea* (86), *Palpomyia* (68), *Atrichopogon* (55) and *Bezzia* (52). Females of nearly 39% of all species are predators on other small insects, while 22% (*Culicoides*, *Leptoconops*, sg. *Forcipomyia* (*Lasiohelea*)) are haematophagous. Present taxonomic efforts are primarily concerned with the latter ecological group, especially *Culicoides*, species of which vector Bluetongue and the Schmallenberg virus. After over 250 years of studies, taxonomy and distribution patterns of biting midges in Europe still remain poorly known. Almost all genera need modern taxonomic revision. Only 32% of the European species are known as larvae and/or pupae (many of these poorly), and we have little knowledge of their specific microhabitats.

Long snouts, short snouts and obscure host associations – phylogeny and systematics of the seed-feeding genus *Ozirhincus* (Cecidomyiidae)

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Keywords: Asteraceae, gall midges, host plants, revision

The genus *Ozirhincus*, described by Rondani in 1840, is restricted to achenes of various asteraceous plants in the tribe Anthemidae. Adult gall midges in this genus are characterized by a conspicuously long rostrum, the function of which is unknown given that the adults are short-lived and apparently do not feed. The genus was originally restricted to the Old World but *O. millefolii* was introduced to North America with its host, *Achillea millefolium*, and is widespread today in the Nearctic region. The only revision of the genus (in 1968) was based on larval characters alone, listing 12 species and reporting some of them from a long list of host plants. In the present study we screened 25 Asteraceae species in Germany, the UK and Israel, and found 11 of them to be hosts of *Ozirhincus* species. We conducted a molecular phylogenetic analysis and a morphological analysis based on larval, pupal and adult characters, which established that the genus includes only four well defined species, both morphologically and genetically, with somewhat complicated host associations. No species is restricted to a single host plant, and in two cases the same host plant supports two *Ozirhincus* species concurrently, which can be differentiated by the length of their rostrum. We explore the possible meaning of the vast differences in rostrum length within the genus and the ways by which cohabiting species share the same plant resource.

Habitat associations of the rare flies *Dolichopus laticola* and *D. nigripes* (Diptera: Dolichopodidae) in the fens of Norfolk, England

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Keywords: *Dolichopus*, UK, habitat requirement, fen quality, conservation

Two dolichopodids, *Dolichopus laticola* and *D. nigripes* are listed in the UK Biodiversity Action Plan which is the government's response to the 1992 Earth Summit held in Rio de Janeiro. They are rare in their entire distribution range and have Endangered status in Britain where they are confined to high quality fenland in the east of the country. More than 300 standardised samples of adult dolichopodids were collected in 2010 and 2011 at 21 sites within Britain's richest fenland in the county of Norfolk. *D. laticola* was more widespread than *D. nigripes* and appeared weakly associated with fens of high botanical interest (based on concurrent botanical survey data), and those rich in other dolichopodid species. It was absent from fens of low botanical value and a lower dolichopodid diversity. Where it occurred, it showed no preference for particular habitats but it seemed to avoid carr woodland (*Alnus*, *Salix*) and commercial *Cladium* beds, and was scarce in fen grazed by cattle. Tree models showed that the only clear microhabitat requirement for this species was damp to wet peat. *D. nigripes* showed a strong preference for grassy fen and was relatively scarce in typical tall-herb fen vegetation, carr and beds of tall *Phragmites* or *Cladium*.

Agglomerative clustering showed that both species were part of an assemblage of dolichopodids including most fenland specialists. Management recommendations based on these results did not require any marked change in practice but did highlight a conflict of managing fens by grazing animals. Such detailed surveys of rare species are important for nature conservation as they identify features that are not apparent from casual recording.

Parasitization of the invasive ladybird, *Harmonia axyridis*, by native phorid parasitoids in Poland

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Keywords: Phoridae, *Phalacrotophora*, parasitoids, *Harmonia axyridis*

Four species of the genus *Phalacrotophora* (Diptera: Phoridae) are known as gregarious endoparasitoids of ladybird (Coleoptera: Coccinellidae) pupae in Europe. Three of them (*P. fasciata* (Fallén), *P. berolinensis* Schmitz and *P. delageae* Disney) have been found to have rather broad host spectra, while the fourth species (*P. beuki* Disney) has so far been reported as parasitizing only one host species, the eyed ladybird (*Anatis ocellata* (L.)). Bearing in mind the relative polyphagy of most ladybird-associated *Phalacrotophora*, we wanted to check whether these parasitoids can contribute to natural control of the recent invasive species in Europe, the harlequin ladybird, *Harmonia axyridis* (Pallas). Between 2008 and 2012 we collected *H. axyridis* pupae from various trees and shrubs in Warsaw and its surroundings. Altogether, we collected 1054 *H. axyridis* pupae, of which 978 (93%) developed into adult beetles. Of the remaining 76 pupae, 56 (5.3% of all collected) were parasitized by the four *Phalacrotophora* species. *P. delageae* was the most frequently recorded (23 *H. axyridis* pupae parasitized) followed by *P. fasciata* (15 pupae), *P. berolinensis* (3 pupae) and *P. beuki* (3 pupae). Furthermore, six host pupae were multiparasitized (four by *P. delageae* + *P. fasciata* and two by *P. delageae* + *P. fasciata* + *P. berolinensis*), and the flies from the other six hosts could not be determined because in the puparia obtained from these hosts, only early developmental stages (larvae and pupae) were found. Our study showed that the rates of parasitization of the harlequin ladybird by *Phalacrotophora* spp. are low, but the species richness of the flies associated with this host is surprisingly high. None of the native European ladybirds has been found to host so many *Phalacrotophora* species and none other than the eyed ladybird has been reported to be parasitized by *P. beuki*.

Cosmopolitan and neglected, *Stomoxys* flies are important vectors of pathogens!

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Keywords: *Stomoxys*, phylogenetics, phylogeography, vector role, control methods

The genus *Stomoxys* Geoffroy, 1762 includes 18 known species (Zumpt, 1973), 17 of which with a tropical distribution and one (*S. calcitrans* (L. 1758)) cosmopolitan. *Stomoxys* flies are haematophagous and are a nuisance because of their painful bites and blood predation, and they are also mechanical vectors of pathogens present in the blood and skin of their animal hosts, especially livestock and dogs but occasionally also humans. A phylogenetic analysis suggests the paraphyly of the genus *Stomoxys*, due to the inclusion of *Prostomoxys saegerae* in the group. The basal branching of *S. indicus* suggests an Oriental origin of the genus, around the end of the Oligocene. A phylogeographic study of *S. calcitrans* shows the presence of an Oriental lineage differentiated from the remainder.

Stomoxys are not only immediate transmitters of pathogens, they are also suspected of delayed transmission by regurgitation of blood from crop or gut, which may considerably impact their role in the epidemiology of the transmitted diseases. Such a mechanism allows inter-herd transmission of pathogens. Equine infectious anemia, African swine fever, West Nile and Rift Valley viruses are known to be transmitted by *Stomoxys*, while others are suspected to be. Rickettsia (*Anaplasma*, *Coxiella*), as well as other bacteria and parasites (*Trypanosoma* spp., *Besnoitia* spp.), are also transmitted by *Stomoxys*. Finally, *Stomoxys* was also found to act as an intermediate host of the helminth *Habronema microstoma* and may be involved in the transmission of some *Onchocerca* and *Dirofilaria* species. Being cosmopolitan, *S. calcitrans* might have a worldwide and greater impact than previously thought on animal and human pathogen transmission.

Based on a better knowledge of their role as nuisance species and their biology, new means of control of *Stomoxys* flies are currently under study to specifically attract these insects to traps or toxic targets.

Comparative study of Diptera in El Musawwarat Area (2012/2013)

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Keywords: Sudan, semidesert, biodiversity, Acacia scurb

In protected areas, where trees and plant cover is conserved and where no human activities are present, both a high diversity and abundances of Diptera is expected. In this study, the diversity of Diptera between two habitats of the El Musawwarat area are compared: a protected area with a high plant diversity, and a non-protected area with acacia scrub. A total number of 219 individuals were collected in the protected area using pitfall traps and dishes 30cm×10cm, and 136 individuals in the non-protected area. These specimens belonged to 24 families, with 20 different families established in the protected area and 9 families in the non-protected area. The results indicate that in both habitats, Muscidae were most abundant, followed by family Calliphoridae, family Asilidae showed highest species diversity in the non protected area, *Promachus bastardii* belong to family Asilidae recorded for first time in Sudan. The statistical analysis revealed a significant difference in Diptera composition between both habitats. Overall, the results suggest that the plant diversity might affect on the Diptera community.

Taxonomic position of a gall midge species (Diptera: Cecidomyiidae) infesting *Suaeda vermiculata* in Alexandria, Egypt

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Keywords: *Suaeda, Stefaniola*, Cecidomyiidae, Egypt

The Palearctic genus *Stefaniola* is one of the largest genera of Lasiopterini (Diptera: Cecidomyiidae) consisting of 110 species associated with plants of the goosefoot family (Chenopodiaceae). In the present study, a gall midge associated with *Suaeda vermiculata* was found in Alexandria, Egypt. The gall midge attack leaves, and sometimes stems and flowers of the host plant, without obvious signs of infestations. Based on morphological examination, the gall midges were found to belong to the genus *Stefaniola* and are considered to be an undescribed species. Descriptions and illustrations of morphological features of this species are presented and compared with closely related gall midges.

Predatory midges (Diptera: Cecidomyiidae) of Egypt, with first records of two species

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Keywords: Cecidomyiidae, predatory midges, *Spilococcus juniperi*, Egypt

The Egyptian fauna of the family Cecidomyiidae is very poorly known with only 43 of the 3113 known Palaearctic species recorded there. *Aphidoletes aphidimyza* (Rondani, 1847) and *Feltiella acarisuga* (Vallot, 1827) were the only previously known predatory midges. In the present study, we confirmed the presence of *A. aphidimyza* and *F. acarisuga,* in addition to recording two new predatory midges for the Egyptian fauna, *Diadiplosis donaldi* (Harris, 1968) and *D. hirticornis* Felt, 1915.

Aphidoletes aphidimyza and *F. acarisuga* were collected from *Nerium oleander* and *Ricinus communis* (respectively) which were infested with *Aphis nerii* and *Tetranychus urticae*, respectively. *Diadiplosis donaldi* and *D. hirticornis* were collected from *Cupressus sempervirens* infested with the mealy bug *Spilococcus juniperi* (Hemiptera: Coccoidea). The latter two are new records for Egypt as well as new prey records. Descriptions and illustrations of both species are presented.

UK surveillance of *Culicoides*

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Keywords: *Culicoides,* seasonality, surveillance, taxonomy, identification

Culicoides Latreille are small biting midges, with some species that are able to transmit a number of animal and human viruses, including Bluetongue virus (BTV) and Schmallenberg virus. Since the outbreak of BTV in northern Europe in 2006, weekly monitoring of *Culicoides* is carried out on a number of farms across the UK. Monitoring is carried out using Onderstepoort Veterinary Institute (OVI) light traps and collections are identified morphologically to species level, as far as possible. Morphological identification of *Culicoides* can be difficult and time consuming, but molecular methods can also be used.

Searle et al. (in press) have analysed the trapping data collected between 2006 and 2010 to determine seasonal activity patterns of *Culicoides.* The length of overwintering period of *Culicoides* in the *Avaritia* group was found to be correlated with the density of hosts and land cover type around the trap. It was also found that the phenology of *Culicoides* in the UK is species-specific, with considerable intra-specific variation between sites and years. Searle et al. (in press) and Sanders et al. (2011) both noted bimodal peaks in activity of *Culicoides* throughout the year. *Culicoides* were most active in early summer and then again in early autumn.

Vectors of Bluetongue virus have different temporal phenologies and may be differentially competent for arboviruses. Both of these factors could influence the seasonality of infection risk in the UK and northern Europe. Future work will involve expanding the surveillance network to a wider variety of habitats including zoos that may support large populations of vector species.

Rothamsted Research has a series of 12 m high suction traps for sampling migratory aphids. These have been running since 1974 and the by-catch includes *Culicoides*. Samples from 1974 to 2012 are currently being processed at Pirbright to see if there are changes in activity and the faunal composition of *Culicoides* over time.

Plenary talk

Standing on the Shoulders of Giants: the past and future of Diptera taxonomy

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Keywords: History, Diptera, taxonomy

Diptera taxonomy has evolved greatly since Linnaeus and its history is here organized in four themes: exploration, description, phylogenetic analysis, and resource synthesis.

Exploration: Voyages of exploration brought home more new and interesting forms that required names for collections. Some were identified by ships' naturalists, but more often they were identified by others.

Description: The first early workers were "generalists" identifying all Diptera. As numbers of specimens and species increased in the 1800s, taxonomic specialists were required, preferring to work smaller units of Diptera. Beginning around the 1900s, specialists increased and the trend continued toward more and more specialization.

Phylogenetic analysis: As species numbers in a genus burgeoned, new genera were employed. These too became large in number and taxonomists now wanted to understand more than just what defined a taxon. Darwin's writings on ancestral relationships led to graphic representations among groups in the form of trees: the most primitive taxon as the trunk and the most advanced as young leaves. In the mid 1900s, a more organized way to estimate relationships was developed (cladistics) and it remains today the primary method used. Initially only morphological characters were used. Since then, DNA has offered a new suite of characters to help estimate relationships.

Resource synthesis: As names of Diptera and associated literature increased, catalogs and checklists were created for easier retrieval by others. The zoogeographical realms were cataloged with the Nearctic first (1965) and others soon followed, ending with the Australian (1989). In 1984, the world database of Diptera project was initiated. Now known as Systema Dipterorum (SD), it continues as the standard to which other names databases aspire. The future for SD has it completely redesigned and community based, interlinking with other databases. The future of Diptera taxonomy will be global input as well as global output.

Taxonomic revision and cladistic analysis of *Acrochaeta* Wiedemann, 1830 (Diptera: Stratiomyidae: Sarginae), with comments on the monophyly of *Merosargus* Loew, 1855

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Keywords: Neotropical region, phylogeny, Stratiomyidae

Among the twelve subfamilies of Stratiomyidae, the Sarginae include 22 genera and 562 described species worldwide, of which 267 are Neotropical. There is still not a cladistic study of the relationships between the genera of the subfamily or between the species of its genera. Many of the genera are poorly delimited, with diagnosis in certain degree based on plesiomorphies. The circumscription of the Neotropical genus *Acrochaeta* is largely based on the elongated flagellar complex, a feature that also applies to some of the species of *Merosargus*. There is taxonomic and morphological inaccuracy in descriptions of species of both genera and lack of illustrations of male and female genitalia of the species. This study makes a taxonomic revision and a cladistic analysis of the genus *Acrochaeta*, redefining the genus from a phylogenetic perspective. *Acrochaeta* now includes 15 species (seven previously described and eight new species). Three *Acrochaeta* species are transferred to *Merosargus*: *M. chalconota* comb. n., *M. longiventris* comb. n. and *M. picta* comb. n.; one species is moved to *Chrysochlorina* (Chrysochlorininae) – *C. elegans* comb. n.; and *M. convexifrons* is transferred to *Acrochaeta* – *A. convexifrons* comb. n. The genus *Acrochaeta* and all previously described species are redescribed and the new species are described. An identification key for species is provided. A cladistic analysis including 45 terminal taxa – of which 27 are outgroups – and 63 morphological characters was performed, resulting in four most parsimonious trees (under equal weight). The monophyly of *Acrochaeta* was recovered by characters of head, thorax and abdomen. An inner clade in the genus was recovered, especially based on characters of the male genitalia. The wide selection of outgroups generate good evidence of the paraphyly of *Merosargus* – some of its species are closer to *Acrochaeta* and to *Himantigera* than to the clade including the type-species of *Merosargus*.

Keroplatidae (Diptera: Bibionomorpha) in Neotropical region and advances in systematics studies

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Keywords: Keroplatinae, Keroplatini, Orfeliini, taxonomy

The worldwide family Keroplatidae is subdivided in four subfamilies: Arachnocampinae, Macrocerinae, Keroplatinae, and Sciarokeroplatinae. Recent topologies show that Keroplatidae constitutes a monophyletic group with Bolitophilidae, Diadocidiidae, and Ditomyiidae. Currently, 950 described species in 92 genera are ascribed to Keroplatidae in the world. The diversity of the family in the Neotropical region has been poorly contemplated, especially due to the lack of specialists in the region, deficiency of identification keys and more revisional studies. After the studies of Loïc Matile, there has been little progress in the knowledge of the Neotropical fauna, like the description of new taxa, faunistic surveys, and genus revisions. Thus, current studies of this fauna are focused on the research of phylogenetic relationships of this family, with emphasis on Orfeliini, and in collections and descriptions of new taxa and revisional studies of genera that have presented themselves “problematic” along the phylogenetic analysis in progress. As a partial result of these studies, a morphological study was carried out to determine the phylogenetic relationships among the genera of Keroplatini and Orfeliini, testing the monophyly of both tribes and establishing the relationships between the genera of both tribes. Until now, the phylogenetic analysis was based on the study of 140 morphologic characters for 135 terminal taxa – of which 12 are outgroups. A total of 20 most-parsimonious trees were obtained with equal weight and two most-parsimonious trees with implied weighting. The results corroborate the monophyly of Keroplatidae, Keroplatinae, and Keroplatini and indicate Orfeliini, as currently defined, to be paraphyletic related to Keroplatini. A group of genera around the genus *Platyura* showed to be a sister clade including *Orfelia* and other genera plus Keroplatini.

Keroplatoidea (Diptera: Bibionomorpha) from States of Mato Grosso (MT), Mato Grosso do Sul (MS) and Rondônia (RO) (Brazil)

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Keywords: Biodiversity hotspots, Taxonomy, Neotropical region

Keroplatoidea comprises the families Bolitophilidae, Diadocidiidae, Ditomyiidae, and Keroplatidae. With exception of Bolitophilidae, all of those families occur in the Neotropics. Diadocidiidae has the lowest number of species in Keroplatoidea, and is known in the Neotropical region from the single taxon *Diadocidia nigripalpis.* Ditomyiidae is represented by 32 Neotropical species placed in nine genera, four of which are found in Brazil (14 species). The family Keroplatidae, with 32 Neotropical genera and over 200 described species, has 40 species recorded from Brazil, particularly in the southern states. In Brazil, most occurrences of taxa in Keroplatoidea were recorded primarily for the southern region, due to the fact that the fauna of the remaining portion of the country is poorly known. As a result of field expeditions related to the project "Diptera of the states of MT, MS and RO: diversity, systematics and distributional limits".

(SISBIOTA-Diptera), other Brazilian biomes were explored (Cerrado, Gran Chaco and Pantanal), and a number of specimens, representing new records and new taxa for these families, were studied. So far 22 new records and five new species have been found. One new species of Ditomyiidae (genus *Rhipidita*) was found for MT and RO. The first record for the family Diadocidiidae in the states of MS and RO was reported. Finally, Keroplatidae has new records for 13 genera, 10 of which are reported for the first time in the entire study area, including new species to be described in the genera *Micrapemon*, *Proceroplatus* and *Lapyruta*. Although Brazilian biodiversity is often praised, most of it is still proportionately poorly studied, and this regional investigation agrees. Unfortunately, the human pressure on natural areas is rapidly increasing, with direct environmental impacts causing devastating results even in a diverse country like Brazil. The fauna of Diptera is only an isolated example of this broader process.

Culicomorpha [poster]

New species of *Forcipomyia* (*Microhelea*) Meigen (Diptera: Ceratopogonidae) from Southern Brazil

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Keywords: Atlantic Forest, morphology, biodiversity, insect-host

A new species of biting midges collected in the Estação Biológica de Boraceia, Salésopolis, State of São Paulo, Brazil is described and illustrated with photos and drawings of mouth parts, head, thorax, legs, abdominal setae and habitus. Photos were taken with a camera mounted on a microscope or on a stereomicroscope, and drawings were obtained using a light dome. Several species of biting midges (especially of the genus *Forcipomyia* Meigen and *Atrichopogon* Kieffer) are known to parasitize other insects. Between 2012 and 2013, during 13 months, 51 nights, 12 hours of light trapping/night, all *Paraphasma paulense* Rehn, 1918 (Phasmida: Pseudophasmatidae) observed were collected. Two females of *Forcipomyia* sp. n. were collected a female specimen of a stick insect attracted to the light trap. One female adult was prepared in a permanent slide and one female adult specimen preserved in an 80% alcohol vial for description (later mounted on permanent microscope slide). The identification of females was based on the Claster and Wirth's key for the species of Neotropical *Forcipomyia* (*Microhelea*) parasites of Phasmida and their characters compared to the descriptions in the same work. Latin American species were checked on Borkent and Spinelli newest checklist, consisting of 49 species for the whole region, including 20 from Brazil. Important diagnostic characters of the species are the asymmetrical maxillae, mandible teeth, and abdominal chaetotaxy. Specimens were deposited in the MZSP entomological collection.

Some morphometric aspects of the eye stalks of the Diopsidae (Diptera)

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Keywords: Sexual dimorphy, homomorphy, allometry, ecological selection

The sexually selective advantage of longer eye stalks has been well established for dimorphic Diopsidae, but other advantages and also constraints need additional study. Here an updated distribution of dimorphic and homomorphic taxa in relation to Diopsidae phylogeny is presented. Use of wing patterns in the homomorphic *Diopsis circularis* species-group as a substitute for use of eye stalks in ritualised fights is illustrated.

As indication for the rate of dimorphism the difference between males and females in allometric slope for eye span on body length is commonly used. The allometric lines in this regard are highly static for both sexes of a species and are useful to check identification of difficult species. Sets of allometric lines can in the Diopsidae be used for morphometric characterisation of genera and species-groups. Static allometries are hard to change, but elevation is assumed more evolvable than slope. In two sets of very closely related dimorphic diopsids, each with a small and a large species, it is shown that in females allometric lines for eye span/body length are exactly in line with each other, while in lines for males only the intercept changed but not the slope.

Little is known about non-intraspecific ecological selection pressure on the eye span in the field. Changes in average eye span during the year in the largely univoltine *Diopsis longicornis* are discussed. In most diopsids, the relation between eye span/body length appears linear. However, in *Diopsis longicornis* eye span reaches an optimum in field-collected flies and does not increase any further in the very large males and females. Based on a small data set the same phenomenon was found in males of "*Diopsis*" *apollo*. Both species are among the largest dimorphic diopsids. Ecological constraints on the largest eye spans form a likely explanation.

Scales microstructures of *Sabethes* (*Sabethes*) *albiprivus* Theobald, 1903 (Diptera: Culicidae)

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Keywords: Exoskeleton, morphotypes, nanostructures

The genus *Sabethes* Robineau-Desvoidy is composed of 39 species, distributed in five subgenera, *Davismyia* Lane & Cerqueira*, Sabethoides* Theobald*, Sabethinus* Lutz*, Peytonulus* Harbach and *Sabethes* Rorineau-Desvoidy. *Sabethes* has the highest diversity within the genus, with a total of 18 described species. *Sabethes* (*Sabethes*) *albiprivus* Theobald, 1903, which is restricted to South America, has been found naturally infected with the yellow fever virus. It varies morphologically in its size and the color of the reflection of the scales that cover its thorax, abdomen, antepronotal lobes and occiput. The objective of this study was characterizing and describing the morphological variations of the samples, as well as studying the existing nanostructures on the scales that cover the body of these Culicidae. In total 210 adult female specimens placed on entomological pins were analyzed with a stereo microscope, and the identified patterns of coloration were described. The samples analyzed using scanning electron microscopy (SEM) were positioned on aluminum stubs, sputter-coated with gold and observed with a JEOL JSM-6360LV microscope. The analysis of the nanostructures of the scales covering the mesonotum, occiput and antepronotal lobes using SEM demonstrated that the observed color variations are due to the distance between the longitudinal lamellae and the presence or absence of nanostructures on the surface of the scales. Based on that, it was possible to describe seven morphotypes for *Sabethes albiprivus*, which were assigned to two groups, defined by the specific characteristics of the scales on the antepronotal lobes, occiput, abdomen and mesonotum. Further analysis should be performed, especially with immature stages, male genitalia and molecular techniques in order to evaluate the possibility that *Sabethes albiprivus* is in fact a species complex.

Personality traits during development in the stalk-eyed fly *Teleopsis dalmanni* (Diopsidae)

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Keywords: Personality, behavioral syndrome, larvae, adults, life history

Stalk-eyed flies are acalyptrate flies with their compound eyes displaced at the end of rigid head projections in both males and females. Personality traits of this group have not been tested yet, and it is unknown whether consistent behavioral syndromes can be observed in a holometabolous insect across different life stages.

During our experiments we have tested 3rd instar larvae every day until they pupariated and adult flies of the same individuals. Tests included personality traits like boldness, explorativeness and various factors of movement (speed, direction, track length).
Analysis of the larval results showed a significant correlation of the boldness trait between data recorded on days 1 and 3 (counted backwards from the pupariation) suggesting their behavior is consistent on these days.

Results will be presented on the larval and adult personality traits of individuals, how they correlate to sex, eyespan size and time of test performance.

Associations between personality traits of different life stages will be discussed with the main focus on both larva and adult being active/ bold/ explorative vs. the two stages showing opposite states of behavioral syndromes.

Relationships of these traits can reveal the evolutionary importance of the connection between the different or similar strategies of early and late developmental stages.

The genus *Phytomyptera* Rondani (Tachinidae) in the Cerrado vegetation, Brazil

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Keywords: Graphogastrini, new record, new species, Tachininae, taxonomy

Tachinidae is between the most specious Diptera families, with approximately 1,520 genera. The tachinid flies *Phytomyptera* are parasitoids of the caterpillar's micro-lepidoptera, e.g., Pterophoridae and Tortricidae. They belong to Graphogastrini tribe and are recognized by a blackish/grayish color pattern, small length, presence of a single large bristle at the base of veins R2+3 and R4+5 and a strongly curved downward proepimeral bristles. Sixty-four species of *Phytomyptera* were recorded around the world, except in the Australasian region; nine of them occurring in the Neotropical Region, and five were recorded in South America. Forty specimens were reared from caterpillars *Chiomara basiguta* (Elachistidae) and *Gonioterma exquisita* (Hesperiidae), collected in the forested areas of Cerrado vegetation, the Brazilian savannah highlands, in Brasília-DF, between 2002 and 2009. This is the first record of *Phytomyptera* in Cerrado. The *Phytomyptera* specimens were not identified with the current literature. They do not fit with the description of any known species and thus were considered as a new species from Brazil.

A world revision of the Schistopterini (Diptera: Tephritidae: Tephritinae)

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Keywords: Schistopterini, diversity, morphology, Asteraceae, flower heads, biology, distribution

The Schistopterini are a tribe of common and unusually ornamented fruit flies that are mostly easy to collect. A world revision of this tribe is ongoing for more than a decade, and several genera and species have been recently treated and described. The group is primarily Afrotropical, with the second largest, but much smaller, fauna in the Oriental region. A few representatives occur in northern Australia, and a few others in the southern Palaearctic region. All reared species develop in flower heads of Asteraceae, mainly from the tribe Vernoniae, and especially in the Afrotropical region. The total number of species already in collections exceeds 200, but only about a third of them are described. Israel's National Collection of Insects in Tel Aviv University (TAUI) currently houses about 30,000 pinned specimens, comprising almost all the described, as well as the great majority of the undescribed species. Preliminary sorting of the available material revealed about ten monophyletic species groups that have no names and may represent undescribed genera. Description of most of these will await a phylogenetic analysis in an attempt to base supra-specific taxa on strong grounds. Here we present the main subtribal taxa, and request and encourage collectors to send us any catches of schistopterines to be included in the revision.

Advanced morphological methods and their application in Dipterology

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Keywords: 3D visualisation, computed tomography, morphological techniques

During the last decade new morphological techniques became available and their combined application was optimized in several projects. This led to a development which was referred to as a “renaissance of insect morphology”. In our presentation we will briefly describe these techniques and outline their advantages and limitations. We address their applicability to specific scientific questions and samples with a special focus on the morphology of dipteran larvae and adults.

The covered techniques include micro-computed tomography (µ-CT), confocal laser scanning microscopy (CLSM), magnetic resonance imaging (MRI), light shed microcopy, focused ion beam (FIB) and recent advances in histological sectioning and scanning electron microscopy (SEM). Specific questions we will address for each method include the adequate size of specimens, the maximum spatial resolution, potential limitations, potential combinations with other techniques, and the invasiveness of the approach.

As most of the presented techniques yield raw data suitable for three dimensional modelling, we will outline the potential of computer-based 3-dimensional reconstructions in the second part of the talk. We critically evaluate the advantages and disadvantages of these models compared to traditional line drawings.

Comparative morphology of the male terminalia of Ulidiidae and Tephritidae

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Keywords: Musculature, male terminalia, Ulidiidae, Tephritidae

The morphology (sclerites and the musculature) of the male terminalia of the Ulidiidae and Tephritidae was examined and their homologies were discussed. We studied sclerites and the musculature of three ulidiid species: *Timia erythrocephala* Wiedemann, 1824, *Ulidia ruficeps* Becker, 1913, *Physiphora chalybea* (Hendel, 1909). These species represent all three genera of the tribe Ulidiini (Ulidiidae). The musculature of the male terminalia of the examined species consists of the following six groups of muscle sets. **I)** Two pairs of muscles connect hypandrium with phallapodeme. Muscle M1 connects laterobasal part of phallapodeme and ventral margin of lateral phallapodemal projections with distal half of hypandrium. Muscle M2 connects lateral margin of medial phallapodeme projection with basal half of hypandrium. **II**) Muscle M5 connects laterodistal part of hypandrium with laterobasal margin of epandrium. **III**) Muscle M4 connects inner lateral parts of surstylus with laterobasal part of epandrium. **IV)** Muscle M7 connects medial part of subepandrial sclerite with cerci. **V)** Muscle M3 connects inner part of epandrium with lateral lobes of subepandrial sclerite. **VI)** Muscle M25 connects anus with medial part of epandrium. **VII)** Paired non-symmetrical muscle M18 connects distal part of hypandrium (1) and basal part of hypandrium (2) with 8th syntergosternite. Single muscle M19 connects basal margin of epandrium with 8th syntergosternite. We homologized all compared muscles with earlier published data on other Cyclorrhapha Diptera.

Efficiency of different colored pan traps for collecting adult Bombylioidea (Diptera)

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Keywords: Bombylioidea, collecting method, pan traps, Iran

Pan trapping is one of the efficient methods for collecting flying insect in natural ecosystems and fields. Usually yellow-colored pan traps are used for sampling flies abundance and diversity. This color is thought to be best for trapping of microbombyliid adults. However the efficiency of other colors for attracting the adults of bombyliids to traps was little studied. In the present study, attractiveness of six colors: yellow, green, black, light blue, white and red are tested based on the complete randomized block design (CRBD) in the Spring of 2008 and 2009. Four replications were conducted for each treatment in a rangeland in Ghazvin province (The north of Iran). The results of the analysis of variance using Spss software, showed that there is a statistically significant difference ($P \leq 1\%$) between traps in both years. The mean comparison of treatments by Tukey's test shows that blue and white colored pan traps capture the highest microbombyliids and are the most effective. Yellow colored pan traps are in the second rank. Other three colors including black, green, red have the least attractivness and the efficiency for collecting adults and are orderd in the third group. It is worth noting that more than 15 new species of microbombyliids were collected by using this finding.

A review of the family Bombyliidae (Diptera: Bombylioidea) in the Northwest of Iran

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Keywords: Bombyliidae, Iran, bee flies, new records

The family Bombyliidae, commonly known as bee flies, are the comprised of species that feed on nectar and pollen in the adult stage so likely play significant role in the pollination of plants; and also in the larval stages they feed on locust eggs or parasitize immature stages of soil dwelling insects consequently having significant effect on the population equilibrium of these insects and the balance of natural ecosystems. Taxonomy and species diversity of bee flies in some areas of northwestern Iran including Ghazvin, Zanjan, East Azerbaijan and Hamadan provinces were studied. A total of 35 species, as listed below, including 2 new species were collected by using Malaise traps, sweeping net and pan traps. In this study three genera and fourteen species are newly recorded from Iran that are marked by two ** and * asterisk respectively.

Usia bicolor Macquart, 1855*; *Apolysis glabrifrons* Gharali & Evenhuis, 2010; *A. pusilloides* Gharali & Evenhuis, 2010; *Phthiria vagans* Loew, 1846; *Ph. minuta* (Fabricius, 1805)*; *Ph. pulicaria* (Mikan, 1796); *Geron asiaticus* Zaitzev, 1967*; *G. griseus* Zaitzev, 1962*; *Conophorus pseudaduncus* Paramonov, 1929*; *C. glaucescens* (Loew, 1863)*; *Bombylius medius* Linnaeus, 1758; *B. analis* ssp. *diagonalis* Wiedemann, 1820*; *B. fuscus* Fabricius, 1781; *B. discolor* Mikan, 1796*; *Bombylella atra* (Scopoli, 1763); *Bombomyia stictica* (Boisduval, 1835); *Triplasius pictus* (Panzer, 1794)**; *Systoechus autumnalis* (Pallas & Wiedemann, 1818); *Prorachthes pleskei* Paramonov, 1927; *Lomatia belzebul* (Fabricius, 1794); *Cytherea obscura* Fabricius, 1794; *Gyrocraspedum pleskei* Becker, 1913; *Amictus firjuzanus* Paramonov, 1931*; *Callostoma fascipennis* Macquart, 1840; *Stomylomyia nigrirostris* Bezzi, 1925*; *Pipunculopsis bivittata* Bezzi, 1925**; *Villa cana* (Meigen, 1804); *Thyridanthrax elegans* (Hoffmansegg, 1818); *Hemipenthes robustus* Zaitzev, 1966*; *H. subvelutina* Zaitzev, 1966; *H. exoprosopoides* Paramonov, 1928; *Oestranthrax karavajevi* Paramonov, 1931**; *Exoprosopa grandis* (Pallas, 1820); *Heteralonia megerlei* (Meigen, 1820).

The *Schistopterum* clade revised – conflicts between molecular and cladistic evidence

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Keywords: Tephritidae, *Schistopterum* clade, phylogeny, cladistic analysis, molecular analysis

The *Schistopterum* clade is a small group of flies within the tribe Schistopterini (Tephritidae), consisting of fifteen species of which nine are new, within four genera, of which one is new: *Schistopterum*, *Brachiopterna*, *Bactropota* and *Damaramyia* n. gen. A comprehensive publication dealing with the entire tribe suggested that the three known genera of the *Schistopterum* clade form a paraphyletic clade together with *Microtreta*. Renewed thinking, based on morphological and biological evidence, made us assume that the previous results do not reflect the true relationships and that the “restricted” *Schistopterum* clade is indeed monophyletic, rather than paraphyletic. Both cladistic and molecular analyses were made. In both analyses almost all fifteen species of the *Schistopterum* clade were included, as well as representatives of all other Schistopterini genera and three representatives of the subfamily Tephritinae. In the molecular analysis a portion of the mitochondrial genome comprising of most of the CoI gene, tRNA-Leu, CoII and tRNA-Lys was sequenced. The sequencing of the entire fragment yielded contigs of 2257–2317 bp in length. The cladistic analysis was based on 45, mainly morphological, characters. According to the molecular analysis, the monophyly of each of the four *Schistopterum* clade genera was retrieved with maximal support whereas, the *Schistopterum* clade as a whole was found to be paraphyletic as it also contained two additional genera of the Schistopterini. Unlike the molecular analysis, the cladistic analysis showed maximal support in the monophyly of the *Schistopterum* clade, while the support of the genera is less distinct.

Notes on the poor known South American genus *Kelloggina* Williston, 1907 (Blephariceridae)

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Keywords: Brazil, Diptera, Neotropical region, systematics

Blephariceridae are a small Diptera family, with 320 species grouped in 27 genera. In the Neotropical region, there are 76 species in five genera, from which 34 species belong to *Kelloggina* Williston. Studies with the genus were few and isolated, and the last paper on this subject was published nearly 60 years ago. The records of the genus were punctual and only 17 localities were sampled, being 13 concentrated in three states of Brazil (SC, SP, RJ). Until now, the distribution of *Kelloggina* is restricted from Santa Catarina state, through Iguazu falls (Misiones, Argentina), to Caparaó, in Minas Gerais state (the most Northern and Eastern records). Also, one species were found in Santiago, Chile. Aiming to enhance the knowledge of the diversity and distribution of *Kelloggina*, material deposited in collections was analyzed. Moreover, field collections focused on Blephariceridae have been made since 2012. Until now, 17 morphotypes were found, from five southeastern and southern states of Brazil (RS, SC, SP, RJ, MG). From those, six undescribed species were found, and also five of the seven Southeastern species described by Lutz in 1920: *K. bocainae*, *K. fascibranchia*, *K. hirtipupa*, *K. horrens*, and *K. mochlura*, expanding their recorded distributions. Also, three species collected in Santa Catarina state are probably also Lutz's, but it is not possible confirm their identification because only larvae were found. The remaining three species cannot be confirmed yet, because they are from Itatiaia and can be species described by Lane and d'Andretta Jr, who only described the adults. It is necessary to rear the imagos from pupae before an accurate identification. Those very early results show us that the number of species of *Kelloggina* and their distribution is highly underestimated in the literature. All the undescribed and the rediscovered old species will be described and re-described, respectively.

What's up with Neotropical *Simulium* subgenera (Diptera: Simuliidae)?

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Keywords: Systematics, Americas, phylogeny, black flies

Of the 2,151 extant species of Simuliidae, 81% belong to the genus *Simulium* Latreille, which is organized into at least 37 subgenera and 110 species-groups around the world. Phylogenetic analyses showed that *Simulium* is monophyletic, but did not determine the same for most subgenera and species-groups. Eleven subgenera of *Simulium* have been recorded in the Neotropical region, including 257 species. Most of those species are well described and represented in collections.

However, the knowledge of the relationships among the supraspecific groups is poor and subgenera diagnoses are unsatisfactory, resulting in divergent systematic arrangements in the literature. Furthermore, most classification decisions have been made exclusively based on personal opinions, without any clear methodology or hypotheses. Thus, previously proposed systematic arrangements are clearly unsatisfactory. This is the case with the subgenera *S.* (*Ectemnaspis* Enderlein) and *S.* (*Psilopelmia* Enderlein). Comparative studies indicate that they are closely related, but there is no consensus in the literature about the boundaries between them, and some species-groups are transferred from one subgenus to the other over the time. Recently, some authors proposed synonymy of both. The two subgenera are traditionally divided into four species-groups: Bicoloratum, Dinellii, Escomeli, Perflavum and Romanai. Recently the species-groups Blancasi and Oviedoi were also incorporated without justification. Moreover, phylogenetic analysis indicate that the subgenus *Chirostilbia* Enderlein is paraphyletic, because the Subpallidum species-group is more closely related to the subgenera *S.* (*Ectemnaspis*) and *S.* (*Psilopelmia*) than to the *Pertinax* species-group. A more inclusive phylogenetic analysis showed that the Blancasi and Oviedoi species-groups are only distantly related to *S.* (*Psilopelmia*). Also, the subgenera *Ectemnaspis* and *Psilopelmia* are not monophyletic, and the only monophyletic species-groups are Dinelli and Romanai. Those results highlight that subgenera and species-groups need more attention, and must be based on an explicit cladistic methodology.

Overview of the Neotropical spider flies (Acroceridae)

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Keywords: Small-headed flies, spider parasitoid, systematics, taxonomy

Acroceridae are a cosmopolitan group of lower brachyceran flies with great diversity of size, shape and coloration. Adults feed on nectar and larvae are endoparasitoids of spiders. Fifty-five extant genera of Acroceridae are presently recognized, containing about 530 described species worldwide. Neotropical fauna comprises all three spider fly subfamilies, and is represented by 19 genera and approximately 110 species. Sixgenera are described in Acrocerinae for the region (*Acrocera* Meigen, *Carvalhoa* Philippi, *Holops* Philippi, *Ogcodes* Latreille, *Pterodontia* Gray, and *Villalus* Cole), while nine genera are described in Panopinae (*Appeleia* Bellardi, *Archipialea* Schlinger, *Camposella* Cole, *Coquena* Schlinger, *Exetasis* Walker, *Lasia* Wiedemann, *Ocnaea* Erichson, *Pialea* Erichson, and *Pteropexus* Macquart). Philopotinae is represented in the Neotropics by four genera (*Megalybus* Philippi, *Neophilopota* Schlinger, *Terphis* Erichson, and *Philopota* Wiedemann). A discussion of the systematics of the Neotropical Acroceridae is presented, including the indication of several Neotropical genera that are still lacking revisions and identification keys. Several new Neotropical species of spider flies are known in collections, mostly in *Lasia*, *Ocnaea*, and the species rich genera *Acrocera* and *Ogcodes*.

Phylogeny and divergence time estimates of spider flies (Acroceridae) using DNA, morphology and fossils

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Keywords: Molecular phylogenetics, morphology, small-headed flies, spider parasitoid

Spider flies (Acroceridae) are a small but morphologically diverse group of obligate spider endoparasitoids. A total-evidence phylogeny of Acroceridae is presented, based on both morphological and DNA sequence data, including fossil taxa as terminals in estimates of relationship and divergence time. The evolution of the spider flies is discussed in a temporal and spatial context, including host use, homoplastic morphological reductionism and considerations of the likely sister group to the family. An overview of the systematics and classification of Acroceridae is presented, with indications of future directions and perspectives, including a cybertaxonomic monograph and interactive keys.

Revision on taxonomy and biology of Lonchaeidae (Diptera): an important family of fruit flies in the Neotropics

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Keywords: Lonchaeidae, lance flies, taxonomy, natural history.

Lonchaeidae are robust moderate size (3–6 mm long) flies, body black, dark blue or green, generally with metallic reflections. Although several species have been associated with fruit or flowers of some Angiospermae species of economic importance, they remain poorly studied. This may be related to the fact that the systematics of this group presents major taxonomic difficulties. The distinction between many species/genera can be quite confusing. In order to elucidate the aspects of biogeography, ecology and taxonomy of the Lonchaeidae, we searched in databases for publications (January 1878 to December 2013), and 201 papers were found. A total of 538 species are described in two subfamilies and ten genera. Two monotypic genera are fossils: *Morgea mcalpinei* Hennig and *Glaesolonchaea electrica* Hennig. There are eight living genera with 536 species: 127 species of *Dasiops* Rondani, 8 of *Protearomyia* McAlpine, 7 of *Chaetolonchaea* Czerny, 23 of *Earomyia* Zetterstedt, 20 of *Lamprolonchaea* Bezzi, 213 of *Lonchaea* Fallén, 98 of *Silba* Macquart, and 40 of *Neosilba* McAlpine. From the nineteenth to the twentieth century, there was a progressive increase of publications about Lonchaeids worldwide. In the twenty-first century there was an increase of interest in their systematics, ecology and biogeography. On the other hand, the evident difficulties in the taxonomy can be a limiting factor for the beginner entomologists in the study of the lance flies. The lack of taxonomic keys, illustrations and the scarcity of research groups specialized in Lonchaeidae hinder the production knowledge about these flies. Even though they are responsible for considerable economic losses in crops, several basic aspects of their biology, ecology and biogeography are still unknown. This revision provides a map of the world distribution of the species, and a taxonomic key for identification of subfamilies and all living genera worldwide.

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Bibionomorpha [poster]

Phylogenetic analyses of the Central European Sciaridae

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Keywords: Black fungus gnats, mitochondrial (COI, 16s) marker, nuclear (28s) marker

The systematics of the family Sciaridae is based mainly on morphological characters and remains quite controversial. In this study we used two mitochondrial (COI, 16s) and one nuclear (28s) marker to elucidate phylogenetic relationships of Central European Sciaridae. A total of 104 species were analysed including two strictly alpine species. Phylogenies of the individual gene datasets based on maximum likelihood and of the concatenated dataset based on Bayesian analyses are presented.

210 new combinations? DNA suggests the Pacific species are separate from *Campsicnemus* Haliday (Diptera: Dolichopodidae)

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Keywords: Dolichopodidae, *Campsicnemus*, Hawaii, French Polynesia, molecular phylogeny

The widespread dolichopodid genus *Campsicnemus* (found worldwide except the Neotropics and Australia) has diversified into the second-largest adaptive radiation of Diptera in the Hawaiian Islands, with 179 Hawaiian endemic species currently described. Another hotspot of diversification appears to be in French Polynesia where preliminary study shows an additional 31 described species. Some 100 new species from Hawaiʻi and French Polynesia have been found and are awaiting description, giving a total of 300 species from just two isolated islands groups. It had been hypothesized by some that the Pacific species are a separate lineage (possibly a separate genus) from *Campsicnemus* sensu stricto. We tested that hypothesis by conducting a molecular phylogenetic analysis of *Campsicnemus*, primarily focusing on the Hawaiian fauna, but also including French Polynesian examples. We analyzed a combination of two nuclear and five mitochondrial loci using Bayesian and maximum likelihood approaches to generate a phylogenetic hypothesis for the genus *Campsicnemus* s.l. Our sampling included a total of 84 in-group species (7 from Europe, 7 from French Polynesia, and 70 from the Hawaiian Islands) and 24 out-group species in Sympycninae and Peloropeodinae. The phylogenies were used to estimate divergence times, reconstruct biogeographic history, and infer ancestral ecological associations within this large genus. The molecular analyses conducted in this study suggest that the Pacific clade appears to be separate from *Campsicnemus* sensu stricto. We found strong support for a South Pacific + Hawaiian clade, as well as for a monophyletic Hawaiian lineage. Divergence time estimates suggest that Hawaiian Islands were colonized approximately 4.6 mya, suggesting that most of the diversity within *Campsicnemus* evolved since the current high islands began forming 5 mya.

Slugs and snails and … sciomyzids: using selected sciomyzid species as biocontrol agents of pestiferous slugs and liver fluke disease

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Keywords: Sciomyzids, biocontrol, pestiferous slugs, fascioliasis

The presence of pestiferous slugs can result in significant crop losses, in addition to which there is a low tolerance among consumers to vegetables with slug damage or contaminated with slug faeces. Similarly, liver fluke disease, the intermediate host of which is the snail *Galba truncatula*, can result in livestock death, reduced animal growth / productivity and rejection of livers for human consumption. Of particular concern is current evidence that climate change will result in an increased number of liver fluke outbreaks in parts of Western Europe. In this presentation we examine optimum growing conditions for two sciomyzid species, in particular, the slug killer *Tetanocera elata* and predator of the snail vector for liver fluke disease *Ilione albiseta*. We also investigate the predatory behaviour of the larval stages of these sciomyzid species vis-à-vis their potential use as biocontrol agents in the context of other control measures currently in use.

Morphological description and notes on the biology of immature stages of three *Peckia* (*Euboettcheria*) species (Sarcophagidae)

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Keywords: Flesh flies, decomposition, Brazil, Neotropical

Peckia Robineau-Desvoidy, 1830 (Sarcophagidae) has 67 described species with mostly Neotropical distribution. The immature stages of some species can be of great value to the forensic field due to its eating habits to be associated with organic matter from decaying animal. Regarding the knowledge of the biology and description of larval stages, most are largely unknown. Thus, morphological descriptions and biological data for the larval stages for species *Peckia* (*Euboettcheria*) *anguilla*, *P*. (*E*.) *australis* and *P*. (*E*.) *collusor* are presented here. Colonies were established in laboratory from field collections carried out in natural environment in several locations in the state of São Paulo, Brazil. Ground beef was used to stimulate the larviposition and to allow the larval development. Samples of 10 individuals were taken every 6 h until pupariation, dissected and preserved in fixative solution to proceed morphological studies. The duration of each instar (first, second and third) at 25°C were, respectively, 6, 18 and 108h for *P*. (*E*.) *anguilla*; 6, 12 and 102h for *P*. (*E*.) *australis*; and 12, 24 and 156h for *P*. (*E*.) *collusor*. A total of 22 internal and external characters were observed in third instar larvae, and those concerning cephalopharyngeal skeleton were relevant for the diagnosis of three species as described: oral hooks with angular curvature in *P.* (*E.*) *anguilla*, or light curvature in *P.* (*E.*) *australis* and *P.* (*E.*) *collusor*; parastomal bar with 2/3 of the length of the intermediate sclerite in *P.* (*E.*) *anguilla*, or representing half of the intermediate sclerite in *P.* (*E.*) *australis* and *P.* (*E.*) *collusor*); tentorial phragm higher than long in *P.* (*E.*) *anguilla* and *P.* (*E.*) *australis*; or longer than high in *P.* (*E.*) *collusor*. These descriptions help to enhance our understanding of Sarcophagidae, beyond making possible the identification of the species in question when are associated with decomposing bodies.

150 million years of Cyclorrhaphan flies and the anatomy of evolutionary radiations

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Keywords: Tertiary, amber, Cretaceous, Myanmar, Schizophora

The Cyclorrhapha consist of 8 basal (aschizan) families and about 60 in the Schizophora (Calyptrata and the acalyptrates). These flies appear to have largely diversified in the Tertiary (65 mya to present) even though the oldest cyclorrhaphan fossils are twice this age. According to the Fly Tree of Life (Wiegmann et al., 2010), which used Bayesian molecular estimates of divergence times, Cyclorrhapha originated approximately 150 mya and Schizophora about 75 mya. These hypotheses are tested using the most comprehensive analysis of fossil (60 species) and Recent (40 species) Cyclorrhapha and >150 morphological characters. All of the fossil taxa are preserved in Cretaceous and Tertiary ambers, fidelity of which provides unique precision with interpretations of phylogenetic relationships. Cretaceous amber species are primarily from Lebanon (Early Cretaceous), Myanmar (mid-Cretaceous), and New Jersey and western Canada (Late Cretaceous); Tertiary species are in amber from the Cambay Shale of western India (earliest Eocene), Baltic region (Eocene), and the Dominican Republic and Mexico (Miocene). The Burmese amber, in particular, is yielding an exceptional diversity of early Cyclorrhapha, the most significant of which are presented. A definitive Schizophoran fly has still yet to be found in the Cretaceous, though the Campanian-Maastrichtian (latest Cretaceous) and Paleocene are poorly known epochs for Diptera in general. The fossil record and relationships of an exemplar group of Schizophora, the Ephydroidea, is presented (these include the Camillidae, Curtonotidae, Diastatidae, Drosophilidae, and Ephydridae, and possibly the Braulidae and Cryptochaetidae). A critique is provided of various estimates of divergence times in Drosophila. Episodes of delayed radiation appear to be universal to all lineages of organisms with a significant fossil record, and a new "adaptive refinement" theory is proposed to explain this.

Biogeography and diversification of northwestern Neotropical Fanniidae: exploring biogeographical patterns in the Andes

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Keywords: Ancestral distribution, estimation of divergence time, *Euryomma*, *Fannia*

Four genera are known in the Fanniidae, two of which are found in the Neotropics: *Euryomma* Stein (19 species) and *Fannia* Robineau-Desvoidy (89 species). Considering the typically high diversity in the Neotropics, especially in the northwest component (Central America + Northwest of South American continent), here we infer phylogenetic relationships among these genera and species in the northwestern neotropics using morphological and molecular information. We then propose an hypothesis of biogeographical diversification of these lineages. In the morphological analysis we used 57 species of Fanniidae and two Muscidae, and in the molecular approach, we used 15 species of Fanniidae and cytochrome oxidase 1 (COI) and 28S genes. We used Bayesian analysis to combine these two approaches. Reconstruction of dispersal and vicariance events was carried out using S-DIVA and estimation of divergence time using BEAST. Our data and analyses support monophyly of the Fanniidae, *Piezura* and *Euryomma*. On the other hand, *Fannia* is paraphyletic due to divergence of the *canicularis* group from the remainder of the *Fannia* species. Reconstruction of the northwestern biogeographical history indicates that the ancestral distribution was in Central America and north of the Andes. Ancestral species of Fanniidae occupied northwestern South America around 41–18 Ma. (Middle Eocene to Early Miocene). Subsequently, several range expansions and vicariance events resulted in the diversification of recent Andean lineages (north of the Andes and the central Andes) and lineages from lowland areas, such as the Chocó, the Amazon, the Guyana Shield, the Chaco and southeastern South America. Events related to the biogeographical evolution of the Fanniidae in the northwestern neotropics are supported by the new model of evolution of the Isthmus of Panama and geological events, such as marine incursions (northern and western South America), and the elevation of the Central and Eastern Ranges (northern Andes).

Ecology and site quality assessment of mangroves using Dolichopodidae and Hybotidae: a case study in Singapore

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Keywords: Dolichopodidae, Hybotidae, Oriental region, Singapore, mangroves, biodiversity, assessment

A month-long sampling campaign with Malaise traps in 2009 in 11 mangroves in Singapore (26 sampling sites) and a non-stop two-year sampling (2012–2014) in 4 locations (13 sampling sites in 3 mangroves, and one terrestrial reference site) revealed the presence of about 150 species of Dolichopodidae and 56 species of Hybotidae. Referring to earlier terrestrial surveys, about 80% of the species are confined to mangrove habitats. Dolichopodidae proved to be good bio-indicator candidates for site quality assessment, being specific for microhabitats as shown with a DCA analysis. This comprehensive biodiversity assessment of wetland Empidoidea has resulted in the creation of a DNA barcode database for all mangrove Dolichopodidae and online public access image catalogue for future research.

Taxonomy and diversity of hybotids (Diptera: Hybotidae) in various types of forest in the Congo Basin near Yangambi (D. R. of Congo)

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Keywords: Hybotidae, Afrotropical region, D.R. Congo, diversity survey, taxonomy

The main objective of the present study is to investigate the relationship between the diversity of insects and the various types of forest in the region of Yangambi (COBIMFO program). Special attention was given to the Hybotidae, a highly speciose group of small predatory flies. However, as is the case for many other non-colonial insect groups, the species diversity is very high but species abundances are very low thus limiting statistical analysis. The number of specimens collected per time unit is much lower in primary forest than in young forest. This might be related to the multilayer stratification of the understory vegetation in young forest, as a consequence of the variety of light intensity that reaches the understory. Primary forests lack a dense understory which is used by predators as hunting ground and as food source for herbivores.

Using DNA barcodes for diversity assessment in Hybotidae (Diptera: Empidoidea)

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Keywords: Hybotidae, barcoding

Empidoidea is one of the largest extant lineage of flies but still the global diversity remains scarcely assessed. Also, phylogenetic relationships among species of this group are poorly investigated. Within the framework of a pilot study, we barcoded about 600 specimens of Old World hybotids belonging to more than 200 species in 25 genera (plus 2 *Empis* species as outgroups). The material originated from the Palaearctic (Belgium, France, Portugal and Russian Caucasus), the Afrotropic (Democratic Republic of the Congo, Uganda) and the Oriental realms (Singapore and Thailand).

Although DNA barcoding generally separated recognized taxa quite well, the study also revealed a number of unexpected phenomena: (i) the presence of new taxa among morphologically very similar or identical specimens of species, often with wide geographic ranges; (ii) morphologically distinct species without genetic divergence; (iii) different patterns of intraspecific divergence that suggests further (life history or spatial) differences between populations or sibling species.

Using COI sequences and simple neighbour-joining tree reconstructions, the monophyly of many species and genus level taxa was well supported, but higher level taxonomic relationships were not significantly supported. It was concluded that in hybotids DNA barcoding is a reliable and useful tool to identify species, but two main constraints must be considered: (i) incomplete barcoding libraries hinder efficient (correct) identification, therefore extra efforts are needed to increase the representation of hybotids in these databases; (ii) the spatial scale of sampling has to be taken into account, and especially for wide-spread species or species complexes with unclear taxonomy, an integrative approach has to be applied to clarify species boundaries and identities.

The morphology of immature stages and the systematics of Muscidae

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Keywords: Muscidae, systematics, immature stages, morphology

Recent results of molecular studies do not confirm the current classification of Muscidae based on adult morphology. Verification of the current classification through incorporation of characters of immature stages of a broad group of taxa is thus desirable. In the 1980s Skidmore suggested several changes to Muscidae classification based on larval morphology.

However, our studies have shown that there is substantial morphological diversity among larvae that has not yet been fully analyzed and synthesized.

According to the literature, third instar larvae of Muscidae are distinguishable from all other Calyptratae by a combination of character states rather than by a single autapomorphy.

We found character states of larval morphology which may be considered as family specific. These data stem from personal examination of specimens. A search of the literature for the presence of these character states in larvae of other Muscidae came to nothing. Because of vague descriptions and inaccurate illustrations provided by earlier authors, previous descriptions require a detailed revision. Our results suggest that the basal split of the Muscidae divides the family into two groups: 1) Muscinae + Azeliini excl. Reinwardtiini, and 2) remaining Muscidae. Because the Reinwardtiini, currently considered as a tribe within the Azeliinae, have a closer morphological similarity to the second group taxa rather than to the first, we consider that this tribe should be raised to subfamily level, i.e. Reinwardtiinae.

Immature stage characters are not thought to be superior to any other data. However, they can provide valuable information on the relationship between taxa and can help resolve questions concerning Muscidae systematics. In the Muscidae, characters of the immature stages support molecular findings, which are at odds with the classification based on adult morphology. We urge dipterists to collect and study immature stage morphology for a better understanding of family systematics.

The application of immature stages of Fanniidae in forensic entomology: prospects and caveats

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Keywords: Fanniidae, larva, morphology, development, forensic entomology

Fanniidae are one of the dipteran families attracted to decaying organic matter. More than 50 species have been reported in carrion succession experiments and forensic investigations worldwide. However, only up to ten species are confirmed as breeding in/on cadavers. Synanthropic fanniid species can colonize a corpse when access to the body is restricted to other forensically important arthropods. Under certain conditions species known from secondary myiasis cases may also be expected to colonize the body before death. Association of fanniids with different stages of cadaver decomposition potentially permits their application for minimum post-mortem interval (PMI) estimation, either with succession or development-based methods.

The vital first step for application of any entomological material in $\mathrm{PMI}_{\mathrm{min}}$ calculation is proper species identification. Currently, application of Fanniidae for medico-legal purposes is beset with problems in the species identification of larvae, and calculation of the age of developing insects on the body. In most species the immature stages have not been described at all. Third instar larvae of only a few forensically important species have been described and the state of knowledge of earlier instars is even more scarce. Lack of detailed developmental data prevents forensic entomologists from calculation of the age of developing Fanniidae on a body.

We discuss here limitations in the larval identification of forensically important Fanniidae. Our preliminary results reveal inaccuracies and even erroneous descriptions in the literature data of fanniid larval morphology. Thus none of the published identification keys for different geographic regions allow for precise species discrimination of the majority of forensically important Fanniidae. We also present the aims of a recently commenced study which will document the occurrence of Fanniidae in forensic entomological casework. This will lead to identification keys for larvae as well as developmental models permitting the age estimation of preimaginal stages.

Confocal laser scanning microscopy as a valuable tool in Diptera larval morphology studies

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Keywords: Larva, morphology, confocal laser scanning microscopy, clearing technique

Insect morphology is traditionally studied using light microscopy. However, in the case of fine structures this method is limited due to problems of resolution, illumination and depth of field. Nowadays scanning electron microscopy (SEM) is also routinely used in morphological studies of Diptera larvae. This technique is very useful for detailed imaging of the insect surface but not for the investigation of internal structures. Confocal laser scanning microscopy (CLSM) is a valuable tool for detailed studies of small, complex structures at high resolution close to diffraction limit. By collecting fluorescence signals from different focal planes within a specimen, a fully three dimensional (3D) dataset can be acquired and used for visualization. CLSM could have a profound impact on the quality of information compared to more traditional methods of imaging. Nonetheless, none of the previous studies on dipteran larval morphology has applied CLSM methods.

We investigated the usefulness of CLSM for the study of cyclorrhaphan larval morphology. We evaluated the CLSM application for examining slides stored in museum collections. These slides were prepared using two standard methods, cleared with potassium hydroxide or chloral hydrate (a key ingredient of Hoyer’s medium). We compared these results with those obtained from freshly prepared larvae. Material for our study were either permanent slides embedded in Euparal or Hoyer’s medium or freshly prepared larvae mounted in water.

Our results indicate that CLSM and 3D reconstruction are excellent techniques for visualizing fine, complex, autofluorescent structures of dipteran larvae, if appropriate clearing techniques, i.e. the application of KOH, are used. When this clearing technique was used the results did not differ between previously prepared slides and freshly cleared material.

Taxonomic revision and cladistic analysis of *Ormiophasia* Townsend, 1919 (Diptera: Tachinidae: Ormiini)

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Keywords: Tachinidae, Ormiiini, *Ormiophasia*, Neotropical, phylogeny

The Tachinidae is a large family of Diptera and all species are parasitoids of arthropods. Their classification is complex and confused, especially in Neotropical region. Tachinidae are classified into Dexiinae, Phasiinae, Exoristinae and Tachininae, the latter including the tribe Ormiini. Ormiine flies occur worldwide and locate their hosts (Orthoptera, Ensifera) phonotactically. They have an inflated prosternum with an acoustic membrane. The genus *Ormiophasia* Townsend includes nine species and it is endemic to the Neotropical region. Its validity has been questioned by many authors, and it has even been considered a junior synonym of *Ormia* Robineau-Desvoidy. This study aims to revise the genus *Ormiophasia*, test its monophyly and reconstruct the phylogenetic relationships among the recognized species. A total of 319 specimens were examined from six Brazilian and five international institutions. A data matrix of 27 morphological characters from 13 species of *Ormiophasia* and 11 outgroup taxa was made in Mesquite 2.75. Characters were treated with equal weights and unordered. *Glaurocara flava* (Glaurocarini) was used to root the tree. Thirteen morphotypes of *Ormiophasia* were recognized, with determination of six species: *O. busckii* Townsend, O. causeyi Tavares, *O. costalimai* Tavares, *O. cruzi* Tavares, *O. lanei* Tavares and *O. travassossi* Tavares. The status of *O. inflata*, *O. morardi* and *O. obscura* is still doubtful. The majority of species are distributed in the Amazon Forest and Central America. Only two species are widespread and *O. lanei* is restricted to Atlantic Forest. Preliminary results corroborate *Ormiophasia* monophyly, with *Ormia* as its sister-group. The monophyly of *Ormiophasia* is supported by larval and male terminalia characters. Since most variation among species of *Ormiophasia* is in male terminalia and the codification of these characters is not yet completed, the species relationships are not fully resolved and some clarification will still be added to the final topology.

Fossil Scatopsidae (Diptera) in Eocene Baltic amber: a preliminary overview

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Keywords: Scatopsidae, Baltic amber, fossil fauna, diversity

Fossil Scatopsidae have been little investigated so far. The oldest known unambiguous representatives of the family are from Early Cretaceous and fossil specimens have been recorded from various deposits, from Cretaceous to Miocene. Strangely, while scatopsids are not very rarely found among dipteran inclusions in Baltic amber (Eocene, 40–50 mya), only few species of Scatopsidae have been described from this fossil rich amber.

The present study is based upon the large collection of over 300 scatopsid inclusions in the Muséum d’histoire naturelle of Neuchâtel, Switzerland (MHNN) and the important material (75 specimens) from the private collection Christel and Hans Hoffeins, Hamburg (CCHH). Few specimens belonging to other collections, including the type material of the species described by Meunier (1907) from the former “Königsberg Bernstein Sammlung” now in Geowissenschaftliches Museum der Universität Göttingen (GMUG), have also been studied.

Three of the four subfamilies of the Scatopsidae (Ectaetiinae, Psectrosciarinae and Scatopsinae) and all four tribes of subfamily Scatopsinae (Rhegmoclematini, Scatopsini, Colobostematini and Swammerdamellini) are represented in studied material of Baltic amber, but their abundance and diversity appear markedly different from that in Present fauna. Representatives of subfamilies Ectaetiinae (23% of examined material), Psectrosciarinae (18%) and of tribe Rhegmoclematini (33%) are abundant and largely dominant in Baltic amber fauna. Eocene representatives of about one fourth of present genera of Scatopsidae have been found, while species belonging to undescribed genera are present in all three subfamilies. An intriguing new genus belonging to the Psectrosciarinae is discussed in connection with the phylogeny of the family.

Myiasis: ante-mortem forensic dipterology

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Keywords: Myiasis, Calliphoridae, *Lucilia,* neglect, development rates

Myiasis is the infestation of living vertebrates with fly larvae. While some species of Diptera will only infest living hosts as obligate parasites, others can infest living hosts as facultative parasites and also develop on dead bodies. It is the facultative parasites, typically species of blowfly (Calliphoridae) or fleshfly (Sarcophagidae), that are most important in a forensic context and often they are the same species that act as the primary indicators of minimum post-mortem interval on dead bodies ($\mathrm{PMI}_{\mathrm{min}}$). If an ante-mortem infestation of a host that subsequently dies is not taken into account, then any $\mathrm{PMI}_{\mathrm{min}}$ calculation will be an overestimate of the actual PMI. However, the major emphasis of this presentation will be on applying knowledge of larval development to determining the minimum period of neglect or abuse in cases of infestation of still living hosts, whether human or animal. Human cases usually involve the young, the elderly or those who are otherwise unable to avoid the attention of gravid flies (e.g. debilitated, in coma). Examples of myiasis of humans and animals will be discussed, where estimations of the periods of neglect were used in the courtroom to support other evidence in the successful prosecution of offenders. The most frequent species encountered in cases of ante-mortem forensic dipterology in the UK is *Lucilia sericata*, whose development is well studied. Until recently the development rates of a closely related species, *L. caesar*, were unknown, but this data has now been collected enabling it to be used as a forensic indicator, demonstrated by a case of dual infestation of a neglected dog with both *L. sericata* and *L. caesar*.

Attractants and traps for collecting Calliphoridae and Sarcophagidae

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Keywords: Traps, attractants, Calliphoridae, Sarcophagidae

Blowflies (Calliphoridae) and fleshflies (Sarcophagidae) are of significant ecological, medical, veterinary and forensic importance and, therefore, there has been a large degree of effort put into developing methods for collecting them in high numbers, both for monitoring and control. The most effective collecting methods rely on natural or synthetic baits, which produce attractant olfactory stimulants, combined with a trap. The trap usually consists of a two-dimensional flat surface coated with adhesive or a three-dimensional non-return container. Both have advantages and disadvantages. This presentation will review the main techniques used and highlight some of the problems that necessitate further research, especially to increase catch size and specificity.

Tephritid Tree of Life: DNA phylogeny and higher classification of the family Tephritidae

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Keywords: Tephritidae, higher classification, molecular phylogeny

In the process of revising the higher classification of the family Tephritidae, we have made a significant improvement based on DNA analysis. In an effort to make a balanced taxon sampling of as many phylogenetic lineages as possible from all over the world, we have so far accumulated fresh samples of 546 species of 214 tephritid genera, covering 13% and 44% of World species and genera, respectively. We have already DNA-barcoded almost all these species, and sequenced some additional genetic markers for a good fraction of these samples. The followings are examples of our findings: 1) two monophyletic groups within the superfamily Tephritoidea were clearly recognized (compatible with Willi Hennig's Pallopteroidea and Otitoidea that are not used in the contemporary higher classification); 2) Resurrection of the family Eurygnathomyiidae including one European species and one new Korean species; 3) Membership of Ctenostylidae in the Tephritoidea; 3) a sister group relationship between *Ortalotrypeta* and *Tachinisca*, and their basal phylogenetic position within Tephritidae; 4) A sister group relationship between the tribes Acanthonevrini and Phytalmiini, and phylogenetic position of *Matsumurania sapporensis*; 5) monophyly of *Taomyia* plus an undescribed new genus, and their basal-most phylogenetic position within the subfamily Tephritinae; 6) a possible sister group relationship of *Cephalophysa* and Adramini; and 7) reconfirmation of monophyletic Trypetini, Carpomyini, Tephritinae, and Dacinae. In addition to these examples, we have discovered many cases of interesting phylogenetic relationships not recognized previously.

Molecular phylogeny and divergence times estimation within Muscidae (Diptera: Schizophora)

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Keywords: Mitochondrial gene, Neotropical region, nuclear genes, systematics

Muscidae is a family of flies with worldwide distribution, comprising about 5000 species in 200 genera. The current classification of house flies divides their members into eight subfamilies. Previous studies based on both adult and immature stages morphology and molecular characters support different hypothesis for the relationships and composition of these groups. Herein we present a hypothesis on the relationships within the main lineages of the family, as well as their divergence time estimation for the main clades. A total of 138 muscid species from 62 genera from all subfamilies and tribes (except for Eginiini) were sampled for this study. They are representative of all biogeographic regions, in particular from the Neotropical region. Phylogenetic analyses were carried out with data from four genes (COI, AATS, CAD e EF1-α) under Bayesian posterior probabilities, maximum likelihood and parsimony criteria. Divergence times were estimated using the Bayesian method. Results recovered three main lineages: one corresponding to the Muscinae, which includes Muscini and Stomoxyiini, Azeliini, Achanthipterinae and *Reinwardtia*. This genus changed its position among different analyses, so its position within the Muscinae is doubtful; a second lineage corresponds to the Cyrtoneurininae, and is composed by the majority of the representatives of this subfamily, Mydaeinae, the remaining Reinwardtiini and Atherigoninae; the last lineage corresponds to the Mydaeinae, and besides representatives of this subfamily, comprises the Phaoniinae, Dichaetomyiini, Coenosiini, and Limnophorini. *Cariocamyia* (a Neotropical Cyrtoneurininae), as well as *Prohardyia* (an Australian Phaoniinae) were positioned in this clade, but in several analyses they were recovered within the Cyrtoneurininae. In some analyses, *Cariocamyia* and *Prohardyia* were recovered as sister-genera. The divergence between Muscidae and Anthomyiidae was estimated between 50 and 60 million years, corresponding to a period between upper Paleocene and lower Eocene. The main lineages of Muscidae diverged between 50 and 35 million years.

Toxin-swilling and millipede-killing: natural history and systematics of the genus *Myriophora* (Diptera: Phoridae)

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Keywords: Kairomone, phylogeny, behavior, parasitoid

Toxic defensive compounds are produced by millipedes in the order Polydesmida and superorder Juliformia. Despite the toxic and potentially lethal properties of these compounds, several insect taxa have evolved mechanisms that allow them to prey on or parasitize chemically defended millipedes. Parasitoid phorid flies in the genus *Myriophora* can even co-opt these compounds as kairomones for host location. Recent fieldwork shows that female flies only oviposit into healthy hosts but will readily feed from wounds of injured millipedes. Investigation into how the toxic effects of the compounds are mitigated is underway. *Myriophora* are found worldwide, and currently 60 new species are being described from the New World. Characters associated with the structure of the female oviscape have proven to be variable throughout the genus and useful for species recognition. Morphological and molecular character data each independently support the monophyly of the genus. The preliminary molecular dataset composed of mitochondrial ribosomal genes as well as nuclear and mitochondrial protein-coding genes are providing finer resolution for studying the evolution of host associations in a phylogenetic context.

Of tapirs and flies – the overlooked connection between the Oriental and Neotropical regions

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Keywords: Biogeography, *Cyphomyia*, Neotropical region, Oriental region, Stratiomyidae.

One of the more unusual and rare connections between the major zoogeographical regions is the connection between the Oriental and the Neotropical regions. One of the few widely known examples is the tapirs, which have representatives in Asian and South America, but are absent from North America. There are few examples from the Diptera, one being the genus *Cyphomyia* Wiedemann, 1819 (Stratiomyidae). But recently more examples have been found. One of the obstacles in the past was the focus of scientists on just one or two zoogeographical regions, although phylogenetic studies, of course, deal with the world fauna. This approach has changed in the past decades, more material is now available and the scientific approach is more a global. The reason for this distribution pattern is very likely extinction events in the Nearctic region.

The Red List of biting midges (Diptera: Ceratopogonidae) in Germany

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Keywords: Ceratopogonidae, Germany, national Red List

The Red List originated with the efforts of scientists and amateur biologists to assess species in Germany according to their degree of risk of becoming extinct.

Initially, there were Red Lists for only a few taxa other than vertebrates. This was surely based on superior data for these large and more popular organisms. Increasingly, the species Red List gained importance as a tool for administration of habitat, litigation, conservation violations etc. More recently, further experts of various animal groups agreed to gather data and to participate in the compilation of Red Lists. While in 1977 the German Red List was a booklet of 66 pages, by 1984 (4th edition), it comprised 270 pages. This volume growth was not only due to the increase in further taxa but also to additional research and inclusion of detailed information. Of approximately 45,000 species present in Germany, the 1998 Red List (with 434 pages) included more than 16,000 species evaluated for their risk of being endangered. The first idea of creating a Red List for the biting midges of Germany emerged in 1982. The List was published in 1984 and included 171 species. In 2014, a new edition of the Red List of biting midges will be published in the series Red List of Endangered Animals, Plants and Fungi of Germany, Volume 4 (Insects). It will include the German checklist of Ceratopogonidae, a total 198 spp., 35 spp. will be indicated on the Red List.

Biting midges (Diptera: Ceratopogonidae) as parasites of dragonflies and amphibians

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Keywords: *Forcipomyia*, Ceratopogonidae, Europe, distribution, phenology, parasitism, hosts, digital photography

Although most Ceratopogonidae have no medical or veterinary importance, our knowledge of some of these in Europe is increasing rapidly. A major trigger for greater interest is digital photography and the co-operation with experts and amateurs outside traditional dipterology.

Forcipomyia (*Pterobosca*) *paludis* (Macfie) is an ectoparasite of Odonata. The female sucks haemolymph from the wing veins of Zygoptera and Anisoptera. Based on analysis of photographs, the actual list of hosts in Europe includes more than 65 species of Odonata, and the flight season in Europe lasts from the beginning of May to the end of August. Recently, the species has been firstly recorded in countries such as Ireland, The Netherlands, Belgium, the Czech Republic, and Spain.

Forcipomyia (Lasiohelea) velox (Winnertz) sucks blood from amphibians in Europe. Examination of digital photographs of amphibians is also a good method for determining biting records. Currently, we made several video-based studies on host-parasite interactions between *F. velox* and green frogs (*Pelophylax* spp.). Based on digital photography and naturalist networks, increasing our knowledge of *F. velox* is a good example of citizen science in the field of dipterology.

Assessing the diversity of wet grasslands using Diptera with special reference to Sciomyzidae

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Keywords: Wet grasslands, Diptera, bioindicators

Farmland covers over 60% of the agriculturally used area in Ireland and it is estimated that over 10–12% of this land contains farmland where agriculture sustains high species richness. Farming in Ireland is predominantly pasture-based and the ecological status of semi-natural grasslands is, therefore, particularly important for biodiversity. Currently, Irish grasslands are classified using plants but there is still a paucity of information regarding how terrestrial invertebrate communities reflect these grassland types. Recent studies indicate that those grasslands with the greatest conservation value in the north-west of Ireland are wet grasslands. The aim of this study was to assess the diversity of selected wet grasslands using plants as bioindicators and compare the findings with the same sites assessed using two invertebrate groups, i.e. Diptera and Carabidae. All Carabidae were identified to species and Diptera to family and morphospecies level, in addition to which Sciomyzidae (Diptera) were identified to species. Assessing each site using only plants or Diptera or Carabidae resulted in different orders of diversity for the sites examined suggesting that using plants only as indicators of wet grassland diversity is limited. Captures of Sciomyzidae at these sites were poor and reasons for this are discussed in the context of their use as biodindicators.

Diversity, phenology and specificity of mealybug preying Cecidomyiidae (Diptera) in the agricultural landscape of Israel

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Keywords: Predators, gall-midges, Pseudococcidae, pests, biocontrol

While the majority of species in the family Cecidomyiidae (gall midges) are phytophagous, numerous genera and species are known as predators of various arthropods, including mites, aphids and scale insects. The taxonomy of predatory gall midges has not been studied extensively since the 1960s and the basic life history of most species is poorly known, if at all. This is the first comprehensive study of predatory cecidomyiids on mealybug pests (Hemiptera: Pseudococcidae) in Israel, which focuses on their life cycle, host range, predation capacity and phenology. We used two collecting methods: spreading ‘baits’ to attract ovipositing cecidomyiid females in different agricultural settings, and direct sampling of mealybug colonies in infested crops. The baits consisted of small mealybug colonies (*Pseudococcus citri* and *Phenacoccus solani*) that developed on potato sprouts placed in small cages (‘traps’). The traps were suspended on the mealybug host plants and left in the field for 1–2 weeks, then brought to the laboratory and kept until emergence of adult gall midges. Traps were spread in 25 localities in citrus, grapevine, pomegranate, banana and persimmon orchards throughout the year, mainly in spring and summer. All 25 sites yielded adult gall midges that we identified as belonging to at least 6 species in the genera *Dicrodiplosis*, *Diadiplosis* and *Trisopsis*, based on morphological and molecular characters. Observations of predation behavior indicated that larvae feed on all developmental stages of the tested mealybug species. We found that during the summer, the gall midges can complete their life cycle within 8–10 days from egg to adult. We conducted prey specificity tests with *Diadiplosis buscki*, *D. donaldi*, *Dicrodiplosis manihoti*, and *Trisopsis* sp. Adult midges of these species that emerged from colonies of *Planococcus citri* and were transferred to colonies of *Phenacoccus solani*, or vice versa, established several generations successfully on the other prey species.

Behavioral ecology

Fooled flies: Chemical mimicry in myiophilous trap and non-trap flowers

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Keywords: Fly pollination, kleptoparasites, food source mimicry

A great number of dipterans are flower visitors and important pollinators. The plant genera *Ceropegia* (Apocynaceae, Asclepiadoideae) and *Brachystelma* are pollinated by flies of several different families, such as Ceratopogonidae, Chloropidae, Milichiidae, Phoridae, Sciaridae, Drosophilidae, Agromyzidae, Lauxaniidae, and Anthomyiidae. *Ceropegia* evolved highly complex non-rewarding pitfall flowers to temporarily trap fly pollinators. In contrast, closely related and syntopic *Brachystelma* has nectar offering non-pitfall flowers.

We analyzed floral scents in the South African species *Ceropegia sandersonii* Decne. Ex Hook and *Brachystelma pulchellum* Schltr. by gas chromatography coupled to mass spectrometry (GC - MS), and identified scent compounds involved in fly-pollinator attraction by electrophysiological and behavioral studies.

C. sandersonii is pollinated by kleptoparasitic *Desmometopa* (Milichiidae) flies, which steal food by feeding on secretions leaking from prey items of predatory arthropods. Honey bees caught by spiders are a preferred food source of *Desmometopa*. Attacked by a predator, honey bees extrude their sting and release their alarm pheromone. Electrophysiological studies showed that several alarm pheromone compounds can be perceived by *Desmometopa* flies, and bioassays confirmed that the honey bee alarm pheromone is highly attractive to these flies. *C. sandersonii* flowers emit several compounds also found in the alarm pheromone of honey bees. We successfully attracted flies to such compounds, which suggests that *C. sandersonii* fools flies into pollinating its deceptive flowers through food source (e.g. preyed upon honey bees) mimicry.

Brachystelma pulchellum is vistited/pollinated by saprophilous flies of several families (e.g. Lauxaniidae and Anthomyidae). The flowers emit a strong putrid scent with high amounts of p- and m-cresol, organic acids, and phenol. Scent analyses, electrophysiology, bioassays, and color measurements point out that *B. pulchellum* mimics dead millipedes to attract its pollinating flies.

Efficacy of different sampling methods of sand flies (Diptera: Psychodidae) in endemic focus of cutaneous leishmaniasis in Kashan district, Isfahan province, Iran

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Keywords: Psychodidae, sand flies, nocturnal activity, trapping, sampling methods

Background: The aim of the study was to evaluate and compare the efficiency and practicality of seven trapping methods for adult phlebotominae sand flies. The results of this investigation provide information to determine the species composition and nocturnal activity pattern of different sand fly species.

Methods: The study was carried out in both plain region (about 5km far from northeast) and mountainous region (about 40 km far from southwest of Kashan City). Seven traps were selected as sampling methods and sand flies were collected during 5 interval times starting July to September 2011 and from 8:00PM to 6:00AM in outdoors habitats. The traps include: sticky traps (4 papers for 2 hours), Disney trap, Malaise, CDC and CO2 Light trap (0.5kg dry ice), Shannon traps (black and white nets) and animal-baited trap.

Results: A total of 1445 sand flies belonging to 15 species of *Phlebotomus* spp. and five of *Sergentomyia* spp. were collected. Females and males comprised 44.91% and 55.09% of catches, respectively. Of the collected specimens, *Se. sintoni* was found to be the most prevalent (37.86%) species, while *Ph. papatasi*, accounted for 31.76% of the sand flies.

Conclusion: Disney trap and sticky traps exhibited the most productivity than other traps. In addition, in terms of the efficiency of sampling method, these two trapping methods appeared to be the most productive for both estimating the number of sand flies and the species composition in the study area.

Diptera in Baltic amber – the most frequent order within arthropod inclusions

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Keywords: Diptera, Baltic amber, family record

Diptera are the most frequent insects in Baltic amber, representing 42–63% of arthropod inclusions. The diversity of flies and midges thoroughly was documented und catalogued earlier. Nematocera are recorded by 29 families: Tipulidae, Limoniidae, Cylindrotomidae, Pediciidae, Trichoceridae, Nymphomyiidae, Dixidae, Corethrellidae, Culicidae, Simuliidae, Ceratopogonidae, Chironomidae, Chaoboridae, Tanyderidae, Psychodidae, Scatopsidae, Ptychopteridae, Bibionidae, Hesperinidae, Anisopodidae, Mycetophilidae, Diadociidae, Ditomyiidae, Bolitophilidae, Keroplatidae, Lygistorrhinidae, Sciaridae, Rangomaramidae* and Cecidomyiidae.

Brachycera are recorded by 59 families: Xylomyidae, Stratiomyidae, Xylophagidae, Rachiceridae, Rhagionidae, Athericidae, Tabanidae, Vermileonidae, Acroceridae, Bombyliidae, Mythicomyiidae, Therevidae, Apsilocephalidae, Scenopinidae*, Asilidae, Empididae, Hybotidae, Atelestidae, Dolichopodidae, Platypezidae, Opetiidae, Phoridae, Syrphidae and Pipunculidae; the section Acalyptratae is recorded by 34 families: Micropezidae, Pseudopomyzidae, Cypselosomatidae, Diopsidae, Psilidae, Megamerinidae, Conopidae, Pallopteridae, Lauxaniidae, Chamaemyiidae, Dryomyzidae, Sciomyzidae, Sepsidae, Natalimyzidae, Clusiidae, Acartophthalmidae, Odiniidae, Anthomyzidae, Aulacigastridae, Periscelididae, Neurochaetidae, Asteiidae, Carnidae, Milichiidae, Cryptochetidae, Chloropidae, Heleomyzidae, Proneottiophilidae, Chyromyiidae, Sphaeroceridae, Camillidae, Drosophilidae, Campichoetidae, Hoffeinsmyiidae. The placement of the latter in the system still is open.

The fossil record of the Calyptratae, omnipresent in the recent fauna, is extremely poor, with one specimen in Anthomyiidae. Two families are extinct: Proneottiophilidae and Hoffeinsmyiidae. Families with a low extant abundance or specialised biology show a low fossil record, whereas families with a high extant abundance are recorded by significant individuals. Chironomidae, Sciaridae and Mycetophilidae represent 65% of all dipteran inclusions, whereas Diptera with specialized preferences are known from few specimens only. The recent Diptera fauna, with about 155.000 species in 189 families, actually face more than 1.000 described taxa within 350 genera and 88 families in Baltic amber.

*unpublished

Vestergaard ZeroFly fabric for fly control in the US

Jerome Hogsette

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Keywords: Stable flies, livestock, exotic animals

Vestergaard ZeroFly pesticide-impregnated fabric has been evaluated in zero-graze swine and cattle farms in Sub-Saharan Africa for management of biting flies, particularly those capable of transmitting Nangana, i.e. tsetse. Other major blood-feeding flies encountered around these units are various species of *Stomoxys* and tabanids. Although this product has shown promise when evaluated under African conditions, some changes in product use can be expected if ZeroFly is to be used in the US. The major target changes in the US from tsetse to *Stomoxys calcitrans*. Farms are much larger in the US and many fly-related problems occur when animals are in pastured situations. In African livestock units the effectiveness of ZeroFly has been related to a decrease in the numbers of protected animals infected with Nangana. In the US, the effectiveness of the fabric will have to be determined in other ways. Because of fly density and mobility, changes in trap counts due to ZeroFly may not occur. In the US, the ability of ZeroFly to protect contained animals has been evaluated as has the interaction between animals, and traps placed nearby to provide a fly population index. Stable flies readily fly over the ZeroFly fabric when attractive traps or animals are placed within a ZeroFly enclosure. However, these flies have an opportunity to rest on the fabric before entering or leaving the enclosure. Placement of ZeroFly along the sides of open dairy barns, where fly pressure is high, results in visible numbers of dead stable flies on the ground, below the base of the fabric. This dramatic effect could not be seen in African conditions because typical stable fly populations were extremely low by comparison. There are potential uses for ZeroFly around US livestock production units, particularly when ZeroFly is incorporated into attract-and-kill devices.

Wolbachia infection in Indian Mosquitoes

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Keywords: *Wolbachia*, microinjection, vector-borne diseases

The *Wolbachia pipientis* bacterium is a gram negative bacterium responsible for reproductive alterations in a wide range of invertebrate organisms. Different strains of *Wolbachia* induce different reproductive manipulation techniques. *Wolbachia* is capable of forming many types of relationships with invertebrates. In some instances this intracellular α-proteobacterium interacts as an obligatory mutualist and at other instances it acts as a facultative parasite. Some strains of *Wolbachia* induce cytoplasmic incompatibility, male-killing, thelytokous parthenogenesis, sperm competition etc. The reason for such disparity in reproductive manipulation across different *Wolbachia* strains is still unclear. These endosymbionts may be transmitted vertically from mother to egg cells and can also be transmitted horizontally among individuals across different species. Infection of mosquitoes, especially transinfection of vector-mosquitoes results in a parasitic interaction between *Wolbachia* and the arthropod. Vector mosquitoes are the primary targets for the *Wolbachia*-led combat. *Wolbachia* cuts the life span of these mosquitoes, preventing the mosquitoes from hosting the viruses and protists that cause these diseases. As a biological weapon, *Wolbachia* may permanently reduce or remove these diseases that claim millions of lives each year. In the present study, I have carried out a survey to determine the prevalence of *Wolbachia* and its phage WO infection in Indian mosquitoes, and classified *Wolbachia* into group A and B based on extensive polymerase chain reaction assay using *Wolbachia* specific wsp and orf7 gene primers. Out of 20 mosquito species caught in the field, eight species were shown to be infected. Single infection with *Wolbachia* group A was found in two species, and with group B in four species, while double infection with AB group was found in two species. The significance of this study is to conduct a survey on the prevalence of *Wolbachia* in Indian Mosquito vectors. Although some of the mosquito vectors are not infected with *Wolbachia* naturally, possibility of artificial introduction using techniques like microinjection and electoporation of *Wolbachia* strains into this open niche has been discussed in order to wipe out the vector-borne infectious diseases such as malaria, dengue fever, yellow fever.

Recent data of the recorded species of the soldier flies (Diptera: Stratiomyidae) from Iran

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Keywords: Checklist, Stratiomyidae, Iran, fauna

The family Stratiomyidae belongs to the suborder Brachycera in Diptera. This family includes more than 2650 species in 375 genera composed of 12 subfamilies worldwide of which 426 species in 55 genera in 7 subfamilies occur in the Palaearctic region. In the recent years some studies have been done in the northern west forests of Iran that added more than 15 species to the fauna of this family in Iran. In this study, the alphabetical checklist of the 27 species and 12 genera of this family occurring in Iran are provided.

Psychodomorpha [poster]

A glossary of morphological terminology of male terminalia in Psychodidae (Diptera)

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Keywords: Morphology, terminology, Psychodidae, homology

Taxonomic and systematic studies of Psychodidae have been hampered by a lack of universally understood and accepted morphological terminology. In particular, structures of the male genitalia have been labeled inconsistently and definitions for some terms have varied among authors. We present a revised terminology framework based on data from recent studies of Diptera morphology and our own observations of Psychodidae and its putative sister group Tanyderidae. A glossary of morphological terms is given, each with a list of synonyms found in the literature. Putative homologies are indicated using colour-coding, and representatives for all psychodid subfamilies are included.

Comparisons between a midgut-resident tachinid and two hemocoel-resident parasitoids: How do food plants of host herbivores affect parasitoids' development?

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Keywords: Endoparasitoid, tachinid, host development, host food plant.

Compsilura concinnata (Diptera: Tachinidae) has an unusual parasitism strategy: the fly larva develops in the midgut of insect herbivores throughout the larval period. No endoparasitoid other than *C. concinnata* has been found to parasitize the host midgut. Because the fly larva is directly exposed to the host's gut contents, including nutrients and toxic allelochemicals in the plants eaten by the host, it may be more susceptible to variation in the chemistry of the host's food-plants. To evaluate this potential disadvantage of midgut parasitism, we examined the influence of foods of the lepidopteran host *Mythimna separata* (Lepidoptera: Noctuidae) on the development of this tachinid species. To provide a comparison, we conducted the same examinations using two endoparasitoids that develop in the host's hemocoel during the larval period: *Exorista japonica* (Diptera: Tachinidae) and *Cotesia kariyai* (Hymenoptera: Braconidae). When the parasitized hosts consumed one of four kinds of plants, all three parasitoid species showed higher survival, a larger body size, and faster development on two natural food plants (maize and sorghum) than on two alternative foods (kidney bean and Japanese radish). Our results suggest that the development of *C. concinnata* in the midgut was affected by the host's food species, but that the effects did not differ from those for the other two endoparasitoids developing in the hemocoel. Hence, the effects of the host's food plants may not represent a severe disadvantage for midgut parasitism by *C. concinnata*, or this parasitoid may have acquired a means to overcome the disadvantage.

Disentangling the effects of agricultural management and landscape on the diversity of tachinid parasitoids

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Keywords: Landscape, Tachinidae, parasitoid, hedgerow, organic agriculture

The conversion of natural ecosystems for agricultural farming is one of the major threats for arthropod diversity. Although many empirical and theoretical studies have elucidated the effects of agricultural management and landscape on the third trophic level, little attention has been paid to the impacts of these drivers on more generalist groups of non-hymenopteran parasitoids. We have used the highly-diverse group of tachinid flies as an alternative model to test the effects of agricultural management and landscape on insect parasitoids. Specifically, our aims were: (i) to examine how within-farm management (organic vs. conventional) and the proportion of organic farms in the landscape affect the diversity of tachinid parasitoids and (ii) to further assess the effects of hedgerow type and proportion of semi-natural habitats at different spatial scales. First, we found a positive effect of organic farming on tachinid species richness at both the local and landscape scale. The diversity of tachinids was always higher at field margins than in field center in organic farms located in conventional landscapes, but in organic landscapes the difference between field center and margin was less evident. Second, we found that increasing the complexity of hedgerows yielded higher species richness at the local scale, while at the landscape level (0.5 km and 10 km) the effect of the semi-natural habitats was irrelevant for tachinid species richness. Our study provides new insights into the consequences of landscape changes on the diversity of a key functional group that has been long overlooked in ecological and conservation studies.

The weird and wonderful – an overview of Afrotropical Chloropidae

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Keywords: Morphology, life history, distribution

This talk presents an overview of the Afrotropical Chloropidae. It is based on work conducted jointly with John Deeming and John Ismay in preparation for the chapter on Chloropidae for the Manual of Afrotropical Diptera. During the talk it will become evident that not all Chloropidae are yellow with black stripes and a large ocellar triangle. This species-rich family is very diverse in its morphology. The apterous genus *Alombus* and the sepsid-like *Mimosepsis* are both endemic to Africa, the life-history of *Alombus* is unknown, while *Mimosepsis* is associated with ants. Some genera resemble beetles – *Nomba* has a long scutellum that covers the abdomen, while *Camarota* covers its abdomen with its curved wings. The seven species of *Nomba* are found from Africa to New Guinea, but their life-histories are unknown. *Camarota* includes only three species and is known from the Palaearctic and Aftrotropical regions. Its species have been recorded from grasses and rice and *Camarota curvipennis* is regarded a pest species of cereals and grasses in some countries. Other genera have spines on their scutum and scutellum and look somewhat like a tiny hedgehog – one species is even called *Anatrichus erinaceus. Anatrichus* is widespread in the warmer parts of the Old World and has been reared from shoots of graminaceous crops. The family also includes *Dactylothyrea,* with long finger-like projections protruding from its scutellum, it occurs in the Afrotropical and Oriental regions, but its life-history is unknown. Other chloropids have pretty wing patterns, e.g. *Chromatopterum* and the African endemic *Pseudochromatopterum,* but their life-histories remain a mystery. *Pachylophus* has thickened hind femora and a thickened arista and has been reared from shoots of Gramineae; although widespread, it is most species-rich in Africa. *Pseudogaurax* is a predator of egg masses of spiders, mantids and moths.

Developments in the genera of Chloropidae

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Keywords: Habitat associations, grasslands, rainforest, species richness, taxonomy

The Chloropidae, a moderate-sized family of acalyptrate Diptera, have about 2500 described and an estimated 5000 species in total. They are found in all regions of the world except Antarctica. In temperate regions many species are associated with grassland habitats and this is also the case in the African grasslands. Genera such as *Chlorops* and *Meromyza* are primary invaders of grass stems while others such as *Elachiptera* secondarily invade damaged plant tissue. Canopy fogging techniques have revealed a rich fauna associated with rainforest habitats. It is thus unlikely that the majority of species are dependant on grasses.

Several genera in all subfamilies have proved to have far more species than previously thought including many undescribed ones. *Apotropina*, known from all major regions, has many species from Australia, New Guinea and the Neotropical region that need to be described. The *Chloropsina* from Africa and Australia have been well covered, but the genus is rich in further species in the rest of the Old World.

Recent work has shown that studies on a global basis are vital. *Psilacrum* and *Notaulacella* were originally described from Africa and South America respectively, but are now known to be distributed from the Neotropical region to Africa and Australia. The genera *Anacamptoneurum*, *Lasiambia* and *Polyodaspis*, which are found in all regions, have recently been synonymized by Cherian. *Gaurax* was originally described from the Nearctic region, but the name has also been used for species in the Australasian region and it is doubtful if this is correct. In the Chloropinae, *Diplotoxa* has been enlarged to include *Pseudopachychaeta* and *Elliponeura*.

In conclusion, many genera are proving to have wider distributions than previously thought.

Annual changes in abundance of aquatic dance flies (Diptera: Empididae: Clinocerinae, Hemerodromiinae)

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Keywords: Empididae, Croatia, water velocity, microhabitat types, water temperature

Aquatic dance flies (Empididae: Clinocerinae & Hemerodromiinae) are important components of freshwater ecosystems, especially running waters. They are predators as larvae and adults and thus relevant for understanding aquatic food webs. The goals of this study were to analyse their preference for various microhabitats, the main ecological factors that affect the composition and abundance of specimens, and emergence of species at different freshwater karst habitats during a seven year period. Also correlations between aquatic dance fly and prey abundances were explored. The study was performed at three sites in the National park Plitvice Lakes, which is situated in a karst region of Croatia. Adult specimens were collected using a semi-quantitative method with 6 emergence traps placed at each location. Specimens were collected monthly from March 2007 until December 2013. In total 16 species were identified. The dominant genus was *Chelifera*, while the most abundant species was *Hemerodromia unilineata* Zetterstedt. Except for the bivoltine *Chelifera precabunda* Collin, *Chelifera pyrenaica* Vaillant and *Chelifera stigmatica* (Schiner) all species were univoltine. The highest abundance of aquatic dance flies at Spring of Bijela rijeka was recorded on moss. The highest emergence rates were recorded above microhabitats with highest prey densities (Chironomidae) and with highest current velocity.

Water temperature and photoperiod are the main ecological factors determining the emergence. Water discharge seems to have the greatest effect on dance fly abundance patterns. Annual changes in abundance were highest in *Chelifera siveci* Wagner and might be related to water discharge or sex ratio variations during the years.

Diverse biology and deep sampling: molecular phylogeny of the Nerioidea and Diopsoidea

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Keywords: Diopsoidea, Nerioidea, molecular phylogeny, Micropezidae

With the 2011 publication of their work on "Episodic radiations in the fly tree of life", Wiegmann et al. challenged the Dipterological community to build upon their proposed evolutionary framework, and continue to examine the relationships within historically problematic groups, like acalyptrate Diptera. Here we begin to do just that, investigating the higher-level relationships of the Diopsoidea and Nerioidea. These groups exhibit a spectrum of biologies, behaviours and morphological adaptations, some of which have attracted significant scientific study while most remain largely unknown, much the same as the higher-level phylogeny of these two groups. By intensively sampling all major lineages within both superfamilies, and estimating species trees using molecular data spanning 10 loci (including ribosomal, mitochondrial, and nuclear DNA), we will provide additional evolutionary context for the taxonomists, ecologists and evolutionary biologists working to understand these fascinating flies.

Measuring costs of sexual dimorphism in stalk-eyed flies

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Keywords: Sexual dimorphism, contest behavior, metabolic costs, stalk-eyed flies

Stalk-eyed flies (Diopsidae) vary hugely across species in eyestalk length and the degree of sexual dimorphism. Discussions of sexual dimorphism and sexual selection often revolve around costs, both in terms of the ornamentation itself and in terms of sexually selected behaviors. Here, we measured metabolic costs of flight in male and female stalk-eyed flies in a sexually dimorphic species, *Teleopsis dalmanni*, and a sexually monomorphic species, *T. quinqueguttata*, using a carbon dioxide probe and a flight apparatus. We also used a similar apparatus in a contest arena to measure the metabolic costs of fighting behavior in *T. dalmanni*. We present these results, relate them to issues of sexual dimorphism and sexually selected traits, and discuss the benefits and limitations of this approach.

An Overview of the traps and attractants used for monitoring and control of Dipteran flies

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Keywords: Traps, visual cues, chemical attractants, monitoring, mass trapping

A very wide range of traps and chemical lures have been used historically for monitoring of pest and non-pest species of Diptera. Some trapping devices use no means of attraction and rely on the insects being caught by blundering into or onto the traps. Others have involved just passive visual cues, while others have used lights of specific wavelengths or flashing frequencies. A great number have also included chemical attractants to provide varying degrees of specificity. The use of these traps and lures in both pure and applied studies and practices will be reviewed and discussed.

The use of DNA barcoding to identify Afrotropical Syrphidae

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Keywords: Syrphidae, COI, DNA barcoding, identification, Central Africa

Currently, there are more than 500 syrphid morphospecies known from the Afrotropical region. For many taxa, however, the taxonomy is very poor and species-boundaries are ill-defined. This hampers a straightforward species identification. Here, we explored the use of the standard DNA-barcode region of the mitochondrial COI gene as a tool to identify Afrotropical syrphid species. Both recent, ethanol-preserved and older (up to 30 years) pinned specimens were examined, and DNA was extracted from single legs. PCR-, and DNA-sequencing, success was very high (>95%) for ethanol-preserved specimens, whereas that for pinned material was much lower (40–60%, depending on the genus and age of the specimens) suggesting that improved storage conditions for pinned material are needed to allow the use of this material in molecular taxonomic studies. For some genera, DNA-barcoding appears a useful tool to identify the species. Yet, for other genera, the poor taxonomic knowledge strongly hampers the evaluation of the COI barcode region as a potential species identifier. These genera first need a sound taxonomic revision before the COI barcode region can be evaluated as a species-identification tool.

Bibionomorpha [poster]

Diversity of fungus gnat – mushroom interactions in the boreal forest

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Keywords: Diptera, Mycetophilidae, host specificity, host preferences

This study investigates the intricate associations between fungus gnats and their mushroom hosts based on quantitative data of their interactions. We show how host diversity, combined with the dietary behaviour of fungus gnat species, affects the fungus gnat diversity in the boreal forest. Differences in fungus gnat communities among mushroom species are affected by the taxonomic and ecological identity, as well as abundance, of the fruiting bodies. About three quarters of the species of both partners were rare, limiting their use in the analyses. Comparison of host species richness distinguished oligo- and polyphages among the seven most common species. The most frequent and abundant species, *M. fungorum*, was defined as an oligophage despite its wide host range among the studied fungus gnats. All other fungus gnat species were too under sampled to be able to estimate their true host richness. The fungus gnat diversity among the three orders of the sampled mushroom-forming taxa appears to correlate with their taxonomic and ecological diversity, decreasing from Agaricales to Boletales and then Russulales. The fungus gnat communities of most of the saprotrophic genera of the Agaricales were more similar to each other than to those of all other genera that comprised only ectomycorrhizal taxa.

Mycetophila ruficollis species-group in Europe: testing morphological delimitation of species

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Keywords: Diptera, Mycetophilidae, fungus gnats, *Mycetophila ruficollis* species-group, COI

Mycetophila Meigen, 1803 is one of the largest and earliest described genera among fungus gnats (Diptera: Mycetophilidae). The first fungus gnat ever described is today known as *Mycetophila fungorum* (De Geer, 1776), a widespread and common species in the Palaearctic region. Since then more than 450 species of *Mycetophila* have been described from all biogeographical realms. One of the most clearly delimited and obviously monophyletic intrageneric clades is the *M. ruficollis* Meigen species-group introduced by Laštovka (1972). Within the limits of the species-group, there are 19 extremely similar species known from the Holarctic, Oriental and Afrotropical regions and reliably identifiable by details of male terminalia only. All species with known biology are mycetophagous as larvae. While discussing intraspecific variability, earlier authors have noted variable coloration of the body, as well as in male terminalia. Therefore, we presumed that the species-group contained some undiscovered diversity. The aim of this study was to test the morphological species limits with molecular methods, and search for possible cryptic species. We analyzed the morphological and molecular characteristics of 69 specimens from eight European species. A 698 bp fragment of the COI gene was sequenced for all species, as well as the ITS2 gene for some species. Bayesian phylogenetic inference, ML, MP and NJ approaches were used to evaluate the phylogenetic relationships and test the species limits. The results of the molecular data showed not cryptic species within the *Mycetophila* species we have examined so far, even though we did see some slight morphological variation.

Lygistorrhina Skuse has branched from the Keroplatidae (Diptera: Sciaroidea) – a new perspective on the phylogenetic relationships in the keroplatid group of fungus gnats

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Keywords: Systematics, Keroplatidae, *Lygistorrhina*

The delimitation of the Keroplatidae from other Sciaroidea is discussed. The *Lygistorrhina* group of genera, as it is here proposed and formerly treated as separate family, represents a component of the Keroplatidae. The prominent features of lygistorrhinid flies are the reduced mid-wing venation and a uniquely developed proboscis. Two new species were described: *Asiorrhina unguicauda* sp. n., from Malaysia and *Asiorrhina balsamica* sp. n., from Baltic amber. The characters shown by amber fossils may improve the arguments for particular evolutionary scenarios. The possible function of the frons of Sciaroidea imagines (Diadocidiidae, Ditomyiidae, Keroplatidae, Mycetophilidae), a component of the head, for controlling the width of the head while feeding on angiosperm flowers, is discussed.

I found that: (1) The *Lygistorrhina* genus group has branched from very early Keroplatidae, restoring their subfamily rank as Lygistorrhininae. (2) Following the position of *A. balsamica* as proposed here, other basal Eocene Lygistorrhininae, such as *Palaeognoriste* Meunier, 1904 and *Parisognoriste* Blagoderov et al. 2010, would have to be placed as descendants of *Asiorrhina* Blagoderov et al. 2009. (3) The following morphological peculiarities have indedependently evolved as morphological adaptations in flower visiting taxa: • antennal socket, mouthparts, frons, face and clypeus have adapted to the enlarged eyes and vice versa • flexible (membraneous) or deeply furrowed (sclerotized) frons in certain taxa is used to control the position of the antennae • elongated mouthparts • medial emargination of eyes • eyes partly moveable under the frons.

Bibionomorpha [poster]

A remarkable new *Trichonta*, *T. costaricensis* (Diptera: Mycetophilidae), from Costa Rica

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Keywords: Taxonomy, Mycetophilidae, *Trichonta*, Costa Rica

This description of *Trichonta costaricensis* sp. n. is based on specimens from the Costa Rica mountain range. A *Trichonta* species from Patagonia (*T. tobasi*) was found to be the closest relative to the Central American species and is redescribed. Further Neotropical and holarctic species were examined, as well as Baltic amber fossils. The delimitation of Neotropical *Trichonta* from Holarctic species is discussed. The newly described species is a member of a group with a conspicuously corrugated wing membrane and unusual body size, even unusual within the entire Mycetophilidae. A further apomorphic condition, shared by all Neotropical *Trichonta* species, so far examined in this study, is the reduction of the mid ocellus. The character set of the Neotropical group of species, together with data on the geological history of Central America and the fossil record, indicates that the common ancestor of the northern and southern group of *Trichonta* existed at most as early as the late Cretaceous. Thus 65 million years B.P. is assumed as the latest point of time for the vicariance event, splitting the range of this ancestor in two groups, boreal and southern.

Biting midges (Diptera: Ceratopogonidae) – putative vectors of Schmallenberg virus in Germany

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Keywords: Ceratopogonidae, *Culicoides*, Schmallenberg virus, vectors

In the late summer of 2011, a new Orthobunyavirus (family Bunyaviridae) was discovered in Europe: the Schmallenberg virus (SBV). Being a member of the Simbu serogroup, which contains about 25 viruses, SBV affects ruminants and new-world camelids where it can cause a variety of symptoms, ranging from a mild and therefore often unnoticed symptomatology, to fever, diarrhea and a decrease in milk production. Infection of pregnant animals can lead to severe malformations of the unborn, abortions and stillbirths. Because it is closely related to Akabane virus, a virus known to be vectored by species *Culicoides* Latreille, SBV was immediately assumed to also be vectored by ceratopogonids. Soon after, studies confirmed the presence of the virus in field-collected biting midges of the genus *Culicoides* in various European countries although vector competences have still not be finally demonstrated. After its rapid spread through many parts of Europe until late 2011, SBV was again observed in 2012. Findings suggest that viral transmission by biting midges is limited to a restricted time period in late summer. Recent literature providing data about SBV-positive midges caught in 2011 and 2012 will be presented and compared with own results on ceratopogonids sampled between 2011 and 2013.

Fossil Diptera [poster]

Subfamily Limoniinae Speiser, 1909 (Diptera: Limoniidae) from Baltic amber (Eocene): the genus *Elephantomyia* Osten Sacken, 1860

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Keywords: *Elephantomyia*, Limoniidae, Baltic amber

The genus *Elephantomyia* is comprising 134 extant species dispersed in four subgenera: *Elephantomyia* (*Elephantomyia*), *Elephantomyia* (*Elephantomyina*), *Elephantomyia* (*Elephantomyodes*) and *Elephantomyia* (*Xenoelephantomyia*) distributed worldwide.

The representatives of *Elephantomyia* occur mainly in Neotropical and Afrotropical regions. Only in the Neotropics, the genus is represented by 3 subgenera and numerous species. In this region, 40 species belong to the typical subgenus, two other represent two different subgenera *E*. (*Elephantomyina*), and *E*. (*Xenoelephantomyia*). Similar number of species is reported from the Afrotropics, but in this region 37 species represent only one subgenus *E*. (*Elephantomyina*). The genus *Elephantomyia* is also known from amber inclusions, mainly from the Baltic amber. In Eocene Baltic amber four species of *Elephantomyia* are known so far: *E. baltica*, *E. brevipalpa*, *E. longirostris*, *E. pulchella*. A species from Miocene Dominican amber remains unidentified. *E. brevipalpa E. longirostris* and *E. pulchella* were previously described as a *Toxorhina* by Loew in 1850 but in later revision these species were placed in the genus *Elephantomyia by* Meunier (1906).

A revision of four species of *Elephantomyia* from Baltic amber and description of two new fossil species is presented. A cladistic analysis of fossil species of the genus is provided.

Similarities and dissimilarities of selected genera of Limoniidae from Baltic amber, Bitterfeld amber and Ukrainian amber

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Keywords: Baltic amber, entomofauna comparison, Limoniidae, morphological variability

The Bitterfeld amber and Ukrainian amber are identical to Baltic amber from Gulf of Gdańsk area, as recognized by physical and chemical analyses as well as palaeofaunistic analyses. However, this opinion is not universally accepted, and some researchers suggest different ages for the above mentioned resins. A comparison of the two most common limoniid genera in Baltic amber, *Cheilotrichia* and *Trichoneura* from particular areas is made based on features of the male hypopygium of these characteristic and easy recognizable species. The results of the analysis are presented.

Multigene phylogeny of fungus gnats (Diptera: Mycetophilidae): where do we stand and what is yet to be done

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Keywords: Sciaroidea, Bibionomorpha, phylogenetic analysis, molecular markers, systematics

The family Mycetophilidae is one of the most species-rich families of Sciaroidea and the entire Bibionomorpha. The relationships within this family are still not sufficiently known. The molecular phylogeny of Mycetophilidae was reconstructed based on the combined analysis of five mitochondrial (12S, 16S, COI, COII, cytB) and four nuclear (5.8S, 18S, 28S, ITS2) gene markers using maximum parsimony, maximum likelihood and Bayesian inference. The current dataset includes more than 70 genera or subgenera of Mycetophilidae sequenced in the years 2011–2014 and some additional taxa from the GenBank database. Our preliminary results revealed subfamilies Manotinae, Leiinae (including *Allactoneura* DeMeijere), Mycomyiinae and Mycetophilinae to be monophyletic groups. The subfamilies Gnoristinae and Sciophilinae appear as paraphyletic groups. The tribe Metanepsiini has not proven to be a monophyletic group, but rather a heterogeneous group of genera within the Gnoristinae. The genera *Docosia* Winnertz, *Ectrepesthoneura* Enderlein, *Megophthalmidia* Dziedzicki, *Novakia* Strobl, *Syntemna* Winnertz, and *Tetragoneura* Winnertz were placed with a group of genera included traditionally in the Gnoristinae. The monophyly of *Dziedzickia* Johannsen and *Phthinia* Winnertz is not supported. The subfamily Mycetophilinae appears as a sister group to the Gnoristinae.

Tipulomorpha [poster]

Taxonomic study of the genus *Epiphragma* Osten Sacken of Japan (Limoniidae)

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Keywords: Crane flies, fauna, Japanese species, distribution

The genus *Epiphragma* of the subfamily Limnophilinae is characterized by having supernumerary crossvein(s) in cell c and distinct wing markings. It consists of 143 species described from all zoogeographical regions except for the Afrotropical region.

In Japan, four species have been recorded so far. However, as they were first described insufficiently and poorly figured, identifications of the species remained difficult and troublesome. Moreover, specimens misidentified by C. P. Alexander, the author of those species, are preserved in the collection of Kyushu University, Fukuoka, Japan, and many Japanese researchers have been referring to these specimens for long time. As a result, some Japanese species have been erroneously named and reported.

In the course of our study on Japanese *Epiphragma*, we examined the types of the Japanese species to resolve the problems. In addition, one Palaearctic species, *E. gracilistylus*, one Oriental species, *E. kempi*, and one undescribed species were discovered from Japan. And it is supposed that *E. trichomerum* described from Shikoku, Japan is a variation of *E. evanescens* described from China and Japan.

In this presentation, we present the diagnostic characters of each Japanese species and their distributions.

Annotated catalogue of Iranian long-legged flies (Diptera: Dolichopodidae)

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Keywords: Dolichopodidae, Iran, species diversity, catalogue

A catalogue of the Iranian species of the family Dolichopodidae is compiled. It includes 104 species within 24 genera. The first studies of the dolichopodid fauna of Iran were conducted by Becker & Stein (1913) and Negrobov & Matile (1974). Later, Grichanov et al. (2010) studied the Iranian fauna of this family and increased the national list of dolichopodids to 33 species in 17 genera which were found mainly in the central and southern provinces of the country. In recent years, several studies in Iran have been carried out by Khaghaninia et al. (2013, 2014) and Gharajedaghi et al. (2013) which added another 21 species new to the country. Based on yet other recent studies, 50 species have been added to this list from northern and northwestern Iran. The Iranian dolichopodid fauna in most parts of the country (particularly the south, east & center), however, remains poorly studied and most presumably features a fauna, distinct from that of northern Iran. It is obvious that more surveys on Iranian Dolichopodidae are necessary. A check-list of dolichopodid genera species of Iran is currently under preparation.

Synopsis of fossil big-headed flies (Diptera: Pipunculidae)

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Keywords: Pipunculidae, fossil Diptera, micro-computed tomography, Baltic amber, palaeoentomology

Fossil Pipunculidae are rarely encountered. Here, all currently known compression fossils and a selection of amber inclusions are presented. The majority of known fossils originate from middle Eocene Baltic amber. Recently, two male amber inclusions belonging to two species of *Metanephrocerus* Aczél, 1948 were studied by means of micro-computed tomography (micro-CT). Inner male genitalic features were partly visualised, allowing a better phylogenetic placement of this extinct taxon. Based on a phenetic comparison of the basic morphological composition of male terminalia on a subfamily level, there is evidence that *Metanephrocerus* and *Protonephrocerus* Collin, 1931, hitherto placed as Protonephrocerini within Nephrocerinae, should be raised in rank, constituting the subfamily Protonephrocerinae.

Catalogue of the Iranian Syrphids (Diptera: Syrphoidea)

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Keywords: Catalogue, Syrphidae, Iran

A catalogue of the Iranian species of the family Syrphidae is provided. Totally about 216 species within the 59 genera are presented. The genera *Eumerus* Meigen, 1822, *Cheilosia* Meigen, 1838, *Paragus* Latreille, 1804 and *Chrysotoxum* Meigen, 1803 respectively with 18, 15, 14 and 12 species have the most number of species among the other genera. Also some of the rare species of the genera *Trichopsomyia* Williston, 1888, *Spazigaster* Rondani, 1843, *Leucozona* Schiner, 1880, *Xylota* Meigen, 1822 and *Myolepta* Newman, 1838 were found in Iran. The genus *Cheilosia* preferred deciduous forests and mountain meadows habitats, formerly 10 species of this genus were reported from Iran. In the recent years, some studies have been done in the Arasbaran Forests located in the northern west of Iran which results have been increased number of species of genus *Cheilosia* to 15 species. The list of the genera and species of syrphids occurring in Iran alphabetically is provided.

A list of the recorded species of grass flies (Diptera: Chloropidae) from Iran

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Keywords: Catalogue, Chloropidae, grass flies, Iran.

The grass flies (Diptera: Chloropidae) with 204 genera and more than 2500 described species, include four subfamilies and belong to the acalyptratae. Kubik and Bartak (2008) described a new species (*Platycephala isinensis*) from Iran, and Modarres-Awal (2012) listed 13 species belonging to 6 genera (*Chlorops* Meigen, 1830; *Elachyptera* Macquart, 1835; *Lasiosina Becker*, 1910; *Meromyza* Meigen, 1830; *Oscinella Becker*, 1909; *Thaumatomyia* Zenker, 1833) from Iran. In recent surveys in northwestern Iran, the number of the Iranian species was increased to more than 30. In this study, the alphabetical catalogue of the 36 species and 20 genera of this family occurring in Iran is provided.

Taxonomic study of *Macrodiplosis* sp. (Diptera: Cecidomyiidae) and the rapid induction of leaf-margin fold galls by first instars

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Keywords: Cecidomyiidae, gall induction, identification

A gall midge that induces upwardly folded leaf-margin galls on *Quercus serrata*, *Q. mongolica* and *Q. dentata* (Fagaceae) was found in Japan and South Korea. This gall midge was identified as a species of the genus *Macrodiplosis* on the basis of larval morphology, gall shape and host specificity. This *Macrodiplosis* sp. is distinguishable from Palaearctic congeners by a combination of morphological characteristics. Molecular analysis supported the results of morphological studies, and indicated that this *Macrodiplosis* sp. is new to science. First instars of this *Macrodiplosis* sp. rapidly folded leaf-margins upward within 32 hrs after they had settled on the leaf margin. Each gall contained one gall midge larva. We demonstrate their gall-inducing behavior and cross-sections of galled tissues at different stages of gall development.

Biodiversity studies of Diptera in the Afrotropical region – past and present

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Keywords: Afrotropical region, biodiversity, collection, curation, sampling techniques.

Surveys of Afrotropical Diptera began following the on-set of European colonialism, when sampling efforts largely targeted Diptera of medical and agricultural importance. European powers, especially Britain, Germany, Belgium, France and Portugal engaged in surveys that generated specimens used today as base-line information for biodiversity studies of the Afrotropical regional fauna. Material generated from such surveys was either deposited directly into European museums, or collections established in African countries were removed by departing colonial powers following independence. In most modern African states this situation has led to the lack of capacity to identify and bio-inventory their respective Diptera faunas. Only a handful of museums in Africa hold Diptera collections (mostly in the more developed countries) and few of these are sufficiently staffed, maintained and actively developed. Unfortunately, vast tracks of Africa remain virtually unsampled and dipterologically unknown, and many unique habitats are subject to rapid and uncontrolled degradation, through urban development and subsistence agriculture. The National Museum (Bloemfontein, South Africa) has been undertaking biodiversity studies for the past five years, in South Africa, Namibia, Burundi, Kenya, Democratic Republic of Congo and Zambia. As a result, the Diptera collection now comprises over 66,000 recent dry-pinned specimens and is the second largest collection of Diptera in Africa. This presentation outlines some of the key biodiversity studies conducted in the Afrotropical region in the past and discusses the model for biodiversity studies and collection development adopted by the National Museum. Sampling and field preparation techniques are outlined and curatorial practices briefly discussed.

Back from the dead II – return of the "terrible hairy fly" *Mormotomyia hirsuta* Austen (Diptera: Mormotomyiidae)

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Keywords: Afrotropical, *Mormotomyia*, Mormotomyiidae, rediscovery, terrible hairy fly

Mormotomyia hirsuta Austen, 1936, is one of the most extraordinary and unusual looking Diptera ever described and was placed by E.E. Austen into a family of its own, the Mormotomyiidae, upon its initial discovery in 1933. The family is endemic to the Afrotropical region. Adults superficially resemble small solifugids (Sun spiders), having extremely long legs that are clothed, especially males, in very long, closely-packed brown hair-like setae. The wings are reduced to dysfunctional straps, the halters to small nodular processes and the eyes are greatly reduced. *Mormotomyia hirsuta* is cavernicolous in all life stages and guanobious at least in the larval stages. The phylogenetic position of the family has long been a subject of much speculation and of disagreement among systematists. Until recently, it had only been collected on two previous occasions: once in May 1933 and again in December 1948, although there have been numerous unsuccessful rediscovery attempts. The species was thought to be confined to the type locality and was, therefore, widely regarded as the "rarest fly in the world". Recently, we reported the rediscovery of adults, larvae and puparia at the type locality, a cave-like rock fissure at Ukasi Hill, Eastern Province, Kenya, in December 2010. This rediscovery was widely reported on in the global media and was one of the highlights of dipterology in 2010. Subsequently, we conducted extensive fieldwork in Kenya to locate other populations. We focused primarily on rocky hills with characteristics similar to those of the type locality. In late 2012 and 2013 we located three additional populations, Ngauluka and Makilu Hills, located (with Ukasi), in the same small chain of hills. The third site, Mbuinzau Hill, is approximately 185 km to the south. Here, we report on these recent finds and add to the limited knowledge of the species' natural history.

Breaching the gaps – fly distribution in the Afrotropical region

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Keywords: Afrotropical region, biogeography, fly dispersal, palaeoclimates, Sahara Desert

This presentation outlines some broad concepts of Diptera biogeography in the Afrotropical region. Examples are provided of Diptera endemism in the ancient Cape Fold Mountains and Cape Floristic Region of South Africa and the Great Escarpment of southern Africa. The significance of the Brandberg Massif in Namibia as a refugium for relict species, including living fossils is discussed, as are links between the ancient Eastern Arc Mountains of Kenya and Tanzania and the Malawi Rift. The expansion and retraction of the Pan-African forests and expansion of savanna grasslands is discussed. It is argued that humid pathways of dispersal *via* the Hogger Mountains, and the megalake catchments of Basin of Chotts, Ahnet-Moyer Megalake, Lake Magafezzan and Megachad of the central Sahara existed as recently as 4000 B.P. and linked the Mediterranean province and southern Africa, allowing dispersal both ways. Examples of Diptera endemism on Madagascar are provided and means of dispersal are discussed.

Progress on the Manual of Afrotropical Diptera project

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Keywords: Afrotropical region, identification keys, Manual, progress report, publication

The *Manual of Afrotropical Diptera* project was launched at ICD7 in Costa Rica in 2010. The mission statement of the *Manual* is "*To encourage the study of dipterology, both on and beyond the African continent, through the production of a high quality* Manual of Afrotropical Diptera*, for the use of practicing systematists, applied entomologists, conservationists, all students of entomology and the public at large*". The project is the first regional initiative of its kind for any insect order on the African continent and is truly an international effort, with 98 contributing authors from 24 countries on six continents. The *Manual* will comprise 13 introductory chapters and 106 systematic chapters dealing with the 108 families of Diptera that occur in the Region. The *Manual* will be richly illustrated with colour photographs of living flies provided by Steven Marshall. Each family chapter comprises a detailed diagnosis of the family and sections dealing with biology and immature stages, economic importance, classification, identification, identification keys to generic (if more than one), or subgeneric level (in some cases), a synopsis of the fauna section arranged by genus and literature cited. The *Manual* will be typeset and published by the South African Biodiversity Research Institute (SANBI) and be published it two hard-backed volumes in full colour. Volume 1 will include the 13 introductory chapters and 43 chapters dealing with the nematocerous Diptera and Lower Brachycera (including Empidoidea), Volume 2 will deal with the remainder of the Brachycera and include 63 chapters. All chapters will be made freely available on-line six months after publication. This presentation provides a report on progress with the *Manual* project, including sponsorship and other funding received, chapters submitted and completed, updates to the *Manual* website and on-line resources available, tables of contents to the two volumes and revised publication deadlines.

Pattern of hoverfly (Diptera: Syrphidae) diversity in the coastal plain of Rio Grande do Sul, Brazil

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Keywords: Species-area relationship, Generalized Linear Model, habitat fragmentation

A fundamental pattern in ecology is the increase in the number of species with the increasing size of the sampled area. This pattern is commonly called species-area relationship (SAR). The understanding of how and why the species number increases with area size is primordial to the study of habitat fragmentation. In order to identify the pattern of Syrphidae diversity in the coastal plain of southern Brazil through SAR we conducted an inventory of the species of hover flies. 140 Malaise traps were set in 35 areas in five regions. For each area, four traps were set equidistantly, according to fragment size, for a uniform and proportional sampling. Each trap was set up for eight days. Sampling resulted in 456 specimens, with a total of 50 species distributed in 17 genera. Representatives of the three subfamilies were collected. Eristalinae has the highest species richness (n=24) with abundance of 187, followed by Syrphinae (n=19) with abundance of 235 and Microdontinae (n=7) with abundance of 34. Only five species occured in three regions: *Pseudodoros clavatus* (Fabricius, 1794), *Syrphus phaeostigma* Wiedemann, 1830, *Copestylum (Phalacromya) spinigerum* (Wiedemann, 1830), *Ocyptamus argentinus* (Curran, 1939) and *Ocyptamus bonariensis* (Brèthes, 1905). As a result, the dissimilarity between areas was high. The lowest dissimilarity was of 30% between two sampling units. Besides, all other areas had more than 50% of dissimilarity. The SAR was evaluated with generalized linear model (GLM), which evaluates the influence of area size in function of richness of species in different regions. Our results demonstrate that the number of species tends to decrease as a function of the sampled area size (distance between traps) with a value of significance for one of the studied regions. Therefore, hoverfly diversity responded negatively to SAR, that is the larger the sampled area, the lower the amount of collected species.

A quarry of fungus gnats in the quarry – a giant insect trap at the gateway to Fennoscandia

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Keywords:Limestone quarry, Sciaroidea, diversity, immigration

The huge man-made limestone quarry ”Limhamns kalkbrott” is situated in the semi-urban coastal outskirts of Malmö in southernmost Sweden, just beside where the Öresund bridge connects Fennoscandia with Denmark and continental Europe. The quarry, excavated between 1866 and 1996, is about 1km long, subrectangular, and 70 meters deep with steep walls, reaching to 58 meters below sea level. Groundwater seeps in through the walls, making the ponds in the bottom semi-brackish, and water is continually pumped out to keep the water levels stable. The climate in the quarry has a distinctly more continental character than the surrounding area, causing a greenhouse effect during summer, with warm air rising in the middle and thereby sucking in colder surrounding air along the edges. The environment is dry and steppe-like in most of the quarry, but with a more lush area with ponds and willow shrubs along the western sun-shadowed edge. The quarry was protected as a nature reserve in 2010. Fungus gnats (Sciaroidea except Sciaridae) in the quarry were Malaise trapped over two years, at four sites, ranging from beside a wet seepage wall, through the lush shrub area, and out in the dry steppe landscape. Some additional material was collected with numerous pan traps. The collected material, totalling 170 species, is surprisingly rich for a steppe-like, semi-urban area. Many rare and little known species were recorded and several are considered to be new to science. The high species diversity is likely related to the rich variety of unique habitats, the central position of the quarry at the immigration route from the continent, and the convection currents of the warm climate in the quarry (i.e. the quarry may function as a giant insect trap for immigrants).

Behavioral ecology [poster]

Dancers in the Dark – Sexual selection acts on wing interference patterns in *Drosophila melanogaster*

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Keywords: Wing Interference Patterns, *Drosophila* mating, sexual selection

When small insects like the *Drosophila* flies mate in lower-reflectance ambient light environments their hyaline wings display vivid and stable structural colour patterns called Wing Interference Patterns (WIPs). Such WIPs are hypothesized to function in sexual selection among small insects with wing displays, but this has not been experimental verified. We measured the variation and heritability of WIPs in a set of 34 isogenic lines of *Drosophila melanogaster.* We found significant variation among the isogenic lines in their WIP-pattern, and a broad-sense heritability of 40%. We then tested whether female mate preference (time to mating = male attractiveness) was influenced by WIP visibility or not. We are now able to present the first experimental evidence, that WIPs in males of *Drosophila melanogaster* are indeed targets of mate choice from females, and that two different colour traits, saturation and hue, experience directional and stabilizing sexual selection, respectively. We found no statistical significant effect of brightness. We think that directional selection on saturation reflects sexual selection for high-quality males, whereas stabilizing selection on hue (and pattern?) might reflect selection for species recognition favouring the modal (wildtype) male phenotype in the population.

New surveillance techniques for the capture of adult *Chyrsops vittatus*

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Keywords: Tabanidae, adults, flight behavior, aspirator, mirrors.

Adult *Chrysops vittatus* have been difficult to collect. Two new techniques have been developed based on their flight behavior. The first technique utilizes a power aspirator. It was observed that the adults of this species will attack moving vehicles, especially the sideview mirror. Therefore, a device was developed consisting of dual power aspirators which will collect adults from both sideview mirrors simultaneous as the vehicle is moving. The second technique is to use an inverted MM-X trap. It was observed that the adults will not be caught a normally oriented MM-X trap, but readily enters an inverted trap.

Development of a cadaver mimicking odour lure for mass trapping of the blowfly pest *Calliphora vicina*

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Keywords: Wind tunnel, synthetic odour, lure development

The blowfly *Calliphora vicina* is a major pest insect in the dried fish industry in Lofoten, Northern Norway. Olfaction is the principal sensory signal to locate resources for most insects. With a viable synthetic odour mimic, mass trapping can significantly reduce the economic loss in the stockfish industry. Due to the cold climate conditions adult blowflies in Lofoten live for more than one year which enables mass trapping outside the drying period without high odour competition from natural sources. A three component synthetic blend already exists. This blend has in a three year study reduced the damage to number of stockfish by 60%. The attraction to the three component blend is, however significantly lower than to natural sources and the potential for increased trapping efficiency with a different odour composition is high.

There is high upwind attraction of *Calliphora vicina* to cadavers in wind tunnel studies. Headspace collections and chemical identification from these odour sources and electrophysiology on insect antennae have revealed several new candidate compounds which could be implemented in a field active odour blend. A number of wind tunnel experiments have been conducted to distill the odour message down to a critical number of synthetic compounds without compromising attraction. Both compound content and blend ratio influence upwind attraction. There is also a distinct difference in upwind responses between male and female blowflies. We have now identified new candidate odour blends which can increase the field efficiency considerably. Deployment of an effective mass trapping strategy in the stockfish production areas is important to increase the utilization of this renewable marine resource.

Overview of recent research on Sciomyzidae

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Keywords:Sciomyzidae, research overview, recent research

The major features of the biology of Sciomyzidae are reviewed. Recent and ongoing research on various aspects are emphasised. A "Passing Parade" of photos of "the giants on whose shoulders we have perched and seen beyond" and the Berg/Sandved film on Sciomyzidae concludes the presentation.

Comparing morphological diversity with genetic structuring in the case of the *Dicranota* (*Ludicia*) *lucidipennis* (Edwards, 1921) (Diptera: Pediciidae)

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Keywords: Biogeography, Carpathians, morphometry, Pediciidae, refugia

Paradigmatically, the European aquatic insects exhibit highly divergent population structures in some extra-Mediterranean mountainous areas which are likely identical with some cryptic refugia during the Pleistocene climate change. During the glacial and inter-glacial periods important area dynamics were also detected in such Central European mountain ranges in a series of arboreal taxa, based on the emergence of highly divergent morphological and genetic structures of the populations from this area. The Carpathians are recognized as one of the most important cryptic refugia of cold-tolerant aquatic insects in Europe, but also a meeting place of some genetic lineages from different extra-Carpathian origin. In the present study we investigate a mountainous aquatic dipteran, *Dicranota* (*Ludicia*) *lucidipennis* (Diptera, Pediciidae) which is quite abundant in Western and Central Europe. The chromatic variability of the species in the Balcan-Dinarian populations has already been used in some previous taxonomic revisions. To test the taxonomic importance of such chromatic divergences we analyzed 216 individuals from the whole range of the species. Important morphological variability was detected between populations, mostly on the size and colour of the individuals. Linear and geometric morphometry support some divergent morphological groups in Europe, mostly on body characters, excluding genital structures. However, our morphometry analysis confirms the presence of two morphological groups in Romania, which were not supported, by genetic evidence (based on mtCOI sequences), but did detect some highly structured genetic lineages from the Apuseni Mountains, which are different from those collected from the Southern and Eastern Carpathians and could be related by important range shifts and isolation of populations during the Pleistocene climate changes.

Taxonomic revision of *Tephritis* Latreille (Diptera: Tephritidae): preliminary results

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Keywords: Tephritidae, *Tephritis*, species groups, host plants, Middle East

The genus *Tephritis* Latreille 1804 includes about 150 species occurring predominantly in the Palaearctic Region, including about 30 undescribed species collected or recognized in collections during this study. The key by Merz (1994) based on thorough revision of Western European species is still the most comprehensive, but it covers the species occurring in Eastern Europe, the Mediterranean region, and Middle East only partially. After two years of taxonomic revision of Western Palaearctic *Tephritis*, some preliminary results have been achieved. Revisions of the two groups of species, those with the entire apical spot, and those with paired apical spots, resulted in the description of nine species, predominantly from the Middle East. Both groups are easily separable by wing pattern details alone, but they are heterogeneous in other morphological characters and taxonomic position of their host plans, and very probably are polyphyletic. A phylogenetic analysis based on a dozen morphological characters, half of which are details of the wing pattern, provides unreliable results. Extensive fresh collections from the Caucasus and Near East in this study, combined with recently accumulated European material for DNA barcoding, provide now a sound base for forthcoming molecular phylogenies. Mass rearing from host plants is the best method to analyze ranges of character variability in populations and discover numerous cryptic species. As in other flower-head infesting tephritids, the length and shape of the aculei is shown to be one of the most important characters to separate sibling species associated with flower buds and bracts of different size.

“Parasitic fruit flies” (Diptera: Tephritoidea: Pyrgotidae, Ctenostylidae, Tachiniscidae)

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Keywords: Parasitic, phylogeny, Pyrgotidae

The Pyrgotidae, Tachiniscidae (or Tachiniscinae if considered a subfamily of Tephritidae), and Tephritidae s.str. form a monophyletic clade, based on both morphological and molecular evidences. The majority of species belongs in the Tephritidae s.str. (Tachiniscinae excluded), a monophyletic group of ca. 5000 species. Its basal groups (Phytalmiinae) have saproxylobiotic larval habits, as observed in most Lower Tephritoidea, while more advanced taxa are phytophagous. The synapomorphy of the Tephritidae s.str., i.e. the presence of the greater ampulla, is primarily lacking in Pyrgotidae+ Tachiniscinae. Pyrgotidae and Tachiniscinae both have acute piercing aculeus, but otherwise of a different structure; it could be either a synapomorphy or resulted from independent adaptation for oviposition into insects: adult scarabs and caterpillars. Earlier studies showed Pyrgotidae and Tachiniscidae (as a family) to form a monophyletic clade based on nucleotid sequences of the 28S, cad, tpi, and aats1 genes. Thus, I take there are two monophyletic lineages, Pyrgotidae + Tachiniscidae, on one hand, and Tephritidae s.str., on another. Some genera of Tachiniscinae are indistinguishable from Pyrgotidae and Tephritidae s.str. except by the structure of female genitalia. Lumping the three families (which have no reliable hiatus in between) into one can be a solution of this problem. Taking Tephritidae s.str. and Tachiniscidae as outgroups turns many character states in pyrgotid taxa into reversals and thus gives a clue of phylogenetic relationships in the Pyrgotidae inferred from the morphology. *Descoleia, Nosferatumyia, Prodalmannia*, and *Maenomenus* and a few undescribed Australian genera represent monotypic basal lineages of unclear relationships, along with Teretrurinae. Most known pyrgotids belong to the subfamily Pyrgotinae. The enigmatic Ctenostylidae are highly specialized aphagous pyrgotids, possibly related to *Toxopyrgota*. Current taxonomic revisions of the genera of Pyrgotidae, Ctenostylidae, and Tachiniscidae will result in rearrangements of the higher classification of these groups of the “parasitic fruit flies”.

Microhabitats and ecological specializations of the Oriental bamboo-inhabiting Gastrozonini and Acanthonevrini (Diptera: Tephritidae: Dacinae and Phytalmiinae)

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Keywords: Bamboo tephritids, larval microhabitats

Gastrozonini and some Acanthonevrini genera are the only Tephritidae breeding in grass (Poaceae). Most species occur in the Oriental Region, some are Afrotropical. Asian species with known larval habitats breed in bamboo, while the African species develop in other grasses. In the present study the ecology of the little-known bamboo-inhabiting Gastrozonini and Acanthonevrini from Southeast Asia is outlined. The focus of the study was on larval microhabitats and ecological or behavioural specializations of the bamboo tephritids. The courtship behaviour was simple or involved the production of a “nuptial gift” produced by the males. Eggs were usually laid below the edges of the protecting culm sheaths or in injuries to the bamboo surface. The freshly hatched larvae entered the bamboo tissue by squeezing in between culm sheaths and bamboo walls or via injuries and holes created by other insects. Larvae of Gastrozonini and some Acanthonevrini mainly fed in the meristem or other soft tissue of living or dead bamboo shoots. Some Acanthonevrini developed in water-filled internode cavities of bamboo culms and scraped food particles from the wall surface. There was a clear zonation in host plant utilization depending on the structural characteristics of the bamboo species, their growth stages and the degree of protection by the culm sheaths.

Preliminary data on the chironomid fauna (Diptera: Chironomidae) of the Pay-Khoy Ridge (Artic Russia)

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Keywords: Pay-Khoy Ridge, Arctic Russia, Chironomidae

CANCELED

Mosquito monitoring in Germany: Detection of mosquito-borne pathogens

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Keywords: Culicidae, autochthonous transmission, Germany, *Dirofilaria immitis, Dirofilaria repens*, filaria, mosquito-borne pathogens, mosquito monitoring, *Setaria tundra*, vector, viruses, zoonosis

Mosquitoes collected within the framework of a nationwide mosquito monitoring program carried out in Germany since 2011 were screened for viruses (Togaviridae, Orthobunyaviridae, Flaviviridae) and filariae (Filarioidea). Roughly 20,000 mosquitoes from numerous sites were pooled to groups of 1–25 individuals according to collection site, collection date and species, and screened for the pathogens by appropriate PCR assays. PCR products were sequenced for identification of the pathogens.

Thirteen pools turned out to be *Flavivirus*-positive although probably insect viruses were detected in the mosquitoes rather than vertebrate-pathogenic viruses since they could not be isolated using common cell culture systems and, thus, not be characterized. In addition, three identifiable filarioid species were demonstrated in the mosquitoes: *Setaria tundra* (4x in *Aedes vexans*), *Dirofilaria repens* (1x in *Anopheles daciae*) and *Dirofilaria immitis* (2x in *Culex pipiens*/*torrentium*), although the mere finding of worm larvae in mosquitoes does not necessarily equalize these with being vectors.

Setaria tundra is a parasite of cervids widely distributed in Scandinavia where it occasionally leads to outbreaks of peritonitis and perihepatitis in reindeer. Data on its occurrence in Central Europe are scarce. The *Dirofilaria* species are zoonotic disease agents with canids as natural hosts. Human infections may cause subcutaneous, subconjunctival and cardiovascular lesions, in rare cases also meningoencephalitis. Both dirofilarial species are endemic in the Mediterranean but a spread to North and East European countries has recently been observed, generally recognized by autochthonous infections in dogs. The additional and repeated finding of *D. repens* in mosquitoes collected in Germany by a second research group together with previous direct or indirect detections in dogs without a travel history suggest that a natural transmission cycle of this species has already established in Germany.

From three spermathecae to seminal receptacle in the genus *Trichocera* (Trichoceridae): stages of evolution documented by five species

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Keywords: Spermatheca, seminal receptacle, Trichoceridae

Within the genus *Trichocera* Meigen a *rectistylus* group of seven species was distinguished by Starý (1998, 2009). Females and males differ from the congeners by the several peculiar features in the genitalia, including modified genital plate and genital fork, and the absence of spermathecae (except for *T. polanensis*). This is a unique character among the genus and the subfamily, whose all members have three spermathecae and similar morphology of female inner and outer genitalia. Moreover, three spermathecae and "usual" trichoceriid genital plates were found also in several fossil genera since the Upper Jurassic times. Thus this configuration appears to be ancestral phylogenetically and also in a geological sense. The present investigations were undertaken to further explore the sperm storage system in the *rectistylus* group. A new structure that has replaced spermathecae is named the seminal receptacle (sensu Pitnick et al. 1999). Two species show possible evolutionary transition states from the plesiomorphic state of three spermathecae to a new sperm storage system. One species has both the spermathecae and the receptacle; the other, *polanensis*, has three poorly sclerotized spermathecae. This is the first case of a seminal receptacle among the Nematocera; the structure was till now known only from the higher Brachycera.

Genus *Ectrepesthoneura* (Mycetophilidae) in Baltic amber: biogeographical implications

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Keywords: Mycetophilidae, *Ectrepesthoneura*, Baltic amber

The genus *Ectrepesthoneura* Enderlein (Mycetophilidae) is a small genus comprising 13 recent species of Holarctic distribution. It appears also to be poorly represented in fossil state: until recently only four species were described. Two oldest representatives come from the Lower Cretaceous (amber of Alava), one species, *E. magnifica*, was described from Baltic amber as *Willistoniella*, and *E*. *rottensis* was described from one imprint of wing from Rott (Oligocene).

Recent investigations of *Ectrepesthoneura* in Baltic amber (Eocene, 40 mya) confirm that the genus was poorly represented also in this epoch: among ca. 4000 of mycetophilids only ca. 120 specimens (mostly males) were found; 15 new species were distinguished.

Morphological and biogeographical comparison with recent fauna is made. Within the genus five groups of recent species are distinguished on basis of male genitalia. Three groups were represented in Baltic amber. Interesting shifts in species representation and biogeography of these groups are observed since the Eocene; for instance, the next relatives of *E. gracilis*, a recent species from the Mediterranean islands, are known from the Baltic amber. Thus this species is probably an endemite after Ice Age.

Fossil Diptera [poster]

The oldest representative of the genus *Gonomyia* (Diptera, Limoniidae) from Lebanese amber (Early Cretaceous): new subgenus and species

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Keywords: *Gonomyia*, Chioneinae, Diptera, Lebanese amber

The genus *Gonomyia* of the subfamily Chioneinae (Limoniidae) is distributed worldwide except Antarctica. The genus is numerous in species, with 652 recent species belonging to nine subgenera. The representatives of the genus occur from boreal to tropical zones.

Fossil specimens of *Gonomyia* are very rare and to date only nine fossil species from the Cenozoic have been described from the Eocene, Oligocene and Miocene. Podenas and Poinar recorded an unnamed female *Gonomyia* specimen from the Lower Cretaceous Burmese amber.

The new subgenus *Gonomyia* (*Azaria*) *lebanensis* subgen. n. and sp. n. is described from Lebanese amber (Early Cretaceous). This is the oldest representative of the genus *Gonomyia* (Diptera, Limoniidae) known so far. Wing venation and morphology of hypopygium distinctly distinguish *Gonomyia* (*Azaria*) *lebanensis* subgen. n. and sp. n. from the other known fossil and recent subgenera and species of *Gonomyia*. These features are: the position of cross-vein m-cu behind the fork of Mb into M1+2 and M3+4, d-cell open by atrophy of the basal section of M3, and simple morphology of aedeagal complex.

Trends in reduction of wing venation in the genus are discussed.

Fossil Diptera [poster]

Homology of wing venation of Mecoptera and Diptera in subcubital and radial sectors

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Keywords: Homology, wing venation, Mecoptera, Diptera

Several systems of wing venation terminology are simultaneously used in particular dipteran families. These various systems have often nothing in common with homology and evolution of the Diptera but are used “traditionally” as a consequence of wrong decisions made ca. 100 years ago. One such misinterpretation concerns the subcostal sector. The original mistake was made by Comstock & Needham (1898), who named only vein Sc, ignoring the crossvein sc-r. This vein was later incorrectly considered as a second subcostal vein (Sc2) by Séguy (1940) and followed by Hennig (1954, 1974). The second problem caused Tillyard (1919) who ignored the crossvein r-r as a vein homological to R2.

Diptera had evolved directly from the Permian Mecoptera and have many characters of wing venation common with scorpion flies. This source of information is still not explored. The next invaluable source is the oldest Diptera described from the beginning of the Middle Triassic (~240 mya years ago) (Krzemiński et al. 1994, Krzemiński & Krzemińska 2003)

Basing on fossil evidence of Mecoptera and Diptera, we present the homology of subcostal and radial sectors of wing venation in these orders and propose to uniform the terminology of Sc and R veins.

The preliminary result of the frit flies research (Diptera: Chloropidae) in Mugla province (SW Turkey)

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Keywords: Chloropidae, Diptera, Mugla province, Turkey, faunistics

The research of Diptera in Mugla province (SW Turkey) is conducted since 2011 with cooperation of Mugla Sitki Kocman University. Most species were collected by means of yellow pan water traps, Malaise traps and sweeping vegetation. Selected specimens are deposited at Czech University of Life Sciences collections. The family Chloropidae (frit flies) is little known in Turkey, only 32 genera and 64 species have been listed up to now. During three years we collected several thousands of specimens of frit flies belonging to 34 genera and 94 species of which 29 genera and 54 species were confirmed for Turkish fauna, 5 genera (*Calamoncosis*, *Eutropha*, *Eribolus*, *Lagaroceras* and *Trachysiphonella*) and 40 species are first recorded from Turkey: *Aphanotrigonum anderssoni*, *A. inerme*, *A. parahastatum*, *A. trilineatum*, *Calamoncosis duinensis*, *C. laminiformis*, *Chlorops limbatus*, *C. serenus*, *Cryptonevra consimilis*, *C. diadema*, *Dicraeus beschovskii*, *D. vagans, Elachiptera graeca*, *E. sarda*, *Eribolus hungaricus*, *Eurina lurida*, *Eutropha fulvifrons*, *Lagaroceras megalops*, *Lasiambia fycoperda, Lasiosina aurea*, *L. albipila*, *L. immaculata*, *L. lindbergi*, *L. paralitoralis*, *Lipara rufitarsis*, *L. similis*, *Meromyza pluriseta*, *Oscinella frit*, *O. pusilla*, *O. trochanterata*, *O. ventricosi*, *O. vindicata*, *Oscinomorpha koeleriae*, *O. minutissima*, *Polyodaspis sulcicollis*, *Rhodesiella fedtshenkoi*, *Trachysiphonella carinifacies*, *Tricimba albiseta*, *T. hungarica* and *T. lineella*. The description of four new species is being prepared. Altogether 37 genera and 104 species are currently known from Turkey. It is likely that this is may represent only 30 % of the total Turkish fauna.

Predatory flies of the genus *Coenosia* Meigen, 1826 (Diptera: Muscidae) supporting biological pest control in greenhouses

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Keywords: Biocontrol, *Coenosia*, pest, predator

The important role of *Coenosia* species (Muscidae: Coenosia Meigen, 1826) as players in a biological pest control system has been increasingly realized in recent years. *Coenosia attenuata* Stein, 1903 in particular is a common and most important species in greenhouses. There are new records of this predatory fly worldwide and several teams of researchers are working on its life cycle, behavior and enhancement. Greenhouses where a biological and integrated mode of husbandry is practiced can be colonised by high numbers of *Coenosia* flies. The flies were found to inhabit vegetables, herbs and ornamental plants. They can establish effective populations in greenhouses, where they find a variety of different pests and innocuous species to feed upon because they are non-specific predators. *Coenosia* are the primary antagonists of the adult stages of black fungus gnats (Sciaridae), whiteflies (Aleurodidae), and leaf miners (Agromyzidae). I investigated the predatory capacity of various *Coenosia* species for black fungus gnats (*B. difformis*) under different climatic conditions. The daily consumption rate of black fungus gnats by the species *C. attenuata*, for example, averaged 7. The remains of the prey can be observed on the surface of the herb leaves. *Coenosia* larvae are also predatory on fungus gnat larvae and can therefore effectively limit fungus gnat populations in the long term. I assumed that insecticides that act on contact (pymetrozin, spinosad and pyrethrum) would reduce the number of the adult *Coenosia* flies, whereas azadirachtin, a stomach insecticide, should have a weak effect. No influence of fungicide treatments on *Coenosia* is expected. Studies on the flies' activity have shown that *Coenosia* predators do not simply colonise greenhouses from the outside for short periods but that they can complete their life cycle in the greenhouse soil and can become established there for a long period of time. *Coenosia* species can build up effective populations under greenhouse conditions, and as non-specific predators can feed on a variety of pest groups and on innocuous species. Their natural occurrence in greenhouses can be considered as potential IPM agents with reduced pesticide applications.

Annual changes of emergence patterns and ecological association of blackflies (Diptera: Simuliidae) at freshwater karst habitats

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Keywords: *Simulium* (*Eusimulium*) *angustipes*, *Simulium* (*Nevermannia*) *costatum*, microhabitats, longitudinal zonation, water discharge

Emergence patterns of blackflies (Diptera: Simuliidae) were investigated in the National Park Plitvice Lakes in Croatia, at three sites: upper reach of Bijela rijeka, tufa barrier Labudovac and tufa barrier Kozjak-Milanovac (tufa barriers = barrage lake outlets). At the upper reach of Bijela rijeka the research was carried out from 2007 until 2010, and at tufa barriers Labudovac and Kozjak-Milanovac from 2007 until 2013. Samples were collected once a month using pyramid-type emergence traps. In all 9 species were identified during this study. Two species were identified at sites close to spring: *Simulium* (*Nevermannia) costatum* Friederichs and *Simulium* (*Odagmia*) *monticola* Friederichs. *Simulium* (*Nevermannia*) *costatum* was found at all sites, but in different proportions. At tufa barriers *Simulium* (*Eusimulium*) *angustipes* Edwards was the most abundant species in all years. Water temperature, water discharge and type of microhabitat are the factors that had the most influence on the blackfly assemblages and emergence patterns. It was found that blackflies do not prefer sites closer to spring, probably to the lower organic input and they prefer microhabitats with greater water velocity and solid substrates. In contrast, there is much larger number of individuals and species at tufa barriers. The blackfly communities at all sites were dominated by species typical of the rhithral zone, but there was a shift in species composition along a longitudinal gradient from the hypocrenal-epirhithral to the epirhithral-metarhithral zone. Multiple generations per year were detected in *Simulium (Eusimulium) angustipes*, whereas in *Simulium (Nevermannia) costatum*, the number of generations differed between upper reach of Bijela rijeka with constant temperature during the year and between the tufa barriers with variable water temperature during the year.

A faunistic account of selected bibionomorph families in Georgia

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Keywords: Caucasus, Georgia, Sciaroidea, Hesperinidae, faunistics

The Caucasus area is considered to be one of the biodiversity hotspots in the Palaearctic region, with a high proportion of endemic species. Due to its habitat diversity, as well as it having been a glacial refugium during the Pleistocene, the area has been a centre of diversification for western Palaearctic taxa. However, the extant Diptera are still rather superficially studied in this area, including Georgia. This study concentrates on the families of the Sciaroidea (excl. Sciaridae) and Hesperinidae in Georgia. Specimens were collected by sweep netting during two recent fieldtrips, as well as by Malaise- and light trapping from 2011 to 2013. A wide range of localities from all over the country were sampled, viz. Lagodekhi NR, Kazbegi NP, Borjomi-Kharagauli NP, Mtirala NP, Kintrishi NR, etc. The collected material includes more than 1750 specimens of 177 species, divided between the families as follows: Hesperinidae 1 sp., Bolitophilidae 2 spp., Diadocidiidae 3 spp., Ditomyiidae 2 spp., Keroplatidae 20 spp. and Mycetophilidae 149 spp. The majority of the species are widely distributed in the western Palaearctic, but at least 10 species are regarded as new to science. The most common species were *Orfelia georgica* Kurina & Jürgenstein and *Synapha fasciata* Meigen. On the basis of the studied material, the second record of *Hesperinus ninae* Papp & Krivosheina (Hesperinidae) and two new *Orfelia* Costa (Keroplatidae) species have been published so far.

The Empididae s.l. fauna of the Caucasus (Diptera: Empididae, Hybotidae, Atelestidae, Brachystomatidae)

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Keywords: Empidoidea, Empididae s.l., Caucasus, biodiversity

The Caucasus occupies a large area between the Black and Caspian seas showing great diversity of natural landscapes varying from high mountains to steppe biotopes that suggests a rich fauna of Empididae (s.l.). However, the first check-list of Empididae (s.l.) from the Caucasus included only 40 species belonging to 11 genera of Hybotidae, and 78 species from 11 genera of Empididae [Shamshev & Kustov, 2006]. Ever since, these data have been significantly updated by descriptions of new species and by new records of known taxa. Currently, Empididae from the Caucasus includes 16 genera and 169 species (41 species newly described); Hybotidae – 18 genera and 81 species (10 species newly described); Atelestidae – 1 genus and 1 species, and Brachystomatidae – 2 genera and 2 species (all recorded from the Caucasus for the first time).

Toward the calyptrate Tree-of-Life: molecular phylogeny of a recent megadiverse branch of Schizophora

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Keywords: Schizophora, Calyptratae, Muscidae, molecular phylogeny

The Calyptratae are with approximately 18,000 described species (12% of known dipteran diversity) a particularly well-known taxon that includes houseflies, tsetse flies, blowflies and botflies. Despite being species-rich, the clade appears relatively young with the oldest confirmed fossil being only 40 million years old. Here we propose a higher-level phylogenetic hypothesis for the group based on transcriptome and Sanger sequencing data. The latter is for ribosomal (12S, 16S, 18S, 28S) and protein encoding (COI, Cytb, CAD, Ef1) genes for 247 species that represent all commonly accepted families in Hippoboscoidea, Oestroidea as well as those of the muscoid grade. Our analyses support the monophyly of Calyptratae. Hippoboscoidea and Oestroidea are consistently found to be monophyletic, and the paraphyly of the muscoid grade is confirmed. We also confirm that the monotypic family Mystacinobiidae is an oestroid, and demonstrate that the previously unplaced and still undescribed “McAlpine’s Fly” is nested within this superfamily. Within the Oestroidea, we confirm the paraphyly of ‘Calliphoridae’. Overall, the Hippoboscoidea is sister group to the remaining Calyptratae, and the Fanniidae is sister group to the remaining non-hippoboscoid calyptrates, whose relationships can be summarized as (Muscidae (Oestroidea (Scathophagidae, Anthomyiidae))). With approximately 5000 species (ca. 180 genera), the Muscidae is one of the most species-rich calyptrate families. As an extension of the calyptrate study, we review the various attempts to classify genera into tribes and subfamilies and find good support for muscid monophyly and a basal split of the family based on data from seven genes for 84 species representing 40 genera. We also find strong evidence for a correlation between predatory larvae and a reduction in larval instars in the Muscidae.

Phylogeny and tribal classification of Psychodinae – a synthesis (Diptera: Psychodidae)

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Keywords: Psychodidae, Psychodinae, phylogeny, classification

The tribal classification of Psychodinae has long been in dispute, with at least three major configurations currently in use. Some nomenclatoral and historical taxonomical issues on the tribe level have been solved by Duckhouse (1987), Jezek et al. (2011) and Kvifte (2012); but a robust phylogenetic framework for classification is still lacking. At present, three major phylogenetic controversies can be identified:

1. Psychodini: Is the subtribe Trichopsychodina Jezek (including *Threticus*, *Philosepedon* and *Trichopsychoda*) more closely related to *Psychoda* s.l. or to the *Telmatoscopus/Paramormia* assemblage?

2. Is *Mormia* s.l. the sister group of the subtribe Brunettiina, or a part of the *Telmatoscopus/Paramormia* assemblage?

3. Do the mainly Southern hemisphere pericomoid assemblages *Clytocerus*, *Tonnoiriella*, and Maruinini/Setomimini belong with the same taxon as the Northern hemisphere Pericomaini?

To address these questions, a phylogenetic analysis was conducted using a combined matrix of morphological and molecular characters. Data were mostly gathered from previous molecular studies of Psychodinae (primarily Curler & Moulton 2012, Espindola et al. 2012 and Kvifte & Andersen 2012), but also from unpublished sequences and examination of fresh specimens. An updated, phylogenetically based tribal classification is proposed.

The SISBIOTA-Diptera Brazilian network. A long term survey of Diptera from unexplored central areas of Brazil

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Keywords: Brazil, Rondônia, Mato Grosso, Mato Grosso do Sul, biodiversity surveys

SISBIOTA-BRASIL is a three-year multimillion dollar research program of the Brazilian government to document plants and animals in endangered/understudied areas and biomes in Brazil. Even in the most studied areas in Brazil, distributional patterns of invertebrates and plants are insufficiently known and the historical events that generated those patterns are even more poorly known. This deficiency brings implications and impediments for conservation policies and for the understanding of evolutionary processes. Conservation decisions are largely dependent upon precise knowledge of the taxonomic and geographic distribution of species. Inside this premise and concerning, we proposed and get approved an ambitious research project to study the Diptera of Central Brazilian areas, in the States of Rondônia, Mato Grosso and Mato Grosso do Sul, which are characterized by four important biomes of the South American continent: Amazon Forest, Brazilian Savannah (Cerrado), Pantanal and Chaco. Besides their ecological relevance and unicity, those areas historically lack satisfactory entomological

surveys. As a result, insects from these areas are strongly under-represented in the main collections. Moreover, they are being exponentially destroyed by the enlargement of the livestock and agricultural areas. This project involves 25 researchers from 16 different Brazilian institutions, and gathers 36 graduate and undergraduate students, and 10 technicians. The project scope encompasses taxonomic, phylogenetic and biogeographical aspects of the studied families. So far, we have processed nearly 300,000 specimens of Diptera, which have been collected with standardized methods in the sampled areas. Thus far, the research output comprises 9 published papers, 23 papers in press, and another 37 in preparation. Taxonomically, 56 families have been recognized, 246 new species are being described and 421 new occurrences are being assigned, so far. As outreach measure to the general public and for researchers with different degrees of expertise and interest on Diptera, we constructed a webpage, a twitter account, a blog, and also a Facebook page.

The life cycle and morphological features of the Natal fruit fly *Ceratitis rosa* (Karsch) (Diptera: Tephritidae), a pest of citrus in South Africa

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Keywords: Tephritidae, *Ceratitis rosa*, life cycle, biology

The Natal fruit fly, *Ceratitis rosa* (Karsch), is a major pest of fruit crops in the subtropical regions of South Africa. Although native to southern Africa, it has spread to other fruit producing regions of Africa and has been reported in the United States of America following accidental introductions. The biology of *C. rosa* has not been formally documented. Instead, it has largely been assumed to closely resemble that of its congeneric *Ceratitis capitata* (Wiedemann) by having several generations per year, depending on climatic conditions and the abundance of food. The lifecycle and some identifying morphological features of the life stages of *C. rosa* were observed in the laboratory. Oranges were used as the food source for the larvae. All life stages were grown at 22±3°C, 60–80% R.H. and a L12:D12 photoperiod. Adult flies were placed with oranges in rearing cages. Oranges that were punctured by ovipositing females were removed and placed into separate cages for individual study. The duration of each stage of development was closely monitored and recorded until adult emergence. Eggs were laid 6–8 days after adult eclosion, with larvae hatching some 6–8 days after oviposition. Larval development took 12–15 days, after which they reached the prepupal stage, which was marked by exit holes on the surface of the oranges. The pupal stage lasted between 10–22 days until the emergence of new adult flies. Hence, the life cycle of the Natal fruit fly can last for 32–50 days, with 6–11 generations per year, depending on the environmental conditions.

Wing venation in Diptera: review of alternative interpretations and proposal of a uniform terminology

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Keywords: Wing venation, terminology, Diptera

The classification of Diptera is heavily based on the wing venation, and most families are characterized by a distinctive venation pattern. Presently a number of different terminologies are in use. They frequently contradict each other even in closely related taxa. This situation greatly impedes the comparison of results obtained in different fields of dipterology (e.g. taxonomy, genetics, paleontology etc.) and even makes it impossible in some cases. Based on literature data complemented with own observations, we critically reviewed the wing venation terminologies used up to now. Up to now three major terminologies have been developed based on several older and more recent studies. If we compare the terminologies used in one of the most important journal devoted to Diptera (*Studia dipterologica*), it becomes evident that while the majority of the articles on brachyceran or recent families followed Comstock's system, other works dealing with nematoceran or fossil families used Tillyard's terminology. Wootton-Saigusa's interpretation is a little bit neglected, but more and more dipterologists recognize its value.

The most remarkable differences are the naming of the medial, cubital and anal veins. Comstock's system recognizes three medial and two cubital veins, Tillyard named four medial and two cubital veins. Wootton-Saigusa suggested four medials, but treated the vein parallel to the first cubital as a pseudovein. We tested the arguments in the Wootton-Saigusa's system and compared it with other terminologies. We concluded that it is a consistent and morphologically sound interpretation, and should therefore be generally applied with slight modifications. As a conclusion we propose the following system: costa (C); subcosta (Sc); radius 1–5 (R1, R2, R3, R4, R5); media 1–4 (M1, M2, M3, M4); cubitus 1 (Cu1); inner cubital pseudovein (iCu); cubitus 2 (Cu2); anal 1–3 (A1, A2, A3).

Exploring species diversity in *Tanytarsus* (Diptera: Chironomidae) with almost 1600 DNA barcodes

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Keywords: Chironomidae, *Tanytarsus*, DNA barcode, diversity, cryptic species

Tanytarsus van der Wulp, 1874, occurring in all types of water, is the most species-rich genus of tribe Tanytarsini within the Chironomidae with more than 400 species worldwide. In this study, we test the effectiveness of the standard 658 bp barcode fragment from the 5’-end of the mitochondrial cytochrome c oxidase 1 gene (COI) in differentiating the species of *Tanytarsus*. The results show that species of *Tanytarsus* are well differentiated by DNA barcodes, enabling the identification of characteristic morphological forms and association of life stages. The Neighbor joining tree based on 1573 DNA barcodes currently available to us in the Barcode of Life Data Systems (BOLD) comprises 135 well separated clusters representing 59 identified and 60 unidentified morphological species of *Tanytarsus*. Among the identified species, DNA barcodes have revealed cryptic diversity in several complexes. In geographically separated populations of the *Tanytarsus chinyensis* species group for instance, overlapping variation in morphological characters are inconsistent with the variation and deep divergence observed in mitochondrial DNA sequences. Species of the *Tanytarsus gregarius* group on the other hand, show significant variation in morphological characters with less divergence observed in DNA barcodes.

A comparative morphology of antennal sensory organs in Calyptratae species from different ecological niches

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Keywords: Calyptratae, sensory organ, antenna

Flies are one of four super-radiations of insects and their remarkable diversity is a challenge to explore. Antennae in Calyptratae are greatly simplified, with unsegmented flagella, indicating their potential role as model olfactory organs. With the ever-deepening ultrastructural study of this diverse group, evolutionary trends and functions of sensilla structures are more clearly revealed. Ultrastructure of the antennae of Calyptratae from different ecological niches were examined with a stereoscopic microscope, scanning electron microscope, and laser scanning confocal microscope. On the scape and pedicel, both microtrichiae and several mechanoreceptors are detected, and two additional types of structures, setiferous plaques and pedicellar buttons, are found on the antennal pedicel. Four major types of surface sensilla are found on the antennal funiculus and are classified as (a) trichoid sensilla, (b) basiconic sensilla, (c) coeloconic sensilla, and (d) clavate sensilla. Sensillar clusters were detected in cuticular invaginations on the antennal funiculus, including sensory pits and sacculi. Coeloconic sensilla identified on the antennal arista are present in almost all parasitic oestrids, which is an unusual phenomenon because of their absence in other Calyptratae species. Combining new results with those of previous studies, unambiguous definitions of the sensory pit and sacculus are proposed. Parasitic species tend to have higher numbers of pits than those of other ecotypes. In the “higher” saprophagous species, highly complex sacculi are present on the antennal funiculus. In predaceous flies, a common type of coeloconic sensilla is absent on the antennal funiculus.

Rarely described antennal sensilla were discovered in different species, such as a perforating pedicellar button and coeloconic-like sensilla in *Lucilia sericata* (saprophagous), branched sensilla in *Portschinskia magnifica* (parasitic), and coeloconic-like sensilla in *Pales pavida* (parasitic). After comparison with previous similar findings, the functions and evolution of these specific structures are discussed in the context of the biology of the species.

Ecological and evolutionary responses of Arctic flies to recent climate change in Zackenberg, Greenland

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Keywords: Biodiversity, climate change, Greenland, Muscidae

Arctic biodiversity is currently pressured by abrupt changes in climatic conditions. True flies are a key ecological group in the Arctic and like other insects, they are particularly sensitive to climate change due to their small size and ectothermy. To determine how recent and rapid climatic changes affect fly biodiversity, we will measure ecological and evolutionary responses of muscid and phorid flies collected yearly since 1996 in north-eastern Greenland through the Zackenberg Ecological Program. This unique data set provides the opportunity to: 1) evaluate and quantify temporal changes in species phenology, diversity and community composition; 2) assess morphological and genetic changes in selected species over time; and 3) determine which climatic factor(s) most affect fly responses over the study period. Our preliminary results highlight important changes in the phenology of muscids, with common species consistently emerging earlier in the season. We also report changes in species succession patterns and an increased synchronization of the emergence peaks of different species.

Phylogenetic analysis of the tribe Winthemiini (Tachinidae: Exoristinae): preliminary results and perspectives

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Keywords: Morphology, biological control, Oestroidea, parasitoids, Neotropical

Tachinidae is one of the most diverse families of Diptera, with about 10,000 species described in 1,521 genera. Although it is widespread in all biogeographic regions, Tachinidae is most represented in the Neotropical region. Species in this family are characterized by being parasitoids, especially in insects, thereby contributing to natural control of many species, especially agricultural pests. While monophyly of Tachinidae is not contested, very few studies have used a phylogenetic approach to understand internal relationships of subfamilies and tribes. Exoristinae comprises about half of all Tachinidae species, divided into six tribes: Blondeliini, Eryciini, Ethillini, Exoristini, Goniini and Winthemiini. The latter tribe comprises 172 species in 17 genera. This study will provide a robust phylogenetic analysis of the tribe Winthemiini based on morphology. Characters were proposed from external morphology and adult terminalia. To examine genitalia, abdominal terminalia were removed and cleared with KOH at 10% and dehydrated in 70% alcohol and subsequently placed in glycerin. The terminalia were dissected and examined under a microscope and then stored in microvials with glycerin and affixed to the corresponding specimen. Outgroup selection was based on previous hypotheses of relationships in the Exoristinae. The matrix was coded in Winclada and characters were left unordered in the analysis. Heuristic tree searches and index estimates were carried out using TNT, version 1.1. Tachinidae has been cladistically understudied due to its morphological variety and wide geographical distribution. Homoplasies are common and they complicate interpretations of the relationships between species and classification of the family.

New data on the pupae of Late Mesozoic Chironomidae

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Keywords: Chironomidae,pupae,systematics,Mesozoic,SEM

Fossil pupae provide a valuable yet almost completely neglected source of data on the biodiversity and morphological evolution of Mesozoic Diptera. Previously, Mesozoic chironomid pupae were described only in three papers (Kalugina & Kovalev, 1985; Kalugina, 1993; Jell & Duncan, 1986). We began to study chironomid pupae from the Upper Jurassic – Lower Cretaceous deposits of Mongolia using the SEM technique, which appeared to be very effective for uncoated impressions and disclosed many important characters not visible under stereomicroscope.

Of the eleven recent subfamilies of Chironomidae, seven or possibly eight are known from the Mesozoic, however up to now pupae are described only for three of them: Tanypodinae and Podonominae are widespread since the Jurassic whereas Diamesinae, known since the Early Cretaceous, are extremely rare in the fossil record. Among the pupae examined, some are indisputable members of recent subfamilies (such as podonomine *Oryctochlus* Kalugina, 1985; revised in Lukashevich, 2012), however, in many cases it is difficult to estimate exact systematic position of pupae. Occasionally they display character states not observed among the recent taxa (e.g. type and positions of setae in the oldest Diamesinae; Lukashevich & Przhiboro, 2014, in press). More often, however, they display unusual combinations of the character states typical or diagnostic of different subfamilies (e.g. Tanypodinae/Podonominae, as in *Jurochlus* Kalugina, 1985, revised in Lukashevich & Przhiboro, 2012). These reasons both, in addition to incomplete preservation, hamper classification. Hence, it is unclear whether the fossil lineages can be separated using diagnoses based on their recent representatives. As examples, we consider morphological features of several Mesozoic genera based on pupae.

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Syrphoidea [poster]

Comparison of the composition of pollen bearing and eaten by Syrphidae

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Keywords: Syrphidae, generalized pollination, pollen feeding

In this research identification and comparison of pollen taken from bodies and stomachs of Syrphidae was made. The study site consisted of Aedogonium podagraria, Anthriscus sylvestris (Apiaceae) and Bunias orientalis (Brassicaceae) were selected. The studies were undertaken at the end of June 2012 and 2013 at the Zvenigorod Biological Station (Moscow region). Pollen composition depends on insect species, but not on plant species, from which insect were collected. Correlation between pollen composition in the gut and at the body surface of the same insect were low, although significant.

Edge size measured by drosophilids assemblage and its application in environmental monitoring

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Keywords: Biodiversity, bioindicator, conservation monitoring, drosophilids, forest destruction

Forest destruction is increasing in tropical regions, and habitat loss is the main threat to biodiversity in these areas. Furthermore, the remaining forest fragments are exposed to several factors that negatively affect biodiversity; i.e., the extent of the remaining area and edge effects. The assemblage of drosophilids, mainly comprising genus *Drosophila*, has been used as a bioindicator in environmental studies due to the characteristic diversity of the group, ease of collection, and, in particular, their sensitivity to environmental variables. This study evaluated the drosophilid assemblages in two semideciduous forest fragments of different sizes using an edge-interior transect to identify the edge size and its correlation to the extent of forest disturbance. The structure of the drosophilid assemblages was significantly different between the fragments, with the larger area having a higher species richness and greater abundance than the smaller area. An interior-edge distribution pattern was found only for the larger fragment, with an observed edge of up to 60 meters in length, whereas this transition was not observed for the small fragment, indicating that edge effects influence a large edge width of up to 200 meters within the fragment. These data demonstrate that the remaining fragments of the smaller area are the most impacted, and edge effects in these environments can penetrate greater distances into the interior of the forest, thus threatening diversity conservation in these areas.

Cecidomyiidae (Diptera) from Atlantic Forest: current knowledge and perspectives

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Keywords: Gall, gall midges, distribution, Brazil

Cecidomyiidae are the most important galling insects in all biogeographic regions, and one of the most speciose families of Diptera, with more than 6,000 species. The Atlantic forest is a typical biome from Brazilian coast, with high index of endemism and a great biodiversity. It comprises about 20,000 plant species (40% endemic). In the past, the Atlantic forest spread over 1.3 million of Km^2. Nowadays, there are only 7% of its original area. This biome is highly endangered, being considered as a prioritary area for conservation. It includes diverse physiognomies: forests, mangroves, restingas, and altitudinal grasslands. The Atlantic forest comprises 149 known species of gall midges (76% of the Brazilian fauna of Cecidomyiidae), and 371 gall morphotypes induced by this family. As each gall morphotype is induced by a single galling species, the number of recorded Cecidomyiidae species should be 371. This difference is due to the great number of records at family level. In fact, 222 species are still not identified. Among the diverse physiognomies, restinga and dense ombrophilous forest comprise 97% of the recorded species. São Paulo and Rio de Janeiro (states of the Southeast region of Brazil) comprise 65% of the gall diversity, whereas Rio de Janeiro comprises 75% of the identified species. *Clinodiplosis*, *Lopesia*, *Asphondylia, Bruggmannia* and *Dasineura* are the best represented genera, with 12, 12, 10, 10 and 8 species, respectively. These values represent 70%, 67%, 71%, 77%, and 80% of the recorded species for each genus in Brazil. So, the taxonomic knowledge of Brazilian gall midges is still incipient, and it is largely restricted to the Atlantic forest (mainly to restinga and dense ombrophilous forest) and to the Southeast region, remaining many gaps in the species distribution.

Bibionomorpha [poster]

Molecular phylogeny of the families Diadocidiidae, Ditomyiidae and Keroplatidae (Diptera: Sciaroidea): preliminary results

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Keywords: Bibionomorpha, phylogenetic analysis, molecular markers, systematics

The infraorder Bibionomorpha constitutes one of the largest clades within Diptera, though exact relationships among its families are still not clear. Here we present preliminary results of our current studies on the molecular phylogeny and affiliation of the fungus gnat families Diadocidiidae, Ditomyiidae and Keroplatidae based on both nuclear (5.8S, 18S, 28S and ITS2) and mitochondrial (12S, 16S, COI, CytB) gene markers. Our current datasets include more than 30 genera of Keroplatidae, 15 species of Diadocidiidae and 10 species of Ditomyiidae sequenced in the years 2012–2014, with some additional taxa from the GenBank database. The Bayesian inference, maximum likelihood and maximum parsimony preliminary analyses revealed several surprising results. The Sciaridae appears as the closest relative of the Diadocidiidae. The closest relative to the Ditomyiidae appears to be the Lygistorrhinidae. The Cecidomyiidae grouped together with the Macrocerinae, rendering the Keroplatidae paraphyletic. Within the Diadocidiidae, the subgenus *Taidocidia* Papp & Ševčík, forms the sister group to all the other taxa of Diadocidiidae. The subgenus *Diadocidia* s.str. is monophyletic with high node support, while *Adidocidia* Laštovka & Matile is paraphyletic. Within the Ditomyiidae, *Symmerus* Walker appears to be paraphyletic and within the Keroplatidae, *Platyura* Meigen is revealed as the sister group to the other Keroplatidae (including Macrocerinae and Cecidomyiinae).

Molecular phylogenetics of Mesembrinellidae (Diptera: Oestroidea): intergeneric relationships and implications for the phylogeny of Oestroidea

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Keywords: Mesembrinellidae, Oestroidea, molecular phylogenetics

The Mesembrinellidae (Diptera: Oestroidea) comprises a small group of calyptratae flies exclusively Neotropical in distribution. Historically it has been considered as a subfamily of the Calliphoridae. More recently, however, the calliphorids have been shown to be polyphyletic, with different sources of morphological and molecular data pointing to the mesembrinellids as a separate lineage more closely related to the tachinids. Some species of Mesembrinellidae have been recently included in broader molecular phylogenetic analyses, but the relationships between the species and genera are poorly understood.

Most certainly at least one genus is paraphyletic. In this study, 20 of the 34 known mesembrinellid species have been sampled for a molecular phylogenetic analysis of the family, belonging to the genera *Mesembrinella*, *Eumesembrinella*, *Laneella*, *Giovanella*, *Souzalopesiella* and *Huascaromusca*. Species of Calliphoridae, Tachinidae, Rhiniidae, Sarcophagidae, Oestridae, Muscidae, Fanniidae and Hippoboscidae were used as outgroups. The study used sequences of COI, 16S, 28S and ITS2 regions. The paraphyly of *Mesembrinella*, suggested in previous morphological analysis, is being studied and will be better evaluated with additional data. Some insights on the position of the Mesembrinellidae within the Oestroidea are provided, with implications for the interpretation of the evolution of viviparity in the group.

Culicomorpha [poster]

How climate change might influence the geographic distribution of vectors (Culicidae) of tropical diseases?

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Keywords: Diversity, new habitats, adaptation, Neotropical

Factors related to the climate and environment are known to be important in the population dynamics of insects, including those classified as vectors, since they directly modulate the lifetime, the reproductive rate, and in particular for Culicidae, the frequency in the deposition of eggs. Mosquitoes of the family Culicidae (Diptera: Nematocera) are holometabolous and many are dependent on water to complete their development in the immature stage. They are among the arthropods that most affect human health to be associated with transmission of various diseases such as malaria, dengue, yellow fever and other arboviruses. Changes in rainfall patterns, the average temperature and rainfall recorded in the last 100 years in Brazil provides an alarming picture of increased abundance and diversity of species of Culicidae, and behavioral changes in the process of occupation of new habitats. As a consequence it has been noted for dengue the intensification of vector activity and expansion of endemic areas during the transmission of diseases. In a review of the literature and from insects collected in field in the South of Brazil we observed an increase in mosquitoes diversity from 74 in 2003 to 96 current species, and this fact is linked, only in part, to increased sampling effort. Anthropogenic changes in the environment also provided part of the change in behavior of the insects. However, the increase in temperature and precipitation (0.3 degrees and 264.4 mm, respectively, from the 60s until now) make clear that these factors were more preponderant in wide distribution observed for *Aedes aegypti* and *Aedes albopictus,* the second first recorded in Brazil in 1986. Projections on the distribution of insects associated with environmental and anthropogenic factors, such as we are conducting in this study, become important to quantify the risks caused by contact with man and vector, in time and space.

Plenary talk

Dipteran diversity through a different lens: digital photography and the democratization of dipterology

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Keywords: Digital photography, democratization, identification, taxonomy, Micropezidae

Although digital macrophotography has only been practical and affordable for around a decade, it has already had an enormous impact on dipterology, especially Diptera taxonomy. Efficient image capture shortens workflows and enhances publications, allowing the distribution of biological and taxonomic information that would previously have been impractical to publish. Growing access to online type photos, images of identified specimens, and growing public libraries of identified living flies further speeds the workflow for professionals, while also enabling and encouraging wider community involvement. This expanding public access, which amounts to a “democratization” of information previously available only to specialists, brings with it challenges and opportunities for professional dipterists. Among the challenges is the need to overcome the taxonomic impediments to public access; among the opportunities is the potential to work with the huge amateur community to improve our knowledge of flies. In both cases, digital images are the key.

This opening up of biodiversity science is a major revolution that dipterists should not only embrace, but also lead. Our community has already shown the way with authoritative yet widely accessible materials such as open access online catalogs and richly illustrated print manuals that set the standard for regional faunal treatments. We now have the opportunity to stay ahead of the curve by rendering flies identifiable and understandable to anyone and everyone. I will illustrate some of the ways that digital photography is driving this “democratization of dipterology”.

A preliminary study of forensically important necrophagous Diptera in Riyadh, Saudi Arabia

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Keywords: Necrophagous flies, carrion, decomposition

This is the first report of an ongoing study of necrophagous flies and their succession on carrion carried out in Riyadh, Saudi Arabia, using rabbit as experimental model. During this period, necrophagous flies belonging to the following families were collected: Calliphoridae (such as *Chrysomya albiceps, Chrysomya megacephala*), Muscidae (such as *Musca domestica*), Sarcophagidae (such as *Wohlfahrtia nuba*). The most important species in respect to abundance and frequency were *Chrysomya albiceps*.

Four decomposition stages were observed (fresh, bloated, decay and dry remains). During the fresh stage, the first insects that appeared were flies of the families Muscidae, Sarcophagidae. During the bloated period, species of Calliphoridae were predominant and the first to oviposit. During decay stage, the most abundant families were Calliphoridae and Muscidae. During the last stage (dry remains), no adult flies were appeared.

Evaluation of larval secretions of two blowflies species (Calliphoridae) in inhibiting the growth of pathogenic bacteria

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Keywords: Larval therapy, treatment, maggots

Larval therapy (LT) is an alternative for the treatment of poorly healing lesions because of its easy applicability and efficiency. During LT, a marked antimicrobial activity has been reported in the literature. However, the actual mechanisms involved in this process are still unclear. This study aimed to evaluate *in vitro* inhibition of bacterial growth of *Pseudomonas aeruginosa* in contact with the secretions from larvae of *Chrysomya megacephala* and *Lucilia eximia* (Calliphoridae). Fly eggs were disinfected in 1% NaClO solution for 3 min and transferred to sterile blood agar. Two experimental groups with the first larval instar were assembled: [Lm] 60 macerated larvae + 60 µL of *P. aeruginosa* concentrate (*Pa*C); [Li] 60 intact larvae + 60µL of *Pa*C. Three control groups were used: [C1] 60 macerated larvae; [C2] 60 intact larvae; [C3] 60 µL of *Pa*C. Centrifugation (4000rpm/8min) of intact larvae in 600µL of sterile water was used to stimulate the release of secretions. Sowings at the times 0, 10, 20, 30 and 60 min were made in BHI agar. After 24h, *Staphylococcus* sp. (negative coagulase), *Bacillus* sp. and yeasts were isolated from C1, while Gram positive cocci, *Streptococcus* sp. and *Bacillus* sp. were found in C2. In the [Lm] group, the same bacteria associated with its control (C1) were isolated, and in the sowing of 60 min, we observed Gram positive cocci and *Proteus* sp. In [Li] group, Gram positive cocci and *P. aeruginosa* were isolated after 30 min of contact with the secretion. The growth of *P. aeruginosa* showed a significant decrease. The growth of *P. aeruginosa* was inhibited in the [Lm] group. Currently, due to the resistance of microorganisms to antibiotics, further research is necessary in order to investigate the process of growth inhibition of pathogenic bacteria.

Biogeography of the tribe Aphrosylini (Diptera: Dolichopodidae)

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Keywords: Dolichopodidae, Aphrosylini, global diversity, biogeography, shoreline

Dolichopodid flies have their greatest diversity near fresh water, but species of the tribe Aphrosylini in the subfamily Hydrophorinae live on rocky, coral, or sandy seashores. This group contains 13 genera and 107 described species that are generally found on sea coasts of the temperate and tropical regions of the world. Because these marine-shore dolichopodids are confined to linear habitats, the distributional ranges of species of this group, including many short range endemics, can easily be represented as lines, instead of polygons (areas) as is the case in non-riparian species. This property is one of the exceptional merits of this group for studying biogeography. As they also inhabit islands, patterns of dispersal and endemism within archipelagoes are also of interest. As part of a broad-scale inquiry about the origin of marine-shore dolichopodid flies, I have conducted surveys of these flies on continental and island seashores around the world, classified the collected specimens, and analyzed their phylogenetic relationships using morphological data and DNA sequence data. In this study, I compare the geographical distributions of 11 genera and 53 species in Aphrosylini with their gene-based phylogenetic tree, using the freshwater-dwelling genera *Diostracus* and *Liancalus* as outgroups, and also discuss the pattern of speciation and the process of dispersal in this tribe. Based on my recent surveys, I also report on the fauna of these flies in the Neotropics, where shoreline dolichopodids have been rarely studied.

The use and usefulness of unique specimen identifiers from a museum perspective

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Keywords: Unique identifiers, museums, legislation, mass-digitisation

Unique identifiers (UIDs) for specimens are essential in this day and age as both a research and a collections management tool. From registering the specimen to monitoring its movement, both within the museum and whilst being sent out on loan, UIDs enable us to track the specimen, and users to discover any history and applicable collecting permits.

This is essential in a time when Access and Benefit Sharing legislations are in force and the upcoming predicted ratification of the Nagoya Protocol will affect the current and future use of the specimens. As well as for legal requirements we can ensure that specimens used for research are locatable. Our collections have been data-mined for years for biological recording Schemes but very few people have added UIDs to the specimens.

The NHM has an exceptionally large collection and at the moment very little of this has UIDs. The Diptera section has many of the types specimen-level databased (SLD) with UIDs but there have been many historical problems with these which will be discussed in the talk. The problems of adding UIDs to the collection, the use of barcodes rather than numbers, and mass digitisation projects will also be discussed.

Acalyptratae

The Drosophilidae of New Guinea

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Keywords: Drosophilidae, New Guinea, taxonomy

The drosophilid fauna of southeast Asia, Hawaii, islands of the South Pacific and northern Australia has been relatively accessible to dipterists for more than a century and the number of described species from these regions reflects this long history. At the biogeographic centre lies the relatively unexplored tropical wilderness of New Guinea – before 1977 only 29 described species were listed (Okada, 1977). This jumped to 76 in 1981 and then to ca. 130 by the mid 1980s. The current tally is 245 described species in 30 genera (Brake & Bächli, 2008). Three drosophilid collecting expeditions to eastern (2003), central (2009) and western (2013) New Guinea have yielded more than 100 undescribed species and some possible new genera. These collections together with the results of the IBISCA 2013 Mt Wilhelm Malaise surveys (yielding ca. 180+ spp. to date) confirm the biogeographically central position of New Guinea. Some of the genera that were considered rare and endemic to Australia are common and diverse in New Guinea (*Bialba, Poliocephala, Tambourella, Mulgravea*). Species possibly belonging to *Balara, Baeodrosophila, Collessia* and *Crincosia* are also present. Like in Australia, the most diverse genus is *Scaptodrosophila.* A number of species are present only at certain altitudes. Large numbers of species collected from flowers or fungus are absent in Malaise traps. The rich fauna of New Guinea has most of the genera present in the Oriental and the Australian Regions and therefore harbours the most diverse drosophilid fauna in the world. The Australian-New Guinean tropics (broadly connected during the Last Glacial Maximum at 18 ka) have 40 drosophilid genera, the Oriental Region has 39 genera, the Neotropics 33 and the Afrotropical Region 29. New Guinea, the Australian mainland and islands of the Pacific (the Australian Biogeographic Region) has 47 genera in total.

Plenary talk

Natural history in the 21st century: technological advance allows taxon specialists to be generalists again

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Keywords: Sepsidae, evolution, natural history, behavior, morphology

Many biologists have bemoaned a decline in the study of the natural history of non-model organism. This decline has led to the undesirable situation where we have little “direct knowledge of organisms – what they are, where they live, what they eat, why they behave the way they do, how they die” (Tewksbury et al.: BioScience 64: 300–310). Indeed, modern biology has emphasized the study of model species over the study of species diversity, favors hypothesis testing over discovery, and has higher support thresholds before observations can be published. In my talk I will argue that the latter obstacle can be overcome by technological advance. More data can be collected at a faster pace which allows taxon specialists to become generalists again; i.e., we can simultaneously study the taxonomy, behavior, phylogenetics, morphology, chemical ecology, and genomics of a taxon. I will illustrate this point by giving an overview over the natural history of Sepsidae (Schizophora). Sepsids are known for elaborate mating behaviors (expect rodeo rides, kissing, and perfuming) and exaggerated sexual ornaments including newly evolved abdominal appendages. I will argue that in sepsid taxonomy and behavior, digital photography and videography in combination with online dissemination have allowed for a faster and better documentation of specimens and behavior. In phylogenetics, next-generation-sequencing yielded trees with better support based on data whose collection was outsourced. In morphology, 3D imaging allowed for the simultaneous capture of external and internal morphology. In chemical ecology, new techniques like DART and LDI-MS allowed for the fast study of pheromones of sepsid legs. However, all these technological advances come at a time when the number of taxon specialists is shrinking fast, so that it is unclear whether there will really be a next generation of ‘taxon specialist generalists’.

Revision of the Neotropical genus *Leptopyrgota* Hendel (Diptera, Pyrgotidae)

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Keywords: Pyrgotinae,Pyrgotini,taxonomy

Pyrgotidae has a worldwide distribution with about 365 species in 55 genera. The Neotropical fauna is composed by 58 valid species names into 12 genera. The genus *Leptopyrgota* Hendel, 1914 was erected to included a single species, *L. amplipennis*, from Bolivia. The *Leptopyrgota* are distributed from Mexico to Uruguay. Actually, there are 33 valid species names in the genus. Most of the species were described based in only one specimen. After analysis of the type species of all valid species names, we recognized 22 valid species, proposing 11 new synonyms. The species recognized as valid were redescribed with illustrations of their mainly taxonomic characters. An identification key to the species is also proposed. The limits of the genus are expanded and now the *Leptopyrgota* can be recognized by the following diagnostic characters: ocellar seta absent; antennal groove without longitudinal carina; postscutellum well developed; R2+3 without apical spur vein; R4+5 bare; alula reduced; hind tibia with dorsal concave and oviscape without apical hook.

Pictorial key to the New World genera of Pyrgotidae (Diptera: Tehpritoidea)

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Keywords: Pyrgotinae, Pyrgotini, Teretrurinae, Toxurini

Pyrgotidae is a small family of Tephritoidea composed by 365 species in 55 genera. The New World fauna is actually represented by 66 valid species names distributed in 15 genera. The members of the family are known by their nocturnal habits and to be internal parasitoids of adults Scarabaeidae (Insecta, Coleoptera). Here we present a pictorial identification key to the New World genera of Pyrgotidae. Illustrations of the mainly taxonomic characters as head, thorax, wing, legs and oviscape are shown. This study presents for the first time an identification key to all known genera of Pyrgotidae to the fauna of New World. The genera included in the key are: *Boreothrinax* Steyskal, *Carrerapyrgota* Aczél, *Descoleia* Aczél, *Idiopyrgota* Aczél, *Leptopyrgota* Hendel, *Lopadops* Enderlein, *Neopyrgota* Hendel, *Pyrgota* Wiedemann, *Pyrgotella* Curran, *Pyrgotosoma* Malloch, *Sphecomyiella* Hendel, *Stenopyrgota* Malloch, *Teretrura* Bigot and *Tropidothrinax* Enderlein.

Phylogenetic relationships of *Asiobaccha* Violovitsh (Diptera: Syrphidae)

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Keywords: Syrphidae, taxonomy, phylogeny, DNA

The concept of the genus *Baccha* Fabricius, 1805 has changed enormously since its original description, being restricted to a small group of species with simple unsegmented aedeagus. *Asiobaccha* Violovitsh, 1976 was originally proposed as a subgenus of *Baccha* but posterior authors have related this taxon with other two genera, *Allobaccha* Curran, 1928 and *Episyrphus* Matsumura & Adachi, 1917. The placement and phylogenetic relationships of *Asiobaccha* are explored using molecular evidence. The mitochondrial protein-coding gene cytochrome c oxidase subunit I (COI) and the nuclear 28S and 18S ribosomal RNA genes are analyzed using parsimony, Bayesian inference and maximum likelihood. Molecular results are discussed with the help of relevant morphological characters to understand the placement of *Asiobaccha* within the Syrphinae.

The handbook for identification of British black fungus gnats (Diptera: Sciaroidea: Sciaridae) – a British-German collaboration

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Keywords: Sciaroidea, Sciaridae, Palaearctic region, Europe, identification keys

The revision of the black fungus gnats (Diptera: Sciaridae) of the British Isles is a British-German collaborative project. This was begun because the existing handbook by Paul Freeman (1983) had become outdated, due to a rapid increase in the number of known species. From 101 species recognised in that handbook, the total had already reached 152 in the British Isles checklist published in 1998. The project has been carried out in two stages. The first stage resulted in a publication in 2006 that provided full data for material examined, as well as notes on ecology and distribution. This included 263 species, of which 111 were new to Britain and 32 new to Ireland, and later papers have increased the British Isles total to 267 species, based on examination of more than 15,000 specimens. Since 2006 work has continued on the second stage, which is a new handbook for the identification of British sciarid species, and this is now nearing completion. As the most comprehensive account of European species yet to appear, it will include keys to all Palaearctic genera, subgenera and species groups. The keys to all species known from the British Isles are fully illustrated with diagnostic characters, and will enable identification of all sciarid species that are of economic importance.

Inferring the phylogenetic relationships of early dipteran lineages based on more than 1,000 orthologous genes from transcriptome data

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Keywords: Lower Brachycera, phylogenomics, 1KITE, transcriptomes

Phylogenetic relationships between the earliest evolving lineages of Brachycera are not resolved while there is no doubt that this is a monophyletic group. We present the first results of our phylogenomic analysis using ~2000 orthologous single copy genes (approx. 500 kb of aligned amino acid sites) derived from transcriptome data from the 1KITE project. Using 40 terminal taxa spanning the phylogenetic region of interest, we performed partitioned analyses of our dataset based on protein domains and optimized partitioning schemes to improve modeling during phylogenetic inference. We reduced the amount of missing data by selecting only partitions for phylogenetic inference that have the necessary taxon coverage for the question at hand. Furthermore, we assess whether our primary dataset matches the compositional and time-reversible conditions assumed in phylogenetic inference.

Importance of bibliographical data of the European Empidoidea fauna (Diptera) demonstrated for regional checklists of species in German federal states and for a New Red List of Germany

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Keywords: Bibliography, Empidoidea, Europe, federal state lists, new German Red List, recording-periods

The main objective of this study is to document the current distribution and threat status of the superfamily Empidoidea in Germany, mainly based on locality data derived from European literature from 1800 to 2012/2013. Records from 1951 onwards are classified as current; records prior to 1950, as extinct or lost. The threat status of terrestrial Empidoidea is classified from records in single German federal states. Currently 1,103 species of Empidoidea occur in Germany. More than 450 species are recorded from Bavaria (711), Thuringia (678), Schleswig-Holstein & Hamburg (592), Saxony-Anhalt (546), Brandenburg and Berlin (482) and Hesse (475). High percentages of older records (up to 1950) are characteristic for the fauna in Bavaria (188: 26.4%), Brandenburg and Berlin (175: 36.3%), Mecklenburg-Western Pomerania (160: 41.7%), Saxony (105: 34.8%) and Baden-Württemberg (101: 23.9%). A total of 986 Empidoidea species with terrestrial larvae are assigned to the German Red List categories 0 "Extinct or lost" 123 species (12.5%), 1 "critically endangered" 87 (8.8%), 2 "endangered" 224 (22.7%), 3 "vulnerable" 278 (28.2%) and G "unknown" 11 (1.1%). Altogether 600 species (60.9%) are threatened, 263 species (26.7%) are currently not threatened. An intensive study of European literature, and evaluation of records of species in different time slots, enabled a comprehensive documentation of both a federal states inventory of species and an evaluation of the threat status of the Empidoidea in Germany.

Comparison of wing venation of five species of *Dasysyrphus* including recently described *D. neovenustus*

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Keywords: *Dasysyrphus*, taxonomy, Syrphidae, wing venation

The species of *Dasysyrphus* Enderlein, 1938 are widely distributed, mainly in the Holarctic region. To date 44 are known, 13 of which occur in Europe. The known *Dasysyrphus* larvae are predators of aphids and other small soft-bodied insects. The species of the *D*. *venustus* group, which include five known from Europe, are highly variable and can be difficult to distinguish. In particular, the species of the *venustus-hilaris* complex are problematic in their identification. Some previous studies have indicated a very high morphological and genetic variability of *D*. *venustus*, suggesting that it is a complex of species.

Nearly all the specimens of *Dasysyrphus* were collected in Poland. 89 male and 83 female specimens were used in the analysis of wing venation. Representing five species: *D*. *hilaris*, *D*. *neovenustus D*. *pauxillus*, *D*. *pinastri* and *D.venustus* The wings were dissected and mounted in glass photographic frames. In every wing image the coordinates of 13 vein junctions were determined. The obtained data were analyzed using methods of geometric morphometrics.

Wings measurements confirmed that the *D. neovenustus* is distinct from other species, and is most similar to *D*. *venustus*. The wing measurements also revealed that *D*. *hilaris* and *D*. *venustus* are very similar and that they cannot be distinguished using wing measurements alone. The percent of correctly identified (with cross-validation) individuals was: *D. neovenustus* (86.8% male, 80.95% female), *D. venustus* (62.1% male, 74.07 female), *D. hilaris* (25% male, 60% female), *D. pauxillus* (85.7% male, 100% female), *D. pinastri* (100% male).

Identification of hoverflies of the genus *Eristalis* based on the wing venation

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Keywords: *Eristalis*, Syrphidae, taxonomy, wing venation

Eristalis Latreille*,* 1804 are relatively big, bee and bumblebee like hover flies. In Europe 21 species are known. The known *Eristalis* larvae are aquatic or subaquatic and saprophagous. Some species of *Eristalis* are highly variable and can be difficult to distinguish, especially by non-specialist. The aim of this study was to develop semiautomatic method of the species identification. The method was based on measurements of wing venation.

The wings were dissected and their images were obtained using photographic scanner. In every wing image coordinates of 13 vein junctions were determined. The obtained data were analysed using methods of geometric morphometrics. The identification was based on Discriminant Function Analysis and average shape of the left and the right wing. There were significant differences between sexes in wing venation, therefore, males and females were analysed separately. Some species were represented by only one sex.

The percent of correctly identified (with cross-validation) individuals was: *E. abusiva* (100% male), *E. arbustorum* (83.33% male, 100% female), *E. intricaria* (83.33% male), *Eristalis obscura* (90% male), *Eristalis oestracea* (100% female), *E. pertinax* (95.16% male, 100% female), *E. picea* (100% male), *E. rupium* (83.33% male, 84.21% female), *E. similis* (100% male, 83.33% female), *E. tenax* (100% male, 98.94% female). The Unweighted Pair Group Method with Arithmetic Mean clustering revealed three distinct groups of species. The first group consisted of *E. abusiva* and *E. arbustorum* the second group consisted species of the "*rupium*" group, and the third group consisted of *E. pertinax*, *E. similis*, *E. tenax*.

Drosophila (Diptera: Drosophilidae) species of the northeastern North America

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Keywords: *Drosophila*, Drosophilidae, Nearctic

The iconic genus *Drosophila* Fallén has been extensively studied because of its centrality to research programs in genetics and evolutionary biology. The genus has recently attracted further attention because of the economic importance of the invasive species *Drosophila suzukii* Matsumura. Despite this, there remain surprising gaps in our basic knowledge of the faunistics and distribution of the Nearctic *Drosophila* species, and there is no current and user-friendly key. Approximately 35 of the 135 recorded Nearctic *Drosophila* species occur in northeastern North America. We here report on a review of the northeastern North American species of the genus based on the examination of over 10 000 specimens from the Canadian National Collection of Arthropods, Ottawa ON, Canada (CNC), The University of Guelph Insect Collection, Guelph ON, Canada (DEBU), The American Museum of Natural History, New York City, NY, USA (AMNH) and The National Museum of Natural History, Washington, DC, USA (USNM).

Results so far suggest that the fauna is larger than expected and that region is home to new and previously unrecorded species of this well-known genus. These species will be included in a new interactive, open access, digital key to the *Drosophila* species of northeastern North America.

Taxonomic revision of the Neotropical fly genus *Sciogriphoneura* Malloch, 1933 (Diptera: Helosciomyzidae), with description of a new species

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Keywords: Taxonomy, *Sciogriphoneura*, Helosciomyzidae, Neotropical

Helosciomyzidae is a small group of flies comprised by 23 species in nine genera, distributed in Australia, New Zealand, Tasmania, Chile and Brazil. According to Barnes (1981), *Sciogriphoneura* Malloch can be distinguished from the other genera of the family by the following characters: dorsocentral setae in four pairs; scutellum convex; costal spinules in one dorsal and one anterior row; veins R_5 and M strongly convergent or fused apically, all characters confirmed in this study. *Sciogriphoneura* is the only Neotropical genus of this family and consists of two species, *Sciogriphoneura brunnea* Steyskall, distributed in Southeast Brazil, and *Sciogriphoneura nigriventris* Malloch that occurs in Chile. This study aimed to do a taxonomic revision of this genus by a comparative morphological study of the body and genitalia of specimens deposited at the Diptera Collection of the Museu de Zoologia da Universidade de São Paulo (MZUSP). The two previously known species were redescribed and a new species (*Sciogriphoneura* sp. n. also distributed in Southeast Brazil) is being described. *S. nigriventris* can be easily characterized by the presence of a dark brown band between postpronotal lobe and wing base, which is lacking in *S. brunnea*. On the other hand, *S.* sp. n. can be distinguished by the presence of a brown color surrounding all thoracic setae, characteristic also absent in *S. brunnea*. Furthermore, the distribution of *S. brunnea* is expanded, as new specimens were recently sampled. In addition to the redescriptions and description, a distributional map and an identification key to the three species are also provided.

Cladistic analysis of Mesembrinellinae (Diptera: Calliphoridae)

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Keywords: Calliphoridae, Mesembrinellinae, cladistic, Neotropical

Mesembrinellinae is an exclusively Neotropical subfamily of Calliphoridae, which includes 36 described species in nine genera. Members of this group are restricted to tropical rainforests and found from Mexico to Northern Argentina. The placement of this subfamily within Oestroidea has generated frequent discussions in the literature, as some authors have suggested the subfamily merits full family status. In addition, the intraspecific relationships of this group remain unclear and some genera appear not to be monophyletic. In this study, all 36 Mesembrinellinae species are sampled as the ingroup, and 26 representatives of the other Calliphoridae subfamilies as well as individuals of Tachinidae, Sarcophagidae, Oestridae, Rhinophoridae, Muscidae and Fanniidae families, as the outgroup. So far, 100 characters were constructed based on a comparative study of morphological structures, including the genitalia, of adult pinned specimens. A preliminary analysis was conducted and resulted in 10 equal parsimonious trees (strict consensus: L=535, Ci=22 and Ri=65). The results indicates that the Mesembrinellinae is a monophyletic group supported by five synapomorphies (interfrontals present in females; posterior spiracle reiniform, with a single lappet; anterior spiracle with dorsal opening teardrop shaped; and female sternite 8 reduced), having *Phumosia promittens* (subfamily Phumosiinae) as its sister group. The genera *Eumesembrinella, Laneella* and *Giovanella* were supported as monophyletic, with *Huascaromusca* being the sister group of *Eumesembrinella* and *Thompsoniella* the sister group of *Giovanella*. However, *Huascaromusca* was paraphyletic by the presence of *Mesembrinella xanthorrhina* inside the clade. Furthermore, *Mesembrinella* was recovered as polyphyletic, but some species formed small monophyletic clades. This indicates that the classification of *Mesembrinella* must be revised. The results will contribute to better understand the relationships of Mesembrinellinae species, its classification and its placement inside Oestroidea.

Syrphoidea [poster]

Taxonomy of *Argentinomyia* Lynch Arribálzaga, 1891 (Diptera: Syrphidae: Syrphinae: Bacchini) from South America

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Keywords: Bacchini, systematic, new species

The genus *Argentinomyia* Lynch Arribálzaga, 1891 (Syrphidae: Syrphinae: Bacchini) is a specious Neotropical genus with 30 species described to date. The genus is recognized by elongated antenna, with scape much longer than wider, basoflagellomere usually elongated; female frons with a pollinose pattern; face generally with transverse grooves, sometimes broadly punctuate and with iridescent reflections; male genitalia with surstyle generally widened and apically irregular. The genus is taxonomically revised and twenty-seven species are redescribed based on type-material, and about 800 non-type specimens. Eight new species are described. The species *Argentinomyia berthae* Lima, 1946 is found again since its description and a neotype is designated. Lectotypes are designated for *Argentinomyia columbiana* and *A. thiemei*. A key to all species is provided. Detailed distributional data with new geographical records, notes on the biology of some species, as well as photographs and genitalia illustrations are included to assist the identification. A cladistic analysis of 43 terminal species (14 outgroups, 29 ingroup species) and 70 adult morphological characters produced two most parsimonious cladograms (length = 120 steps, consistency index = 65, retention index = 90). According to the resulting hypotheses, this study also discusses the biogeographic patterns of *Argentinomyia* in a phylogenetic context.

Revision of the Neotropical genus *Talahua* Fluke, 1945 (Diptera: Syrphidae) with the description of three new species

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Keywords: Flower flies, generic diagnose, new species

Talahua Fluke, 1945 (Diptera: Syrphidae: Bacchini) is a small Neotropical genus of Flower Flies, previously known by two species from Ecuador and Colombia. The genus is recognized by a large face without transversal grooves; metacoxa pilose posteromedially on apical angle; scutellum with a deep groove next to the apical rim; abdomen generally broad, with large maculae, and male genitalia with surstyle and cerci elongated. The genus is re-diagnosed, including re-description of *T. fervida* and description of three new species. A key to species, illustrations of male genitalia and habitus imagines are also provided. The new distributional records as well as the discovery of the new species in Mexico and Costa Rica, extends the genus distribution to the Northern Central America.

The flower flies of the Andes: Effects of global warm on patterns of distribution and the conservation of their biodiversity based on predictive models

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Keywords: Flower flies, Andes distribution, fauna conservation

The Andes comprise more than 30% of South American landmass. These continental islands are characterized by an astounding diversity of microhabitats and extreme environmental conditions favorable for the establishment of a unique combination of taxonomic linages. The geographical barriers among the three highland masses have led to the isolation, radiation and have promoted the adaptation of an incalculable number of species, turning them into the main biogeographic area of endemism in the World. Spite of the importance of these hot spots, in the last decades, human alteration and global warm have emerged as a critical threat to the biodiversity in these areas. As a consequence, an important number of species are endangered or becoming extinct in an unexpected and unknown rate. These constitute an important attribute that promote, as priority, the study and conservation of their fauna and flora.

From this perspective, the biogeographical patterns of the Andean Syrphidae genera *Macrometopia* Philippi, *Meropidia* Hippa & Thompson, *Orphnabaccha* Hull, *Talahua* Fluke, *Tropidia* Meigen and *Tuberculanostoma* Fluke were studied by track analysis. Generalized tracks were determined when individual tracks were congruent among them. The intersection between two or more generalized tracks was considered as potential biogeographical nodes or endemic areas. A modelling of distribution was also created using maximum entropy ecological niche in MAXENT. According to the resulting maps, the distributional patterns and the potential effects of climatic changes in Andean Syrphidae populations is discussed as a baseline to understand and to identify priority areas and habitats for conservation within the tropical Andes.

Aphidophagous flower flies (Diptera: Syrphidae) as agents for biological control in Brazil

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Keywords: *Allograpta,* Neotropical region, predators, Syrphinae, *Toxomerus*

There are many species of Syrphidae which could be important to the biological control of pests, but little is known about their behavior, especially in the Neotropical region. Most of Syrphidae predators are placed within the Syrphinae and their most common preys are species of Hemiptera, mainly aphids. In Brazil, few studies have been conducted on the activity of predatory species of Syrphinae. Moreover, some of these studies showed the importance of several Syrphidae species on biological pest control based only on the survey of adults, regardless the presence of immature stages in the crops. Therefore, this study aimed to contrast the diversity of adult syrphids collected with Malaise trap, with the diversity of the immature stages collected in an organic crop of *Brassica oleracea* var. *acephala*. The experiment was conducted from August to October 2013, in Lavras (21°13'51.5"S 44°58'35.9"W), Brazil, in a crop of 10X20 plants, and maintenance of surrounding spontaneous plants. A Malaise trap was placed two meters from the crop edge for adult collection; and at every harvest, all harvested leaves were inspected for immatures. A total of 1305 adult syrphids belonging to seven genera were collected; *Toxomerus* was the most abundant (1107). From the harvested leaves 62 immature syrphids were collected, from which three adults of *Allograpta exotica* and three of *Toxomerus dispar* emerged; thirty pupae were parasitized by *Diplazon laetatorius* and nine by *Syrphophagus* sp. The number of adult syrphids collected with the Malaise trap, related to the number of immatures, indicates the importance of keeping spontaneous plants for insect attractiveness. However, it is clear that not all adults of Syrphidae flying nearby the crop might play a role in aphid predation. To know which species can be useful for biological pest control, studies on the biology and behavior of the immatures must be developed.

A phylogenetic analysis of Eristalini sensu lato (Diptera: Syrphidae) based on combined morphological and molecular characters

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Keywords: Flower flies, cladistic analysis, Eristalinae

Syrphidae is traditionally divided into three subfamilies: Eristalinae, Syrphinae and Microdontine. Eristalinae currently comprises about 3000 described species in 114 genera, which is half of the known species diversity in the family. Among recognized tribes of Eristalinae, Eristalini sensu lato – including Sericomyina as subtribe – is the second largest regarding number of genera (32), with ca. 820 described species and with a worldwide distribution. In this study, phylogenetic analyses were carried out to infer the relationships among genera which were originally part of Eristalini sensu lato. The phylogenetic relationships were investigated based on combined analyses of morphological and molecular characters of the mitochondrial COI and nuclear 28S rRNA sequences. The ingroup comprised 93 taxa of Eristalini sensu lato, totalling 22 genera. The outgoup taxa comprised eleven taxa belonging to other Eristalinae tribes and one taxon belonging to Microdontinae. The trees were rooted between *Peradon bidens* (Microdontinae) and the remaining taxa. A preliminary analysis was carried out under the parsimony criterion. The results corroborated the monophyly of Eristalini sensu stricto, not including the Sericomyina taxa. 'Sericomyina' was also recovered as a monophyletic group, but not as sister to Eristalini sensu stricto. The present subtribal classification within Eristalini is not supported. The Eristalini subtribal classification is discussed in light of these results.

Modelling carcass visitation by sarcosaprophagous Diptera: a comparative analysis in temperate and tropical areas

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Keywords: Accumulated degree days, computer modelling, heterotrophic succession, *postmortem* interval

Despite an urgent need of validation methods in courtroom proceedings and significant progress in the development of computer modelling tools to examine the succession of carrion-related insects on carcasses, succession-based entomological estimates of the *postmortem* interval (PMI) are still largely calculated by hand. This presentation reviews the succession-based statistical models of PMI estimation, with particular emphasis on emerging new models, and uses data from studies conducted on pig carcasses in Canada and the Philippines to model and compare carcass colonization and visitation by sarcosaprophagous Diptera. Results indicate that the occurrence, diversity, and role of larval and adult Diptera during carcass decomposition differed considerably between the temperate and tropical settings. Nevertheless, in both settings, generalized linear models based on accumulated degree days performed well, efficiently identified habitat-related differences, and generated combined odds that permitted the development of probability-based PMI estimations. The performance of these models and other models of PMI estimation in terms of training carcasses, variability explained, capacity to deal with reoccurring species, statistical adequacy, and ecological realism will be discussed.

Spatio-temporal dynamics and preference for type of bait in native and introduced blowflies (Diptera: Calliphoridae)

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Keywords: Necrophagous insects, *Chrysomya albiceps, Chrysomya megacephala, Lucilia eximia*, population dynamics

We performed a year-long survey of blowflies (Diptera: Calliphoridae), using carrion-baited traps (fish, beef liver, or chicken gizzards) in the municipality of Campinas and five adjacent municipalities with diverse urbanization profiles in the state of São Paulo, Brazil. The collections were carried out in rural, urban, and forest environments. Our objectives were to study the spatio-temporal variability and preferences for type of bait of three calliphorid species that are forensically and medically important in Brazil: *Chrysomya albiceps* (Wiedemann), *Chrysomya megacephala* (F.) and *Lucilia eximia* (Wiedemann).

Chrysomya albiceps and *C. megacephala* originated in the Old World tropics and were introduced into Brazil in 1975–1976, with the large influx of Angolan refugees. *Lucilia eximia* is a Nearctic and Neotropical species that is commonly found in rural and urban areas. The definitive establishment of species of *Chrysomya* in Brazil affected the dynamics of the native blowfly populations, which is an important factor in the assessment of demographic aspects of biological invasions. All three species preferred chicken. *Chrysomya albiceps* and *L. eximia* preferred the urban environment, while *C. megacephala* preferred the rural environment. No clear seasonal patterns could be recognized for the three species. The associations of species/municipality, species/environment and species/bait will be discussed from the ecological and forensic standpoints.

A novel kind of mating trophallaxis behavior (nuptial feeding) in Diptera, as demonstrated by *Ceroxys urticae* (L.) (Ulidiidae)

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Keywords: Mating trophallaxis, nuptial feeding, Ulidiidae, *Ceroxys urticae*

Mating trophallaxis (MT) is trophallaxis (= transmission of food from one individual to another) between mates, connected to copulation and taking place shortly before, during or after copulation. The origin of the transmitted food may be prey, body secretions or even the body of the mate. The significance of premating trophallaxis is *prima facie* obvious – it increases the chance of mating. On the other hand, what may be the benefit of MT taking place during or after copulation? A variety of these phenomena were previously studied in several species of Tephritoidea.

A unique and novel MT behavior was observed in *Ceroxys urticae*: About half an hour after the termination of copulation, *C. urticae* females secrete a substance from the ovipositor and feed on it. My observations show that this substance originates in the male who transmits it to the female during copulation. The phenomenon of *C. urticae* females to feed on this secreted substance raises questions about its nutritional value and its contribution to the fitness of the female and\or her progeny. In the lecture I will give a detailed description of this MT behavior and compare it to similar cases.

Biodiversity richness and water quality in natural and constructed wetlands: what can Sciomyzids tell us?

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Keywords: Constructed wetlands, natural wetlands, Sciomyzidae

Often built for municipal and agricultural wastewater treatment, constructed wetlands (CWs) aim to reduce the effects of organic pollution entering rivers and streams by acting as a polishing stage after conventional treatment. Natural wetlands are considered as some of the most ecologically and economically important habitats worldwide. However, despite the continued global loss of natural wetlands, the design of CWs primarily focuses on nutrient reduction with little reference to their role in the maintenance/enhancement of biodiversity, about which little is currently known.

This research focuses on comparing the biodiversity of constructed and natural wetlands by providing research-based evidence to promote biodiversity in CWs while enhancing their wastewater treatment capabilities.

CW and natural wetlands, similar in terms of dominant plant species composition, were selected within the Western River Basin District (Ireland). The use of sciomyzid flies (Diptera: Sciomyzidae), as indicators of wetland biodiversity, is investigated. Aerial invertebrates were sampled using a malaise trap placed at each site and sciomyzid flies (Diptera: Sciomyzidae) were identified to species level. Wetland performance was investigated: water samples were collected at the inflow and outflow of all sites and analysed for total nitrogen and total phosphorus in addition to biological and chemical oxygen demand and total suspended solids.

Preliminary results comparing sciomyzid species composition at natural and constructed wetlands in the context of plant species composition and water quality are presented. The data which will determine the efficacy of using sciomyzids as bioindicators of wetland biodiversity will also provide an essential tool in the future design and management of wetlands on an international scale.

Tephritoidea [poster]

Long term monitoring of the temporal abundance of *Bactrocera invadens* (Diptera: Tephritidae) in Eastern Central Tanzania

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Keywords: Abundance, monitoring, *Bactrocera invadens*, Tanzania

The invasive *Bactrocera invadens* is a strong competitor that has been reported to have traits of r-strategists, including heavy population fluctuations over time and space. Most studies were based on short term monitoring, and such observations could have occurred by chance. Here we present the results of a long term monitoring program that quantified the abundance of *B. invadens* in Tanzania and its relationship with meteorological conditions. Abundance patterns of *Bactrocera invadens* were monitored from October 2004 to February 2013 in Morogoro Region, Eastern Central Tanzania. Abundaces were monitored using modified McPhail traps that were hung on trees in the three sub-orchards of the Sokoine University of Agriculture. Two sets of the traps (one baited with protein bait and another with methyl eugenol) were placed on each of mango and citrus sub-orchards and one set of traps in the guava sub-orchard. A total of five replicates were maintained with data collected weekly and abundance of *B. invadens* recorded as the n. of adult flies per trap per week. The abundance of *B. invadens* varied across seasons with high abundances recorded during the rainy, warm periods of the year. Generally, the abundance of *B. invadens* correlated positively with rainfall, relative humidity and temperature. However, at higher temperatures (beyond 32°C) the population of *B. invadens* fell sharply to near zero. In contrast, the population of *B. invadens* seems to stabilise at relative humidity of 75%. Furthermore, the correlation of *B. invadens* abundance with rainfall was positive throughout the studied rainfall range. The population of abundance of *B. invadens* increases with rainfall, temperature and relative humidity, which corresponds to the periods when major fruit hosts are available. Management programs should thus be initiated at the start of such periods to avoid subsequent crop losses.

Phoomyia, a new genus of Dolichopodinae (Diptera: Dolichopodidae)

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Keywords: Dolichopodidae, *Phoomyia*, Oriental region, taxonomy

The recently newly described genus *Phoomyia* Naglis & Grootaert, 2013 is presented. It can be distinguished from all other genera of the subfamily by the following combination of characters: body non-metallic; 5th pair of dorsocentral setae offset medially; wing vein M with strong anterior bend; hind basitarsus with one dorsal seta; male cerci strongly reduced. The genus includes actually two species from the Oriental region: *P. srilankensis* Naglis & Brooks, 2013 and *P. thailandensis* Naglis & Grootaert, 2013. Adults of *Phoomyia* are found on sandy coastal beaches often in the burrows of ghost crabs. Differential diagnoses are presented for *Phoomyia* and the closely related genera *Argyrochlamys* Lamb and *Pseudargyrochlamys* Grichanov.

Microtype Tachinids possess thousands of eggs: Do they have any oviposition strategies?

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Keywords: Tachinidae, interspecific competition, microtype, reproductive strategies

Microtype tachinids lay eggs containing a first instar larva on food plants of the host and then the eggs must be ingested by the host for parasitization. As those tachinids have a large number of eggs, people tend to doubt whether they have oviposition/reproductive strategies to enhance a parasitization possibility. We investigated oviposition behaviour of two species of microtype tachinid flies, *Pales pavida* and *Zenillia dolosa*. Responses of two species to odours from maize leaves infested with the parasitoids' common host, the larvae of the noctuid moth *Mythimna separata* were investigated in a wind tunnel. Naive females of *P. pavida* showed a higher rate of landing on *M. separata* infested maize plants than on artificially damaged or intact maize plants, whilst *Z. dolosa* landed on both of the infested and artificially damaged plants with higher rate than on intact maize plants. We also examined which part of an infested maize leaf the flies oviposit. Females of *P. pavida* scattered eggs on the whole part of the leaf, in contrast, *Z. dolosa* concentrated oviposition around an area of host infestation or an artificially damaged spot. The eggs of *P. pavida* laid on maize leaves survived over 10 days, but most of the eggs of *Z. dolosa* died within 5 days. We are going to discuss on a role of Herbivore-induced Plant Volatiles with oviposition behaviour of those microtype tachinid flies.

Tipulomorpha [poster]

The apterous crane fly, *Chionea*, is an under snow crawler (Limoniidae)

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Keywords: Flightless insect, habitat, Shirakami Mountains

Flies of the genus *Chionea* are virtually apterous, the adult of which is often found on the surface of snow during the winter. It is known that adults of *Chionea* are very sensitive to temperature, not only to warmth but also to coldness. They are active at –4 to 0°C, and it is said that they can't live when the air temperature fall lower than –10°C. However, in the habitats of *Chionea,* air temperatures far below the lower limit are frequent. Some authors assumed the existence of shelters, such as gaps in the snow around tree trunks, explain its biology. We had some doubt about the idea that *Chionea* inhabits mainly the snow surface and escapes into cracks when the weather is severe. In order to investigate their habitat, we placed pan traps filled with propylene glycol together with data loggers recording temperature under the snow cover, and collected the specimens every 1 or 2 weeks from November 2013 to April 2014, at Shirakami Mountains, northern Honshu, Japan. In this site, the snow usually amounts to more than two meters high, and *Chionea kanenoi* is present.

Our results confirm that the environment under thick snow cover is stable for the season and suitable for *Chionea* species, and that they are actually active, moving around between the snow cover and the ground. Burrows of wild rodents, such as *Apodemus speciosus*, are supposed to be playing a major role for providing the flies spaces to move.

Discovery of a male only flightless crane fly in Japan (Limoniidae)

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Keywords: Brachypterous, sexual dimorphism, *Hexatoma*, *Eriocera*

An undescribed species of *Hexatoma* (*Eriocera*) was found in Kushidagawa River, Mie Pref., Honshu, Japan. This species is brachypterous and flightless in male, while in female wings are fully developed. Males are entirely flightless, and move around in large number very quickly, like ants do when their nest is disturbed, to seek newly emerged virgin females on sandy river banks. Females are less active runner, and stay on wet sand near water after copulation. They are inactively but still positively capable to fly for a short distance.

Wing reduction in Diptera is often explained in relation to parasitic life cycles, or as adaptations to severe environments (such as oceanic islands, high mountains, boreal habitats, winter season, etc.). In the cases when wings are reduced only in the female, it is usually regarded to save energy and to increase reproduction ability. However, as the present fly was found along a calm river in temperate mainland of Japan at low elevation under 100 m (of course, it is not parasitic), it seems to be not in these cases. Loss of flight ability only in male is very rare. Future investigations on behavior and ecology of this species may provide new information to understand wing reduction in Diptera.

In the presentation, we will demonstrate the peculiarities of morphological and behavioral features of this species.

I.A. Portschinsky – one of the first Russian dipterists

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Keywords: Calyptratae, larvae, Russian dipterist, biography

Iosif Aloizovich Portschinsky (9.02.1848–16.05.1916) was born in the Ukraine. His father was a military medical doctor. Iosif spent his childhood in Central Russia, surrounded by a rather rich nature and fauna. He studied biology at St. Petersburg University. After graduating at university he worked at the Ministry of Agriculture, where he organised the Bureau of Entomology. He traveled a lot throughout Russia and worked as an applied entomologist, studying various pests of agricultural crop plants. His special interest was in the study of the biology and larvae of Diptera, mainly calyptrates, especially those developing in flesh and dung: *Wohlfahrtia*, *Sarcophaga*, *Musca*, *Pyrellia*, *Cynomyia* and others, as well as warble flies. He described Bombyliidae as secondary parasites of Orthoptera. He also worked as a taxonomist in Diptera, describing 10 new genera, 130 new species and 7 new varieties, most of which are still valid today. His type specimens are kept in the Zoological Institute of Russian Academy of Sciences in St. Petersburg. He also described one new species of Orthoptera, two of Lepidoptera, and three of Hymenoptera, and published several faunistic lists of Diptera. Worthy of notice are his papers on mimicry in flies and Lepidoptera. Iosif Aloizovich was an pioneer of cultural entomology. He studied drawings of insects on Egyptian monuments and antiques, popular beliefs and superstitions associated with insects. He worked closely with the Russian Entomological Society, founded in 1861. He was a very active member of the Society from 1872, was its scientific secretary and librarian from 1874 until 1895 and was elected Vice-President in 1896. Together with F.N. Keppen and S.M. Solsky, he wrote the Catalogue of the Library and two additions to the Catalogue (1873–1877). His list of publications contains 124 scientific papers.

The seasonal activity of the genus *Forcipomyia* (Diptera: Ceratopogonidae) in the Italian Alps

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Keywords: *Forcipomyia*, Italy, biodiversity, Alps, Ceratopogonidae

Ceratopogonidae were collected from May to October 2005 at different altitudes between 930 to 2,013 m, in Stilfer Joch National Park, Italy using Malaise traps. A total of 1,000 specimens belonging to twenty-one species of the genus *Forcipomyia* Meigen (Diptera: Ceratopogonidae) from seven subgenera were identified.

This study has expanded the current knowledge of the genus *Forcipomyia* of Italy and has brout to light the presence of five subgenera and 17 species recorded for the first rime. The results are significant in faunistic terms and for understanding the seasonal activity of each species.

A comparison of robber fly (Diptera: Asilidae) communities found in native and non-native plant associations in the Great Basin of western North America

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Keywords: Asilidae, biodiversity

We inventoried robber fly composition (Diptera: Asilidae) at three sites in the eastern Great Basin of western North America. Plant communities in these vast habitats often consist of Utah juniper woodland, sagebrush shrubland, cheatgrass grassland, and crested wheatgrass grassland. Juniper woodland and sagebrush shrubland are native associations in the region while cheatgrass grassland is a more annually timed invasive community that often establishes after fire or severe grazing pressure. Crested wheatgrass, a non-native bunchgrass is often planted in disturbed sites (after fire or severe grazing) to stabilize the abiotic habitat and allow reestablishment of more native biotic associations as a bridge species. We sampled these four communities where they were contiguous in three widely separated locations using malaise traps evenly arranged across the sample area. A total of 2,438 robber flies were collected from the traps over the course of two years. We identified the asilids as belonging to 24 genera and 58 species. Composition was significantly different between all habitat types with the greatest diversity occurring in juniper woodlands, followed by sagebrush, cheatgrass, and crested wheatgrass. Thus the native woody communities were richer than the non-native grasslands. The conversion of native habitats to cheatgrass favors robber flies in the genus *Dicropaltum* but that preference is not found in the superficially similar grassland community dominated by crested wheatgrass. Other patterns in the robber fly communities will be explored as well. The enhanced richness and abundance of robber flies in native juniper woodlands and sagebrush shrubland compared to the two exotic grassland systems sheds light on their contribution towards regional biodiversity in this faunal group overlooked by land managers and researchers.

Cuticular muscle attachment sites in forensically important blowflies

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Keywords: Muscle attachment sites (MAS), species determination, *Lucilia*, PMI

One essential task of forensic entomology is minimum post-mortem interval (PMI) calculation based on insects and their larvae collected from the body found at a crime scene. Blowflies are among the first colonizers, the age of their larvae therefore correlates closely to the PMI. Interspecific morphological similarity of the larvae and differences in growth rate make species determination an essential prerequisite for an exact PMI calculation.

As we showed earlier, muscle attachment site (MAS) patterns can be used for species identification as well as age estimation in forensically important dipteran larvae. Species determination in genus *Lucilia* has proven to be difficult even when employing genetic methods due to the relatively recent divergence of the species such as *Lucilia caesar* and *L. illustris*.

We compared MAS patterns of three frontal segments in six *Lucilia* species and found three levels of differences in the patterns which can be grouped in obvious, intermediate and subtle differences. A walk-through keylist helps determine the species even in difficult cases.

As in previous studies, only segments 2–4 were analyzed to find differences. For further studies it might be necessary to analyze all available segments, as was already conducted in a MAS study of boneskipper flies.

Neotropical Tachinidae: where are we and where are we going to?

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Keywords: Neotropical region, Tachinidae, taxonomy, systematics

Tachinidae is a large family with 9,899 species worldwide. In Neotropical region, the number of described taxa considered is that one provided in the outdated catalogue of Guimarães and stands at 2,864 species, 944 genera. Neotropics bear the highest diversity compared with other regions: Afrotropical 1,006 species – 228 genera; Australasia 850 – 228; Nearctic 1,345 – 303; Oriental 725 – 259; and Palaearctic 1,600 – 409 (World 9,899 – 1,517). The number of Neotropical species is down-estimated. First, because after 40 years species number should be over 3,000, and second, the actual size of family is much larger as some regions (Neotropical, Afrotropical, Oriental and Australasian) contain high number of undescribed species. As for genera, Neotropical numbers are certainly over-estimated and artifactual. Most genera are monotypic and described by Charles Townsend during six decades of intense and prolific activity, when he described 1,491 genera, 1,555 species, the great majority in Tachinidae. This means that revising tribes or genera is the same as revising all the species. Add to that, the lack of identification keys to tribes or genera, lack of sufficient number of local experts, outdated catalogue, and underrepresented collections, and, the result is the Neotropical Tachinidae as a real and extreme example of taxonomic impediment. However, some progress has been done in the last century with revisionary works by Curran, Aldrich, Reinhard, Sabrosky, Arnaud, and more recently, Guimarães, Wood and Toma. Despite all significant progress, much work still remains to be done, namely, to adjust regional tribal classification to the world classification (many endemic tribes with uncertain validity); to place monotypic genera into tribes (all non-examined genera which became either unplaced or doubtfully placed after recent splitting and lumping of tribes); to prepare identification key to genera; to perform phylogenetic analyses at different hierarchical levels to test current tribal arrangement and new generic definitions; among others.

Diversity and systematics of the world Tachinidae (Diptera)

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Keywords: Geographic distribution, evolution, classification

The Tachinidae are the most successful and diverse of all parasitoid fly families with about 8500 described species and thousands of undescribed species. In the current classification they are divided into four subfamilies, about 50 tribes, and 1515 genera. The oldest fossils were long thought to be of Eocene age but a re-examination of the evidence changes this to the Oligocene (ca. 30 mya). It appears likely that the rapid evolution of the Tachinidae took place after the major radiation of their most common host order, the Lepidoptera, and tachinids may have ancestrally parasitized another insect order. Tachinids colonized the world so successfully during the Tertiary, after the breakup of Gondwana, that all subfamilies and most tribes are well-distributed in each of the six biogeographic regions. Certain tribes, such as the Rutiliini in the Australasian Region and Tachinini in the Neotropical region, are markedly more diverse in some parts of the world but as a general rule tachinid tribes are well distributed among multiple regions. At the generic level there are clear patterns of distribution that reflect the proximity of the current continents. Under the current classification, pairs of regions sharing more than 100 genera are the Palaearctic–Oriental (178 genera), Nearctic–Neotropical (175 genera), Palaearctic–Nearctic (134 genera), and Palaearctic–Afrotropical (114 genera).

Not all biogeographic regions of the world have received equal taxonomic treatment during the past 200 years and this is evident in the regional classifications. Efforts are underway through the “Phylogeny and Evolution of World Tachinidae” project to better understand tachinid relationships as a requisite to reclassifying the more problematic taxa and assessing the historical biogeography of the family. Progress towards a well-supported phylogeny of the Tachinidae based on morphological and molecular evidence will be discussed in related ICD8 presentations on the “Phylogeny and Evolution of World Tachinidae” project.

The utilization of adult house flies, *Musca domestica* (Diptera: Muscidae), in the production of hair dye using oil produced from sesame plants (*Sesamum indicum*)

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Keywords: Housefly, albino rat, synthetic

CANCELED

Finding the Leiinae: monophyly, problem genera and broader issues in Mycetophilidae phylogeny (Diptera: Bibionomorpha)

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Keywords: Bibionomorpha, Mycetophilidae, Leiinae, phylogeny

The Mycetophilidae includes 233 genera and about 4.500 species, and is known from all biogeographic regions. The oldest fossil records are from the early Cretaceous with a modern fauna appearing in the late Cretaceous/Early Cenozoic. The family has been divided into the subfamilies Sciophilinae, Gnoristinae, Mycomyiinae, Leiinae, Manotinae, Allactoneurinae, and Mycetophilinae, though the monophyly of the subfamilies and the relationships between them are still poorly understood. Leiinae is one of the subfamilies that has received little attention in the literature. Knowledge on the relationships between its genera is poor and even its monophyly is questionable, making it difficult to determine the limits of the group. Some of the included genera – *Docosia* Winnertz, *Tetragoneura* Winnertz, *Ectrepesthoneura* Enderlein, *Novakia* Strobl, *Sticholeia* Søli, *Aphrastomyia* Coher & Lane – are often placed in other subfamilies. *Allactoneura* de Meijere has been treated as either a subfamily of its own, a member of the Manotinae, or of the Leiinae. Therefore, a phylogeny of Leiinae would help clarify intrageneric relationships and some general aspects of Mycetophilidae phylogeny. We examined the phylogenetic relationships between Leiinae genera using morphological data, with wide ingroup and outgroup sampling, in order to properly test the monophyly of the subfamily, and determine the placement of questionable genera. A total of 135 morphological features, for 110 terminal taxa, including two new genera, were used in the study. All recovered topologies show a monophyletic, though more restricted, Leiinae, characterized by the presence of the mesopleurotrochantin and having the mesepimeron not reaching the ventral region of the thorax. *Docosia*, *Novakia*, *Ectrepesthoneura*, and *Tetragoneura* are not placed in a monophyletic group with the Leiinae. *Sticholeia* does not belong to the Leiinae and consistently appears as sister to *Allactoneura*, in a clade that also includes the Manotinae.

Ecology of bat flies (Nycteribiidae) in North Palaearctic

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Keywords: Bat fly, Nycteribiidae, *Penicillidia monoceros*

We investigated the distribution, specificity of host-parasite relationship and winter ecology of three species of bat flies (Diptera, Nycteribiidae): *Penicillidia monoceros* Speiser, 1900, *Nycteribia quasiocellata* (Theodor, 1966), *Basilia rybini* (Hurka, 1969) across Eastern Europe, the Urals, Western and Central Siberia. Respectively, 148, 234 and 196 individuals of each species were collected. The bat flies belonging to the family Nycteribiidae are oligo- or monophagous bat ectoparasites in the North Palearctic (Theodor, 1967). Specificity of *P. monoceros* depends on the abundance of its primary host (Orlova et al., 2014). In areas where *Myotis dasycneme* (Boie, 1825) is at low density or absent, *P. monoceros* can parasite other *Myotis* species. Within most of the host area it can be considered as monophagous since it found on the pond bat only. On the contrary, *N. quasiocellata* and *B. rybini* are associated exclusively with the eastern water bat *Myotis petax* (Hollister, 1912), which occurs in the Central and Eastern Palaearctic. The decrease (due to mortality or emigration) in density of blood-sucking flies non-monotonic during host wintering and optimally can be described as an S-shaped curve; and besides, its “step” corresponds to the time of host pairing (Orlova et al., 2012). Both studied bat species fall to 1.5 (95% CI 1.04–2.0) times its bloodsucking flies load by the end of wintering. Females of *M. dasycneme* have 3.4 (1.4–8.3) times higher odds of being infected, and 2.4 (1.5–3.7) times higher average number of *P. monoceros*, than males. Similarly, *M. petax* females have 1.7 (1.2–2.4) times higher density of *N. quasiocellata* and/or *B. rybini*. We hypothesize the existence of host-sex-recognition mechanisms in bat flies (Lourenço & Palmeirim, 2008), providing “ecological profit” for ectoparasites as a consequence of “anisotropic” sex-biased dispersal among adult hosts during wintering and, later (following summer), the chance to infect host juveniles.

Comparative morphology of the ovipositor of Tephritidae and Scathophagidae (Diptera) with reference to the larval habits

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Keywords: Tephritidae, Scathophagidae, evolution, ovipositor musculature

Transformations of the female ovipositor mechanism in two families of Diptera (Tephritidae and Scathophagidae) have been compared in connection with the developmental adaptation for oviposition in different substrates. The structure of the ovipositor sclerites and musculature was investigated in tephritid flies, whose larvae develop in decaying wood (*Lenitovena*), in soft tissues of various fruits (*Ceratitis, Bactrocera, Rhagoletis* and *Carpomya*) or in hard flowerheads of asteraceans (*Campiglossa, Urophora*). New data (*Oxyna*) were also obtained. Species of the genera that lay eggs in hard flowerheads and galls have evolved more complicated adaptations, such as a more complex structure of the basal part of syntergosternite VII with different apodemes and strong muscles, and an apodeme of sternum VI. The origin of the additional flexible thin apodeme has been traced in the following series of genera: *Lenitovena* – *Bactrocera* – *Carpomya* – *Ceratitis* – *Campiglossa* – *Urophora*. The structure of the ovipositor sclerites and musculature was also investigated in Scathophagidae (*Cordilura*, *Scathophaga*, *Pogonota* and *Spaziphora*). Adaptations of the ovipositor sclerites and muscles associated with changes of the oviposition substrate caused by new larval habitats (plants and semi-liquid material) are analyzed. Proposed schemes of the evolutionary transformations of the ovipositor in the two families are compared. Morpho-functional similarities of the ovipositor structure are a result of adaptive rearrangements. Changes of the ovipositor structure of scathophagids with phytophagous larvae compared to ovipositor structures in scathophagids with other types of larval feeding habits are mainly found in the skeletal structures rather than in the associated muscles.

Plenary talk

Europe as a frontier in fly diversity research

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Keywords: Diptera, taxonomy, systematics, curation, innovation, funding

Dipterology is the scientific study for the advancement of knowledge on Diptera. Knowledge of the living world is paramount for human well-being, and knowing about the ten percent of planetary life classified as Diptera promotes prosperity, sustainability and health. Our science is both international in scope and inherently collaborative. Still, Europe has the largest concentration of natural history museums in the world, and more than half of all scientific Diptera specimens may reside in European museums. With such a unique resource base, Europe should be in an ideal situation for being at the cutting edge and providing major contributions to dipterology. Indeed, European dipterology is delivering high-quality output from canopy-research to avant-garde 3D-modelling of morphology, and the inventory of European Diptera, along with the remaining fauna, has been considered a prosperous 'test bed' in biodiversity exploration. Interestingly, more than half of the newly described European species are delivered by people not specifically paid to do so, i.e., by either amateurs or retired taxonomists, which can be seen as a successful synergy between academia and citizen science – but also as a result of diminishing funding and demographic changes. European research is influenced by a growing demand for scientific innovation from institutions and funding agencies, which conflicts with the need for long term funding (often seen as asking for 'more of the same'), which is vital to the success of large-scale inventories, detailed documentation of species, and collection maintenance for megadiverse taxa like Diptera. Many European museums have recently been renovated or reshaped, but the need to serve as "iconic" urban landmarks often conflicts with their purpose of housing our growing collections and making the most of taxonomic research. So, where is the frontier, and what are the stakes?

Sarcophagidae (Muscomorpha) attracted to decomposing carcasses of *Sus scrofa* L. in a rural area of the State of Minas Gerais, Brazil

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Keywords: Cerrado biome, biodiversity, decomposition process, checklist

This study presents a list and determines the diversity and abundance of adult Sarcophagidae (Muscomorpha) collected from eight pig carcasses (*Sus scrofa* L.) exposed in two different environments: forest and pasture range, at the campus of Federal University of Uberlândia, Uberlândia City, Minas Gerais State, Brazil. The experiment was carried out through carcasses decomposition, and lasted 49 days during the 2012 dry and cold season, and 30 days during the 2013 wet and warm season. A total of 44,446 adult Sarcophagidae, belonging to 18 genera, 46 species and two morphotypes was collected, mostly during the decay stage of decomposition. *Blaesoxipha* (*Acanthodotheca*) *acridiophagoides* was collected exclusively on the bloated stage; *Dexosarcophaga ampullula*, *Oxysarcodexia occulta*, *Sarcophaga* (*Lipoptilocnema*) *crispina*, *Sarcophaga* (*Lipoptilocnema*) *crispula* and *Tricharaea* (*Sarothromyia*) sp. were collected exclusively on the decay stage and *Peckia* (*Squamatodes*) *trivittata* and *Titanogrypa* (*Sarconeiva*) *fimbriata* exclusively on the dry stage. The most abundant species was *Peckia* (*Sarcodexia*) *lambens*, followed by *Oxysarcodexia thornax*. *Blaesoxipha* (*Acanthodotheca*) *acridiophagoides*, *Blaesoxipha* (*Acridiophaga*) *caridei*, *O*. *occulta, Nephochaetopteryx orbitalis* and *Ravinia effrenata* were reported for the first time for the Cerrado biome. In addition, 389 Sarcophagidae were reared from the carcasses, and *Peckia* (*Pattonella*) *intermutans* was the most abundant species with 379 specimens. *Nephochaetopteryx orbitalis* may be a potential forensic indicator for the forest, and *B*. (*A*.) *caridei*, *Oxysarcodexia aura* and *Oxysarcodexia terminalis* may be potential indicators for the pasture. *Blaesoxipha* (*Acanthodotheca*) *lanei* may be a potential indicator for the wet and warm season, whereas *B*. (*A*.) *caridei*, *Dexosarcophaga paulistana*, *Helicobia rapax*, *N*. *orbitalis*, *O*. *aura*, *Oxysarcodexia fluminensis*, *Oxysarcodexia simplicoides* and *Titanogrypa* (*Cucullomyia*) *larvicida* may be potential indicators for the dry and cool season. However, only *P*. (*P*.) *intermutans* was reared from the carcasses, making this species a forensic indicator for the Experimental Farm of Glória.

Identification of microRNAs in *Cochliomyia hominivorax* and *Cochliomyia macellaria*: Implications for parasitism studies in Calliphoridae (Diptera: Brachycera)

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Keywords: miRNAs, screwworm fly, secondary screwworm fly, evolution of parasitism, next generation sequencing

MicroRNAs (miRNAs) are small non-coding RNAs that act as post-transcriptional modulators of gene expression in Eukaryotes. Imperfect complementarity between miRNAs and messenger RNAs inhibits translation in animals, thus making them key genes for expression control. The investigation of miRNAs can provide a better understanding of a variety of biological processes as well as the evolution of morphological, physiological and life history traits. The family Calliphoridae is a group of myiasis-causing flies with varied feeding habits, which includes the species *Cochliomyia hominivorax* (screwworm fly) and *Cochliomyia macellaria* (secondary screwworm). The screwworm fly is one of the major pests in the Neotropical region. Their larvae infest and feed on live tissues of warm-blooded vertebrates, resulting in severe livestock industry losses. In contrast, the closely-related secondary screwworm exhibits a saprophagous habit, feeding and breeding on carcasses and dead tissues, and is crucial for forensic entomology and public health. Because of their close evolutionary relationship and contrasting habits, they represent worthy models to study the molecular basis of parasitism and feeding specialization in Calliphoridae. To identify miRNAs of both species, the small-RNA transcriptomes of adults and larvae were sequenced using Illumina platform. Reads were mapped against the *Drosophila melanogaster* genome and screened in miRBase. We identified 84 evolutionary conserved miRNAs, of which 80 were found in *C. hominivorax* and 78 in *C. macellaria*, and traced the evolution of these miRNAs through time back to the Nephrozoan ancestor (641 mya). An expression profile analysis revealed 79 differentially expressed miRNAs between species, gender and life stages based on hierarchical clustering and statistically significant change fold analysis. The results presented here provide new information about the genetic background of parasitic habits in *C. hominivorax* and *C. macellaria*, with potential application to functional and evolutionary studies in Calliphoridae.

Making small data big: Towards next generation, data and narrative text integrated, publishing for biodiversity

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Keywords: Data publishing, data sharing, semantic enhancement, community peer-review

The "publishing bottleneck" in biodiversity is comparable to the "taxonomic impediment" and is caused by:

(1) increasing amount of data to be analysed and published due to the intensification of scientific exploration; (2) use of non-machine-readable publishing formats, e.g. paper/PDF; (3) increasing overload of peers; (4) pressure to publish in "high-impact" journals which often have inconsistent policies and insufficient technologies for data publishing.

The Biodiversity Data Journal (BDJ) (http://biodiversitydatajournal.com) and associated Pensoft Writing Tool (PWT) (http://pwt.pensoft.net) build on the experience of the ZooKeys journal. The basic idea behind BDJ is to mobilise, review, publish, make interoperable and re-use small and large biodiversity data through the act of scholarly publishing.

BDJ and PWT present the first work flow ever to support the full life cycle of a manuscript, from authoring, through community peer-review, publication and dissemination within a single, online collaborative platform. PWT provides a set of pre-defined, but flexible, article templates, and import function from external databases (Darwin Core compliant data, data tables, bibliographies), including track change and comments tools, revision history, online collaboration between authors and external contributors (e.g., mentors, potential reviewers, linguistic editors). Submission to the journal is simply at the click of a button.

Text and data submitted to BDJ are formally evaluated through a novel community-based pre-publication and also post-publication peer-review. Authors may also opt for an entirely public peer-review process.

Upon publication, Darwin Core Archives are being automatically generated and harvested by GBIF and Encyclopedia of Life. Occurrence data and other in-text data tables can be downloaded straight from the article text.

BDJ publishes taxonomic, morphological, genomic, ecological, etc., articles, with no lower or upper limit to manuscript size, such as: (1) single taxon treatments; (2) data papers describing biodiversity-related databases; (3) sampling reports and inventories; (4) ecological and biological observations of species/communities; (5) identification keys; (6) descriptions of biodiversity-related software tools.

Applied Dipterology [poster]

Diptera pollination in agriculture

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Keywords: Diptera, pollination, agriculture, economic value, Syrphidae, Acalyptrata

Diptera can be important pollinators with a high economic value. A well known example is the pollination of cacao flowers by a small ceratopogonid midge, *Forcipomyia sp*.. More examples of pollination by Diptera that are of economic importance are shown.

Syrphidae in Brazilian Southern Highlands: an overview of the occurrence of species in a *Pinus taeda* affected area

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Keywords: Syrphidae, biodiversity, abundance

We studied the Syphidae fauna from southern highlands (between 1000 and 1300m) located in "Refúgio da Vida Silvestre dos Campos de Palmas" – RVS-CP, a conservation area in Paraná State, South of Brazil.

This is the first study of Diptera in the area. Two Malaise traps were set up in an area where all the representatives of *Pinus taeda* were removed for restoration of native field. We collected fortnightly for 15 months in a total of 58 samples. 45513 insects belonging to 15 orders were collected. From those, 37142 (81.4%, r=0.969) were flies and 1129 syrphids of 15 genera. The genera accumulation curve reached an apparent asymptote on 9th collection. Syrphidae distribution along the year shows variance, although more flies were collected in the warmer months of the year (r=0.78). The most abundant genera are: *Syrphus* Fabricius, *Toxomerus* Macquart and *Allograpta* Osten Sacken (89.46% of all syrphids collected). *Syrphus*, the most abundant genus, is represented by the species *S. phaeostigma* Wiedemann. This species was collected along all year but more abundantly between September and February; there was no significative correlation with the variables temperature or humidity. Six species of *Toxomerus* were collected and their distribution along the year also oscillated. The highest abundance was between September and May. There was a positive correlation with temperature (r=0.57) and a negative with humidity (r=–0.51), similar with information in literature. 148 individuals of four species of *Allograpta* were collected and *A. exotica* Wiedemann was the most abundant (52.02%). The genus distribution along the year presented peaks in March, July and October/November. Other genera collected were: *Argentinomya, Sterphus (Ceriogaster)*, *Copestylum, Leucopodella, Myolepta, Notosyrphus, Ocyptamus, Palpada, Platycheirus, Pseudodoros, Salpingogaster* and *Xanthandrus.* The survey will continue for 15 months in different environments such as open native fields, edge and forest fragment.

Current issues in the taxonomy of the winter gnat genus *Trichocera* (Trichoceridae)

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Keywords: Taxonomy, Trichocera, Trichoceridae

The genus *Trichocera* Meigen 1803 currently comprises about 112 species, mostly from the Palaearctic region, with about 25 species in the Nearctics and 12 in the Oriental region. Several species were accidently introduced into some South-Atlantic and Australian islands. The Palaearctic fauna of winter gnats is the best-studied one, although central and northern Europe saw considerably more research effort than Asia.

The main issues in taxonomic studies of *Trichocera* are the following: some of the species are not illustrated at all or illustrations are practically unusable; the identity of some species is ambiguous; even comparatively better studied European countries lack sufficient material to infer distributional patterns, and many species from other regions are known only from their type material.

Several species, mostly known from type specimens alone, were not illustrated in their descriptions (*T. abieticola*, *T. arisanensis*, *T. auripennis*, *T. bellula*, *T. bisignata*, *T. glacialis*, *T. tenuicercus*, *T. variata*) or had only wings illustrated (*T. mexicana, T. minuta, T. punctipennis*). Several other species, even as common as *T. dahlae* or *T. parva*, did not include illustrations of females. Moreover, illustrations of specimens of several species are rather ambiguous (females of *T. columbiana*, *T. mackenziei, T. ursamajor*, males of *T. arnaudi, T. banffi*) and require correction, and the females (or males) of many species are still to be discovered and described.

During the identification of winter gnat material from Russia, a question of the identity of *T. columbiana* and *T. mendli* arose. Some specimens of *T. borealis* and *T.arctica* from Canada (CNC) were erroneously identified as *T. columbiana* by Ch. Dahl, showing that the identity of *T. columbiana* is not clear. Moreover, Ch. Dahl stated in her description of *T. mendli* that it is very similar to *T. columbiana*, so it is obvious that more clarification is needed.

Additional studies, especially in Tian Shan and the Himalayan mountain systems as well as the Nearctic region will probably yield more new species even in such a small group as *Trichocera*.

Tipuloidea of Iturup Island (the South Kuril Islands)

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Keywords: Tipulidae, Limoniidae, Pediciidae, Kuril Islands (Russia), zoogeography

Iturup Island is the largest of the Kuril Islands (far eastern Russia) and is characterized by highly diverse habitats. The Tipuloidea fauna of Iturup is poorly studied as compared to other parts of the southern Far East of Russia. Alexander and Savchenko recorded 24 Tipulidae, 32 Limoniidae and 5 Pediciidae species from Iturup. In August – September 2011, we conducted an expedition, during which we collected adults of Tipuloidea in all major landscapes and habitats in different parts of Iturup. About 2000 specimens of Tipuloidea were sampled from 46 localities, mostly with net and Malaise traps.

In total, we recorded 30 species of Tipulidae in 8 genera, 39 species of Limoniidae in 23 genera, and 6 species of Pediciidae in 3 genera. Seventeen Tipulidae, 22 Limoniidae and 5 Pediciidae species are recorded for the first time from the island, bringing the species number of Tipuloidea of Iturup to 105. Two species of Tipulidae are recorded from Russia for the first time. The most interesting records are*Tipula* (*Acutipula*) *hokusaii* de Jong, *Tipula* (*Pterelachisus*) *pauli* Mannheims and *Tipula* (*Pterelachisus*) *daitenjoensis* Alexander. *Tipula* and *Dicranomyia* are the most diverse genera represented by 26 and 7 species, respectively. *Antocha* (*Antocha*) *dentifera* Alexander and *Dicranophragma* (*Brachylimnophila*) *nemorale* (Meigen) were the most abundant species in our samples.

According to the updated but still incomplete knowledge, the Tipuloidea fauna of Iturup includes 13 zoogeographic components (according to Savchenko), of which species with the Japanese-Manchurian, Kuril-Japanese and Sakhalin-Kuril-Japanese ranges are most numerous, accounting together for 60% of the total species number. The Tipuloidea fauna of Iturup is most similar to the faunas of the adjacent islands Shikotan (Czekanowski-Sorensen index 0.64) and Kunashir (0.58), and differs more with that of Sakhalin (0.47) and Hokkaido (0.33).

The composition and structure of Empididae, Hybotidae and Brachystomatidae communities in Thailand – how did they arise?

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Keywords: Biogeography, Brachystomatidae, Empididae, Hybotidae, Thailand

Current knowledge of Empididae, Hybotidae and Brachystomatidae in Thailand is summarized and likely diversity estimated. Biogeographic affinities at generic level and community-level distribution of taxa along environmental gradients (habitat, ecological characters, seasonality, altitude, *etc*.) are combined with endemicity mapping and parsimony analysis of endemism to infer how empidoid communities might have responded to historical environmental changes. A General Historical Model of empidoid communities in Thailand is proposed in which (i) the onset of the monsoon cycle forced altitudinal migration of “rainforest” biota to higher elevations where seasonality was relaxed and moist conditions prevailed throughout the year, (ii) orogenesis promoted speciation as mountain ranges became higher and more isolated, (iii) developing mountain chains provided continuity and immigration “corridors” effectively connecting Thailand’s mountains with others further north and south, and (iv) oscillating climatic conditions, especially during recent glacial periods, caused repeated changes in sea-level and expansion and contraction of lowland seasonal forests encouraging migration from north and south.

Crane flies (Diptera: Tipuloidea) of the Korean peninsula

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Keywords: Tipulidae, Limoniidae, Cylindrotomidae, Pediciidae, Korea, diversity

Studies of Korean crane flies started in 1933 by two papers of Jujiro Masaki. From 1934 onwards, the American entomologist Charles P. Alexander started publishing on Korean crane flies. Most of his specimens were collected by A. Yankovsky in 1936–1939 in Seren Mountains and Ompo, currently situated in North Korea. The total number of discovered species encompassed 63 Tipulidae, 97 Limoniidae, 19 Pediciidae, and one single Cylindrotomidae.

We started the study of Korean crane flies in 2012 together with researchers from the National Institute of Biological Resources, Incheon, South Korea. As a result of these investigations, the total amount of discovered species increased significantly. Judging on groups, that were studied most intensely (subfamily Limoniinae, most genera of Pediciidae, family Cylindrotomidae, few genera and subgenera of family Tipulidae), the number of crane fly species in the Korean Peninsula is estimated at about 400.

Most of the Korean crane flies also occur in Japan, and less species are shared with mainland China, with the Far East of Russia (islands of Sakhalin, Kuriles and South Primorye) and with Taiwan.

The proportion of endemic species in Korea is very high, close to 20 percent. Most endemic species (n=33) were described from North Korea (mostly from Seren mountains and Ompo). Types of these species are preserved in the National Museum of Natural History, Washington DC, USA. Our investigations revealed that one third of these species also occurs in South Korea and some of them are even rather common in suitable habitats. *Chionea mirabilis* is the single species only described from South Korea; types are preserved at the Museum national d'Histoire naturelle, Paris, France.

Immature stages of the crane fly genus *Phyllolabis* (Diptera: Limoniidae) with discussion of the systematic position of the genus

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Keywords: Larvae, pupae, *Phyllolabis*

Phyllolabis is one of the few Holarctic genera of the family Limoniidae for which immature stages were previously unknown. Recent fieldwork in Mongoliawith subsequent rearings of the larvae has provided associated larval and pupal specimens for *Phyllolabis mongolicus* Podenas and Gelhaus 2011. Despite the fact that *Phyllolabis* is currently placed in subfamily Chioneinae, the overall appearance of its larvae and general features of head capsule are more similar to that of subfamily Limnophilinae, especially to the genus *Austrolimnophila*. The overall appearance of the *Phyllolabis* pupa is also more similar to that of the subfamily Limnophilinae, but it lacks rows of spines along the posterior margin of abdominal segments. The immature stages of *Phyllolabis* were collected in wood debris of *Larix* a habitat also similar to that of *Austrolimnophila* and *Epiphragma*.

At the cutting edge: Micron-scale phenotypic engineering reveals genital function

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Keywords: Genital morphology, *Drosophila* genital spines, function, sexual selection, laser surgical manipulation

The remarkable evolutionary diversification of male genital morphology has been recognized for centuries. Postcopulatory sexual selection, as cryptic female choice and sperm competition, is generally regarded as the evolutionary driver of this diversity, but direct empirical tests of this hypothesis are infrequent. An important challenge facing research into the function of insect genitalia is the small, often microscopic, size and difficult-to-access placement of morphological traits, whose functions have been of interest since Darwin but which remain unresolved because of the practical impasses that limit trait manipulation. To surpass this problem, we have developed a laser surgical technique permitting the experimental manipulation of genital traits previously inaccessible with standard mechanical cutting tools, such as even the finest of micro scissors. We used this laser technique to experimentally manipulate the genital spines in different species of *Drosophila*. The genital spines are claw-like projections from the male ventral cercal lobe (secondary clasper) and they exhibit a pattern of pronounced diversification among closely related species, rendering them of notable taxonomic importance. Males with spines reduced in size or entirely eliminated had sharply reduced copulation success, arising from failure to couple their genitalia with that of the female. In those cases where surgically-manipulated males did succeed to mate, they were not less successful at sperm transfer or competitive fertilization success, contrary to the postcopulatory sexual selection hypothesis for genital function and evolution. The results imply that the evolution of the genital spines in Drosophila is driven by precopulatory sexual selection and sexual conflict.

Problematic groups in the Holarctic fauna of fungus gnats (Diptera: Mycetophilidae)

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Keywords: Mycetophilidae, Holarctic, taxonomy

Fungus gnats are one of the most diverse groups of Diptera, numbering over 4000 species in the world fauna. This group has been quite intensively studied in the Holarctic since 19th century. However, the fauna of this region can still not be considered comprehensively known. Every year a number of new taxa are described and new data on poorly known species are published.

Identification of fungus gnats to the species level in most cases is only possible on the basis of male genitalic characters. This relies on the availability of detailed high quality illustrations, which (with few exceptions) started to appear in the literature only towards the end of the 20th century. The lack of good drawings often led to incorrect identification or misinterpretation of some species. Such issues can be relatively easily solved in cases where the type specimens are available, otherwise serious problems may arise. Examples of unclear cases can be seen in several groups of species e.g. those near Trichonta terminalis Walker, Boletina nigricoxa Staeger, Exechia spinuligera Lundström.

Since the 1960s many large and small Mycetophilidae genera have been revised, but only a few (*Acomoptera*, *Coelosia*, *Leptomorphus*, *Katatopygia*, *Mycomya*, *Sciophila*, *Speolepta*, *Trichonta*) over the entire Holarctic region. Moreover some revisionary works (e.g. *Sciophila* and *Trichonta*) are substantially out-of-date, as many new species have been described. Such diverse genera as *Boletina* and *Mycetophila* are particularly in need of revision, and there are certainly gaps in other groups too. Taking into account the considerable affinity of the Nearctic and Palearctic faunas, studies covering both regions are desirable, ideally requiring the combined efforts of scientists from different countries.

The position of the Chilean dolichopodid fauna in the Neotropics (Diptera: Dolichopodidae): a first assessment

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Keywords: Chile, Valdivian temperate rain forest, Andean cordillera, Dolichopodidae, biodiversity

For many insect taxonomic groups, Chile harbours a yet largely undiscovered and highly endemic fauna. Indeed, its natural barriers in the north (Atacama desert), east (Andean cordillera), south (Antarctic conditions) and west (Pacific Ocean) make this country a virtual island within the South American continent. Also, it provides excellent circumstances to study the latitudinal diversity gradient (LDG), i.e. the increase in species richness from the poles to the tropics, thanks to its topography.

During a survey in January 2013, 17 different sites in 3 Chilean regions (VIII – Bío-Bío, IX – Araucanía, X – Los Lagos) between 35°S and 41°S in the central Chilean Andes (70°–72°W) were sampled with traps. Nearly all sites encompassed Valdivian temperate rain forest and most were situated in or near national parks (PN) or reserves (RN). At 9 different sites near Ñuble RN, and within Conguillío PN, Puyehue PN and Alerce Andino PN, a complete trap unit was installed, consisting of one Malaise trap and 10 blue, yellow and white pan traps. In addition, these and a considerable number of other sites were sampled with sweep nets.

A total of 362 traps were in operation during 3,819 trapping days. Yields per trap type and sampling site were pooled in the field producing 47 trap samples. Also 132 sweep net samples were collected. In the lab, over 20 taxonomic groups were separated from the samples and subsequently disseminated to a network of taxonomic specialists around the world.

A total of 8,247 dolichopodid specimens were collected during this survey, representing 135 species. The subfamilies Sympycninae (30 species, 59% of specimens) and Peloropeodinae (*Chrysotimus*, 22 sp., 8%) appeared the most speciose, followed by Achalcinae (14 sp., 12%). The genus *Somillus* also proved surprisingly diverse with 11 species. During this survey, we came across some unexpected circumstances in the field.

Red Lists sensu IUCN: a bridge too far for Dolichopodidae (Diptera) of Flanders?

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Keywords: Dolichopodidae, Flanders (N Belgium), Red List, IUCN, conservation

The documented Red List (RL) of Dolichopodidae (Diptera) of Flanders (N Belgium – Pollet 2000) used a compilation of all ecological and distributional data on this dipteran family in Belgium between 1850 and 1997. Data on nearly 263,000 specimens were analyzed using the regional Red List criteria in Flanders (Maes et al. 1995). This study revealed the presence of 260 of the 295 Belgian species in Flanders. Twenty-two species were considered regionally extinct, whereas another 10, 14 and 16 species were categorized as *critically endangered*, *endangered* and *vulnerable* respectively. Eighty-six species were estimated as *fairly rare*, *rare* or *very rare*. The analyses also stressed the need for additional inventories as records originated from only 40% of the Flemish UTM 5x5 km grid cells.

Between 1997 and 2005, an additional 246,000 specimens from 211 different Belgian localities (including 63 previously unexplored ones) were processed allowing us to validate previous estimates of rarity and decline. Six species that were previously assumed extinct in Flanders were rediscovered and 28 threatened species were encountered fairly to very abundantly. Furthermore, 8 species were recorded in Flanders for the first time, and another 11 proved new to Belgium; nearly all 19 species were collected in very low numbers. Fifteen species were assigned a more threatened RL status, and 50 a less threatened one (Pollet & Maes 2005).

In 2003 IUCN adjusted its Red List criteria to make them applicable on a regional scale (IUCN 2003), which was subsequently implemented in each new Red List of Flanders. The new approach focuses more on quantitative data on populations and trends then before and encompasses new RL categories. Moreover, trends must be calculated during shorter, more recent periods, which implies monitoring. An attempt to apply the new regional IUCN criteria to the recently extended dolichopodid dataset of Flanders raised new challenges.

The Muscidae of Armenia

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Keywords: Muscidae, Caucasus, Armenia, biogeography, faunistics

Armenia is a small landlocked country between the Black Sea and the Caspian Sea, on the southern flank of the Caucasus Mountains. The north and west of the country are mountainous and rugged, with the highest peak Mt Aragats at 4095 m; there is a depression with Lake Sevan in the centre; and a dry plain in the south and south-west. Habitats are therefore many and varied.

Over the last decade Armenian scientists have been studying the water quality of the rivers and streams by monitoring blackfly and mosquito populations. We have participated in five expeditions with the Armenians between 2003 and 2012, and have collected many Muscidae, Anthomyiidae and other Diptera. Almost all parts of the country have been visited and samples collected mainly in the vicinity of aquatic habitats.

Back in 2003, only 20 species of Muscidae were known from Armenia. We now know 132 species, and the total continues to rise as our collections are more completely worked up. Of these, 23 species (17.5%) are pan-Palaearctic species, 42 (31.8%) are temperate Palaearctic species (from the coniferous and broad-leaved forest zones), 23 (17.5%) are southern Palaearctic, 18 (13.6%) are temperate West Palaearctic, i.e. European species, 6 (4.5%) are Mediterranean species, 9 (6.8%) are upland or montane species, and 11 (8.3%) are endemic Armenian or Caucasian species.

Scuttle Flies (Diptera: Phoridae) in caves in Rhineland-Palatinate (Germany)

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Keywords: Phoridae, caves, *Triphleba antricola*

In several surveys of the fauna of caves in Rhineland-Palatine (Germany) numerous scuttle flies (Phoridae) were found. Some species were caught very frequently. This indicates that several Phoridae species may be eutroglophile, which means that caves are their preferred habitat, in which they build stable populations. Other species may be subtroglophile. This implies they live regularly but not permanently in caves (i.e. for hibernating). Here we introduce the Phoridae species we often found in caves.

Studied were natural caves and artificial underground rooms in Germany west of Rhine and southeast of Mosel Rivers. As trapping method Barber traps are used. Small samples were taken with a small brush.

We classify *Triphleba antricola*, *Megaselia posticata*, *M. tenebricola*, *M. sericata*, *M. costalis* and *M. vernalis* to be eutroglophile species. They are common in caves and were seldom found outside from caves. *Triphleba antricola* is the principal species characteristic for caves in Europe (Disney 1994). Also we add *Megaselia ciliata* and *M. rufipes* to the list of eutroglophile species because of numerous findings in European caves. We consider *Triphleba hyalinata*, *Megaselia albicaudata*, *M. melanocephala* and *M. pleuralis* as subtroglophile species. They were often collected in caves but were also frequently caught outside caves. The larvae of Phoridae in caves develop e.g. in carrion (from bats, snails or insects) or dung. In caves, *Triphleba antricola* is known to breed in bat dung and the larvae of *Megaselia melanocephala* feed on the eggs of cave spiders (Disney 1994).

Immature Diptera in semiaquatic shoreline habitats of hypersaline lakes: diversity and adaptations to extreme conditions

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Keywords: Crimea, salt lakes, larvae, semi-aquatic shoreline habitats, taxonomic richness, adaptations

Salt lakes are predominant waterbodies in steppes and semi-deserts of the Palaearctic region. Shorelines of hypersaline lakes are extreme habitats with poorly known dipteran diversity.

During 2005–2013, Diptera were investigated that develop in shoreline habitats (water margin zone) of two hypersaline lakes, Koyashskoe and Kirkoyashskoe, situated in eastern part of the Crimean Peninsula. The study combined a quantitative assessment of macroinvertebrates (numbers and biomasses) with the rearing of dipteran immatures to adults (about 3000 specimens). Samples were taken from 16 sites of the water margin zone strongly differing in substrate, vegetation and water mineralization (20–430 g/l). Some tendencies in composition and structure of dipteran immature assemblages are discussed.

Diptera comprised 65–90% of macroinvertebrate biomass in all habitats. The taxonomic and ecological diversity of Diptera in the shoreline zone of the investigated lakes is comparable to that of many freshwater lakes of European Russia but shows a stronger variation between habitats. Species in 18 dipteran families develop in the shorelines of the two lakes. Most species are halophilous; some of them develop in extremely wide ranges of salinity. Ceratopogonidae, Stratiomyidae and Ephydridae were represented by more than five species. Surprisingly, many closely related species (in *Nemotelus*, *Stratiomys*, *Culicoides*, *Dasyhelea*) inhabit same extreme habitats and sites. Taxonomic structure at generic and familial levels is similar to that in other extreme semi-aquatic habitats (sea intertidal zone, hot springs, shores of polluted waterbodies).

Adaptations in six halophilous species of Stratiomyidae, Tabanidae and Ceratopogonidae were examined in comparison with related species confined to cold freshwater habitats. In halophilous species, larvae display a higher thermotolerance and maintain higher concentrations of heat shock proteins (HSP70) both before and after heat shock. Halophilous species of Stratiomyidae differ in organization of HSP70 and HSP83 genes from species living in cold freshwater bodies.

Immature Diptera in small lakes of northwestern Russia: tendencies in colonization of shallow aquatic and semiaquatic habitats

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Keywords: Russia, aquatic environment, semiaquatic habitats, lakes, larvae, life habit

Immatures of Diptera were studied in three groups of small freshwater lakes situated in NW Russia at latitudes from 66° to 55°N. From north to south, lakes changed from oligotrophic to macrophyte-dominated eutrophic. Within each lake, major habitats of the upper littoral and water margin zones were sampled. The study combined quantitative assessment of immatures and reliable species' identifications based on rearing immatures to adults using three techniques.

Over 380 species in 33 families were recorded in 12 lakes. Latitudinal tendencies in taxonomic composition, habitat and depth distribution, abundance and life histories of non-chironomid Diptera are described.

Vegetation and bottom sediments are the main complex factors that govern composition and abundances of Diptera in the littoral zone. In littoral communities, Diptera are represented mainly by insectivorous predators, detritivores and phytophages of emergent macrophytes.

The number of families with larvae living in semiaquatic mesohabitats at lake shorelines is higher than mentioned in reviews and handbooks. In particular, some species of Sciaridae, Mycetophilidae and Cecidomyiidae seem to be specialized inhabitants of lake shorelines. On the other hand, immatures of several families often referred to as “aquatic” actually inhabit only semi-aquatic mesohabitats within the water margin zone but not the littoral zone of lakes. Among them are all members of Cylindrotomidae, Ptychopteridae, Psychodidae, Forcipomyiinae (Ceratopogonidae), Dolichopodidae, Hybotidae, Sciomyzidae, Scathophagidae and Muscidae associated with lakes. Immatures of several more families (e.g. Limoniidae, Stratiomyidae, Syrphidae) colonize in lakes few aquatic mesohabitats, mostly dense stands of emergent higher vegetation, but many semi-aquatic mesohabitats.

Apparently, colonization of aquatic habitats by most families of Diptera is limited by restricted respiration in larvae and pupae under the water surface. Patterns of colonization of aquatic environment by different taxa of Diptera in lakes differ considerably from those in running waters.

Mating behavior evolves faster than sexual morphology: An integrative approach to studying population divergence in a widespread neotropical fly, *Archisepsis diversiformis* (Sepsidae)

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Keywords: Sepsidae, population divergence, speciation, mating behavior, morphometrics, COI

Rapidly evolving reproductive traits often play a part in generating sexual isolation, restricting gene flow and reinforcing species boundaries. Pre-mating discriminating mechanisms, such as courtship behavior, can evolve particularly fast even among populations of widespread species. Here, we present a detailed study of mating behavior and sexual morphology in two populations (Costa Rica & Panama) of the neotropical fly *Archisepsis diversiformis* (Diptera: Sepsidae), focusing on differences in behavioral, morphometric and molecular data. We find that (i) despite overall similarities in courtship repertoires, some behavioral elements performed during mating are clearly population-specific, and (ii) when tested one-on-one, focal females from both populations mated preferentially with males of the same population. Nevertheless, mass-container population crosses (no-choice) produce F1 offspring after extended exposure. (iii) Furthermore, morphometric analysis indicates that the populations differ significantly in male and female wing shape but only moderately in the shape of the sexually dimorphic male fore femur, and not at all in the male genital clasper shape. (iv) Finally, a comparison of the fast-evolving cytochrome oxidase subunit I (*COI*) gene fragment indicates that individuals from Costa Rica & Panama are genetically highly similar, forming a strong monophyletic cluster with uncorrected pairwise distances ranging from 0.5–1.6%. This study documents that mating behavior evolves faster than morphology, which may restrict gene flow between populations. We argue that integrative studies taking into account fine-scaled behavioral work is important when studying incipient sexual isolation and ongoing processes of speciation among widespread species.

Sexual selection, sperm competition and incipient speciation in a widespread dung fly, *Sepsis punctum* (Sepsidae)

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Keywords: Sepsidae, sexual selection, sperm competition, mating systems, population divergence

Theory predicts that males have limited resources to invest in reproduction, which they must allocate to mate acquisition as well as insemination and competing for fertilizations. Because adaptations to both episodes of selection may be costly, trade-offs are predicted to arise between traits that influence pairing success and those that enhance fertilization success (Parker et al. 1997). Using fitness component assessments, we recently demonstrated that sexual selection for large male body size accounts for a geographic reversal in sexual size dimorphism (SSD) in the widespread dung fly *Sepsis punctum* (Diptera: Sepsidae), where males are larger than females in Europe (EU) and females are the larger sex in North America (NA) (Puniamoorthy et al. 2012). Here, we address continental variation in mating behavior, volatile organic compounds (including cuticular hydrocarbons), internal reproductive morphology and sperm traits in light of phylo-geographic information to assess differential investment in reproductive traits. We find that EU populations are not only larger in body size but females exhibit higher (re-)mating rates and males invest disproportionally more in testes and have longer sperm length. NA populations, in sharp contrast, invest more in mate acquisition with courtship displays that are absent in EU and vary in intensity across NA. We also find that there is great variation among populations within both continents with respect to cuticular hydrocarbons. Finally, the underlying genetic variation in a *COI* gene fragment and six microsatellites recovers distinct clusters that show clear isolation-by-distance within the continents. As such, the associated changes in pre- and post-copulatory traits suggest a shift in mating systems and incipient speciation in this species.

Acalyptratae [poster]

Can *Fergusonina* galls be founded by multiple mothers?

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Keywords: COI, *Eucalyptus*, host specificity, Myrtaceae, nematode

Fergusonina flies (Diptera: Fergusoninidae) and *Fergusobia nematodes* (Tylenchida: Neotylenchidae) form galls in the bud tissue of myrtaceous trees and have a mutualistic relationship. Their unique association is the only known mutualism between insects and nematodes, and *Fergusobia* is the only nematode with parthenogenetic and sexual plant-living generations followed by an insect-parasitic generation.

Because of the host specificity of each *Fergusobia* species to one particular *Fergusonina* species, and to their tree host species, this system provides an excellent model for studies of coevolution. A previous study of three *Fergusonina-Fergusobia* species from multilocular snow gum galls found that the fly and nematode phylogenies correspond at species level, but the correspondence breaks down at an intra-specific level. Multiple flies founding galls may be one reason for this incongruence, as it could allow nematodes to migrate between fly hosts within the gall. It has often been speculated that multiple foundresses occur in *Fergusonina*, but this has never been tested until now. I sequenced 233 flies from 27 galls collected from four host plant species, compared the mitochondrial COI sequences, and found that more than a quarter of the galls in the study contained multiple haplotypes, each representing a maternal line. Given the sensitivity of the marker, this is a conservative estimate of the frequency of multiple foundresses, and the incidence of multiple founding is likely to be much higher.

Applied Dipterology [poster]

Ecological impact of antiparasitic medicines in relation to the population dynamics

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Keywords: Diptera, cattle, macrocyclic lactone, antihelmintics, dung insects

Veterinary pharmaceutical drugs are used widely to control diseases and promote production in the agricultural sector. The drug will after its internal therapeutic utilization in the animals, be excreted mostly via dung dropped on the field, by grazing animals. Authorization of antiparasitic medicinal products follows, like other veterinary drugs, a tiered approach, where Tier 1 is based upon a simple generic risk assessment based on laboratory studies, and Tier 2 is a more advanced assessment of the environmental impacts, which normally is very laborious and economically burdensome. Most antiparasitic substances will, due to their high toxicity to dung living insects, fail to pass Tier 1 leading to a need for higher Tier assessment. We have therefore started the development of a simulation program to assess impacts on biodiversity of dung-living Diptera. Our aim it is to develop and parameterize a model, which can be used to assess some of the population dynamic effects of antiparasitics on selected insect species living at the dung. At present a literature search for parameters and relevant species has been conducted. A first preliminary version of the program has been developed and coded. Several Diptera families had been found in Europe to have parts of their life-cycle associated to bovine dung (Trichoceridae, Tipulidae, Psychodidae, Ceratopogonidae, Culicidae, Chironomidae, Anisopodidae, Bibionidae, Mycetophilidae, Sciaridae, Scatopsidae, Cecidomyiidae, Stratiomyidae, Empididae, Phoridae, Rhagionidae, Asilidae, Hybotidae, Empididae, Dolichopodidae, Syrphidae, Sepsidae, Sphaeroceridae, Drosophilidae, Ephydridae, Oestridae, Gasterophilidae, Sarcophagidae, Calliphoridae, Scathophagidae, Anthomyiidae, Fanniidae, Muscidae); beside beetle and earthworms species. Output from the ToxDung Simulation model will be presented. Simulation programs, like ToxDung seems to be a feasible possibility to diminished cost of higher Tier testing within the approval process of veterinary pharmaceuticals in Europe.

Rural and Urban comparation of attractants formulations and trap designs to capture adults of *Musca domestica* L. (Diptera: Muscidae) in the Tovar Colony, Aragua, Venezuela

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Keywords: *Musca domestica*, attractants, Diptera ethological control, entomological traps

Musca domestica L. (Diptera: Muscidae) population growth at the Tovar Colony, had an impact on human and animal health, besides tourist activity. Purpose was to characterize the efficacy of attractants and trap design to catch *M. domestica*. We evaluated two locations: rural area (RA) (1352 msnm.) and Urban Area (UA) (1.876 msnm.). Three attractant formulations were assessed eight weeks: FAGRO-UCV-10 [Soluble concentrated protein (Comprosol1)+bórax], FAGRO-UCV-11 [Aqueous solution of *Sardinella aurita* (Teleostei: Clupeidae)] and TOVAR-UCV-1 [milky sugared solution 2:2:1 (milk+Chicha)+water] and a control (water+borax2%) and other eight weeks, four kind of trap designs were assessed: Plastic McPhail® w/yellow cup (YC), Plastic McPhail® w/clear cup (CC), JD-EUGO-97® y EUGO-2010®. Captured species of Diptera were treatment arranged. A non-parametric statistical Fisher test was used. Level of significance chosen was α=0.05. Solutions attracted adults of *M. domestica*, and FAGRO-UCV-11 was more effective than the rest for female flies, but not for males between treatments. At the UA there was no difference between trap design in plastic McPhail ® YC and CC, but in numeric values the plastic McPhail® CC was the more effective to capture females, males and (females + males) of the species, with statistical differences against other designs assessed. At the RA the trap design JD-EUGO-97® did not had statistical significance to plastic McPhail® YC and CC, but captured the highest number of females, males and (males+females) of the species. Predominant families of Diptera were: Tipulidae, Otitidae, Neriidae, Micropezidae, Muscidae, Calliphoridae, Sarcophagidae, Tachinidae. The best combination trap/attractant for *M. domestica* resulted different between localities: for UA was plastic McPhail® CC/FAGRO UCV-11 and for the RA was JD-EUGO-97®/FAGRO-UCV-11. EUGO-2010® had an alternative to obtained fresh material to identification. With

this study, it could be establish an adequate ethologic control management for *M. domestica*, encompassing the environment characteristics of each locality

Teleopsis dalmanni, the genomic model Diopsid

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Keywords: Genomics, sexual selection, meiotic drive

The stalk-eyed fly, *Teleopsis dalmanni* (Family Diopsidae), has become a model organism for the study of sexual selection, meiotic drive, and sex chromosome evolution. However, until recently little genetic data existed for this species or any other diopsid. We have recently created a high quality genome assembly using an inbred line of *T. dalmanni*, and have annotated it using a separate high quality transcriptome assembly composed of RNAseq data from six tissues and an expressed sequence tag library from three stages of pupal development. This genome contains tens of thousands of genes, including about 10,000 that can be identified as Drosophila orthologs. We are currently using these resources to track the evolutionary changes associated with sex-chromosome meiotic drive to basepair resolution, and to study genetic differences between populations and species in the family Diopsidae. We are sharing our findings with the community on our own JBrowse server, and publishing the genome with Ensembl. We hope that these resources will be of use to researchers worldwide interested in comparative genomics of flies.

Description of a new fruit fly species within the genus *Bactrocera* Macquart (Diptera: Tephritidae: Dacinae) from Pakistan

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Keywords: Fruit, pest control, Tephritidae

CANCELED

Global diversity patterns in crane flies (Diptera): sampling bias and biogeographical signal

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Keywords: Birds, global diversity patterns, Latitudinal Diversity Gradient, mammals, Species-Area Relationship, Tipulomorpha

Global patterns of crane fly (Diptera: Tipulomorpha) diversity are investigated, with respect to the Species-Area Relationship (SAR) and the Latitudinal Diversity Gradient (LDG), and interpreted in light of the patterns of mammals and birds. Species richness for the three taxonomic groups agreed with the expected SAR pattern of high diversity in broad areas. Regarding LDG, mammal and bird curves demonstrated the expected pattern of decreasing richness from the Equator to higher latitudes in a strongly congruent manner. However, the LDG curve obtained for the crane flies showed a contrary trend, which was interpreted as being caused by a bias, due to a global imbalance in research efforts within the group. Better knowledge on the tropical faunas is likely to provide a more realistic picture of the Latitudinal Diversity Gradient in the group in the future.

However, as measured by its congruence in the ordering of clustering world countries, the biogeographical signal of crane fly distributional data did not differ significantly from the signal provided by these data from the well-known vertebrate taxa. The most obvious implication is that, albeit the urgent need of diminishing the global study effort imbalance, there appears to be sufficient data about crane fly distribution for the rigorous testing of broad-scale biogeographical hypotheses.

New *Leptotarsus* from the Early Cretaceous of Brazil and Spain: the oldest members of the family Tipulidae (Diptera)

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Keywords: Las Hoyas, *Leptotarsus*, Lower Cretaceous

New species of *Leptotarsus* (Tipulidae s.str.) are described from the Lower Cretaceous beds of Brazil (Santana Fm. Aptian/Albian, ca. 112 mya) and Spain (La Huérguina Fm., Late Barremian, ca. 126 mya), vis. *L. grimaldii*, *L. cretaceus*, *L. martinsnetoi, L. buscalioniae*., *L. ibericus,* and *L. contractus*. Males of three species possess extremely long antennae. The fossils are the oldest representatives of the genus *Leptotarsus*, and the oldest known members of the family Tipulidae.

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The world's biogeographical regions revisited: global patterns of endemism in Tipulidae (Diptera)

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Keywords: Endemism, biogeographical regions, Diptera, VNDM, Tipulidae

This paper explores the distributional data of 4,224 Tipulidae (Insecta: Diptera) species to search for endemism patterns on a worldwide scale and to test the extent to which the global patterns of endemism of the group fit into previously proposed regionalization schemes, particularly Wallace's system and recent revisions of it. Large scale areas of endemism are assessed using the grid-based method implemented in VNDM. VNDM depends on the prior definition of the grid size for analysis, but the criteria for choosing a particular grid size beforehand is not clear. The same holds for the choice of the level of similarity in species composition selected for the calculation of consensus areas. In our study, we developed a methodological approach that helped define objective criteria for choosing suitable values for these critical variables. Large-scale areas of endemism around the globe are identified and ranked according to endemicity levels: 1 – West Palaearctic, 2 – Nearctic, 3 – East Palaearctic-Oriental, 4 – West North America, 5 – Australia, 6 – Neotropical, 7 – Sub-Saharan Africa, 8 – Palaearctic, and 9 – Middle East. Our main conclusion is that there are still some limitations in applying biogeographical classifications proposed mostly on the basis of vertebrate distribution to other taxonomic groups, such as the Tipulidae. While there is a general congruence of the broad-scale areas of endemism of tipulids with previously proposed regionalization schemes, for some areas, the sharpness of boundaries between traditional regions is not so acute, due to a greater level of overlap of part of its biotic elements.

Morphological and molecular insights into the taxonomy of *Xanthogramma* Schiner (Diptera: Syrphidae) in Europe

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Keywords: Greece, Syrphinae, new species, male genitalia, DNA analysis

From the start, the genus *Xanthogramma* has been controversial, since it was erected without included species. In addition the taxonomy of some species has proven difficult and their validity is still being questioned. Currently, 21 Palaearctic species are considered to belong to this genus. Although only six species have been recorded from Europe, the genus is in need of revision. For many years we have compiled adult *Xanthogramma* hoverflies (250+) from the Greek islands to the Italian Tuscany, through the Former Yugoslavia. Our experience with the taxonomy of other syrphine hoverflies (e.g. *Chrysotoxum* spp.) and the morphological variability displayed by the studied specimens prompted us to provide a new approach to the taxonomy of *Xanthogramma* in Europe.

A total of seven species has been identified within the species groups of *X. citrofasciatum* (De Geer) and *X. pedissequum* (Harris). DNA of named specimens of *X. dives* Rondani, *X. pedissequum*, and *X. stackelbergi* Violovitsh clustered together, suggesting that they all belong to a single taxon. Two additional DNA clusters were obtained for two separate species of the *citrofasciatum* group. The male genitalia were examined for all the studied species. The validity of some morphological characters widely used by other authors (e.g. wing pigmentation) is discussed and a preliminary key to the studied species of *Xanthogramma* is provided. Further molecular analyses are required to clarify the taxonomic status of certain studied taxa.

Progress in understanding the megadiverse syrphid genus *Copestylum* (Diptera, Syrphidae): species breeding in plant stems, fruits and flowers

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Keywords: Neotropics, biodiversity, new species, male genitalia, breeding sites

Taking place in a wide range of habitats, including deserts and forests and centred on the Neotropics, *Copestylum* Macquart represents one of the most extensive radiations known within the Syrphidae. For more than a decade, we have found and reared *Copestylum* species in many countries from Bolivia in the south to Mexico in the north. Much new biology and many new species have been discovered. The study described here, of species reared from understory stems, fruits and flowers, represents a third contribution to knowledge of *Copestylum* following work published on faunas associated with bromeliads and cacti.

A total of 34 species belonging to 12 species groups are dealt with, including 24 species new to science. Holotypes in collections from all over the world were studied and concepts of poorly defined species, such as *C. musicanum* Curran, stabilized. As with previous studies, we use a combination of gross morphological and particularly, male genitalia characters to define species and delineate species groups (putative monophyletic groups). Biological data acquired through rearing, represent an important contribution towards species conservation.

Advances in the knowledge of Neotropical Chloropinae (Diptera: Chloropidae): the status of the group *Ectecephala*

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Keywords: Cladistics, grass flies, Neotropics

The subfamily Chloropinae has 75 genera, 20 of which occur in Neotropics. Only six of these genera are exclusive from the region – *Bothynocerus* Paganelli, *Bricelochlorops* Paganelli, *Coroichlorops* Paganelli, *Ischnochlorops* Paganelli, *Psilochlorops* Duda, *Urubambina* Paganelli. The first study of the Neotropical Chloropinae was made by Paganelli (2002), who presented a phylogenetic analysis including only the genera from the Neotropical region. A constraint of the analysis is that some Neotropical genera are more related to non-neotropical genera – i.e., the Neotropical chloropines do not compose a clade. The group *Ectecephala*, erected by Paganelli (2002) is composed by four genera, *Ectecephala* Macquart, *Ectecephalina* Paganelli, *Bothynocerus*, *Homaluroides* Sabrosky. *Bothynocerus* is exclusively Neotropical, while the remaining genera have additional some Nearctic species. This group has an uniform male genitalia, with rectangular mesolobus, fused gonites, basiphallus drop-shaped or oval, anterior lobe of surstyli distinct, and median lobe of surstyli conic. These species are associated to Poaceae and some present viviparity. More than 20 first instar larvae have been found inside the female abdomen. The species of the group *capillata* of *Ectecephala* were transferred by Paganelli to a separate genus *Ectecephalina*. A preliminary study of the phylogenetic relationships within *Ectecephalina* showed the genus to be non monophyletic. More species of *Ectecephala*-group were included to test its monophyly. The ingroup sampling used here includes all ten described species of *Ectecephalina* and 11 undescribed species, four species of *Ectecephala*, the only *Bothynocerus* known species, and one species of *Homaluroides*. The analysis was performed using the software TNT. The data matrix has 43 morphological characters. The result shows eight most parsimonious trees. The paraphyly of *Ectecephalina* in relation to *Ectecephala* is corroborated. Otherwise, the species gathered in *Ectecephala* by Paganelli compose a clade. This group of genera appears well supported and seems to be related to the non Neotropical group *Platycephala*.

The tachinids (Diptera: Tachinidae) of the tundra of Siberia and the Far East

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Keywords: Tachinidae, tundra, Siberia, Far East

The report is based on the works of Yu.I. Chernov on the fauna of Taimyr, the paper of D.M. Wood and the author on Yakutia, the author’s papers on Polar Urals and Wrangel Island, and a new material from Chukotka.

The following tundra tachinids are Holarctic: *Chetogena gelida* Coq., *Steleoneura novemmaculata* Wood, *Prooppia strigifrons* Zett., *Ceromasia hybreas* Walk., *Onychogonia flaviceps* Zett., *Linnaemya varia* Curran, *Macquartia obscura* Coq., *M. pegomyioides* Richter et Wood, *M. plumbea* Richter et Wood, *Solieria borealis* Ringdahl, *Gnadochaeta fulvicornis* Zett., *Trafoia arctica* Sack, *Periscepsia stylata* B.B., *Rondania dimidiata* Mg.

On the Wrangel Island *Chetogena gelida* is reared by O.A. Khruleva from larvae of *Gynaephora rossii* Curtis (Lymantriidae), and *Aesia acerbiana* (a genus and species described by the author) is reared by O.A. Khruleva from a larva of *Acerbia alpina* Quensel (Arctiidae), collected in the tundra landscape. The genus *Aesia* seems to be endemic to the Wrangel Island. It belongs to the tribe Blondeliini and is not similar in morphological aspect to any Palaearctic genus of tachinids.

The most part of species found in tundra is distributed widely in Siberia and are usual in Central Yakutia.

The gut microbiota of alpine soil dwelling dipteran larvae analysed by next-generation sequencing

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Keywords: Diptera-microorganisms interactions, litter decomposition, 454-sequencing

The importance of interactions between faunal and microbial components in soil organic matter turnover has become increasingly recognised. However, several studies analysing the intestinal microbiota associated with decomposer animals have led to conflicting results. While the gut microbiota of diplopodes was found to be mostly resident, microbes in the gut of earthworms are often transient.

Here, we analysed the gut microbiota of bibionid larvae from alpine soils. Soil-dwelling larvae of Diptera are important decomposer species. However, Diptera are among the least-studied soil animal taxa, mostly because soil-dwelling larvae require a special extraction technique from soil samples, they do not conform well to the conventional distinction between mesofauna and macrofauna, and most dipteran larvae cannot be identified to species level. Therefore, knowledge on interactions of microorganisms and soil-dwelling larvae of Diptera is scarce. Our results obtained with next-generation sequencing suggest a resident microbial community.

Bibionomorpha [poster]

Research on fungus gnats diversity and their trophic relation in Lithuania

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Keywords: Lithuania, fungus gnats, trophic relations

The Lithuanian list of fungus gnats (Diptera: Bolitophilidae, Diadocidiidae, Ditomyiidae, Keroplatidae, Mycetophilidae) now comprises 230 species, including 11 species of Bolitophilidae, 2 species of Ditomyiidae, 2 species of Diadocidiidae, 24 species of Keroplatidae and 191 species of Mycetophilidae The comprehensive investigation of fungus gnats in Lithuania was carried out from 1997. Trophic relations with fungi of various taxa, relations with *Orthocentrinae* parasitoids, seasonal activities and habitat distribution have been investigated. The first data on Lithuanian fungus gnats (Mycetophilidae) was given in the checklist of Lithuanian Diptera in 1992 where 3 species of fungus gnats were mentioned and 12 species of fungus gnats (Mycetophilidae) were listed as present in Lithuania in the Catalogue of Palaearctic Diptera. Three species of Keroplatidae, one species of Ditomyiidae and 48 species of Mycetophilidae are listed on the Fauna Europaea Web Service for Lithuania. The investigation of fungus gnat distribution and trophic relation were presented in various scientific papers in recent years.

Trophic relations have been established between larvae of fungus gnat species and orders of fungi as follow: 42 species with the Agaricales; 15 species with the Boletales; three species with the Hymenochaetales; nine species with the Pezizales; 10 species with the Polyporales; 19 species with the Russulales; two species with the Thelephorales; and one species with the Tremellales.

Historical Biogeography of *Stylogaster* Macquart, 1835 (Diptera: Conopidae)

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Keywords: Biogeography, Conopidae, dispersal, Gondwana, *Stylogaster,* tracks, vicariance

This study aims to recover the history of the geographical distribution of the thick-headed fly genus *Stylogaster* Macquart, which contains 115 described species recorded to date. Species of *Stylogaster* are potential pollinators as adults and parasitoids of flies, cockroaches and orthopterans as larvae. *Stylogaster* is widely distributed over the world, being absent only in the Palaearctic Region, Pacific islands and polar regions. Six hundred and forty distribution records were sampled and used to determine areas of endemism of *Stylogaster*, by the track analysis method. A previous phylogeny of nearly all known species, plus some undescribed taxa, including a fossil, were used to create the cladistic biogeographic analysis, using the Dispersal-vicariance analysis method. Approximate times of divergence were speculated with the available fossil information. Sixty-five generalized tracks and 33 biogeographic nodes were found, eight tracks having associated speciation events. Fourteen areas of endemism were proposed based on the patterns of the tracks. The DIVA analysis recovered a history with 98 dispersals, 33 vicariant events and 3 extinctions, suggesting a combined ancestral area of Madagascar and southern South America. *Stylogaster* may have originated in the Early-Mid Cretaceous (ca. 120–110 mya), or near the K-T boundary (ca. 65 mya). According to the dating, it may have vicariated with the separation of Madagascar from Gondwana, or made a transoceanic dispersal from Antarctica to Madagascar. The Old world clade dispersed from Madagascar four times and arrived in Africa, India, South-east Asia, Oriental islands, Papua-New Guinea, Australia and New Caledonia. The American clade moved north from Patagonia and diversified into two species-groups, reaching the Brazilian Atlantic Forest before dispersing to Amazonia, Caribe, Central America, Mexico and the Nearctic region.

Phylogeny of *Stylogaster* Macquart, 1835 (Diptera: Conopidae) based on morphological characters

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Keywords: *Stylogaster*, taxonomy, fossil, phylogeny

Conopids are a worldwide group of parasitoid flies. The remarkable genus *Stylogaster* Macquart, 1835 is recorded from all zoogeographic regions except for the Palaearctic, but is poorly studied in phylogenies due to the low sampling of species, especially outside the New World. *Stylogaster* species are nectarivorous as adults and have a characteristic morphology and behavior compared to other conopids, making them considered a separate family by many authors. Here, a set of 120 *Stylogaster* species, representing about 98% of the known diversity of the genus, is analyzed. An implied weighting parsimony analysis was performed, using a concavity constant *k*-value of 11.68. From a total dataset of 134 terminal taxa and 269 morphological characters, a single most parsimonious tree with 2859 steps, F=99.7%, CI=10 and RI=59 was recovered. The resulting topology divides *Stylogaster* in two large clades, one in the New World and one in the Old World, both proposed as new subgenera. The American species, previously divided into four species-groups, are largely reformulated taxonomically and divided between a short ocellar triangle and a long ocellar triangle clades, which are considered as the new species-groups. The basal position of the fossil species in one of the New World species group indicates a minimum age of 23 mya at least for this clade.

Advances in the knowledge of Ecliminae Hall, 1969 (Diptera: Bombyliidae): morphological and systematics studies

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Keywords: Asiloidea, Bombyliidae, morphology, phylogeny

The worldwide subfamily Ecliminae belongs to the family Bombyliidae and includes 59 species in nine genera: *Alepidophora* Cockerell, *Cyrtomyia* Bigot, *Eclimus* Loew, *Lepidophora* Westwood, *Marmasoma* White, *Palintonus* François, *Paratoxophora* Engel, *Thevenetimyia* Bigot and *Tillyardomyia* Tonnoir. Traditionally, the Ecliminae genera were classified among the Toxophorinae or the Cylleniinae, depending on the author, until the official establishment of the subfamily proposed by Hall. Relationships within Bombyliidae were recently postulated by Yeates, who ranked Ecliminae to tribe status within Bombyliinae, according to cladistics analysis based on morphological characters. Posteriorly, Evenhuis and Greathead revalidated the group as a subfamily based on morphological differences. The Ecliminae has the body elongated, usually with scales and have a modified sand chamber in the female terminalia. Recently, a phylogeny for *Lepidophora* was proposed and confirmed the monophyly of the genera *Lepidophora*, *Cyrtomyia* and *Palintonus*, as well as the sister group relationship between *Lepidophora* and *Cyrtomyia,* corroborating previous, intuitive or based on cladistics analysis, hypothesis. *Palintonus* appears as the putative sister group of this clade, corroborating one of the groups proposed by Greathead from a phenetic analysis for Ecliminae. Considering the historical problems surrounding the classification of Ecliminae and the dubious positioning of their genera, we expanded the study group to test the monophyly of the subfamily and its supraspecific taxa, as well as to infer the relationships among them. Until now, 171 morphological characters were coded for 42 terminal taxa, of which seven are outgroups. The characters related to integument projections (hairs, scales, tubercles, bristles) represent approximately 75% of the data available and were selected on the basis mainly of relevance that have shown with the systematic study in progress. As expected result, these characters must have a great influence on the phylogenetic hypothesis for Ecliminae, contributing to the systematic knowledge of the group and future biogeographycal studies.

Frog flies (*Caiusa* Surcouf, 1920) (Diptera: Calliphoridae)

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Keywords: *Caiusa*, Calliphoridae, Anura, Rhacophoridae, foam nests

A progress report on an ongoing revision of the taxonomy of the Oriental, Australian and Oceanian frog fly genus *Caiusa* (Surcouf, 1920) (Calliphoridae: Phumosiinae) is presented. The genus has previously been treated as a synonym under *Phumosia* Robineau-Desvoidy, 1830, but several peculiarities of the male genitalia, especially the shape of the pregonites, justify a separate status. Seven nominal species have been assigned to the genus in the past, two of which are still unplaced because based on females (*violacea* Séguy, 1925 and *dubiosa* Villeneuve, 1927). Two others will be synonymized under the fifth species *indica* Surcouf, 1920 (*nigronitens* Senior-White, 1923 and *surcoufi* Bezzi, 1927). The two remaining names are *testacea* Senior-White, 1923 and *coomani* Séguy, 1946. All three names have been misapplied frequently in the past because too much reliance has been put on external colour differences, and insufficient attention has been given to the male genitalia. Recent collection of *Caiusa* flies from the foam nests of various rhacophorid tree frogs in South East Asia has revealed the existence of four new species, all clearly recognisable by the male genitalia only. Eight valid species will be recognised, including a fifth new species from the Japanese Ryukyu island chain, bred from a rhacophorid frog species only found there (*Rhacophorus owstoni*). Seven species oviposit on the foam nests of rhacophorid frogs and the fly larvae devour the developing frog embryos. One species, *Caiusa indica*, has so far not been collected from rhacophorid frog foam nests. It has a wide distribution in Asia, and also occurs in Papua New Guinea, Solomon Is and Australia where rhacophorid frogs do not occur. Photographs of the male genitalia of all the eight valid species will be presented.

Tertiary Anthomyzidae (Diptera): a review of described taxa, with discussion on habitat association and diversity

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Keywords: Diptera, Anthomyzidae, Tertiary, Eocene, Baltic amber, Dominican amber, habitat and diversity, Eocene amber forest

All known ancient (Tertiary) taxa of Anthomyzidae (Diptera) are reviewed with a total of four genera and 13 species as currently recognized. Most of them (nine) belong to the exclusively fossil subfamily *Protanthomyzinae* Roháček, 1998 with the single genus *Protanthomyza* Hennig, 1965 which according to Roháček (2013) contains one unnamed (*P.* sp.) and 8 named species, viz. *P. collarti* Hennig, 1965, *P. hennigi* Roháček, 2013, *P. hoffeinsorum* Roháček, 2013, *P. krylovi* Roháček, 2013, *P. loewi* Roháček, 2013, *P. meunieri* Roháček, 2013, *P. presli* Roháček, 2013 (all from Baltic amber) and *P. tschirnhausi* Roháček, 2013 (from Bitterfeld amber). Because the amber from Bitterfeld is actually considered to be a re-deposited Baltic amber, all these amber inclusion fossils are dated to Middle Eocene (38–50 mya). The remaining four ancient species belong to three different genera of the largely extant subfamily Anthomyzinae Czerny, 1903. The Middle Eocene genus *Lacrimyza* Roháček, 2013 is represented by two species, viz. *L. lacrimosa* Roháček, 2013 (Baltic amber) and *L. christelae* Roháček, 2013 (Bitterfeld amber). Also of the same age is *Reliquantha eocena* Roháček (in press), recently discovered in a Baltic amber inclusion, a fossil species belonging to the genus *Reliquantha* Roháček, 2013 which was established for the extant *R. variipes* Roháček, 2013 from Great Britain. Only the genus *Grimalantha* Roháček, 1998, with the single species *G. vulnerata* Roháček, 1998 is younger; it was described from Dominican amber (Mid Miocene, 17–20 mya). All but this latter ancient species of Anthomyzidae originate from the Eocene Baltic amber and, consequently, had to live in the 'Baltic amber forest', probably in wet habitats of forest undergrowth not very different from those of contemporary Anthomyzidae as indicated by syninclusions found in amber samples with Anthomyzidae (repeatedly Chironomidae, Sciaridae, Dolichopodidae). However, because the members of the extinct Protanthomyzinae are so markedly different morphologically from the Anthomyzinae (note e.g. the presence of A_2, setose mesopleuron), their habitat association could possibly also be somewhat different from those of ancient and recent Anthomyzinae. The most striking feature of Baltic amber Anthomyzidae proved to be their unexpectedly high species diversity: apparently, more species lived in the Eocene amber forest than is known from the whole of Europe today.

Biodiversity surveys [poster]

A shitload of flies: surprisingly rich alpine fauna of dung flies in Switzerland (Diptera: Sepsidae)

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Keywords: Sepsidae, altitudinal gradient, diversity, species richness

The Sepsidae are a relatively species poor family of acalyptrate flies strongly associated with vertebrate excrements and decaying organic matter. Recent studies on sexual selection, thermal adaptation and ecotoxicology document a steadily growing interest in this family as a model organism in evolutionary ecology. However, thus far we have a very poor understanding of the basic ecology and distribution of sepsid flies in Central Europe.

We identified more than 5000 individuals from ethanol collections and present first data on the distribution and diversity of sepsids in Switzerland. Individuals were sampled over the years from 1980 to 2012 at more than 150 locations covering most of Switzerland, representing the northern and southern lowlands as well as the central alpine regions. The 19 recorded species include representatives of all native genera (*Meroplius, Nemopoda, Saltella, Sepsis, Themira*).

We found a surprisingly rich alpine fauna consisting of up to 12 sympatric *Sepsis* species at one particular high altitude site (Lenzerheide, Graubünden) representing all *Sepsis*-species known to Switzerland. Such a high extent of sympatric species was never observed before and suggests elaborate and yet uninvestigated niche partitioning. Species richness, evenness and diversity correlate significantly with altitude and climate variables. Differences in community composition between the lowlands and the alpine regions, species distribution patterns and possible niche differentiation are discussed.

Cross-continental variation in sexual selection and its effect on the contrasting reversal of sexual size dimorphism in closely related sepsid fly species (Sepsidae: Diptera)

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Keywords: Sepsidae, sexual selection, body size, population divergence

Sexual size dimorphism (SSD) arises when the net effects of natural and sexual selection equilibrate differently in males and females. Species and even populations within a species can exhibit quantitative variation in the extent of SSD, but qualitative reversals in SSD are rare. In a previous study, we document that sexual selection accounts for a geographic reversal of SSD in the widespread sepsid fly *Sepsis punctum*. Here, we study the variation in sexual selection acting on male body size in three further closely related species with contrasting reversals of SSD in Europe (EU) vs. North America (NA). In all three species, laboratory-reared offspring indicate clear genetic differentiation among populations in body size and development time. Using common garden experiments, we document female-biased SSD in all EU populations of *S. cynipsea*. However, in its sister species *S. neocynipsea* females are larger in EU, whilst NA populations exhibit male-biased SSD. This is in sharp contrast to our earlier work on *S. punctum*, NA populations of which display female-biased SSD, whereas in EU males are larger. Yet in another species, *S. biflexuosa*, SSD is consistently absent, the sexes having similar body sizes in both EU and NA. We conducted mating experiments under three increasing male-biased operational sex ratios in the laboratory to calculate selection differentials based on pairing success to estimate sexual selection acting on body size. Although sexual selection on males was overall positive, contrary to *S. punctum* there was quantitative but no significant qualitative relationship between the intensity of sexual selection and male body size in *S. neocynipsea*. It is possible that the potentially counteracting effects of viability selection acting on both sexes and/or fecundity selection acting on females could be stronger than sexual selection on males, which requires further investigation.

Genetic data confirm the species status of *Sepsis nigripes* Meigen (Diptera: Sepsidae) and thus adds a species to the Alpine fauna while questioning the synonymy of *Sepsis helvetica* Munari

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Keywords: Sepsidae, molecular identification, phylogenetics, *Sepsis nigripes, Sepsis luteipes*

Sepsid flies (Diptera: Sepsidae) are becoming increasingly important model organisms in evolutionary biology because of conspicuous sexual dimorphisms and the ability to conduct elaborate experiments with many species that breed well under laboratory conditions. Accurate species boundaries and phylogenetic relationships are thus of interest to many biologists. Here we resolve the conflict surrounding the taxonomic status of the European *Sepsis nigripes* Meigen, which is shown to be a valid species using morphological and molecular data based on multiple species concepts. The species is also placed onto a phylogenetic tree for the genus *Sepsis* that includes most European and North American *Sepsis* species. In addition, we assess the genetic variability between two populations of the Holarctic *Sepsis luteipes* Melander and Spuler from Europe and North America and find conflicting evidence between morphology and DNA sequences. Different species concepts here yield different inferences, and if two species were to be accepted, *Sepsis helvetica* would have to be resurrected from synonymy. We provide high-resolution images for all species in order to aid in accurate identification.

Diversity of mosquito species (Diptera: Culicidae) in three ecosystems from the Colombian Andes: identification through DNA Barcoding and adult morphology

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Keywords: Culicidae, Colombia, barcoding

The family Culicidae contains approximately 3,500 species of mosquitoes distributed over a diverse range of habitats around the world. Mosquito identification has been traditionally conducted with morphological features; however, the development of molecular techniques, such as DNA-barcoding, provides opportunities for gaining higher resolution in species determination. Colombia, one of the world's megadiverse countries, has a highly diverse mosquito fauna and a high prevalence of mosquito-borne diseases such as malaria and dengue. This study provides relevant up-to-date information about the diversity, taxonomy, and occurrence patterns of mosquito species in Colombia. To do so, our research tests the usefulness of combining adult morphology and barcode sequences to identify and describe 22 different mosquito species from eight genus collected over different gradients in the Departments of Antioquia and Caldas. Our study shows the importance of combining methodologies to accurately identify the diversity of mosquitoes.

2 in 1: DNA Barcoding reveals new host-parasitoid relations

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Keywords: Pipunculidae, Auchenorrhyncha, COI, GBOL

Information about host-parasitoid relationships is limited, especially for Diptera acting as parasitoids. But such kind of biological data is absolutely essential needed for understanding interaction of taxa within our environment. Within the German Barcoding Campaign (GBOL) new host-parasitoid relations between big-headed flies and cicadas were detected and analyzed. Some practical advice was given how to get both of the barcodes.

Molecular identification of Diptera [poster]

German Barcode of Life Project: first dipterous results

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Keywords: DNA barcoding, Diptera, GBOL

The GBOL (German Barcode of Life) project is a national DNA barcoding campaign to capture the genetic diversity of animals, fungi and plants in Germany. GBOL has been granted a funding of approximately 5 million Euros by the German Federal Ministry of Education and Research (BMBF) for an initial period of 3.5 years. The GBOL project is a step towards collecting, processing, data sharing and deposition of samples in conventional and molecular collections in order to facilitate the compilation of an open-access DNA barcode library of biodiversity.

GBOL is a national consortium of natural history museums and other research institutions which will provide their professional taxonomic expertise and existing infrastructure (collections/biobanks, databases, bioinformatics platforms and laboratories) to comprehensively collect, catalog, describe, and sequence the eukaryotic species in Germany. Professional taxonomists in GBOL depend on the enthusiastic and active support of qualified amateur taxonomists to establish a comprehensive library of biodiversity.

Though far away from a comprehensive genetic library covering all German diversity of Diptera a first overview of surprising results from our national DNA barcoding campaign is given.

AMTC: Automated Malaise Trap Changer

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Keywords: Flying insects, monitoring biodiversity, metabarcoding, DNA barcoding

Progress of molecular investigations, for instance so called metabarcoding, requires for efficient realization automated sampling in the field. The AMTC is combined with a standard malaise trap. Due to a solar panel buffered by rechargeable batteries it can be run autonomous in remote areas for weeks. Time frame of changing collection bottles is adjustable. In combination with climate data logger it may open a new dimension within ecological research (of Diptera).

Technique and microscopic preparations of first-instar larvae of Psychodinae (Psychodidae, Diptera)

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Keywords: Psychodidae, Psychodinae, first instar larvae

Newly hatched larvae of Psychodinae (Psychodidae) have important characters that can help to find a more stable classification of these insects. The technique for preparing these larvae is based on the number and position of spines and setae as well as on other characters. In the present study, females were collected with a net and kept individually in small glass vials with a drop of water. The mated females lay eggs a few days later. Some of the newly hatched larvae were mounted on slides and others were kept alive in a suitable environment to obtain the 4th instar larvae and adult males for identification.

The taxonomy of some species of Psychodinae (Diptera: Psychodidae) based on the characters of newly hatched larvae

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Keywords: Larva, morphology, Psychodidae

The second, third and fourth instar larvae of the subfamily Psychodinae (Psychodidae) have important characteristics that can help to find a suitable classification for these flies. It was found that the newly hatched larvae were different from those of the 2nd, 3rd and 4th instars, possessing characters that distinguish them from genera of other subfamilies within the Psychodidae. This work contributes towards a key for the 1st stage larvae of several species. It also suggests that the taxonomy of these flies based on male characters must be reviewed.

Surveying Diptera in Finnish Lapland – a case study from a conservation area

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Keywords: Lapland, species inventories, conservation value

Natural Heritage Services (NHS) of Metsähallitus is a governmental authority managing state owned conservation areas in Finland. National Parks, Wilderness Areas and other conservation areas cover ca. 3,2 million hectares of Finnish Lapland. NHS is responsible of protecting and monitoring species and habitats in state-owned conservation areas. Since 2012, dipterans have been surveyed in Lapland by NHS. The aim of using Diptera in species inventories is to have an additional biotic group in the assessment of conservation values of terrestrial and freshwater habitats. During 2012 and 2013, Malaise trap samples were taken in the Törmäoja conservation area (FI1301512). Törmäoja is situated in eastern Lapland, belonging to the River Tuloma catchment area (waters end up in the Barents Sea). Mining activities are planned to the immediate vicinity of Törmäoja, and large-scale changes in land use may have negative effects on the biodiversity in the conservation area. A total of nine traps operated from the beginning of June till the end of September in both years. Mycetophilids (sensu lato), tipuloids and chironomids were identified from the samples. So far, 430 nematoceran species have been identified (by Lauri Paasivirta and Jukka Salmela). A total of 15 Red List nematocerans have been found, including species such as *Orthocladius abiskoensis* Thienemann & Krüger, 1937, *Greenomyia baikalica* Zaitzev, 1994 and *Rhabdomastix parva* (Siebke, 1863). Fifteen fungus gnat species have been encountered for the first time in Finland, e.g. *Mycomya thula* Väisänen, 1984, *Pyratula subcanariae* Chandler & Blasco-Zumeta, 2001 and *Boletina intermedia* Lundström, 1915. Diptera, as a diverse group in the boreal zone, may have a great potential in the assessment and monitoring of the state of northern nature. Due to their high species richness in northern Fennoscandia, families such as chironomids and mycetophilids may shed new light on the conservation value of habitats in the north.

Molecular identification of *Tabanus glaucopis* (Diptera: Tabanidae) from Eskisehir-Turkmenbaba mountain

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Keywords: *Tabanus glaucopis,* COI, molecular identification

It is seen that infinite gene replacements have occurred when millions of generations are taken into account. The reasons of these replacements are mutations, selections and recombinations. These replacements are not always observed in phenotype. Consequently, different species can be evaluated as the same species. To overcome this complexity of the classification, molecular identifications are needed. Classification of Arthropoda has been based on the basis of the morphological characters for years, but recently this phenomenon has been replaced with molecular characters. Mitochondrial DNA was isolated from the collected samples, and PCR was carried out to amplify the desired gene region by using an appropriate primer. The 658 bp long COI gene of interest to be amplified, was monitored by using gel imaging analysis, and after determination of the desired size, purification was performed. Sequence information of the gene region that has been purified was obtained by sequence analysis method. Sequence analysis results of PCR products, which is collected from *Tabanus glaucopis* (Diptera: Tabanidae) individuals, was compared with data from NCBI data bank, and showed a high level of similarity. In this study, the COI gene region, which is a molecular character, was used for identification of the species, *Tabanus glaucopis*, which was previously identified morphologically, from Eskisehir, Turkmenbaba Mountain area, and accuracy of the morphological identification was supported by molecular data.

Culicomorpha [poster]

Comparative morphology of the larval hypostomium and postgenal cleft of the subgenera of *Simulium* Latreille 1802 (Diptera: Simuliidae) in the Neotropical region

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Keywords: Systematic, immature, aquatic insects

Simulium Latreille (Simuliidae, Diptera) is a cosmopolitan and monophyletic genus that included 2,151 valid species distributed in 37 subgenera. In the Neotropical region ten subgenera are present (sensu Adler & Crosskey, 2011). Most species of *Simulium* in the Neotropics are well described, however, knowledge of the larval stage is merely descriptive and comparative studies are lacking. For this reason the diagnostic characters of the *Simulium* subgenera larvae and their species are not satisfactory. For identification, the last instar larvae are normally used but the number of larval instars in black flies is variable, being reported from 6–8 in the Neotropical region. Most larval features vary across the larval life, however, two structures appear to remain relatively constant during the larval development, the hypostomium and the postgenal cleft, although the size of these structures naturally increases as the head capsule grows. In *Simulium* the postgenal cleft varied from very deep to not evident and the hypostomium have the hipostomial teeth almost similar being the median tooth approximately at same level as the laterals. We present a comparative study of these structures for *Simulium* larvae belonging to the Neotropical subgenera were we denoted that the combined use of these two characters may be useful to identify the larvae in subgenera or even species groups, regardless of in which instar they are. Examples: (1) shallow postgenal cleft and hypostomial medial tooth at same level as lateral teeth distinguishes the subgenus *S*. (*Aspathia*) from *S.* (*Inaequale*), who presents a deep postgenal cleft and the hypostomial medial tooth lower than the lateral teeth); (2) *S*. (*Chirostilbia*) – postgenal cleft bell shaped or subovoidal distinguishes the Pertinax species-groups from the Subpallidum species-groups. This study provides morphological data for a better understanding of the *Simulium*, contributing to systematic studies.

A biographical profile of Nelson Papavero

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Keywords: Dipterology, Hennig, history of science, Neotropical region, phylogenetic systematics

Nelson Papavero is one of the major Brazilian dipterologists. His contribution to Neotropical zoology began in the second half of the twentieth century, when he started publishing in the areas of entomology, systematics, biogeography, and history of science, while working at graduate courses and training teachers and students. Papavero was one of the earliest Brazilian advocates of Hennig's phylogenetic systematics. In his entomological work, his first widely recognized works were the Catalogue of South American Diptera and his essays on the history of Neotropical Dipterology. Papavero's greatest contribution, however, is in his Special Courses on Zoological Systematics, as well as his numerous administrative positions during his academic career. All these were fundamental to the development of zoology and comparative biology in Brazil and other Latin American countries. Papavero retired in 1997. He is currently working on a dictionary of popular animal names, and is a collaborator of the Research Center for Entomology and History of the Portuguese Language. Papavero is also consistently publishing on the history of systematics and biogeography. Here we present a biographical profile of Nelson Papavero, discussing his role in the development of Brazilian biological systematics over the last 50 years.

Higher-level phylogeny of Diptera [poster]

Supertree approach and the phylogeny of Diptera (Hexapoda: Holometabola): methodological and taxonomic considerations

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Keywords: Brachycera, heuristics, monophyly, Nematocera, supermatrix

Supertree is a technique to combine phylogenies resulted from the analysis of different primary data. It is built by the combination of the topologies of primary studies, and does not deal with characters per se. The supertree topology reveals which clades remain stable and well explained, and which ones need more attention in further analyses. Herein, we review the main topics concerning the supertree approach, especially the matrix representation with parsimony approach (MRP approach), and present a supertree for the order Diptera. The main aim of the analysis is to improve the supertree presented by Yeates et al. (2007) by adding two other source matrices. In our supertree, “Nematocera” is paraphyletic, as traditionally considered in literature, with the families of Psychodomorpha inserting instability on the phylogenetic hypothesis. Also, the relationships among Culicomorpha, Ptychopteromopha, Limoniidae and Blephariceromoprha remains uncertain. Brachycera is monophyletic, and the main ambiguities within the group concern Asiloidea and Nemestrinoidea, both considered paraphyletic groups. The supertree technique shows flaws, as other heuristic methods, but is a powerful tool to deal with more inclusive phylogenetic hypothesis, as those dealing with the megadiverse order Diptera. Its results also suggest the need for subsequent studies to elucidate the unsolved relationships revealed in the supertree.

Culicomorpha [poster]

Mosquitoes (Diptera: Culicidae) in an Atlantic Forest fragment in Southern Brazil

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Keywords: Atlantic Forest, environmental factors, hematophagy, seasonality

Estimating mosquito richness in forest fragments is important for evaluating the conservation state of protected areas, as well as identifying species of potential disease vectors in those habitats. The aim of this study was to estimate the species richness of Culicidae in one 80-hectare Atlantic Forest fragment in Rio Grande do Sul State, Southern Brazil. Insects were sampled monthly between October 2012 and September 2013 in the morning, afternoon, and evening. Mosquitoes were actively collected using human bait during the day, and Shannon traps at night. A total of 572 specimens of adult mosquitoes, classified in 16 species and 11 genera, were captured. The most represented species were *Psorophora ferox* (32%), *Aedes crinifer* (23%) and *Coquillettidia venezuelensis* (23%). Mosquitoes were most abundant in the autumn (42%), followed by spring (34%), winter (16%) and summer (8%). Similarly, the highest species richness was observed in the autumn (n=10), followed by spring (n=9), summer (n=9) and winter (n=7). With regard to the collecting period, the highest number of mosquitoes occurred in the afternoon (46%), followed by night (32%) and morning (22%). *A. crinifer*, *Sabethes purpureus* and *Culex dolosus/eduardoi* were collected in all seasons, however, only *A. crinifer* was present in large numbers in all sampling periods. A Canonical Correspondence Analysis indicated that mosquitoes had their hematophagous activity affected by environmental factors, such as temperature, relative humidity, and rainfall. Some species found in the study commonly develop in large puddles, such as *Aedes scapularis*, *Aedes serratus* and *P. ferox*. The presence of species of *Sabethes* suggests that the area surveyed is well conserved. Despite being collected less frequently, *Haemagogus leucocelaenus*, responsible for the maintenance of the wild cycle of yellow fever, was found in the fragment, indicating the need for more studies in this area.

Overview of tabanids inhabiting in Hokkaido, Japan (Diptera: Tabanidae)

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Keywords: Hokkaido, tabanids, fauna, Japan, diversity

Tabanids or deer flies are a serious nuisance to livestock and damages by tabanids are not only caused by blood sucking but also the transmission of diseases. Cattle in Hokkaido is assumed to be strongly infected by Bovine Leukemia Virus that is transmitted mainly by tabanids.

Hokkaido is the second largest island in Japan, located at the North end, and has coastlines facing the Sea of Japan, the Sea of Okhotsk, and the Pacific Ocean. Its geographical coordinates are 43°N and 142°E and the total area is 83,450 km^2. Currently, 33 species and 4 subspecies in 7 genera are recorded from Hokkaido. Most of these species are shared with Honshu (main island of Japan), only *Hybomitra takahasii* is endemic to Hokkaido. Nearly half of the species also occur in Siberia, East China and Sakhalin. Tabanids in Hokkaido show 4 different distribution patterns: they occur either on the entire island, or only in the central and western parts, the eastern and northern parts, or the southern part. In Hokkaido, tabanids are active from June to September and reach an abundance peak between July and early August. *Chrysops japonicus* emerges earliest in the season, and *Tabanus rufidens* latest. *Tabanus nipponicus* and *Chrysops suavis* have the longest activity periods. Eight species are recorded as autogeny and some of them are known to be serious pests to livestock in Hokkaido. *Tabanus nipponicus*, the major pest species of cattle, also feeds on wild deer. Concerning their attraction to colour, tabanids in Hokkaido prefer black, blue and red, and avoid yellow; only *Haematopota tristis* prefers white and blue.

Relation between seasonal abundance of tabanid flies and bovine leukemia virus infection in pasturing cattle

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Keywords: Japan, tabanids, BLV, *Tabanus nipponicus*

Bovine leukemia virus is transmitted mechanically by haematophagous insects, especially tabanids. The parallel surveys were performed on the municipal pasture in “Q” town of Hokkaido, the northern island of Japan. Seasonal abundance of tabanids was surveyed fortnightly from early July to early September in 2012 and 2013. The CO_2 lured Nzi trap was used to capture the flies at the pasture. Trap was set from 9:00 to 16:00 in every working day. Captured tabanids were killed by ethyl acetate, and identified and recorded the numbers according to the species. Blood samples of pasturing cattle were collected in May, July, August and October of the two years. All serum samples were processed to detect antibodies against BLV gp 51 with a commercial indirect enzyme-linked immunosorbent assay. PCR were also conducted to obtain reliability data for doubtful samples in ELISA test. DNA from peripheral blood samples were isolated by the Whatman FTA cards. A 598-bp and a 444-bp fragment of the env gene were amplified by nested PCR using two pairs of primers according to Fechner, 1997. As a result of field survey, a total of 7,958 flies, belonging to 13 species in 5 genera were collected during summer in 2012 and 2013. The most abundant two species were *Tabanus nipponicus* (5,891 individuals and 74%) and *Haematopota tristis* (1,403 individuals and 18%). The seropositive rate of BLV in cattle was 16.2% and 28.9% in the beginning of pasturing, increased to 24.3% and 35.4% at the end of pasturing in 2012 and 2013 respectively. There is a clear link between seasonal abundance of tabanids and BLV infection. Therefore, it was concluded that the most possible main vector of BLV infection in cattle is tabanids at the surveyed area.

Calyptratae [poster]

Discriminating between species of root-maggot flies (Anthomyiidae: *Delia*) using near-infrared spectroscopy

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Keywords: Near-infrared spectroscopy, species identification, Anthomyiidae, *Delia*

The correct identification of agricultural pests is important for control methods, as these often do not have the same effect against different species. Unfortunately, the identification of many insect pest species such as maggot-root flies of the genus *Delia* using morphology is difficult and time consuming, especially without extensive training. Considering the time investment and how difficult it is to identify *Delia* species, the development of a fast and accurate method for *Delia* specimen identification would be a great asset for onion growers in Québec (Canada), as they are currently experiencing much *Delia*-related damage to their crop. The objectives of this project were therefore to test the ability of near-infrared spectroscopy (NIRS) to discriminate between three species of *Delia* flies often collected in onion crops in Québec and the rest of Canada (*Delia antiqua*, *D. platura*, and *D. radicum*), determine the optimal number of scans for generating average spectral signature, and evaluate the influence of different data transformations on identification accuracy. Our results indicate that even when both sexes are included in the same model, NIRS has the ability to discriminate between pairs of closely related species of *Delia* flies with at least 86% accuracy (80% accuracy when all three species are included in the same model) and that 15 scans and mean-centering appear to be the optimal combination of equipment setting and data transformation.

The evolution of head structures in lower Diptera

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Keywords: Head, morphology, anatomy, evolutionary scenario

The knowledge of adult and larval head anatomy of Diptera is very fragmentary. The understanding of crucial evolutionary events is impeded by the severe lack of morphological data. Therefore, we compiled an extensive morphological dataset of adult and larval head features. Cephalic characters of Diptera are generally greatly affected by homoplasy and therefore of limited value for phylogenetic reconstruction. Thus, the morphological data were mapped on a recently published robust phylogeny based on an extensive molecular dataset. With this approach, an evolutionary scenario was developed for adult and larval head structures. The head of adult dipterans is mainly characterized by reductions, linked with the minor role of feeding and the specialization on liquid substrates. By contrast, the compound eyes and the antennae, sensory organs used for orientation and for finding a suitable mating partner and oviposition site, are well developed. A number of profound modifications took place at the base of the Diptera (groundplan) and also in Brachycera, but head structures are relatively uniform among the lower dipteran lineages. The larvae of the lower dipteran groups differ more strongly in their head structures than the adults but are also affected by convergences and are therefore insufficient for resolving basal dipteran relationships. The mouthparts are only slightly modified compared to the holometabolan groundplan, whereas the larval eyes show a clear tendency towards reduction. Larvae of presumably basal groups, notably Deuterophlebiidae and Nymphomyiidae, live in streams and feed on algae and microorganisms. Adaptations to this life style are the toothed hypostoma and the presence of a mandibular comb and a specifically arranged labral fan. An unusual specialization among dipteran larvae is the predacious life style in Chaoboridae: they possess raptorial antennae inserted on the anterior margin of the head and compound eyes that are suitable for coordinating the catch.

A tussle with Tachinidae

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Keywords: Tachinidae, New Zealand, identification

Tachinidae are considered to be the most speciose family of the order Diptera in the world. There are currently about 140 described species in about 58 genera in New Zealand of which the majority were described by Malloch 1938. The last description by Dugdale dates from 1961, and an attempt to place genera at higher taxon levels was carried out by Dugdale 1969. Many more undescribed species are known and more remain to be discovered. Not much different from many parts of the world, New Zealand Tachinidae are very much understudied. This is despite their ecological importance in regulating herbivore populations and in structuring both natural and managed ecological communities. I will report on the making of the Department of Conservation (DoC) funded Terrestrial and Freshwater Biodiversity Information System (TFBIS) project ‘Virtual guide to the tachinid flies (Tachinidae) of NZ’ which will be but one stepping stone towards a better understanding of New Zealand Tachinidae and hopefully will encourage future research and funding. I present examples of an interactive key to genera of New Zealand Tachinidae, relevant character and imago images, as well as fact sheets. These will be made available on the Landcare Research, Manaaki Whenua website upon completion. Tachinidae are considered to be one of the most difficult families of Diptera in which to make practical identifications and I will discuss some challenging observations and perils faced during the development of the key. An overdue revision at the genus level is recommended for New Zealand Tachinidae.

Systematics of the family Lauxaniidae (Diptera: Acalyptrata)

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Keywords: Lauxaniidae, systematics, immature comparative morphology, molecular markers, phylogenetic analysis

Systematics of the family Lauxaniidae is unsatisfactory. Several taxa are considered as paraphyletic; however, phylogenetic analysis is still missing. Here we used two approaches to systematics: comparative morphology of immature stages and phylogenetic analysis of molecular characters. The immatures were obtained by laboratory rearing. Larvae were than prepared for scanning and light microscopy. For phylogenetic analysis we used two molecular markers: mitochondrial 16S rRNA and nuclear elongation factor 1-alfa. Trees were constructed by three methods: maximum parsimony, maximum likelihood (both constructed in MEGA5) and Bayesian inference (constructed in MrBayes). The immatures were obtained for 30 species, sequences for 55 species. Molecular and morphological characters show that *Cnemacantha muscaria* should be included in genus *Homoneura*, *Tricholauxania* should be possibly included in genus *Meiosimyza*; *Calliopum*, *Lauxania*, *Schumannimyia* (subg. of *Sapromyza*) and *Sapromyza obsoleta* species group form a distinct clade; *Sapromyzosoma*, *Sapromyza sexpunctata* species group and *Pachycerina* form another distinct clade. High number of systematic changes suggested by our results underlies the poor state of knowledge of systematics within this family.

New World Neriidae: diversity and systematics

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Keywords: New World fauna, cactus flies, systematics, taxonomy

Neriidae are a small acalyptrate Diptera family with approximately 111 species in about 19 genera in two subfamilies: Neriinae and Telostylinae. These long-legged flies feed on sap and decaying plant tissues and are found in all biogeographic regions, tending to predominate in the tropics. Only Neriinae is distributed in America, with 38 valid species in 9 genera divided in two groups of species: *Eoneria*-group and *Nerius*-group. In the last few years, the research on Neotropical Neriidae has increased, with revisions and descriptions of new species, including new records for Costa Rica, Colombia, Venezuela, Guyana, Ecuador and Brazil, and a number of synonymies have been discovered. Today, only two New World genera have not been revised: *Antillonerius* and *Nerius* and generic definitions are improving but still needs to take full advantage of phylogenetic methodology. At the time, we are working on the revision of *Nerius*, one of the most conflicted genera in the Neotropical region and one new genus is described from Colombia. In order to place the New World fauna in context, new diagnosis and a key for identification of the genera and its species have been provided and both taxonomic and phylogenetic studies have been conducted, in order to present a preliminary classification within the family.

The study of genera and species of Neriidae from other continents is planned, seeking to understand the delimitation and relationships of the family worldwide.

Calyptratae [poster]

A new record for the Turkish blowfly fauna: *Pollenia rudis* (Fabricius, 1794) (Diptera: Calliphoridae)

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Keywords: *Pollenia rudis,* Calliphoridae, cluster flies, blow flies

Calliphoridae is a cosmopolitan calyptrate family. This family contains over 1000 described species worldwide and almost 115 of them are present in Europe, also a great species richness which is more than known is expecting by researchers. Members of the genus Pollenia are commonly referred to as cluster flies. Taxonomy of some species groups and their life history are well documented. They are Calliphorids that have very diverse habits, especially the larvae. While the adults generally visit flowers, faeces and carrion, there are species whose larvae feed on dead animals, faeces or other decaying organic matter. On the other hand this family has great importance for ecological, medical and forensic science. Their maggots quickly invade the areas of the corpse and grow in size and weight. Information about the size, weight and age of blowfly larvae and adults on a corpse can be used to identify the time, and sometimes place, of death. Distribution, variability and forensically importance of *Pollenia rudis* (Fabricius, 1794), which is the new record for Turkish Calliphoridae fauna, are briefly discussed.

Diversity of fungus gnats (Diptera: Sciaroidea) in a primary lowland rainforest of Brunei: proportion of undescribed species and comparison of sampling methods

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Keywords: Mycetophilidae, Keroplatidae, Borneo, tropics, biodiversity

Diversity patterns of fungus gnats (Diptera: Mycetophilidae, Keroplatidae, Diadocidiidae and Ditomyiidae) were studied in a primary lowland rainforest in Ulu Temburong National Park (Kuala Belalong Field Studies Centre), Brunei, as a part of a broader ecological study undertaken within a joint project of the Universiti Brunei Darussalam and two Czech universities (University of Ostrava and Palacký University).

Within this project, several quantitative sampling methods were used to establish the species composition of selected groups of invertebrates, with special focus on Diptera. They included Malaise traps, coloured pan traps, pitfall traps, rearing from fungi and sweep netting.

More than 50 species of Mycetophilidae, 12 species of Keroplatidae, 1 species of Diadocidiidae and 1 species of Ditomyiidae were collected in February 2013 and January 2014 by means of 6 Malaise traps situated in 3 different microhabitats. Diurnal and night activity of several species was also studied.

The overall proportion of undescribed species was rather high. More accurate estimates will be given during the presentation, together with the Chao 1 estimates of expected species richness of fungus gnats in Ulu Temburong National Park. Concerning the species rich genus *Manota* Williston, a total of 15 species have been found in Brunei, of which six species will be described as new to science in the near future.

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Molecular phylogeny of Bibionomorpha (Diptera): current state of knowledge

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Keywords: Sciaroidea, phylogenetic analysis, molecular markers, systematics

The infraorder Bibionomorpha represents one of the most species-rich clades of Diptera, but phylogenetic relationships among and within its families are still insufficiently known. The molecular phylogeny of the Bibionomorpha has been reconstructed based on the combined analysis of two mitochondrial (12S, 16S) and two nuclear (18S, 28S) gene markers using maximum parsimony, maximum likelihood and Bayesian inference.

The monophyly of the Bibionomorpha was established with high support in both the parsimony and model-based analyses. The monophyly of the Sciaroidea was less supported. Most of the currently recognized families of Sciaroidea proved to be monophyletic. The Keroplatidae appears paraphyletic, with the genera of Macrocerinae being more related to the Cecidomyiidae than to the other taxa of Keroplatidae, however, the support for this arrangement is low.

Both the Bayesian and likelihood analyses of 12 families of Bibionomorpha revealed the Sciaridae as the closest relative of the Diadocidiidae, with the Mycetophilidae as a sister group to this clade. The well-supported clade (Ditomyiidae + Lygistorrhinidae) forms, together with (Cecidomyiidae + Macrocerinae), a moderately supported group that also contains the other taxa of Keroplatidae. The Bolitophilidae is revealed as the sister group to all the other families of Sciaroidea. The (Bibionidae + Pachyneuridae) clade is a sister group to the Sciaroidea. When we included *Nepaletricha* Chandler in the dataset, as a representative of the enigmatic Sciaroidea incertae sedis, most of the support values decreased and this genus occupied a rather isolated position within the Sciaroidea. The families Anisopodidae and Scatopsidae were used as outgroups in this study.

These results continue to be improved and optimized by adding both genes and taxa to the dataset.

Faunistic study of tachinid flies (Diptera: Tachinidae) in northwestern Iran

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Keywords: Tachinidae, fauna, new records, Iran

The fauna of tachinid flies was studied in northwestern Iran (East Azerbaijan, West Azerbaijan and Kordestan provinces) during 2009–2013. A total of 52 species from 4 subfamilies were identified, of which 12 genera and 22 species belong to the subfamily Phasiinae. Ten genera and 17 species of the subfamily Tachininae were recognized, of which three genera, *Ceracia* Rondani, *Triarthria* Stephens, and *Zophomyia* Macquart, and 10 species, *Ceracia mucronifera* Rondani, *Linnaemya frater* (Rondani), *Macquartia chalconota* (Meigen), *Macquartia praefica* (Meigen), *Nowickia ferox* (Panzer), *Nowickia atripalpis* (Robineau-Desvoidy), *Peleteria abdominalis* Robineau-Desvoidy, *Tachina magna* (Giglio-Tos), *Triarthria setipennis* (Fallén) and *Zophomyia temula* (Scopoli), are recorded for the first time from Iran. In this survey nine species belonging to eight genera of the subfamily Dexiinae were also identified. Of these, three genera, *Eriothrix* Meigen, *Dexia* Meigen and *Hypovoria* Villeneuve, and six species, *Athrycia trepida* (Meigen), *Dexia rustica* (Fabricius), *Zeuxia cinerea* Meigen, *Zeuxia erythraea* (Egger), *Eriothrix rufomaculatus* (De Geer) and *Hypovoria hilaris* Villeneuve, are new records for the fauna of Iran. Only four species of the subfamily Exoristinae were identified in this study, two of which, *Belida angelicae* (Meigen) and *Phryno vetula* (Meigen), are recorded for the first time from Iran.

DNA polymorphism in mosquito species (Diptera: Culicidae)

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Keywords: Culicidae, DNA polymorphism, DNA markers

Exact identification of morphologically similar or identical mosquito species is essential for the controlling of human and animal infections. It is particularly challenging to distinguish representatives of species complexes, such as *Anopheles maculipennis* and *Culex pipiens* (Diptera: Culicidae). The problem can be solved by application of molecular-genetic analysis and development of DNA markers that identify species and subspecies of these groups. Both nuclear and mitochondrial markers are commonly used for these purposes. Nuclear markers allow us to detect potential hybrids and mitochondrial – the origin of species. Both have advantages and limitations.

The usefulness of simple PCR-based assays for molecular identification of species from four genera, *Culex, Aedes, Ochlerotatus* (subfamily Culicinae) and *Anopheles* (subfamily Anophelinae), is discussed. We found that nuclear markers are more useful for distinguishing *Anopheles* species, whereas mitochondrial markers are better suited to distinguish *Culex* species in temperate climates. In areas of proposed hybridization it is necessary to use both types of markers.

New data on the genus *Hybos* Meigen (Diptera: Hybotidae) from the Palaearctic region

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Keywords: Empidoidea, Hybotidae, *Hybos*, Palaearctic region, taxonomy

The taxonomy and distribution of the genus *Hybos* Meigen in the Palaearctic region is reviewed. Twenty-five species have been recorded from the Palaearctic, of which 4 species are known from Europe. We describe 2 new species from Portugal and Middle Asia and clarify 2 doubtful species described from Algeria and Iran. Numerous new data on distributions of *H. culiciformis* (Fabricius, 1775), *H. femoratus* (Müller, 1776), *H. grossipes* (Linné, 1767) and *H. vagans* Loew, 1874 are given. COI barcoding helped in reconstructing the phylogeny of the West-Palaearctic species.

Mining Genbank to resolve Orthorrhapha: a supermatrix analysis of lower Brachycera

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Keywords: Evolution, diversification, orthorrhaphan phylogeny

Fly evolution has undergone at least three rapid bursts of diversification, one occurring within the lower Brachycera approximately 180 Ma. This region of the fly tree includes 23 families with a diversity of life histories: large flower visiting flies, blood feeders (Tabanidae, Athericidae, Rhagionidae), parasitoids (Bombyliidae, Acroceridae, Nemestrinidae) and predators (Asilidae). Though most of lower Brachycera has traditionally been grouped together in Orthorrhapha, it has widely been considered a paraphyly lacking both morphological and molecular support. Recent large-scale molecular analyses of higher-level fly phylogeny, however, found a monophyletic Orthorrhapha (excluding Empidoidea) to be well supported. To test this unexpected result of orthorrhaphan monophyly, we have compiled a supermatrix of existing molecular markers from Genbank for a taxon dense sampling of lower brachycerans. This data set, including over a thousand of taxa and up to 18 genes, is the largest compiled to date for the resolution of fly phylogeny.

A molecular phylogeny of the family Sciaridae (Diptera: Sciaroidea), focused on the *Pseudolycoriella*-group and related genera

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Keywords: Sciaridae, *Pseudolycoriella*-group*,* *Rhynchosciara,* phylogeny, classification

The *Pseudolycoriella*-group was proposed in an earlier molecular phylogenetic study, and is the most controversial group of genera within the Sciaridae. This group includes the taxa *Bradysiopsis, Camptochaeta*, *Dichopygina*, *Lycoriella*, *Pseudolycoriella*, *Xylosciara*, *Keilbachia*, and *Corynoptera boletiphaga* species-group. A recent molecular phylogenetic study showed that the *Pseudolycoriella*-group + Megalosphyinae is monophyletic. However, the monophyly of *Pseudolycoriella*-group has not been supported in any morphological or molecular study. To solve this complex relationship, we reconstructed the molecular phylogeny of the Sciaridae, with emphasis on the *Pseudolycoriella*-group and related genera. The monophyly of genera *Dichopygina* and *Claustropyga* were strongly supported. However, the genera *Camptochaeta*, *Corynoptera*, *Cratyna* (*Peyerimhoffia*), *Lycoriella*, and *Xylosciara* were revealed as non-monophyletic. In the Megalosphyinae, a species of *Rhynchosciara* appeared as sister taxon of *Bradysia* + *Phytosciara*. The classification of the Sciaridae is discussed based on the results of these molecular analyses.

Phylogeny and biogeography of *Labrundinia* Fittkau, 1962 (Diptera: Chironomidae): evidence from morphological and molecular analyses

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Keywords: Pentaneurini, Tanypodinae, Bayesian inference, parsimony, CAD

The genus *Labrundinia* (Diptera: Chironomidae) was erected by Fittkau based on *Tanypus longipalpis* Goetghebuer as the type species. It comprises 39 species, all except *Labrundinia longipalpis* described from areas outside the Palearctic region: five from North America, four from Central America and 29 from South America. Relationships among *Labrundinia* species were postulated by S.S. Roback, who recognized four groups of species based on morphological characters of immatures. In the present study, phylogenetic relations among known *Labrundinia* species are inferred using partial DNA sequences of the nuclear protein-coding gene CAD and morphological characters. Both maximum parsimony and Bayesian analyses suggest that the genus is monophyletic and robust species groups in the molecular phylogenies are supported by morphological characters. The historical biogeography of *Labrundinia* is analysed based on the phylogenetic reconstructions. Brooks Parsimony Analysis (BPA) and dispersal-vicariance Analysis (DIVA) both favoured the *Labrundinia* ancestor as having its initial diversification in the Neotropical region and that current presence in the Holarctic region is due to later dispersal.

The species of *Physegenua* Macquart, 1848 (Diptera: Lauxaniidae) from Brazil, with a key to the Brazilian species

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Keywords: Brazil, Lauxaniidae, new species, *Physegenua*

The genus *Physegenua* was described by Macquart (1848). During the period of 1868 to 1902 many authors dealt with the genus, describing new species or just transferring others to it. Hendel (1908) was the first to give a more complete characterization of the genus; he included eight species, with an African, South American and Oriental distribution. All the non-Neotropical species of *Physegenua* were examined by different authors along the time and were transferred to other genera by Curran (1938), Shewell (1977) and Pape & Thompson (2010). After all those changes, the distribution of its species returned to be strictly Neotropical. So far, the genus is composed of 11 valid species (Gaimari & Silva, 2010), occurring mostly in Central and Northern South America: *P. eronis*, *P. ferruginea*, *P. lineata*, *P. striatopunctata*, *P. vittata*, *P. annulata*, *P. banksi*, *P. centralis*, *P. obscuripennis*, *P. urina*, and *P. vittifrons*; the first five species are known to occur in Brazil. This study was done with material from 12 collections around the world. As a result, a new status, a new combination, and a new synonym are proposed; also, a new species, from Brazil, is described. *Physegenua* may be distinguished from other lauxaniid genera by its face strongly convex, protruding beyond eye in profile; frons broad, anteriorly concave; anterior fronto-orbital seta strongly medioclinate; acrostichal setulae biseriate; and scutellum almost as long as wide. The new species is distinct due to body yellow; frons with two small blackish spots; face without markings; thorax with small spot on anepisternum and two short vittae on mesonotum; legs yellow, but tibiae brownish black, fore femur with subapical black ring; wing brownish hyaline, darker at anterior margin. A key to the Brazilian species of *Physegenua* is presented.

Nearctic balloon flies: resolving the diversity of *Empis* (*Enoplempis*) (Diptera: Empididae)

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Keywords: Empididae, *Empis*, balloon flies, dance flies, mating behavior

The *Empis* subgenus *Enoplempis* Bigot includes the only balloon-making species in the Empidini. The subgenus is restricted to North America with 35 described species. Nineteen species occur east of the Rocky Mountains and 17 west of the Rockies (including one widespread species). In addition, some 47 undescribed western species have been identified, making *Enoplempis* the dominant subgenus among Nearctic *Empis*. The subgenus includes species with short and fleshy labella, frequently modified male hindlegs (tubercles, lobes, prominent setae or bristle pencils), spine-like ventral setae on tarsomeres of all legs, and females without pinnate scales or expanded darkened wings. The diversity of morphological modifications will be illustrated and the three broad species groups defined. Swarming behaviour and distribution of balloon-making abilities within *Enoplempis* will be discussed.

Distribution and ecological aspects of sand fly (Diptera: Psychodidae) species in India

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Keywords: Phlebotominae, *Leishmania*, distribution, India

Phlebotomine sand flies (Diptera: Psychodidae: Phlebotominae) are unique among insect vectors of disease by the co-occurrence of a large number of competent vector species in Old World endemic transmission foci of leishmaniasis. Visceral Leishmaniasis is caused by infection with the protozoan parasite *Leishmania donovani* with female *Phlebotomus argentipes* considered as the vector. The seasonality of the vector species directly affects the transmission of the infectious disease. Species composition, distribution and diversity of *Phlebotomus* species were used to study the ecological information to develop tools for the control of this disease. Sand flies were collected from various localities monthly between 1800–0600 hours with the help of sticky traps and aspirators, they were processed in 70% alcohol and mounted in Berlese' medium. Identification of species was according to the keys formed by Lewis (1978). A total of 8,131 sand flies were collected with a female/male ratio of 5.6/4.4. Nine species were identified, of which 3 belonged to the genus *Phlebotomus*, 6 to *Sergentomyia*. The increase in leishmaniasis cases is due to a combination of multiple factors, involving changes in climate, human behaviours, vectors and reservoirs. The changing pattern of dispersal and the spatial distribution of sand flies to new locations are critical factors that may implicate an increased risk of human-vector contact.

The results revealed seasonal variation in sand fly prevalence, with the highest peak in July. Soil samples collected were characterized by alkaline (pH 7.6). Thus, the aims of the present study were to determine the composition, geographical distribution and diversity of visceral leishmaniasis vectors in the endemic regions of India. Additionally, this study sought to verify the association between the characteristics of the areas studied and the communities of phlebotomine sand flies inhabiting them. On-going surveys of the sand fly insect fauna are important to increase our knowledge of the areas where these insects occur, as the comprehension of the population dynamics of this group might be an important factor for the implementation of policies for the epidemiological control of leishmaniasis.

Research on Calyptratae in India: a wheel of fire from past to present

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Keywords: Calyptratae, research, India

Research work on Indian insects along modern scientific lines was first started with the advent of the East India Company and Christian missionaries during the mid-eighteenth century. Some enthusiastic Medical Officers of the Colonial Government collected insect materials from several parts of India and supplied them to renowned European systematists. This study is considered as the pioneer scientific contribution on Calyptratae research in India. Flies related to severe economic loss like tachinid flies as pests in sericulture and bot flies related to myiasis in camels and horses were studied and reported mainly during the second half of the nineteenth century. Inauguration of the journal of the Bombay Natural History Society and the Records of the Zoological Survey of India contributed a lot to Calyptratae documentation in India. In the post-independence period, though a number of Indian workers made remarkable contributions on Calyptratae following the British Officials and foreign workers, not all the families have been covered extensively to date. The existing inadequacy of experts in most of the families under the Calyptratae is a serious matter to be reviewed.

Recording and mobilising data for Diptera – a UK perspective

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Keywords: Diptera recording, data mobilisation, data verification

Diptera records are generated by a sparse community of specialists and enthusiasts around the world. Collecting such data is basic prerequisite to understanding Diptera biogeography, however, collating and verifying data from such disparate and sometimes unfamiliar sources can be a major challenge. This presentation will review how we gather Diptera data and examine support systems enabling researchers, policy makers and land managers to access and make use of these datasets. Taking the UK as an example, we will look at new measures being put in place to streamline the data verification process and explore efforts being made to encourage and stimulate more Diptera recording.

Pipunculidae phylogenetics: Preparing the ground for an updated classification and a wave of host research and ecological discovery

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Keywords: Pipunculidae, phylogeny, classification, host use

We are collecting data from five genes (COI, cytB, 12S, CAD and AATS) and morphology to create a new hypothesis of relationships for Pipunculidae. We sampled 161 taxa originating from all biogeographic regions and all but two genera and subgenera (excluding fossil genera) in our attempt to create a thorough analysis. In line with recent work incorporating fossil data, we find support for retaining four subfamilies of Pipunculidae. However, the traditional view of a basal Chalarinae is challenged and molecular evidence suggests that Nephrocerinae is the basal pipunculid lineage. The existing tribal classification is largely supported, requiring only a few tweaks to maintain monophyletic groups. Phylogenetics of the tribe Eudorylini has been the most difficult to penetrate historically and it is now clear that several new genera need to be created to maintain a predictive classification. Despite considerable inroads, more data are still needed to resolve the relationships between Eudoryline lineages. In part to fill in gaps in this analysis, we have created a library of COI sequences (4977 sequences from 862 species). This library of sequences is also being used to guide taxonomic hypotheses and can be queried by anyone when attempting to identify larvae from hosts. The latter is one of the most important areas of pipunculid research and is in dire need of attention. Big-headed fly host relationships have been poorly studied in the past, with host records being obtained exclusively through rearing. Rearing is fraught with difficulty and molecular diagnostics of larvae promises to rapidly improve our knowledge of host relationships.

Syrphidae phylogenetics

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Keywords: Syrphidae, phylogeny, anchored phylogenetics, DNA barcoding

Syrphids are increasingly being used as models and study organisms in ecological research. The demand for predictive phylogenies at both generic and species levels has thus increased substantially. We are coordinating a global effort involving 26 scientists from 13 countries to assemble these phylogenies. Six genes are being used to form the backbone of the effort (all of COI, 28S D2-3, 18S, 2 regions of CAD, AATS and Period, for a total of ~6 kB of data). We are also using anchored phylogenetic techniques on a subsample of syrphids to build a strong phylogenetic hypothesis for higher-level relationships. At this point we have nearly 500 species of over 100 genera included in the six gene project and 30 species of 29 genera sampled using a 500 probe dataset (>200,000 kB of data). Additionally, we are building a large dataset of 5’ COI obtained from pinned museum specimens for use in supplementing phylogenetic hypotheses and for help with taxonomy and association of life stages and sexes (12,817 specimens of 1,499 species). Preliminary phylogenetic results and an overview of the project will be provided during the talk.

Fossil Diptera [poster]

Evolution of the family Tanyderidae in the Jurassic period

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Keywords: Tanyderidae, oldest members, Jurassic period

The family Tanyderidae is one of the most ancient families of Diptera. Currently, this small family mainly inhabits tropical and subtropical regions. Tanyderids are characterized by the highest number of plesiomorphic features in the order Diptera. In the Mesozoic Tanyderidae used to live in the whole area of Eurasia, but as fossils are uncommon we assume that the abundance of individuals was not high.

The oldest record of this family, *Nannotanyderus oliviae* was described on the basis of a wing venation imprint in the sedimentary rock from Lower Jurassic of England (Sinemurian) about 190 mya ago. Dating back to 180 mya are two species form Lower Jurassic of Germany (Toarcian): *N. krzemińskii* and *N. grimmenensis*. Other fossils are reported from Middle and Late Jurassic of Mongolia: *N. kubekovensis* and *N. incertus*. Juxtaposition of wing venation of Jurassic representatives allows us to observe evolutionary tendency within the family Tanyderidae and its relationship with the family Psychodidae.

Sarcophagidae (Muscomorpha) attracted to different baits in a region of “Cerrado”, Southeastern Brazil

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Keywords: Flesh flies, checklist, abundance, attractiveness

Approximately 870 species of Sarcophagidae (Muscomorpha) are known to occur in the Neotropical region. They occur in all Brazilian regions, and the adults are attracted to different substrates, such as urban garbage, feces and carcasses. Studies concerning the abundance of species occurring in the Cerrado are scarce, and studies focusing on this subject are important in order to provide a better knowledge of the dipterofauna present in this biome. The present study aimed to determine the occurrence of flesh fly species composition in a Cerrado area belonging to the Biological Reserve of Mogi Guaçu (Campininha), on Mogi Guaçu City, São Paulo State, Southeastern Brazil. Three active collections were done during the warm and wet season, using four different baits: dog feces, raw minced beef, chicken gizzard and raw fish, exposed in line with a distance of 50 m from each other. Only male specimens were identified to species, using dichotomous keys, and by comparison with voucher specimens deposited on the Laboratory of Entomology, Department of Animal Biology, University of Campinas. A total of 198 specimens was collected, comprising 20 species and 6 genera: *Dexosarcophaga* (1 species, n=1), *Helicobia* (2 species, n=8), *Oxysarcodexia* (8 species, n=90), *Peckia* (*Patonella*) (1 species, n=16), *Peckia* (*Squamatodes*) (2 species, n=28), *Peckia* (*Eubottcheria*) (4 species, n=41), *Ravinia* (1 species, n=1), *Sarcophaga* (*Lipoptilocnema*) (2 species, n=13). *Oxysarcodexia admixta* (n=33) was the most abundant species. Chicken gizzard was the most attractive bait (n=76), followed by dog feces (n=56), raw minced beef (n=48) and raw fish (n=18). The knowledge of the occurrence of Sarcophagidae species in biomes poorly studied, such as the Cerrado, and the biological information, such as attractiveness, contribute significantly to the understanding of the diversity of flies in Neotropical areas.

Bamboo inhabiting Tephritoids in South America (Diptera: Tephritoidea)

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Keywords: *Ozaenina*, Richardiidae, *Pterocerina, Ulivellia*, Ulidiidae, Poaceae, *Guadua*

The Amazonian rainforest is, contrary to general belief, far from a stable habitat. Tree-falls, floods and forest fires constantly cause disturbance and rejuvenate parts of the forest. In southeastern Peru the most important pioneer plant species on these disturbance patches is bamboo *Guadua* sp. (Poaceae). In some parts the forest is even predominated by bamboo. Not surprisingly, there is a whole community of animals adapted to this spiny forest type, amongst other some Tephritoids. In the course of several years fieldwork was carried out in different parts of Latin-America but above all in southeastern Peru. Countries visited include Costa Rica, Colombia, Ecuador, Bolivia, Paraguay and Brazil and additional material was received from Surinam and French Guyana. Specimens were collected from damaged young shoots of bamboo, mainly *Guadua weberbaueri*. A total of 13 genera have been collected, the most common were *Coilometopia* Macquart, 1847, *Richardia* Robineau-Desvoidy, 1830 (Richardiidae) and *Euxesta* Loew, 1868, *Pterocerina* Hendel, 1909 (Ulidiidae). Three species have been reared from young bamboo shoots: *Coilometopia longicornis* Hendel, 1911 (n=8), *Euxesta* sp. (n=1) and *Pterocerina* sp. n. (n=>200). The females of the latter displayed a peculiar pre-oviposition behavior. Rearing this species revealed a distinct sexual dimorphism in wing-pattern, raising questions on the status of several of the species described only based on one sex and revealing a genus in bad need of a revision. Two other striking genera were found in bamboo dominated forest, but whether these utilize bamboo remains questionable: a new genus close to *Ozaenina* Enderlein, 1912 (Richardiidae) and *Ulivellia* Speiser, 1929 (Ulidiidae). The first is striking because of its appearance and the second by its behavior.

Diptera and the taphonomy of amber

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Keywords: Mexican amber, Dominican amber, copal, resin

Diptera are the most common group as amber inclusions, thus the best taxon to study amber taphonomy. We might regard sticky tree resin, the precursor to amber, as a type of biotic "trap" that records the flora, fauna, and debris that are accidently stuck and entrapped. Diptera are abundant in amber because so many taxa are associated with tree trunks, thereby increasing their chance of becoming accidently entombed as inclusions. Using tree trunk sticky traps as an amber analogue, we can study the taphonomy of recent tree trunk associated faunas and compare this to amber faunas. We compared Diptera collected with sticky traps on the recent forest trees *Hymenaea courbaril* and *Bursera simaruba* in Mexico and *H. verrucosa* in Madagascar, with fossil Diptera fauna from *H. mexicana* and *H. protera* (Miocene Mexican and Dominican ambers). The present work aims to review key questions about taphonomic biases and filters of the fossilization processes based on Diptera taxa in amber. The project is supported by German Science Foundation (DFG) SO 894 3/1 and the Spanish Ministry of Economy and Competitiveness GL2011-23948 AMBARES 2012-2014

Blood-sucking vector flies of nesting birds

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Keywords: Culicidae, Ceratopogonidae, blood-sucking flies, vector, bird

Vector-spread diseases of birds are popular research subjects, however, the vector–bird relationship at species level is rather poorly known yet. A simple and cheap method for collecting blood-sucking flies in bird nest boxes was tested.

Three artificial colonies of Red-footed falcon (*Falco vespertinus* Linnaeus, 1766) were studied at Kardoskút, South Hungary between 2010 and 2012. Transparent plastic plates (10×15 cm) covered with baby oil gel on one side were fixed on the inner roof of the nest boxes for 24 hours during the three different phases of the incubation period (eggs, young and old nestlings). The flies were removed by clean petrol and later stored in 70% ethyl-alcohol. The washing down of the specimens did not damage them, thus the identification of these fragile flies was possible.

A total of 16,668 diptera specimens (from 23 families) were caught during the study. More than 90% of the specimens collected were mosquitoes (Culicidae). Four biting midge (Ceratopoginidae) species proved to be new to the Hungarian fauna (*Culicoides duddingstoni* Kettle & Lawson 1955, *C. alazanicus* Dzhafarov, 1961, *C. manchuriensis* (Tokunaga, 1941), and *Leptoconops bidentatus* Gutsevich, 1960).

Significant correlation was found between the numbers of the mosquitoes and the nestlings; the rate of blood-feeding flies was larger in young nestlings than in old(er) ones.

An important finding was the detection of the West-Nile Virus (lineage 2) in *Culex pipiens* Linnaeus, 1758 in the sampling area.

Molecular identification of Diptera [poster]

Adhoc: an R package to calculate ad hoc distance thresholds for DNA barcoding identification

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Keywords: DNA barcoding, JEMU, ad hoc

Identification by DNA barcoding is more likely to be erroneous when it is based on a large distance between the query (the barcode sequence of the specimen to identify) and its best match in a reference barcode library. The number of such false positive identifications can be decreased by setting a distance threshold above which identification has to be rejected. To this end, we proposed recently to use an *ad hoc* distance threshold producing identifications with an estimated relative error probability that can be fixed by the user (e.g. 5%). Here we introduce two R functions that automate the calculation of *ad hoc* distance thresholds for reference libraries of DNA barcodes. The scripts of both functions, a user manual and an example file are available on the JEMU website (http://jemu.myspecies.info/computer-programs) as well as on the comprehensive R archive network (CRAN, http://cran.r-project.org).

Seasonal and daily activity of the Oriental latrine fly, *Chrysomya megacephala* (Fabricius) (Diptera: Calliphoridae) in Chiang Mai, northern Thailand

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Keywords: *Chrysomya megacephala*, seasonal activity, daily activity, Thailand

The Oriental latrine fly, *Chrysomya megacephala* (Fabricius), is a medically important blowfly species worldwide, with it not only being a fly of forensic importance, but also a mechanical carrier of numerous pathogens. This study aimed to determine the seasonal and daily activity of adult *C. megacephala* in the rainy season (July to October 2013) and winter (November 2013 to February 2014) in Chiang Mai province, northern Thailand. Fly collections were performed every two weeks at Mae Hia Agricultural Research, Demonstrative & Training Center, Mueang Chiang Mai district using automatic traps invented by Kom Sukontason, and 1-day tainted beef offal (300 g) as bait. Three land use types were involved in this study – a forested area, longan orchard and palm garden. Five traps were placed to collect flies over a 24-hr period. Seasonal activity in the rainy season and winter revealed that the fly number decreased gradually from July to January, which was when the lowest number of flies were collected. The number increased sharply in February. Daily activity showed that most *C. megacephala* were collected from 3:00 P.M. to 6:00 P.M., followed by 12:00 noon to 3:00 P.M., 9:00 A.M. to 12:00 noon, 6:00 A.M. to 9:00 A.M. and 6:00 P.M. to 6:00 A.M., consecutively. Collection in the summer of 2014 is on-going. The relation between daily activity of this fly and forensic entomology is discussed.

Ultrastructure of male genitalia of Thai blow flies of medical importance (Diptera: Calliphoridae: Chrysomyinae)

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Keywords: Male genitalia, blow flies, Chrysomyinae, scanning electron microscopy, Thailand

Male genitalia of blow flies (Calliphoridae) are peculiar in their morphological features and are often used for species identification. The aim of this work was to investigate the male genitalia of blow flies of medical importance from Thailand at the ultrastructural level, using scanning electron microscopy (SEM). Species of the subfamily Chrysomyinae were examined, including *Chrysomya pinguis* (Walker), *Chrysomya chani* Kurahashi, *Chrysomya thanomthini* Kurahashi et Tumrasvin, *Achoetandrus rufifacies* (Macquart), *Achoetandrus villeneuvi* (Patton) and *Ceylonomyia nigripes* (Aubertin). Particular attention was paid to the main distinguishing features such as the shape of the cercus, surstylus and phallus including the juxta, vesica, harpes and median stylus. The differentiation of the male genitalia of these species at the SEM level is discussed and compared to conditions in closely related species such as *Chrysomya megacephala* (Fabricius).

Faunistic relationships of the Muscidae (Diptera) of the high altitude of the Altai Mountains and the latitudinal tundra of Russia

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Keywords: Muscidae, Arctic, Altai, Russia, tundra

In order to determine the historical biogeographic relationships of the Muscidae of the high mountains and of the latitudinal tundra of Russia, the local faunas of the Altai Mountains in Central-south Siberia and the faunas of the arctic Taimyr Peninsula and Chukotka Autonomous Okrug were compared.

The number of muscids known from the Altai Mts now totals 215 species in 36 genera. It has been established that only 34 of these species (16%) occur throughout the entire Altai. The high-mountain tundra has the greatest species diversity of Muscidae. This Altai fauna consists of arcto-montane (52%) and arcto-boreo-montane (21%) species, whilst the remaining species (27%) have a Trans-Palaearctic distribution or are known only from the Altai. 130 species in 25 genera have been found at high altitude, and 97 of these have been found only above the tree-line.

In the latitudinal tundra, 110 species in 17 genera have been found, including 72 species on the Taimyr Peninsula and 69 species in Chukotka.

43 species in 13 genera have been found in both the high mountains and the latitudinal tundra. Most of them (67%) have an arcto-montane (19 species) or an arcto-boreo-montane (10 species) distribution. However, 10 species are known to have a distribution restricted to the Altai Mts and in the arctic are present mainly in Siberia and/or in North America.

Spilogona species are dominant in both the high-mountain and the latitudinal tundra (11 species in common). However, the highest species-richness of *Spilogona* is in the arctic regions (45 species) whilst only 28 species are known from the Altai. *Drymeia* is dominant in the high-mountain tundra, both in the number of species and in the number of individuals. 18 species of *Drymeia* are found in the high-mountain tundra whilst only 8 are found in the Arctic.

Reproductive strategy of snow recorded winter crane flies (Diptera: Trichoceridae)

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Keywords: Trichoceridae, winter-active fauna, reproductive strategy

Trichoceridae are well known for their winter activity. In the temperate climate of Poland they begin to swarm in October, and during the winter are often observed flying and/or sitting on the snow cover depending on the air temperature, humidity and wind (windless days with temperature around 0oC and higher are favourable). Our studies of snow active insects were carried out during four winter seasons (2010–2014) in the Beskid Sądecki Mountains in southern Poland. To obtain representative results, a semi-quantitative method was used. Among all sampled Diptera, as well as other snow recorded groups, Trichoceridae have clearly predominated. The flies were present on the snow during the entire period of snow cover, when air temperature was higher than –4°C. Our studies resulted in almost 1400 collected flies. In the sampled material *Trichocera dahlae* Mendl 1971 and *T. regelationis* (Linnaeus 1758) were the most abundant by far. The stage of maturity of at least 600 female abdomens was examined. The two species differ significantly in abundance throughout winter; *Trichocera dahlae* emerged earlier and reproduced most probably from the end of January to the beginning of February. After that, their activity suddenly decreased to almost none. By contrast, two peaks of activity were noted for *T. regelationis*: at the beginning of February and in the first part of April. The observed differences in female maturity level attests to the mid-winter reproductive strategy of these two dominating trichocerids.

Snow active Heleomyzidae – a case study in lowland and mountain areas of Poland

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Keywords: Heleomyzidae, Poland, winter activity, snow fauna

Diptera are the most abundant group of snow active insects. However, the ecology of this group is still insufficiently known. Heleomyzidae are considered cold adapted flies, winter active and are regularly encountered in the snow cover in Scandinavia, as well as in Poland. Thus, heleomyzids are members of the supranivean fauna.

We present the results of long term investigations on heleomyzids recorded on snow in Poland. The investigations were carried out regularly from 1999 to 2013 in a lowland area of central Poland and in the Beskid Sądecki Mountains in the south of Poland. More than 120 insect samples including Heleomyzidae were collected from the snow using a semi-quantitative method.

Two Diptera families were dominant in the samples. Trichoceridae were most abundant, while Heleomyzidae were most speciose. Almost 400 individuals belonging to 28 species of Heleomyzidae were recorded as active on snow. Among them *Heleomyza modesta* (Meigen 1835), *Heteromyza rotundicornis* (Zetterstedt, 1846), *Scoliocentra (L.) brachypterna* (Loew 1873) and *Tephrochlamys rufiventris* (Meigen, 1830) clearly predominated. Heleomyzidae were found on the snow during the whole period of snow cover. However, the highest number of specimens was caught from the end of November to the beginning of February. In the second part of winter and in early spring the snow activity of heleomyzids decreased. Most of the individuals were active on the snow at air temperatures between –2.0 and +2.5°C. Lowland and mountain assemblages of snow recorded Heleomyzidae are compared.

A new species of *Japanagromyza* Sasakawa (Diptera: Agromyzidae) from Brazil

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Keywords: Leaf-miners, taxonomy, Rio de Janeiro

Agromyzidae is a family of Diptera with about 2800 species in the world and are known as leaf-miners flies because during the immature stages they feed on plants forming tunnels on the plant surface. The fauna of Agromyzidae in Brazil is little known and the species richness underestimated, with 90 species recorded only in five states in the country. The material was collected in Casimiro de Abreu and São Francisco de Itabapoana municipalities in Rio de Janeiro, Brazil. The specimens were captured using Malaise trap and preserved in alcohol 98%. All specimens were mounted in entomological pins and deposited in the collection of Museu Nacional, Universidade Federal do Rio de Janeiro. The identification was based using a key for Neotropical species and original descriptions. The specimens were identified as *Japanagromyza* Sasakawa, a genus with approximately 80 species in the world, being 30 known in Neotropical region and two in Brazil. The genus is considered morphologically close to *Agromyza* Fallèn and *Melanagromyza* Hendel, by characters as: one pair of prescutellar setae, halter yellowish (*Agromyza*), two strong dorsocentral setae (rarely three), fore tibia with lateral seta and dark halter (*Melanagromyza*). About 25 species of *Japanagromyza* have their interaction with plants known, some are known as gallers and others cause mines. The new species is characterized by: frons shining black, orange brown at ori level; face, fronto-orbital plate and ocellar triangle shining black; palpus, proboscis and labellum paller yellow; halters entirely yellow; calypters light yellow with margin and fringe black; three postsutural dorsocentral setae, first pair short and fine. This species is morphologically close to *J. maculata* Spencer and *J. spadix* Spencer, but can be easily segregated from them by the male terminalia morphology.

Calyptratae [poster]

Intra-puparial development in *Peckia lambens* (Diptera: Sarcophagidae)

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Keywords: Intra-pupal development, Sarcophagidae, metamorphosis

The chronology of the intra-puparial development of *Peckia lambens* (Diptera: Sarcophagidae) is described based on 310 pupae. The pupae were fixed in Carnoy's solution at intervals of six hours until the emergence of the adult. Later they were immersed in 5% formic acid for 48 hours and preserved in 70% alcohol. Two events were observed in the process of pupation. The first was the larval-pupal apolysis, the separation process of the last larval cuticle from the epidermis of the pre-pupa. This process occurred three hours after pupariation. The second process involved the following phases: (1) the Cryptocephalic pupa, where the body resembles that of a larva; (2) the Phanerocephalic pupa, where the head, thorax and abdomen of the imago can be distinguished and (3) the Pharate adult, where the imago is developed. This was the longest phase of the entire development. The pharate phase was in turn subdivided into four chromatic stages of the compound eyes: transparent, yellow, pink and red. The time of intra-puparial development of *P. lambens* lasted 156 hours.

Taxonomic issues and male asymmetry in *Oxysarcodexia* (Sarcophagidae)

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Keywords: Dung-breeding, flesh flies, Neotropical region, rotational scanning electron microscopy

Oxysarcodexia is one of the most species-rich genera of Neotropical flesh flies. A taxonomic conspectus based on male specimens recognized 85 valid species, including six new to science. The distribution of *Oxysarcodexia* is markedly Neotropical, with 63 species exclusively from this region, two species recorded from both the Neotropical and Australasian/Oceanian regions, 15 from the Neotropical and Nearctic regions, and five restricted to the Nearctic region. Species within this genus are considered to be dung-breeding, although biological information is still very sparse. The conspectus presents diagnosis, synonyms, geographical distribution, biological data (when available), and a pictorial database of all species, with data assembled from the literature and from examination of museum specimens and newly collected material. Males of *Oxysarcodexia* can be recognized by the presence of a setose postalar wall; a mid-femoral ctenidium of flattened spines; tegula blackish; basicosta orange; sternite five deeply cleft; phallic tube unsegmented; acrophallus with three conducting styli; phallic vesica well-developed and conspicuous; and phallic tube with a lateral triangular (“tooth-like”) extension proximal to the vesica. The latter character state is the only autapomorphy supporting the monophyly of the taxon. The occurrence of asymmetry in the male genitalia was documented using rotational scanning electron micrographs for three species and investigated with a phylogenetic approach based on a character matrix for 54 species. Sinistral directional asymmetry in the terminal lobes of the phallic vesica is recorded for eight species, and asymmetry appears to have arisen several times in *Oxysarcodexia*, while it is otherwise found rarely in the remaining flesh flies. Subgroup arrangements within the genus are revised based on the preliminary phylogenetic analysis. There are few well-supported subgroups, and a classification into subgenera is considered as premature on the present evidence.

The hoverfly fauna (Diptera: Syrphidae) of the Saarland (West-Germany)

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Keywords: Diptera, Syrphidae, fauna, Saarland, Germany

The Saarland is a relatively small federal country in West-Germany with only 2570 km², bordering France and Luxembourg. While the highest elevation is only 695 m. a.s.l. and therefore high mountain habitats are missing, open habitats inlcude a wide variety of species-rich dry to wet grasslands; forests are potentially mainly beech and to a limited extend oak forests. The hoverfly fauna (Diptera, Syrphidae) of the Saarland was almost unknown until 2005 and virtually no historical records existed. After a revision of the existing collections of the Saarland, including some by-catch of a Lepidopterologist (De Lattin), the collection R. Ullrich and some material from student excursions (ZfB collection) a first list resulted in 85 species only. More systematic field collections since 2005 and a limited number of Malaise traps in different habitat types made a preliminary checklist possible in 2008, based on data up to the end of 2006. This approximately doubled the number of known hoverfly taxa (164 species) within only 2 years of systematic collecting. Additional sampling with Malaise traps and more field collections were done in the following years and the syrphid list now has more than 205 species including undescribed taxa.

Collecting effort, methods and completeness of the actual checklist of hoverflies will be shortly discussed in relation to the fauna of adjacent countries. A comprehensive hoverfly fauna of the Saarland is in preparation.

The same old gene fragments: impact of considerably improved taxon sampling for Syrphidae classification

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Keywords: Syrphidae, molecular phylogeny, COI, 28S

The Syrphidae is traditionally divided into three subfamilies: Eristalinae, Syrphinae and Microdontine. The family of hover flies comprises >6000 species worldwide. We carried out molecular phylogenetic analyses using parsimony, maximum likelihood and Bayesian inference on a dataset of mtDNA COI and nuclear 28S rDNA gene regions comprising 345 syrphid taxa to explore the monophyly of the subfamilies and currently recognized tribes. Additionally, for a smaller taxon set of 300 taxa we conducted the analyses including also a fragment of the 18S rDNA gene in combination with the COI and 28S. The outgoup taxa comprised multiple taxa of Pipunculidae, Platypezidae and Phoridae, and the trees were rooted on Phoridae. The results are presented and discussed focusing on the monophyly of the subfamilies and tribes of Syrphidae.

Palaeobiogeography and Palaeoecology of Nematocera from Early Eocene Indian amber

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Keywords: Indian amber, Eocene, Nematocera, biogeography, ecology

India´s peculiar and highly diverse biota combined with its unique geodynamical history has generated much interest in the patterns and processes that might have shaped the current distribution of India´s flora and fauna and their biogeographic relationships. Several different theories concerning India´s geological history have been established but none of these models provide satisfying answers to questions about the origin of Indian and Asian biodiversity. A recently discovered fossiliferous amber deposit from the Early Eocene of India for the first time provides the opportunity to study fossils of the most species rich group of terrestrial organisms – the insects – to investigate India´s geological history and get insight in a terrestrial ecosystem in tropical latitudes at the beginning of the Early Eocene Climatic Optimum. The present project focusses on the Nematocera which are represented by more than 500 inclusions from eleven families and thus comprise the most common and diverse inclusions in this amber. First analyses of selected taxa reveal high potential for biogeographic and ecological studies. The psychodine subfamily Sycoracinae for example – which is represented by five specimens in Indian amber – is generally rare in the fossil record and has only a few disjunct distributed extant species, none of which known from India; and a fungus gnat in Indian amber reveals affinities to the lygistorrhinid genus *Palaeognoriste* from the Eocene Baltic amber. Additionally, almost all nematoceran groups in Indian amber include taxa of ecological importance in terms of feeding or habitat requirements, like the aquatic larvae of Chaoboridae and Chironomidae or the blood feeding Corethrellidae and Sycoracinae.

Anopheles plumbeus (Diptera: Culicidae): habitat shift from natural to artificial breeding sites

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Keywords: Culicidae, *Anopheles plumbeus*, habitat shift

The Palaearctic mosquito species *Anopheles plumbeus* (Stephens, 1828) is widely distributed throughout Europe, the Middle East and North Africa. Specimens can be found in forested areas from sea level to altitudes of 2,000 m. As a typical dendrolimnic species, *An. plumbeus* inhabits water-filled cavities in a variety of tree-species, but in periods of extreme drought, this species is also able to breed in containers with stagnant rain water and groundwater such as manure pits, discarded tyres and cemetery vases. Contrary to natural habitats where the population density is limited due to the restricted availability of potential breeding sites, populations from artificial breeding containers can reach high densities. In Germany, nuisances caused by massive abundances of *An. plumbeus* have been recorded from the federal states of Baden-Wurttemberg, Bavaria, Saxony and North Rhine-Westphalia.

To compare mosquito population development in man-made containers with that in tree-holes and to investigate the processes which contribute to high population densities of *An. plumbeus*, artificial breeding containers such as car tyres and plastic cups have been set up in different areas in Germany. Areas with a known *An. plumbeus* nuisance will be compared to those with normal abundances of this species. The examination of different habitat types (deciduous and coniferous forest, open field and urban areas) within a single study area facilitates the comparison of the mosquito composition in artificial and natural breeding habitats.

Assessment of Culicoides (Diptera: Ceratopogonidae) abundance in bovine dung: a comparison of methods

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Keywords: *Culicoides*, larvae, emergence trap, sugar-flotation, Berlese, cow dung

There are few comparisons of relative efficacy of larvae extraction methods and emergence traps for species of *Culicoides* Latreille. We compared sugar-flotation and a modified Berlese funnel with the use of emergence traps, in order to analyse the colonisation of cow pats by *Culicoides chiopterus* (Meigen) and *Culicoides dewulfi* Goetghebuer (Diptera: Ceratopogonidae). With all three methods considerable numbers of individuals were obtained. Significantly more individuals were recovered via sugar-flotation and Berlese funnel-extraction as compared to the emergence traps. These differences, likely due to natural mortality and sample processing are discussed. We recommend Berlese funnels as a superior method for extracting *Culicoides* larvae from bovine dung. It produces data rapidly, and extracted larvae are viable. Sugar-flotation yielded more larvae when compared to Berlese funnels but was very labour and time intensive.

Whence the Tachinidae?

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Keywords: Oestroidea, Calliphoridae, molecular phylogeny, parasitoid, *Pollenia*

The relationships among fly families in the superfamily Oestroidea represent one of the most phylogenetically intractable areas of the order Diptera. The origins of the family Tachinidae are particularly obscure, with nearly every family of oestroids being forwarded as its possible sister taxon based on morphological and molecular data, including the Rhinophoridae, Sarcophagidae, Oestridae, and Calliphoridae. Understanding where Tachinidae arose within this group, and what their sister group is may provide insight into the origins of the parasitoid habit in this family, which represents the largest clade of insect parasitoids outside the hymenopteran "Parasitica".

Recent molecular phylogenetic analyses focused on the order Diptera, the Calyptratae, the Oestroidea, and the Calliphoridae have failed to clarify relationships between Tachinidae and other oestroid families. In some cases, analyses have even indicated that Tachinidae are poly- or paraphyletic, a result that seems highly unlikely based on morphology. Here we briefly review proposed relationships within the Oestroidea, focusing on the placement of Tachinidae, and present the results of a recent molecular phylogenetic analysis of relationships among major tachinid groups and related taxa based on nine genes (11.4 KB). In a combined maximum likelihood analysis, we find strong support for a monophyletic Tachinidae and for a close relationship between Tachinidae and one clade of Calliphoridae, the Polleninae. The implications of a Polleninae-Tachinidae sister relationship for the origins and early development of the parasitoid habit in tachinids is discussed.

Towards a molecular phylogeny of World Tachinidae: a progress report

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Keywords: Parasitoid, host use, CAD, 28S

The Tachinidae are one of the richest families of flies. All species are parasitoids of insects and other arthropods and they parasitize a great range of host taxa, notably members of the Lepidoptera. Systematic evidence suggests that the family is relatively young and actively radiating. This radiation has resulted in both great morphological diversity and a high level of homoplasy among taxa, obscuring relationships within and among major lineages. Despite their diversity and taxonomic difficulty, there have been few attempts to reconstruct the phylogeny of the family using morphological or molecular data. Recently, we have embarked on an international collaborative effort to understand the phylogenetic relationships of World Tachinidae. Here, we outline some of our current progress using molecular data to reconstruct a phylogeny of the family.

Thus far we have obtained sequences of two genes (28S and CAD) for over 200 tachinid genera, spanning all major tribes and most minor ones. Preliminary maximum likelihood analyses of these data strongly support a major split between the subfamilies Phasiinae+Dexiinae and Tachininae+Exoristinae. In each of these major clades the former subfamily is reconstructed as paraphyletic with respect to the latter. However, this paraphyly is caused by one small clade in each case. In addition, a Coleoptera-attacking lineage of the subfamily Tachininae, including members of Myiophasiini and Macquartiini, is reconstructed as sister to the remaining Tachinidae. Several major tribes are supported as monophyletic or nearly so, including Tachinini, Siphonini, Dexiini, Voriini, Exoristini and Blondeliini, however several others are para- or polyphyletic including Leskiini, Eryciini, and Ernestiini. As in recent morphological analyses, our results suggest that the ancestral hosts of Tachinidae were not Lepidoptera, but rather Coleoptera or hemimetabolous groups. We are currently obtaining sequences from additional nuclear genes to resolve these relationships more clearly and robustly.

Searching for biting midges – evolutionary relationships and the Swedish fauna

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Keywords: Sweden, phylogeny, new records

As a part of the Swedish Taxonomy Initiative's efforts to increase the knowledge of less known organism groups, the diversity and evolutionary relationships of biting midges (Ceratopogonidae) are investigated. Specimens collected from multiple locations in Sweden have resulted in more than twenty species and several genera previously not recorded from Sweden. These new records along with previously recorded species from the literature have been assembled for an overview of the currently known Swedish fauna, which now stands at 22 genera and 127 species. The phylogenetic relationships of the family with all extant subfamilies and tribes represented have been analyzed using nuclear and mitochondrial protein-coding gene fragment. The result reveals all subfamilies but Leptoconopinae as monophyletic and within the well-supported Ceratopogoninae only Culicoidini, Heteromyiini and Stenoxenini are supported.

The biology of Conopid larvae – a summary of the underestimated published knowledge

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Keywords: Conopidae, larval biology, hosts, morphology, egg laying, bibliography

Knowledge concerning the larval biology of Conopidae is usually estimated as being poor. While working on a bibliography of the Conopidae, some 299 works were found with information concerning either larval biology or the morphology of larvae or eggs. An overview is given of the knowledge and ignorance concerning the larval biology of Conopidae.

The first record of a conopid larva as an endoparasite of a bumblebee (*Bombus* sp.) was published in 1809 by Latreille. Up to now there are host "records" at the species level reported in about 222 papers for some 86 conopid species (11% of the currently known 782 valid species worldwide). For 12 genera there are host "records" available (21% of the 56 currently known genera worldwide). At least 200 host species are reported as being parasitized by conopid larvae, the great majority of which are Hymenoptera. The problems in assessing these records are discussed. In this context the question of whether or not [non-stylogasterine] Conopidae also parasitise Orthoptera is addressed.

The first description of a conopid larva was published in 1812 by Bosc d'Anticone – who did not recognise that he had described a conopid larva at all. Up to now there are "descriptions" published in 38 papers of about 24 species of conopid larvae or puparia, covering only 9 genera. Morphological adaptions of the eggs, the larvae and the puparia of Conopidae are discussed and the mode of egg laying of different conopid taxa is compared. An overview is also presented of the enemies of conopid larvae recorded so far.

Key questions for further work concerning conopid larval biology are proposed.

Future prospects and lessons learned from 8 years of Chironomidae DNA barcoding

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Keywords: COI, non-biting midges, diversity

The family Chironomidae has about 6200 species described world-wide and is among the most widely distributed families of Diptera. Chironomids are found in almost all kinds of terrestrial and aquatic habitats, but are particularly species rich and abundant in freshwaters. Many species have specific habitat requirements and chironomids are therefore well suited for biological monitoring as well as research projects focused on evolution and biogeography. However, the full potential remains unleashed as many species are difficult to identify and a large number still is undescribed. DNA barcoding of Chironomidae therefore represents a great tool for the advanced use of non-biting midges in research and nature management. In this presentation we will summarize our work on DNA barcoding of Chironomidae over the last 8 years, what we have learned and how we see the future of chironomid barcoding. Particular focus will be on analytical success, the importance of vouchers, association of life stages, detection of cryptic diversity, the lack of genetic variation and how a DNA barcode library provides a common base for species interpretation and paves the way for a broader use of Chironomidae in environmental studies and biosystematics.

An updated phylogenetic hypothesis for Sepsidae (Diptera: Cyclorrhapha) based on improved taxon sampling and phylogenomic analyses of transcriptome data

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Keywords: Sepsidae, phylogenomics, mitogenomics

With more than ca. 320 described species in 37 genera, Sepsidae is a moderately species-rich family of cyclorrhaphan flies with an almost worldwide distribution. Males of many species in this acalyptrate family possess spectacular sexual dimorphisms and courtship behaviours. As such, flies of this family are an emerging model system for comparative studies in behavior, morphology and development. Although several attempts have been made to reconstruct the relationships within this family, the positions of some key clades remain poorly understood. There is low support for internal nodes and several suprageneric relationships show topological conflict when analyzed using maximum likelihood or maximum parsimony. Here I will present some of our recent efforts to resolve the sepsid phylogenetic relationships. We first attempted to address these issues through increased taxon sampling, where we sequenced five nuclear and five mitochondrial markers (totalling 8,813 bp per species) for almost 30% of all known diversity of Sepsidae (105 sepsid taxa). Nonetheless, we still found topological conflict and low internal node support. We then tried to resolve these issues through increased character sampling using next-generation sequencing technology. We have now generated and analyzed mitochondrial genome sequences for 28 sepsid species and transcriptome sequences for 18 species representing all major clades of Sepsidae.

Biodiversity surveys [poster]

Dipteran diversity of the Ogasawara Islands

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Keywords: Biogeography, oceanic island

The Ogasawara (Bonin) Islands are an archipelago with more than 30 islands, 104 km^2 in area, and located ca. 1,000 km south of Tokyo, Japan, in the Pacific Ocean. These subtropical and tropical islands were nominated to a natural world heritage in 2011 because of their unique fauna and flora in an oceanic environment. The Diptera fauna of the islands was first studied in 1916 and at present approximately 250 species of 45 families are recorded from the islands. A recent Diptera inventory based on several museum collections revealed a number of new localities and records of several taxa. The families Empididae, Dolichopodidae, Strogylophthalmyidae, Nannodastiidae, and Canacidae are newly recorded from the islands. The family Ephydridae, of which only a single genus *Ephydra* has been recorded, is represented by 10 genera in this study. Compared to two Pacific islands, the Galápagos and the Hawaiian Islands, the dipteran fauna of which are well documented, the Ogasawara Islands have the following characteristics in Diptera fauna: they share more than 35 families with the Galápagos and the Hawaiian islands, lack members of several families (like e.g. Scenopinidae, Hybotidae, Neriidae, and Piophilidae), and have members of the families Acroceridae, Strogylophthalmyidae, and Nannodastiidae. The fauna is poor in aquatic dipteran taxa and lacks half of the water-inhabiting families recorded from Japan. The family Lauxaniidae is represented by at least five genera, whereas it encompasses less than four genera on the Galápagos and the Hawaiian Islands. The family Sphaeroceridae with more than 10 genera on the Galápagos and the Hawaiian Islands, holds only three genera on the Ogasawara Islands.

Identification of armyworms (Diptera: Sciaridae) occurring in Japan by rearing larvae to adulthood

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Keywords: Sciaridae, armyworms, Japan

Since the 19th century, strange mass movements of the larvae of sciarid flies, called "armyworms", have been frequently observed worldwide. The armyworms of Europe have been identified as *Sciara militaris*, but those of other regions are very poorly known. Some Japanese residents recently took photographs of armyworms in Japan, demonstrating that armyworms occur in this country. I have examined specimens of armyworms from the central and north-eastern Japan. All larval colonies were found and collected by local residents. I received several larval specimens in ethanol. The morphology of sciarid larvae is very simple and cannot be used to distinguish species. However, DNA barcoding identified these larvae as *Sciara kitakamiensis*. A local resident also sent me live larvae and I sought to rear to adulthood. Nineteen adults (1 male and 18 females) were reared successfully and the male morphology was determined to be that of *S. kitakamiensis*. Thus, this study reports that the molecular identification of armyworms of Japan was also confirmed by rearing larvae to adulthood. In addition, I update the inter-specific and intra-specific genetic distances within the genus *Sciara*, using DNA barcodes mined from public databases, and discuss the utility and difficulties of molecular identification when obtaining and rearing live larvae.

Neural mechanisms underlying aggression in stalk-eyed flies

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Keywords: Stalk-eyed fly, aggression, monoamines, serotonin, HPLC

The outcome of contests over limited resources such as mates, territories, and food has significant fitness consequences. Therefore, it is of great theoretical and practical importance to understand the mechanisms that modify different agonistic behaviors. In several invertebrate groups, neural serotonin (5-HT) has been linked to heightened aggression and conflict escalation. Stalk-eyed flies (*Teleopsis dalmanni*) provide an excellent model system to study mechanisms underlying the expression of aggressive behaviors, because males readily engage in aggressive contests in which the escalation occurs in a stereotypic manner. To investigate how changes in central monoamines, including octopamine (OA), dopamine (DA), and serotonin (5-HT), contribute to modifying the expression of aggression in these flies, we developed a dissection and sample preparation method sufficiently sensitive to measure monoamine concentrations from whole brain samples of small insects. Furthermore, we developed a noninvasive, pharmacological method that significantly augments brain 5-HT by administration of the precursor, 5-hydroxytryptophan (5-HTP), in food media. We will present data from contests between size-matched and size-mismatched males and between size-matched females in which one contestant has been pre-treated with 5-HTP. Individuals with higher brain 5-HT levels displayed greater levels of high-intensity aggressive behaviors and fewer retreats and, in the case of size-matched males, increased the probability of winning contests. In size-mismatched contests, smaller treated males were not more likely to win a contest despite a significant increase in initiation and aggressive escalation. Interestingly, pre-treatment of the smaller male also induced an increase in aggression in their larger untreated opponent. Pretreatment with 5-HTP did not significantly alter OA or DA concentrations. The finding that 5-HT enhances aggression in stalk-eyed flies suggests future studies investigating the role of 5-HT and other monoamines will contribute to understanding neural mechanisms modulating rival assessment and individual variance in aggressive behavior.

A new species of *Alhajarmyia* Stuckenberg (Diptera: Vermileonidae), the first wormlion fly described from East Africa, and its biogeographical implications

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Keywords: Afrotropical, *Alhajarmyia*, biogeography, *Isalomyia,* Vermileonidae

In 1999 Stuckenberg & Fisher described *Lampromyia umbraticola* from the Al Hajar Mountains of northern Oman, being the first recorded species of the family Vermileonidae from the Arabian Peninsula. Later, in 2003, Stuckenberg erected the new monotypic genus *Alhajarmyia* to contain it. Stuckenberg suggested that *Alhajarmyia* and the endemic, monotypic Malagasy genus *Isalomyia* represent sister-groups and discussed possible means of dispersal of the two. No species of Vermileonidae are currently known from East Africa, although Stuckenberg suggested that dispersal from an East African ancestor may have produced the *Alhajarmyia* lineage in Arabia. He predicted that undescribed species of *Alhajarmyia* may occur in the mountains of Yemen and the Somali Peninsula. The discovery of a closely-related new species of *Alhajarmyia* from two localities in the Coastal Province of Kenya affirms Stuckenberg's prediction of the occurrence of related species in East Africa. The new species differs from its congener in the wing venation and characters of the male and female terminalia. The material of the new species was sampled in indigenous cloud forest from two localities: Kasigau Mountain, at an elevation of 1065–1117 m, and the Taita Hills, at an elevation of 1614 m. The two localities are only 50 km apart, but both represent isolated Precambrian mountains that form the northernmost part of the Eastern Arc Mountains. These mountains are isolated refugia that are well known for their endemic flora and fauna. Biogeographical implications of this range extension are discussed.

Fossil records of mosquitoes (Diptera: Culicidae)

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Keywords: Mosquitoes, fossil, taxonomy, evolution

The Culicidae is a well-known family of nematocerous flies. In the extant world fauna over 3,500 species are described and classified in two subfamilies, Anophelinae and Culicinae, and 112 genera. They are frequent parasites of warm blooded vertebrates (mammals and birds); the female proboscis is long and adapted for puncturing skin and sucking blood directly from small vessels – capillaries. Traces of a blood meal in Eocene *Culiseta* and *Plasmodium* in Miocene *Culex* were recently reported. Fossil records of dipterans indicate that the Culicidae is a young monophyletic group which evolved during the Lower or Upper Cretaceous from much older family Chaoboridae dating back to the Jurassic (ca. 200 mya). Fossil records of mosquitoes are poor and include 19 more or less recognisable species; however, many named fossils are barely preserved and characters visible are showing nothing more they are mosquitoes. The oldest true mosquito *Paleoculicis minutus* is reported from Upper Cretaceous Canadian amber (c. 75 mya). In the Eocene, Culicidae still are extremely rare, while became more common in Oligocene and Miocene deposits (0.64% of nematocerans in Miocene Dominican amber). Within subfamily Anophelinae, the extant genus *Anopheles* and two fossil species from Oligocene and Miocene are reported. In the subfamily Culicinae, 16 fossil species have been reported in the following genera: two extinct – *Eoaedes* (Eocene, 1) and *Aetheapnomyia* (Eocene, 1), and five extant – *Culex* (Eocene, Oligocene, Miocene, 6), *Culiseta* (Eocene, 3), *Ochlerotatus* (Eocene, Oligocene, 2), *Coquillettidia* (Eocene, Oligocene, 2), *Toxorhynchites* (Miocene, 1).

Fossil Diptera [poster]

Family Chironomidae in Baltic Amber from the collection of the Museum of the Earth, Polish Academy of Sciences in Warsaw

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Keywords: Chironomidae, inclusions, Baltic amber, Eocene

The Museum of the Earth’s collections of amber (over 26,000 specimens) have been systematically accumulated since 1951. Inclusions of Chironomidae are dominant in the order Diptera in amber. In the Museum of the Earth’s collection, more than 3,100 inclusions of chironomids have been analysed to date. Based on the completed research, Orthocladiinae is the most abundant subfamily, followed by Chironominae and Tanypodinae.

Chironomids frequently are reported as syninclusions along with Nematocera as Sciaridae and Mycetophilidae, and also with Dolichopodidae, Rhagionidae, Phoridae and another Brachycera, with many individuals often found in a single piece of amber. The number of females largely exceeds that of males; this is not advantageous for research because the morphology of fossil Chironomidae males is more reliable in taxonomic research

New perspectives in morphological identification of fleshfly larvae (Diptera: Sarcophagidae)

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Keywords: Sarcophagidae, larva, morphology, identification, forensic entomology

Larvae of Sarcophagidae are a significant part of the insect community driving decomposition processes of vertebrate carrion. Their impact is especially high in dry habitats. Forensic importance, defined by development on dead human bodies, is well documented for several species of flesh flies. However, a broad application of Sarcophagidae ranging from medico-legal purposes to a full understanding of their role in decomposition processes is complicated by taxonomic problems. Species identification of larvae of fleshflies is constrained by: 1) high level of morphological similarity between closely related species, 2) lack of data for large subsets of important species or particular instars, and 3) available morphological data are of insufficient quality for taxonomic application.

To improve this situation we have implemented the following actions: 1) application of a novel approach to studies of larval morphology focusing on the form and distribution of cuticular structures present on the integument, 2) systematic collection and careful preparation of larval material in selected geographical regions, 3) application of a standardized protocol of description in order to obtain comparable data for taxonomic studies, integrating light microscopy and SEM.

As the first result of our studies, an identification key is presented for the third instar larvae of European fleshflies of forensic importance. The key is user-friendly and with no need to dissect larvae, as soaking the material in methyl salicylate will allow observation of all diagnostic details of the cephaloskeleton. A simple stereomicroscope (magnification about x 50) is sufficient for the observation of all characters present in the key. This key will be systematically extended by addition of species present in adjacent geographical regions.

First attempt at reconstructing a molecular phylogeny of Miltogramminae (Diptera: Sarcophagidae)

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Keywords: Miltogramminae, phylogeny, Cyt-B mtDNA

Miltogramminae are a diverse group of Sarcophagidae with more than 600 described species. Surprisingly, the phylogeny of Miltogramminae has only been superficially studied. Recently published information concerning the larval morphology of Miltogramminae points to significant flaws in existing approaches to the systematics of this taxon. There is an urgent need to reconstruct miltogrammine phylogeny using molecular data in order to solve the conflicts coming from various types of phenotypic data. We used the 700 bp part of the mitochondrial cytochrome b gene (cytB) to reconstruct the phylogeny of 46 species representing all tribes of Miltogramminae with the addition of 6 species of Paramacronychiinae, 2 species of Sarcophaginae and 9 species from other families of the Oestroidea. We built the phylogeny using maximum likelihood as implemented by RAxML, applying the GTR+I+Γ model of nucleotide substitutions.

The reconstructed phylogeny did not support a monophyletic Miltogramminae, and the majority of internal nodes had low bootstrap support (BS). The basal split of the entire family Sarcophagidae separated a clade containing the genera *Phylloteles*, *Mesomelena* and *Eumacronychia* from the remaining Sarcophagidae. Sarcophaginae and Paramacronychiinae did not form sister groups and they were grouped with different species of Miltogramminae. Additionally, Paramacronychiinae emerged as polyphyletic. The monophyly of *Taxigramma*, *Metopia* s.str. and *Sphenometopa* was highly supported. Moderate values of BS were obtained for a few nodes of Miltogramminae: *Apodacra*, *Macronychia*+*Oebalia* and *Miltogramma*+*Pterella convergens*. Other species of *Pterella* were grouped with *Protomiltogramma*. Noteworthy is the paraphyletic constitution of *Senotainia*.

The results obtained are strongly conflicting with the traditional classification of Sarcophagidae by questioning the monophyly of Miltogramminae and Paramacronychiinae. However, the basal position of Phyllotelini to all other Sarcophagidae is in agreement with recent data pointing to saprophagy as an ancestral breeding habit of Miltogramminae.

Life in the Palaeogene amber forests

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Keywords: Amber forest, palaeohabitats, faunistic composition, fossils

The Palaeogene (66–23.03 mya), the time after mass extinction ending the Mesozoic era, is the crucial period for the understanding of the formation of the modern biotas. The Paleocene (66–56 mya) was a critical time in the evolution of numerous groups of plants and animals and the modernization of ecological communities. The Eocene (56–33.9 mya) began as a time of global warming, with temperatures across the planet soaring. Forests thrived and trees grew even in the polar regions. Eventually, the Eocene became cooler and drier. The following epoch, the Oligocene (33.9−23.03 mya) is often considered an important time of transition, a link between the archaic world of the tropical Eocene and the more modern ecosystems of the Miocene.

Only a few of known Palaeogene fossil resins deposits contain sufficiently numerous and diverse fossils to permit detailed investigations of ambers, inclusions and biotas.

The oldest biota, Oise amber forest (55–53 mya), originating from Fabales trees and Eocene Thermal Maximum-2 times, presents relatively 'modern' fauna, with very few genera shared with Baltic amber.

Fushun amber forest biota (53–50 mya) are documented by resin from Cupressaceae trees, exuded during Early Eocene Climatic Optimum. Some taxa recorded have affinities with Baltic amber inclusions.

Baltic amber is the best known and the largest studied fossil resin, but still being the most mysterious. Its origination is often coincided with the Middle Eocene Climatic Optimum. Its botanical origin is still unresolved. Explanation of the assortment of organisms preserved in Baltic amber is far from complete, and with new answers – new questions are raised.

The unique images of the life in the amber forest could help to estimate and understand the climatic changes and challenges of the present time.

A revised evolutionary history of female reproductive (oviposition) strategy in the subfamily Exoristinae (Calyptratae: Tachinidae)

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Keywords: Oviposition, phylogeny, reproductive strategy

The Tachinidae are parasitoids of insects and other arthropods and are one of the largest families of Diptera. Several reproductive strategies beyond the typical direct oviparity have been adopted by tachinids to parasitize their hosts. The Exoristinae, one of the four subfamilies of Tachinidae, have diverse morphological characters and female reproductive habits. In particular, oviparity, ovolarviparity and micro-ovolarviparity are known in this subfamily. We inferred the phylogenetic relationships among genera and tribes of Exoristinae using 4 genes (white, 18S, 28S and 16S rDNA), and evaluated the transformation of female oviposition strategy of the Exoristinae on the resulting phylogeny (Tachi & Shima, 2010). However, the evolutionary history of the micro-ovolarviparity was not well-resolved due to the unclear relationships of the Eryciini.

Here, we revise our understanding of the phylogenetic relationships within Exoristinae by adding taxa and genes to the previous dataset. In particular, the placement of the oviparous genus *Aplomya* Robineau-Desvoidy was examined. The transformation of the female reproductive system of the Exoristinae was re-analyzed based on the generated tree. It indicates as follows: 1) oviparity is the primitive state. 2) ovolarviparity has independently evolved in multiple clades. 3) The Goniini are monophyletic and their female reproductive system (micro-ovolarviparity) originated from one of the ovolarviparous clades. However, we also provide evidence that micro-ovolarviparity may have evolved multiple times.

Biodiversity surveys [poster]

Spatial dynamics of blowflies (Diptera: Calliphoridae) in a urban-rural gradient, Altos Mirandinos, Venezuela

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Keywords: Calliphoridae, Venezuela, species composition, forensic entomology, urbanization

Due to their necrophagous habits, blowflies are among the most important groups of insects in forensic entomology, medicine and public health. They are also active decomposers and recyclers of organic matter in ecosystems. However, in the Neotropics, especially in the Caribbean countries, there are few studies related to biodiversity and ecology of these flies. The development of urban areas induces physical changes in the environment that usually cause the decrease in diversity of insects, and leads to the extinction of native species and colonization of alien and/or synanthropic species. This study determined the spatial fluctuations in the diversity of species of Calliphoridae (Diptera) in an urban-rural gradient in the Altos Mirandinos, Cordillera de la Costa, Venezuela. We made monthly collections for 6 months during November 2012 to April 2013 in 3 different areas with increasing degree of human intervention: rural, semi-urban and urban. Three sets of two modified Van Someren Rydon traps were in operation for 3 consecutive days in each area, totalling 18 trap samples per month. Bait consisted of 250 g of decaying chicken liver and sardines. In each month and locality, environmentalariables were recorded, and the richness and abundance of species was determined. We collected 3,783 calliphorids, in the rural area showing a higher abundance (2062 ind.), followed by the semi-urban (1025 ind.) and urban (696 ind.) areas. The most common species were *Lucilia cuprina* (25,57% of the total number of individuals), *Chrysomya megacephala* (14,38% ind.) and *C. albiceps* (12,64% ind.) in the urban ecosystem, and *Hemilucilia semidiaphana* (54,17% ind.), *H. segmentaria* (14,74% ind.) and *L. peruviana* (13,29% ind.) in the rural area. Most species were also present in the semi-urban ecosystem but usually with intermediate abundances. This study provides information about the response of blowflies to urbanization, thus contributing to the knowledge necessary for both ecological and forensic entomology.

DNA barcoding for identification of species of *Oxysarcodexia* (Sarcophagidae) in Brazil

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Keywords: Barcoding, morphology, identification

DNA barcoding and DNA taxonomy have recently been proposed as an alternative tool to assist in the identification of species. Some flesh flies have represented a great taxonomic challenge, due to the high diversity and morphological similarity. In addition, the identification can become difficult because is based primarily on the morphology of the male genitalia. In the case of immatures, the difficulty comes from the few characters available with diagnostic value and scarce description of larval forms. *Oxysarcodexia* (Sarcophagidae) is one of the most species-rich genera of Neotropical region. Several species seem to be associated with dung and other decaying materials, including animal carcasses. In this study we evaluated whether DNA barcoding sequences can be useful for identification of 10 *Oxysarcodexia* species. Adult specimens were collected predominantly in urban and natural areas in Brazil using traps and decaying flesh as bait. Approximately 700 bp from portion of the cytochrome oxydase of mitochondrial DNA was amplified and sequenced for *Oxysarcodexia admixta, O. avuncular, O. bicolor, O. carvalhoi, O. culmiforceps, O. paulistanensis, O. riograndensis, O. terminalis, O. thornax* and *O. varia.* Analyses were conducted using Kimura 2-parameter model. Evolutionary analyses were conducted in MEGA5. It was possible to consistently delimit species based on tree-based and on pairwise distances. Considering the species profiles based on a 3% threshold, 98% of all profiles are consistent with currently accepted species limits, except *O. admixta* and *O. carvalhoi* which remain below the threshold (only 1%). We concluded that the future use of DNA sequences in a modern taxonomy could be useful for avoiding misidentifications among closer species.

Drosophilids in the Brazilian savanna: fifteen years of study

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Keywords: Biodiversity, Brazil, community dynamics, *Drosophila*, seasonality

Drosophilids are frequently used as biological models in genetics, evolution and more recently in conservation biology. We have been focusing on the structure and dynamics of drosophilid assemblages in the Brazilian savanna biome, using multivariate analysis in order to identify patterns of variation in different temporal and spatial scales. This biome is one of 34 global biodiversity hotspots, due to its high biodiversity, endemicity, and because it is threatened by human activities. It consists of savanna with variable structure on the well-drained interfluves with gallery forests or other wetland vegetation near the watercourses. Precipitation in this biome is highly seasonal, characterized by a well-defined dry season from May to September.

A massive amount of data (more than 100.000 individuals and 100 species) has been analyzed since 1998, showing that fly assemblages vary throughout time and space. The richness and abundance of drosophilids suffer a strong bottleneck in the dry seasons, and a recovery during the rainy seasons. At the spatial scale, gallery forests are richer in drosophilid species than the savanna. The open vegetation, in turn, presents a higher abundance of individuals and a dominance of exotic species.

This general pattern has been confirmed at different temporal and spatial scales, not only for adults but also for immature stages. The causes of these dynamics are clearly multifactorial, but the fluctuation in resource availability (variation in richness and abundance of rotting fruits across a year) is a good predictor of fly assemblage structure. Finally, we are convinced that drosophilids can be useful to study patterns and processes related to biodiversity and biological invasions. They can contribute to the elaboration of conservation strategies, and can improve projections about what might happen in the future.

Study of Middle East Dolichopodidae from the collection of National Museum in Prague

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Keywords: Dolichopodidae, Middle East, diversity, faunistics

The long-legged flies of the Middle East are generally not very well known, with only a few exceptions (e.g. Israel). In the past decade, several authors have started to investigate the dolichopodid faunas of Iran and Turkey. Currently, 44 species are known from Iran, and 171 species from Turkey. In addition, one single species has been reported from Socotra Island (Yemen), namely the widely distributed *Tachytrechus tessellatus* Macquart, 1842.

The Diptera collection of the National Museum in Prague (NMPC) holds extensive material from these areas acquired from the following actions/sources: 1) historical expeditions of the NMPC staff to Turkey (1947) and Iran (1970, 1973, 1977); 2) a recent insect survey of Socotra Island conducted by Czech entomologists; and 3) the dolichopodid collection of Jiří Olejníček, also housed in the NMPC. The study of the material started in 2013 and the preliminary results are presented. Also, information about the collecting sites and expeditions are provided in detail and potentially new records are discussed. Some species of special zoogeographical interest are presented with a discussion about their origin.

Phylogeny of Platypezidae: Is *Microsania* a platypezid?

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Keywords: Cyclorrhapha, Platypezoidea, molecular data

Studies of phylogenetic relationships of Platypezidae were based almost exclusively on morphological characters of adults or larvae, and no comprehensive molecular systematic study across the family has been published. Here, we present results of a molecular phylogenetic study with 47 species of Platypezidae of 18 genera (from 19 world known genera) based on nucleotide sequences for genes from the mitochondrial (12S, 16S, COI) and nuclear (28S) genome. Although the tree topologies are generally consistent with the previous morphological studies, there are still several dissimilarities, which are pointing out to the problematic parts of the previous studies and are stating new questions about the flat-footed flies phylogeny and systematics. The results were highly congruent with recent morphological analyses except for the position of Microsaniinae and shows that the family Platypezidae consists of three well-supported clades: the subfamilies Platypezinae, Callomyiinae and Melanderomyiinae. Microsaniinae form a unique lineage distant from Platypezidae. At the generic level, the genus *Agathomyia* was not resolved as a monophyletic lineage and seems to be paraphyletic. Family Platypezidae (*Microsania* excluded) is monophyletic. According to molecular analyses, subfamily Microsaniinae should be excluded from the Platypezidae and its new systematic position is debated and hypothesized. The important morphological apomorphies defining Platypezidae *sensu novo* are presented and debated. Is there also enough morphological and ethological evidence to exclude *Microsania* from the Platypezidae? If the *Microsania* forms unique clade of cyclorrhaphan evolution or is part of some other bigger taxonomic group (e.g. Phoridae) is still a question and some possible hypotheses are presented.

Wing asymmetry of males and females in three species of *Eristalis*

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Keywords: *Eristalis*, asymmetry, dimorphism, wing venation

In *Eristalis* there are marked differences between sexes in flight behavior. In general males spend more time in flight than females. Moreover there are some differences between species in the flight behavior of males. In *E. tenax* and *E. pertinax* males are territorial. They hover few meters above the ground and chase other males by performing dashing flights. Males of other species, for example *E. arbustorum*, are seen less often hovering and usually they are found on flowers where they probably search for females.

If insects with symmetric wings fly better it can be expected that, in *Eristalis*, males will be less asymmetrical than females. Moreover, it can be expected that the asymmetry will be particularly indistinct in hovering males. In order to verify these hypotheses we have measured size asymmetry and shape asymmetry of wings in 260 individuals belonging to three species: *E. tenax*, *E. pertinax* and *E. arbustorum*. Size asymmetry was measured as the absolute difference between the centroid size of the left and the right wing. Shape asymmetry was measured as Procrustes distance between the left and the right wing.

Wings of females of all three species were significantly larger than wings of males. In *E. tenax* and *E. pertinax* asymmetry of male wing size tended to be smaller in comparison to females. In *E. arbustorum* the opposite was true. However, the difference in asymmetry was only statistically significant in *E. pertinax* and not in the two other species. In all three species asymmetry of male wing shape tended to be smaller in comparison to females. However, the differences were not significant. The results indicate that wings of hovering males can be less asymmetrical than wings of females. However, a larger sample size is required to confirm this with higher certainty.

Taxonomic study of the subtribe Schizomyiina (Diptera: Cecidomyiidae: Asphondyliini) in the eastern Palaearctic region

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Keywords: Asphondyliini, Cecidomyiidae, gall midge, Schizomyiina

The subtribe Schizomyiina (Diptera: Cecidomyiidae: Asphondyliini) consists of 164 described species belonging to 27 genera worldwide. Among them, four genera and 16 species are distributed in the eastern Palaearctic region, comprising 12 species of *Asteralobia*, two species of *Schizandrobia*, one species of *Kiefferia*, and one species of *Oxycephalomyia*. The genus *Asteralobia*, which was erected by Kovalev (1964), is an endemic genus in this region and it is distinguished from the type genus *Schizomyia* by shallow constriction of male flagellomeres. In this study, we examined adult and larval morphological features of the type species of these genera, *Schizomyia galiorum* and *Asteralobia doellingeriae*, as well as of other species of *Asteralobia*. As a result, we confirmed that at least some individuals of *S. galiorum* possess shallowly constricted male flagellomeres, which has been considered as the synapomorphy of *Asteralobia*. In addition, we found that two species of Japanese *Asteralobia* have unique characters in larval morphology. Based on these findings, we discuss taxonomic treatments of eastern Palaearctic Schizomyiina.

Tipulomorpha [poster]

The European widespread *Ptychoptera albimana* Fabricius, 1787 (Diptera: Ptychopteridae): deep morphological divergences, low genetic variability

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Keywords: Genetic analysis, COI, linear and geometric morphometric analysis, Ptychopteridae

Aquatic insects with large distribution area exhibit highly divergent allopatric structures through their ranges as a consequence of Pleistocene climate changes. This paradigmatic pattern has frequently been demonstrated in cold-adapted mountainous species, while a number of euritherm species are consequently neglected. Dipterans are of major importance in almost all types of aquatic ecosystems. In the current study a comparative morphological analyses and molecular tools (mtCOI sequences) were used to test taxonomic hypotheses in the case of the European widespread *Ptychoptera albimana* which presents highly divergent morphological structuring throughout its range. However, such morphological divergent structures are sympatric in some cases, but are clearly separated along an altitudinal gradient. The typical *P*. *albimana* were identified mostly at low elevations in Europe (Luxembourg, Germany, France and Hungary, but also in Romania, in Dobrogea and Bulgaria in Stara Planina) between 50–300 m (lowland-hilly area). In contrast, divergent morphological structures were identified from the Carpathians and Rhodope Mts., up to 500 to 800 m (mountainous area). In contrast the standard BOLD mtCOI sequences (650 bp) frequently used in molecular taxonomy did not reflect a similar pattern and suggest recent area dynamics of populations from different isolated refugia in Europe with secondary contact and genetic introgression. The present integrative study confirms the species status of *P. albimana* and detects postglacial morphological divergences due to some local adaptations in more or less isolated wet habitats through its range.

A phylogenomic estimate of fly evolution

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Keywords: Higher-level phylogenomics, transcriptomes next-gen

The evolutionary relationships of flies are increasingly well understood due to the application of molecular systematics over the past decade and due to large collaborative efforts such as FlyTree (AtoL). Over the course of more than 260 million years of evolution, flies experienced three episodes of rapid radiation: within lower Diptera, lower Brachycera, and Schizophora. As the backbone of fly phylogeny becomes more clear, many relationships within these rapid radiations remain ambiguous. With the application of high-throughput sequencing, resolving these rapid radiations within fly phylogeny may become feasible. Here we present a new higher-level estimate of fly relationships based on new and existing transcriptome data that addresses the placement of several key lineages across the fly tree of life.

Some like it fast, some take it slow: the evolution and potential drivers of copulation duration in Sepsidae (Schizophora)

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Keywords: Copulation duration, mating, sexual selection, Sepsidae

The duration of copulation can greatly influence male fertilisation success while reducing female fitness and generating sexual conflict between the sexes. Despite its importance, the evolution of copulation time remains poorly understood due to a lack of comparative studies. Here, we adopt a comparative approach using sepsid flies as a model to bridge this gap and understand how copulation duration changes over evolutionary time, as well as what factors drive these changes. We examine 50 species of sepsids from across the family, and find that copulation time evolves fast, with times ranging from 5 minutes to 5 hours. While the phylogenetic signal within several smaller clades may be strong, there is a general lack of phylogenetic pattern in copulation time across the family. Only a few species have independently evolved extended copulation times, and such long copulation durations are surprising as they can impose significant mating costs. Additionally, we observe a wide repertoire of mating behaviour and complex variation in their morphology, and so we ask: are there behaviours and morphologies that significantly extend or reduce copulation time? Specifically, we examine the male stimulatory and female rejection behaviours, as well as the male aedeagus and clasper morphology as potential drivers of copulation time. We analyse the synergistic influence of these factors on copulation time while correcting for phylogenetic history.

Fruit flies (Teprhitidae) on two species of Sapotaceae in the Southwest of Brazil

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Keywords: *Anastrepha*, seed feeder, pulp feeder, infestation indices

Tephritidae and Lonchaeidae (Tephritoidea) are denominated fruit flies because their larvae feed in plant tissues of Angiospermae, mainly in fruits and flowers. The fruit flies have global economic importance due their damage in cultivated species of fruits and vegetables, being a quarantine concern. Sampling of wild species of fruits are fundamental for the knowledge of the host plants and trophic interactions of fruit flies species in nature, since in the Neotropical region are unknown the hosts of about 50% of the species of frugivorous Tephritoidea. In this study two species of Sapotaceae were sampled: *Mimusops coriacea* (A.DC.) Miq., in the locality Praia da Lagoinha, Ubatuba, São Paulo, Brazil (23°26'13"S, 45°04'08"W), and *Pouteria ramiflora* (Mart.) Radlk., in the locality Sítio Pena Verde, Assenta-mento Marcos Freire, Dois Irmãos do Buriti, Mato Grosso do Sul, Brazil (20°41'06"S, 55°17'31"W). From *Mimusops coriacea* we sampled 167 fruits (4,525 g, January 24, 2011), and obtained 214 adults of *Anastrepha serpentina* (Wiedemann), with the respective indices of infestation (no. of adults / no. fruits and no. of adults / grams of fruit): 1.281 adults/fruit, and 0.047 adults/g of fruit. On Dec. 27, 2013 and Jan. 29, 2014 we sampled 116 fruits (3,100 g) of *Pouteria ramiflora*. From this host fruit emerged 256 Insects: 91 *Anastrepha serpentina*, 2 *Anastrepha* sp. 1, 8 parsitoids (Braconidae), 118 *Neosilba* spp., 36 Ulidiidae, and 1 *Atherigona orientalis* (Schiner). The infestation levels were: 2.206 adults / fruit and 0.082 adults/g of fruit. *Anastrepha* sp. 1, probably a new species, was found feeding inside seeds, while *A*. *serpentina* consumes the pulp of the fruits. The Ulidiidae and *A*. *orientalis* are probably saprophagous, from fruit already in the decomposition process.

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Description of eight new species of Stomatosematidi (Cecidomyiidae: Diptera) from Brazil

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Keywords: Bibionomorpha, Cecidomyiidae, Diptera, Mato Grosso do Sul State, Stomatosematidi, taxonomy

Cecidomyiidae is one of the most diverse families of the order Diptera, with 6,131 known species and is organized into five subfamilies: Catotrichinae, Lestremiinae, Mycromyinae, Porricondylinae, and Cecidomyiinae. In this family there are a variety of habits, from mycophagous, galling, or inquilines to predators of aphids. The mycophagous habit, present in the basal Sciaroidea, remains in the Catotrichinae, Lestremiinae, Mycromyinae, Porricondylinae and some species Cecidomyiinae, such as Stomatosematidi, Brachineuridi, and a few species of Lasiopteridi. There have been few studies on the family throughout the Neotropical region, especially related to non-galling species. The Stomatosematidi supertribe has 12 fossil species in three genera and 20 living species. The living species are cosmopolitan and placed in two genera, *Didactylomyia* with 3 species and *Stomatosema* with 17 species. In this study eight new species of Stomatosematidi are presented, six species of *Stomatosema*, and two of *Didactylomyia*. The material studied is from the Sisbiota-Diptera Project, collected with malaise traps in the Pantanal, Cerrado and Semideciduous Forest environments of Mato Grosso do Sul State, Brazil. All of the new species are distinguished from previously described species by the unique shapes of the male terminalia.

The first description of the male of *Oxycera quadrilineata* Üstüner and Hasbenli, 2007 (Stratiomyidae: Oxycera) from Turkey

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Keywords: Stratiomyidae, male of *Oxycera quadrilineata*, taxonomy, Turkey

The study is based on a single male specimens of this species was collected at Kindiralık Village in 2002. The male of *Oxycera quadrilineata* Üstüner and Hasbenli, 2007 is described for the first time. Antennae entirely black. Thorax shinnig black. Humeral and postalar callus are yellow. Yellow subnotopleural stripes widened posteriorly and extend to base of halters. Legs mainly yellow, fore tarsi entirely black. Abdomen shinnig black with starting side markings on lower corners of tergum 2 and consisting of side-markings on terga 3 and 4 terga and apical spot on tergum 5. Those on tergum 4 well-separated but not fused medially. Male terminalia: Genital capsule with pronounced medium height and round medial process at hind margin. The male of *Oxycera quadrilineata* are compared with male of *Oxycera pardalina* Meigen, 1822 and male of *Oxycera limbata* Loew, 1862.

Behavioral ecology [poster]

The evolution of striped coat patterns in African mammals – what function do the stripes have?

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Keywords: Tabanidae, attractiveness, stripes, African mammals

Several families of mammals have stripes and many hypotheses have been proposed to explain the evolution of the striped coat patterns. However, there is very limited experimental evidence to support which hypotheses are the most likely to explain the evolution of the striped patterns. Therefore, what adaptive function the stripes serve in all these species is still largely unknown. Some explanations have been proposed such as a striped coat pattern may act as camouflage and a defense against predators. Alternatively, they are perhaps a system for personal identification, social attachment, a cooling device or a display to avoid insect pests.

In this study I investigated the characteristics of stripes such as stripe width for both white and black stripes on 36 striped African mammals' coats collected in museums. I also demonstrated the relationship between width of stripes and attractiveness to tabanid flies increasing with stripe width except for patterns imitating what is found in family Hyaenidae. My study further revealed that appearance of stripes on mammalian coats is most likely not involved in sexual selection, as there were similarities in stripes number or stripes width between sexes for *Equus grevyi* and *Tragelaphus imberbis*. In order to evaluate the effects of stripes on tabanids attractiveness, two experiments designed to test tabanid attraction were performed.

The findings revealed that the stripes in all striped patterns were extremely important in stimulating tabanid flies' repellency. My results suggest that appearance of stripes on different mammalian coats could be an evolutionary force reducing tabanids attractiveness to many striped animals. Thus, the disease transmission risk caused by the biting from tabanid flies may be reduced in host animals evolving a striped coat pattern.

Distinction of the Sciomyzidae larvae in relation to their morphology, prey microhabitats, and prediction of their feeding specificity

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Keywords: Snail-killing flies, larval adaptation

The Sciomyzidae, with 541 worldwide described species exhibit many remarkable adaptive morphologies and larval feeding categories. Their life-cycle, immature stages, larval attributes including microhabitats, specific, morphology, differences of attack and host/prey are important ecological adaptations. This is confirmed by recent molecular analyses. The aspects of the posterior spiracular disc lobes, development of the interspiracular processes, and size of the sensillum setae are useful to predict their polyphagous or monophagous feeding specificity.

Aquatic polyphagous larvae have long triangular spiracular lobes, long branched interspiracular processes, and long sensilla. Those living at the bottom of the water, attacking bivalves, have a lot of long lateral respiratory expansions. Species whose larvae live mainly on the aquatic edges have spiracular lobes and interspiracular processes that are reduced. Some species, such as *Sepedon* spp., have dorsal hairs used in swimming.

Terrestrial species feeding on terrestrial snails, slugs, or, *Pelidnoptera fuscipennis* on Diplopoda, have short spiracular lobes, and the interspiracular processes are fine, very small fishscale-like (many *Pherbellia* spp.). Species feeding on hygrophilous Succinidae spp. have rounded spiracular lobes, and poorly developed interspiracular processes. For all terrestrial species, the sensilla are short. All have short sensilla.

Sciomyzids displaying terrestrial prey specificity show tiny scale-like interspiracular processes with a single spike (*Pherbellia limbata*) unlike polyphagous species in which several spikes were observed (*Euthycera cribrata*). As the above, their sensilla are short.

Morphometric landmarking to disentangle the *Ceratitis* FAR complex (Diptera: Tephritidae)

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Keywords: *Ceratitis rosa, Ceratitis fasciventris*, wing landmarks

Species within cryptic complexes are often difficult, or impossible, to differentiate using classic morphological examination. This is the case with female specimens of representatives of the *Ceratitis* FAR complex (a complex of three agricultural pests that can be further subdivided into five genotypic clusters), especially of *C. rosa* and *C. fasciventris*. We investigated the use of wing morphometrics (including the geometric position of intersections of wing veins and cross-veins, and the demarcation of wing bands) as a possible tool to resolve the complex. Seventeen homologous type I landmarks of the wing venation, and six partial wing bands of both male and female specimens were chosen to conduct generalized procrustes analysis. The results were analyzed using Principal Component Analysis (PCA), Canonical Variate Analysis (CVA), and Permutational Multivariate Analysis of Variance (PERMANOVA). PCA of the landmarks showed clear sexual dimorphism. Yet, differences between morphospecies and, to some extent genotypic clusters, could only be observed when maximizing group differences through CVA. PCA and CVA for the surface areas of the wing bands were generally less resolved than for the wing landmarks. Yet, in all cases, PERMANOVA showed significant differences between morphospecies and genotypic clusters.

Mechanisms of gust rejection in stalk-eyed flies

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Keywords: *Teleopsis*, stalk-eyed flies, kinematics, flight, gusts

Insect flight requires considerable aerodynamic reserves to perform behaviors such as maneuvering, predator-evasion and load-carriage, as well as fly in heterogeneous environments characterized by gusts and turbulence. Stalk-eyed flies, however, generally appear less agile than many popular dipteran model species, and their capacity for passive aerodynamic damping is counteracted by the increased inertia resulting from their elongated eye stalks (Hedrick et al. 2009). How then might stalk-eyed flies (*Teleopsis dalmanni*) respond to simple, lateral wind gusts during flight? We investigated and analyzed the time-course of body attitude (roll, pitch and yaw) and wing kinematics (stroke position and amplitude, geometric angle of attack) using 3D high-speed videography. The gusts perturbed the body attitude about the roll, pitch, and yaw axes simultaneously. Flies quickly responded (16.5 ± 5.4 msec) to these body rotations through bilateral asymmetry in stroke amplitude and wing angle of attack; quasi-steady aerodynamic models suggest these kinematics generate significant roll moments, but only mild pitch and yaw moments, to aid the arrest of gust-induced body motions and restoration of body attitude during the gust response (Vance et al. 2013). Symmetric wingstroke kinematics at the onset of gust-induced body rotations and towards the end of the gust response comprise a significant percentage (40.9 ± 8.0%) of the perturbation and recovery flight sequence where passive aerodynamic damping may mitigate the effects of the gust prior to and following the active kinematic response. Despite our preconceptions, we observed *T. dalmanni* to be extraordinary hoverers and very capable fliers in response to perturbations. Future research investigating flight performance across variation in eye stalk length, thorax muscle mass, and wing size may further characterize the costs of ornamentation with respect to compensatory mechanisms.

Cuticular hydrocarbons as a tool for the discrimination of fruit fly species complexes

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Keywords: Cryptic species complex, *Ceratitis, Anastrepha*, cuticular hydrocarbons, chemotaxonomy

Discrimination of particular species within the species complexes of tephritid fruit flies is a very challenging task. In this fruit fly family, several complexes of cryptic species have been reported, including African *Ceratitis* cryptic species complex (FAR complex) and South American *Anastrepha fraterculus* cryptic species complex. Cuticular hydrocarbons (CHCs) appear to be an excellent tool for chemotaxonomical discrimination of these cryptic species. CHC profiles have been used to discriminate among three important agriculture pests from the FAR complex, *Ceratitis fasciventris*, *C. anonae* and *C. rosa* and among six geographically distinct *Anastrepha fraterculus* populations. Hexane body washes of mature males and females were analysed by two-dimensional gas chromatography with mass spectrometric detection and differences between species and sexes tested through multivariate statistics. Quantitative as well as qualitative differences between sexes and species are reported. Our results represent an important first step in the development of a useful chemotaxonomic tool for cryptic species identification of these important agricultural pests.

Morphological and behavioral novelties in Costa Rican *Hilarempis* (Diptera: Empididae)

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Keywords: Empididae, *Hilarempis*, Costa Rica, taxonomy, behavior

Cumming and Sinclair (2009) previously reported an undescribed species of *Hilarempis* from Costa Rica. An examination of genital and other morphological features in specimens in the collections of INBio (Instituto Nacional de Biodiversidad, Costa Rica) seem to suggest that a second undescribed species of *Hilarempis* is present in the country. Males of these two Costa Rican species exhibit novel characters in the apex of the fore tibia, namely a brush of very long hairs. These modified tibial hairs might be used for hunting prey, a behavior reported in males of other species within the tribe Hilarini.

Behavioral observations of both sexes of these *Hilarempis* species were carried out in Tapantí National Park near Cartago, and Cascajal de Coronado in San José (Costa Rica). It was seen that males exhibited a skimming behavior on the water surface of a brook, moving themselves with their wings. Females, that were more difficult to find, seem to hovered over the males along the stream.

Bibionomorpha [poster]

The Sciaridae (Diptera: Sciaroidea) of Greenland

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Keywords: Bibionomorpha, Sciaroidea, Sciaridae, Nearctic region, Arctic areas, Greenland, Canada

In view of the current climate change, the biota of the Arctic areas is regarded as one of the most vulnerable, and the insect species and their distribution are essential in tracking these changes. The Sciaridae fauna of Greenland and some other Arctic areas was investigated. Twenty species were identified from Greenland, including four new species to Science. In addition to these, five species are known from literature. The most species-rich genera were *Lycoriella* (eight species) and *Camptochaeta* (six species), most with arctic-boreal-alpine distribution. The material was mainly obtained from the ZMUC collection in Copenhagen, but material from recently made collections in Northeast Greenland, Zackenberg Nature Reserve, were also available, resulting in 15 species. The Zackenberg Sciaridae make a part of a larger-scale food-web study by a Finnish research group, including constructing a DNA library of all identified invertebrates from the area. Regarding its climate, the area is among the harshest in the ice-free Greenland and its fauna will make a good indicator of potential changes.

Some materials from the Arctic Canada were also studied, resulting in six sciarid species from Ellesmere Island, including an undescribed one.

The study continues with identification of more available materials, including the study of the types from the historical collection of E. H. Rübsaamen (ZMHB, Berlin), describing the new species, and solving the existing taxonomic problems.

Phylogenetic patterns in the greenbottle flies (Calliphoridae: Luciliinae)

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Keywords: Forensic dipterology, phylogeny, adaptive radiation

The blowfly subfamily Luciliinae is globally distributed. Its four currently recognised genera – *Dyscritomyia* Grimshaw, 1901, *Hemipyrellia* Townsend, 1918, *Hypopygiopsis* Townsend, 1916, and *Lucilia* Robineau-Desvoidy, 1830 – contain many species that have species that have medicolegal forensic significance. Nucleotide sequences of parts of the *28S rRNA*, *COI* and *Period* genes of 20 species of *Lucilia*, three species of *Hemipyrellia* and three species of *Dyscritomyia* were used to estimate a phylogeny. The placements of *Dyscritomyia* and *Hypopygiopsis* were ambiguous, since both made *Lucilia* paraphyletic in some analyses. Recognising *Hemipyrellia* as a genus consistently left *Lucilia* s.l. paraphyletic, and the occasionally recognised (sub)genus *Phaenicia* was consistently paraphyletic. Analysis of morphological characters scored for adults of all genera and most of the species included in the molecular analysis confirmed several of these findings. *Lucilia* showed radiations in the Holarctic, the Nearctic and the Palaearctic. Within *Lucilia*, different feeding habits were phylogenetically clustered and did not form a graded series of evolutionary stages.

Tephritoidea [poster]

An electronic identification key to African fruit infesting Dacines (Diptera: Tephritidae)

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Keywords*:* Lucid keys, multi-entry key, Dacini

The morphological identification of African Dacines (including representatives of economically important genera such as *Bactrocera*, *Ceratitis* and *Dacus*) relies on the use of classical single-access (dichotomous) keys. The quite specific terminology used in the published single-access keys is a serious obstacle for non-specialist users who are not particularly acquainted with tephritid morphology and taxonomy. Additionally, species identification through single-access keys necessarily fails whenever the user is not able to identify any of the dichotomous character states (e.g. due to inadequate taxonomical expertise, lack of clarity of the key, damaged specimen, etc.). Here we present a multi-entry identification key for African fruit-infesting Dacines specifically developed to (1) facilitate morphological identification by non-specialists and (2) provide a single and updated identification tool. The key, available on a Lucid3 platform, includes a total of 394 species and comprises an initial key for genus identification and individual keys to African representatives of eight fruit fly genera (*Bactrocera*, *Capparimyia*, *Carpophthoromyia*, *Ceratitis*, *Dacus*, *Neoceratitis*, *Perilampsis*, *Trirhithrum*). Separate character sets are considered for each genus (range 11–95 characters, 22–280 character states). Images and drawings are provided for (1) characters (showing where the character is found and how it looks like), (2) character states (showing the degree of morphological variability across species with the same character state) and (3) species (providing information about species morphological features). A formal description is provided for each species according to the published literature. Information regarding the taxonomic status, geographic distribution and collection specimens for species is available through hyperlinks to Encyclopedia of Life and to the Belgian Biodiversity Platform (as Belgian portal to GBIF). Links to the Barcoding of Life Database website (BOLD) allow verifying the availability and geographical sampling of DNA barcodes for each species.

Higher phylogeny of frugivorous fruit flies (Diptera: Tephritidae: Dacini) as inferred from mitochondrial and nuclear gene fragments

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Keywords: Ceratitidina, Gastrozonina, *Zeugodacus, Bactrocera, Ceratitis*

The phylogenetic relationships among subtribes of the tribe Dacini (Ceratitidina, Dacina, Gastrozonina) were investigated by sequencing of mitochondrial and nuclear gene fragments. Analyses were implemented on two datasets. The first, aiming at obtaining the largest taxonomic coverage, included 161 concatenated COI+16S gene fragments, the second, aiming at obtaining the strongest phylogenetic signal, included 82 concatenated COI+16S+ND6+*per* sequences. Taxon sampling included 134 species belonging to (a) six of the 12 Ceratitidina genera, (i.e. *Capparimyia*, *Carpophthoromyia*, *Ceratitis*, *Neoceratitis*, *Perilampsis* and *Trirhithrum*), (b) two of the three Dacina genera, (i.e. *Bactrocera* and *Dacus*) and (c) two out of the 27 Gastrozonina genera (i.e. *Bistrispinaria* and *Clinotaenia*), with strong emphasis on African representatives. The subtribal position for all genera sampled concur with their current taxonomic placement. All three subtribes were recovered as monophyletic clusters with Gastrozonina (*Bistrispinaria* and *Clinotaenia*) in a basal position with respect to the two other subtribes. Within Ceratitidina only *Perilampsis* and *Capparimyia* formed well-resolved monophyletic groups while *Ceratitis*, and *Trirhithrum* do not form reciprocally monophyletic clades. *Carpophthoromyia* is paraphyletic due to *Trirhithrum demeyeri* being included in this clade. Complex phylogenetic relationships were observed within Dacina with *Dacus*, representatives of subgenera of the *Zeugodacus* group and representatives of subgenera of the *Bactrocera* group forming separate clades. The recovered phylogeny, as well as previously published data, show that *Zeugodacus* (and related subgenera) represent a separate entity with respect to the other *Bactrocera* subgenera. Yet, the exact phylogenetic relationship between these three entities cannot be properly resolved.

Diversity of florivous flies (Diptera: Tephritoidea) in the Southwest of Brazil

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Keywords: Asteraceae, host association, Tephritinae

The Tephritoidea oviposit in Angiosperm tissues (fruits, seeds, flowers, leaves, stems, roots), and they can cause direct and indirect damage. Several species Tephritinae (Tephritidae) consume the seeds of Asteraceae and can act on the population suppression of Asteraceae weeds in cultivated areas. The main aim of this study was to investigate the occurrence of Tephritoidea species associated with head flowers of Asteraceae in three vegetation types in the region of Dourados-MS, Brazil, to check which species of Asteraceae are host of Tephritidae and Lonchaeidae in physiognomies of Cerrado, Semidecidual Forest and Agricultural Area. Head flowers were collected from 37 Asteraceae species, being about 500 inflorescences were packed in containers and emerging flies or their parasitoids were fixed after 48 hours of the emergence in 80% ethanol for later identification. Were obtained a total of 2,706 adults, being 833 Tephritinae (Tephritidae) belonging to seven genera and nine species. The species of Tephritinae reared from their respective host flowers, were: *Cecidochares fluminensis* (*Chromolaena arnottiana*, *Chromolaena ivifolia*, *Vernonia cognata* and *Vernonia polyanthes*), *Dictyotrypeta* sp. (*V. polyanthes*), *Dioxyna chilensis* (*Bidens pilosa*, *C. arnottiana*, *Porophyllum ruderale*, and *V. polyanthes*), *Tetreuaresta* sp. (*Pterocaulon virgatum*), *Trupanea jonesi* (*Chaptalia integerrima*, *C. arnottiana*, *C. ivifolia*, *P. ruderale* and *V. cognata*), *Tomoplagia brasiliensis* (*Vernonia bardanoides* and *V. polyanthes*), *Tomoplagia reimoseri* (*C. arnottiana*, *V. bardanoides* and *V. polyanthes*), *Xanthaciura biocellata* (*C. arnottiana*, *C. ivifolia*, *Eupatorium multicrenulatum*, *Pterocaulon virgatum*, *V. cognata*, *V. polyanthes* and *Zinnia elegans*), and *Xanthaciura unipuncta* (*Baccharis triplinervis*, *C. arnottiana*, *V. polyanthes* and *Z. elegans*). From the sampled Asteraceae flower heads also have emerged 1,097 adults of *Lonchaea* spp. (Lonchaeidae), and 776 parasitoids (Hymenoptera). This is the first record for Tephritinae in capitula of Asteraceae in the Midwest of Brazil and from Lonchaeids associated to Asteraceae flower heads in Brazil.

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Psychodomorpha [poster]

Faces behind names – a short history of research on Psychodidae

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Keywords: Psychodidae, history, predecessors

Psychoda was the first mothfly genus named by Latreille (1796) based on '*Tipula phalaenoides*' Linné. J. W.

Meigen contributed 8 more species to '*Psychoda*' in the first half of the 19th century. During the following decades Macquart (1838) distinguished *Nemopalpus* Haliday (1839), *Sycorax*, and *Trichomyia*. *Ulomyia* and *Pericoma* were named by F. Walker (1856). Around the turn of the century E. A. Eaton described about 30 species and distinguished the genera *Clytocerus* (1904), *Philosepedon* (1904), *Telmatoscopus* (1904), *Threticu*s (1904), and *Panimerus* (1913). A.L. Tonnoir named approx 130 species and published for example a remarkable study on the genus *Psychoda* (1922). His further studies were on Afrotropical, Neotropical and Australian taxa. Enderlein (1935/36) attempted a tribal arrangement. After World War II research activities developed in Japan (Tokunaga/Komyo), Great Britain/ Australia (A.L. Tonnoir/G.H. Satchell/D.A. Duckhouse), France (F. Vaillant) Italy (M. Sarà/G. Salamanna) and the United States (L.W. Quate). The bulk of species and genera known to date were mainly described in the second half of the 20th century by these colleagues and their followers. To date promising new faces and names turn up in Europe, North and South America, who with all the new methods will continue the work on this adorable family, and solve problems concerning phylogenetic concepts in the future.

Psychodidae subfamilies – answers and questions

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Keywords: Psychodidae, subfamily, relations, evolution

Approximately 2.500 psychodid species (excl. Phlebotominae) have been described to date. Phlebotominae, Bruchomyinae, Trichomyinae, Sycoracinae, Horaiellinae and Psychodinae are the six generally accepted subfamilies. However, some doubts on the position of some taxa with combined radius 4+5 vein (Trichomyiinae, Sycoracinae) remain. An attempted phylogenetical analysis of subfamiliar morphological features, particularly of the genera *Sycorax* Haliday, *Parasycorax* Duckhouse, *Aposycorax* Duckhouse and other Neotropical species should provide hints whether the subfamiliar structure of Psychodidae (s.l.) may be assumed stable.

Documenting systematic relationships among the Australian blowfly fauna

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Keywords: Calliphoridae, Australia, systematics

Taxonomic and phylogenetic studies of Australia's blowflies have a long history, dating back to the descriptions by Fabricius in 1775 of *Amenia leonina* and *Calliphora augur*, species collected by Banks and Solander during Cook's voyage along eastern Australia in 1770. Nonetheless, documentation of the Australian fauna was not significantly advanced until the work of Macquart in the 19th century, and Malloch and Norris in the 20th century. Despite the efforts of these and other workers and the relatively conspicuous nature of most Australian blowflies, probably at least half of the endemic fauna remains undescribed. Such fundamental taxonomic research must be a priority in order to fully appreciate the pattern of evolutionary diversity of the family in Australia, as well as their radiation within the continent and immigration from neighbouring regions. Of additional assistance in this regard must be the expansion of molecular analysis to encompass more Australian species, especially to help resolve the relationships between subfamilies that have recently been suggested to be polyphyletic.

This paper reviews the state of systematic knowledge of the Australian Calliphoridae, identifies the main gaps and research opportunities, and lays a plan for developing a more sophisticated level of understanding of this important group of flies.

Forensic application of Australian flesh flies

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Keywords: Sarcophagidae, Australia, forensic entomology, identification, systematics

Flesh flies of the genus *Sarcophaga* are prominent and important components of the Australian fly fauna. Immature sarcophagids of carrion-breeding species are potentially useful for estimating the minimum time since death of victims of violent crimes. The potential for using sarcophagids in forensic entomology has however been limited because species cannot be reliably identified, especially as immatures. Flesh flies have notoriously uniform adult and larval morphology.

This paper reviews recent research that has aimed to redress this situation by 1) developing new identification tools for all genera of Australian flesh flies and males of all species of *Sarcophaga*; 2) revising the Australian distributions of sarcophagid species and recording species new to Australia; 3) recognising species new to science and revising the morphology of others in the process of including them in a new key; 4) pioneering the application of mitochondrial ‘barcoding’ in sarcophagids by analysing this region of COI, and showing that it can also be used to identify immatures; and 5) undertaking phylogenetic analysis of flesh flies by incorporating COI along with CAD (a nuclear marker) and morphological characters. The future scope for research on Australian flesh flies in a forensic context is summarised.

Systematic study of the subfamily Phasiinae from China (Diptera: Tachinidae)

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Keywords: Diptera, Tachinidae, Phasiinae, taxonomy, biogeography, China

Phasiinae (Diptera: Tachinidae) is the smallest subfamily of the Tachinidae, with about 500 species in 150 genera and 6–16 tribes are recorded in the world. As parasitic natural enemies of pest Heteroptera they are an important group in agriculture and forestry protection. The monophyly of Phasiinae was recently confirmed by Cerretti et al. (2014). In this study, about 1,000 specimens of Phasiinae collected from 32 Provinces, Autonomous regions and Municipalities of China are identified and described. A revised checklist including 105 species in 21 genera belonging to 5 tribes is recognized, in which 25 species are new to science, 18 species are recorded in China for the first time, 3 species are newly recorded to the Palaearctic and 2 species are new to the Oriental region. A key to genera and keys to species in China are given. Based on the species distribution and collecting data, information on life history and potential use as natural enemies in biological control are added. Faunal and biogeographic features, especially for China, are preliminarily analysed. Based on 112 morphological characters the phylogenetic relationships within Phasiinae are currently under analysis.

Flight strategies of *Coenosia attenuata*: a high speed video study

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Keywords: Vision, aerial attack, 3D trajectory

The tiny (3–4 mm) Calyptrate, *Coenosia attenuata,* challenges the notion that visually driven predation in insects is restricted to species with large brains and eyes. However, extreme size constraints still apply, imposing the need for behavioral tradeoffs. For example, since a small brain is limited in computational power, *C. attenuata* might simplify the predatory attack by employing a “pure pursuit” strategy, in which the predator flies directly towards the prey until contact is made. Although computationally simple, this strategy suffers three drawbacks: it is energetically expensive because the trajectory is long; the flight speed must be high; and the prey has time to detect the attacker. In contrast, interception offers the shortest pathway and requires the fewest maneuvers, but it is difficult to achieve because both position and angular velocity must be estimated accurately and quickly. To determine the attack strategy employed by *C. attenuata*, we filmed their aerial-attack trajectories in the wild and in captivity with high-speed video cameras, and later reconstructed the 3-D trajectories. Indeed, *C. attenuata* usually took off directly towards the prey (pure pursuit). However, later in the flight, *C. attenuata* headed towards the future prey location (interception). Thus, the pursuit trajectory flown by *Coenosia* results from a novel insect flight strategy, which we term “partial lead” (borrowed from fighter-plane terminology). It is not known how the neural system in *C. attenuata* achieves the performance necessary to employ this strategy. In captivity, *C. attenuata* suffer from large errors in the estimation of prey location, even when the prey is stationary, perhaps due to a featureless visual background. It is possible that in the wild, the background clutter created by gravel and vegetation provides useful cues for such calculations.

Paleogene Diptera compression fossils as valuable information source for evolutionary history

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Keywords: Fossil Diptera, paleobiogeography, paleoecology

Investigations on fossil biota from the Paleogene show that Diptera were a highly speciose part of the former biocoenosis during that time. Due to taphonomic influences, only a selected taxa representation is given, both in compression fossils and in amber fossils. For example, the preserved size spectra in compression fossils and in amber often differ significantly, the specimens in amber being usually smaller than in compression fossils. Taphonomic influences among different fossil sites delivering compression fossils are for example the significant scarcity of Diptera fossils in Maar lake deposits.

Compression fossils have given unexpected insights. For example, the fossil record of a tsetse fly (Glossinidae) in the Oligocene of Enspel in Germany documents a formerly very different distribution of these flies, which today occur only in Africa. The only other fossil record of fossil glossinid flies is from Florissant, USA. These fossil records are very informative in biogeographical respect, but paleoecological implications can only be drawn with caution because one has to keep in mind that the ecological preferences could have changed in evolutionary history, which seems to be the case for tsetse flies. From Messel a tangle-veined fly (Nemestrinidae) was recorded, which were speciose during the Mesozoic, but whose abundance declined during the late Mesozoic and Cenozoic. Bee flies (Bombyliidae) of the genus *Comptosia*, which closest relatives today occur only in Australia, were recorded from compression fossils from Messel and Florissant. The investigation of fossils gives unique insights into their former biogeography and and adds significantly to the understanding of the evolutionary history of flies.

An example of paleoecological importance is the investigation of Diptera remains in fish coprolites which gave insights into the former food web structure of former Lake Messel.

Culicomorpha [poster]

Community-based passive mosquito monitoring in Germany by the citizen science project “Mückenatlas”

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Keywords: Culicidae, citizen science, Germany, invasive species, mosquito distribution, Mückenatlas, passive mosquito monitoring

Changes in the mosquito fauna are usually perceived for the first time by the human population, not by scientists or authorities. As part of a German nationwide mosquito monitoring program, the citizen science project “Mückenatlas” (www.mueckenatlas.de) was initiated in early 2012 as an instrument of passive mosquito monitoring based on the assistance of the general public. Supported by extensive media work, the public is requested to collect mosquitoes in private surroundings and submit them for scientific analyses. The data will supplement data obtained by trapping, and both will be combined into a common database. The advantage of the “Mückenatlas” is the cost-efficient coverage of large numbers of collecting sites, which allows for a considerable improvement of mosquito distribution maps and provides the possibility to detect early changes in the mosquito fauna, such as the introduction and establishment of invasive species.

In 2012 and 2013, a total of approximately 4,500 postal items including some 18,000 mosquitoes were received by the “Mückenatlas” team. Out of 50 culicid species supposedly occurring in Germany, 39 belonging to six genera (*Anopheles*, *Aedes*, *Coquillettidia*, *Culex*, *Culiseta*, *Ochlerotatus*) were identified. In addition to abundant and wide-spread species, some rare species were recorded. Most strikingly, the “Mückenatlas” led to the detection of two unknown populations of the Asian bush mosquito *Ochlerotatus japonicus japonicus* in West and North Germany.

While the collections and analyses continue, the “Mückenatlas” proves to be a valuable tool for passive mosquito monitoring.

Mosquito monitoring in Germany: detection of invasive and rare indigenous species

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Keywords: *Aedes albopictus,* Culicidae, invasive species, mosquito monitoring, Mückenatlas, *Ochlerotatus japonicus japonicus,* rare species, trapping, vectors

To update data on the German culicid fauna, a mosquito monitoring program was launched in 2011. BG sentinel and EVS traps equipped with CO_2 sources were set up at 120 locations distributed all over the country, catching mosquitoes from April to October for 24 hours per week. Irregularly, additional collections were conducted on adults from winter shelters with aspirators and on larvae and pupae from breeding sites with dippers. The citizen science project “Mückenatlas” served as an instrument for passive monitoring by requesting the submission of mosquitoes captured by private persons. The mosquitoes were identified to species morphologically or, in the case of damaged specimens or cryptic species, genetically.

In addition to huge numbers of individuals of abundant and wide-spread species, invasive and rare indigenous species were also found. Thus, several adult specimens of both the Asian tiger mosquito *Aedes albopictus* and the Asian bush mosquito *Ochlerotatus japonicus japonicus* were trapped in southwestern Germany in 2011. In 2012, *Oc. j. japonicus* was also collected as preimaginal stages in western and northern Germany, leading to the discovery of two hitherto unknown populations of this species in Germany. A third invasive species, *Culiseta longiareolata*, was repeatedly trapped in southwestern Germany. Three *Culiseta* species not reported from Germany for decades were re-discovered: *Cs. alaskaensis*, *Cs. ochroptera* and *Cs. glaphyroptera*. So far, the monitoring has produced 44 species, 43 now considered indigenous in Germany plus a non-established one (*Ae. albopictus*).

The further introduction and spread of *Ae. albopictus* and *Oc. j. japonicus* need to be thoroughly surveyed since these are regarded as competent vectors of pathogens.

Diversity and behaviour of the kleptoparasitic satellite flies (Diptera: Sarcophagidae: Miltogramminae)

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Keywords: Flesh flies, Miltogramminae, natural history, diversity, kleptoparasitism

The Miltogramminae, or satellite flies, are one of the three subfamilies of Sarcophagidae, and account for just under a quarter of the known species in this family. They are distributed worldwide and are particularly diverse in the arid and subarid habitats of the Old World. Most species develop, in the larval stages, as kleptoparasites in the nests of solitary Apoidea, where they feed on the provisions stocked in the nest for the bee's or wasp's offspring. Females of different species have evolved different behavioural mechanisms for infesting the nests of their hosts, as well as for destroying the host's immature stages. Kleptoparasitism was initially thought to be a groundplan biological feature of the subfamily; however, recent findings suggest that it may have evolved from a plesiomorphic necrophagous lifestyle. From a phylogenetic point of view, recent works have shown that much information can be found in the larval morphology; also, targeted molecular studies are yielding the first solid phylogenies for the group. Recent sampling around the world has shown that miltogrammine diversity is probably still heavily underestimated, especially in sub-Saharan Africa, the Middle East, and Asia. This talk summarises our current knowledge of the Miltogramminae, providing an overview of their morphology, classification, diversity and ecology, with particular emphasis on their kleptoparasitic habits.

A review of the taxonomy and distribution of species of the genus *Lucilia* Robineau-Desvoidy (Diptera: Calliphoridae) in the Neotropical region

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Keywords: *Lucilia*, Calliphoridae, taxonomy

The taxonomy of Neotropical *Lucilia* is currently in a state of confusion and badly in need of revision. The current study was initiated to address the following issues: to establish the valid species in the region; to examine types to determine valid species names; to develop a key to aid in species identification; to redescribe the existing species; and to describe any undescribed species found in the region. The identification and distribution of each species will be briefly reviewed and distinguishing characters for each species will be discussed.

Archiving, mining, and analyzing genomic data for NEXT-GEN Dipterology

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Keywords: GENBANK, genome, transcriptome, databases

Genomic data are now widely applied in systematics, taxonomy, population genetics, ecology and behavior of flies. NEXT-GEN sequencing has dramatically increased the pace of data accumulation and researchers are faced with a growing number of specific data repositories to archive and manage the primary genetic data from diverse studies. Here, we review and provide examples to illustrate the availability of genomic information on Diptera, emphasizing the availability and use of public data repositorties. Specifically, we describe the work-flow for deposition of transcriptome data into public databases, highlight the challenges of archiving primary data from NEXT-GEN sequencing, and present details of our use of existing data for phylogenetics and functional genomics. A large comparative phylogenetic analysis of data from EST libraries, genomes, and transcriptomes is used to highlight the potential of use and re-use of existing genomic data for addressing key questions in dipterology.

Morphological identification of *Lucilia sericata, Lucilia cuprina* and their hybrids (Diptera: Calliphoridae)

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Keywords: Greenbottle blowflies, morphology, discriminant analysis

Hybrids of *Lucilia sericata* and *L. cuprina* have been shown to exist in previous studies using molecular methods, but no study has shown explicitly that these hybrids can be identified morphologically. Published morphological characters used to identify *L. sericata* and *L. cuprina* were reviewed, and then scored and tested using specimens of both species and known hybrids. Ordination by multi-dimensional scaling indicated that the species were separable, and that hybrids resembled *L. cuprina*, whatever their origin. Discriminant function analysis of the characters successfully separated the specimens into three unambiguous groups – *L. sericata*, *L. cuprina* and hybrids. The hybrids were morphologically similar irrespective of whether they were from an ancient introgressed lineage or more modern. This is the first evidence that hybrids of these two species can be identified from their morphology.

Review of the fossil spider flies (Acroceridae): a surprising prehistory of morphological and biological diversity

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Keywords: Spider-fly, parasitoid, fossil

Spider-flies (Acroceridae) are a morphologically bizarre and diverse group of obligate spider parasitoids. There are presently over 520 described species in about 53 genera, divided into three subfamilies, Acrocerinae, Philopotinae and Panopinae. Fossil acrocerids have been described from Cretaceous to Miocene-aged deposits, both as compression fossil and amber inclusions. The overwhelming number of genera and species are known from Baltic amber, and yet all fossil acrocerids known are placed in the subfamilies Acrocerinae and Philopotinae; no Panopinae fossils have been discovered. We review the fossil Acroceridae in the context of recent phylogenetic studies on the family, including identification of new genera and species from Baltic Amber.

Mesembrinellinae (Calliphoridae) from Colombia: taxonomic diversity and ecological approach

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Keywords: Colombia, diversity, Mesembrinellinae, taxonomy

Mesembrinellinae is a Calliphoridae subfamily with nine genera and 34 species restricted to the Neotropical region and found mainly in areas with undisturbed native vegetation. In Colombia, this group has just recently been studied from the sea level to high altitude in Maracaibo, Choco, Magdalena, Cauca, Napo Imeri and Northern Andean provinces. Traps using decomposed fish and fruit as well as human feces were used to collect the specimens. The results showed great diversity with 20 species of seven genera: *Mesembrinella* Giglio-Tos with eight species; *Huascaromusca* Townsend and *Eumesembrinella* Townsend with four species; *Giovanella* Bonatto, *Laneella* Mello, *Souzalopesiella* Guimarães and *Thompsoniella* Guimarães with one species each. Colombia has an equatorial climate with bimodal rainfall: March–May and September–November. The mesembrinelids were collected mainly during rainfall periods; *G. carvalhoi*, *H. aeneiventris*, *H. decrepita*, *H. semiflava*, *H. vogelsangi*, *L. perisi M. patriciae*, *M. currani* and *Thompsoniella* sp. n., in the Northern Andean province between 1400–2900 m; *M. bellardiana*, *M. pictipennis*, *E. cyaneicincta, M. currani, H. vogelsangi* and *E. randa* at the foothills of the Amazon in the Napo province 400–900 m; *M. batesi* in Imeri province at 400 m; *S. facialis* in pluvial forest, in Choco at 30 m, Magdalena and Cauca provinces between 500–600 m. All are found mainly in undisturbed native forest. However, for *M. bicolor*, *M. abaca* and *M. townsendi* the habitat pattern was different. They were most widely distributed and were collected mainly in areas with disturbed vegetation or semi-urban areas with human intervention in the Cauca and Magdalena provinces. This is the first study on the ecology of the species of this Neotropical group in Colombia. I hope this could be used as a parameter to be taken into account in programs that evaluate preserved areas, as well as part of the policies for environmental studies as are used today for birds, plants and soil organisms.

Bibionomorpha [poster]

Review of the genus *Camptochaeta* Hippa & Vilkamaa (Diptera: Sciaridae) from China

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Keywords: Sciaridae, new species, new record, China

The genus *Camptochaeta* in China is reviewed and ten species are recognized. Among them, three new species, *C. robusta* sp. n., *C. helanshana* sp. n. and *C. tumidula* sp. n. are described, and four species, *C. bournei* (Shaw, 1941), *C. consimilis* (Holmgren, 1869), *C. subcamptochaeta* (Mohrig, 1992) and *C. uncifera* Hippa & Vilkamaa, 1994 are reported for the first time from China. In addition, the geographical distribution of the ten Chinese species is provided, as long with a key to all these Chinese species. This study raises the number of the species of Chinese *Camptochaeta* from three to ten.

Systematic of Phthiriini and revision of Neotropical species of *Phthiria* Meigen, 1820 (Diptera: Bombyliidae: Phthiriinae)

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Keywords: Bombyliidae, *Phthiria,* taxonomic revision, cladistic analysis, Neotropical

The Phthiriinae is a bee fly subfamily that includes two tribes: Phthiriini and Poecilognathini, together, consisting of 10 genera. The Phthiriini encompasses six genera: two exclusively found in the Nearctic region (*Acreophthiria* Evenhuis and *Neacreotrichus* Cockerell), and three exclusively Australian (*Acreotrichus* Macquart, *Australiphthiria* Evenhuis and *Pygocona* Hull) and *Phthiria* Meigen, main focus of this study, which has 63 species distributed through Afrotropical, Neotropical, Paleartic and Oriental regions. A taxonomic review of Neotropical species of *Phthiria* is conducted, including a cladistic analysis and redescriptions and illustrations of species. Six valid species are recognized from the Neotropics: *Phthiria austrandina* Edwards, *P. cana* Philippi, *P. chilena* Rondani, *P. exilis* Philippi, *P. homochroma* Hall and *P. tristis* Bigot. An identification key to species based on distinctive morphological features is also presented. The main question of this project is whether the six Neotropical species previously included in *Phthiria*, belong, to this genus or if they will form a different monophyletic group which, should be placed in another genus of Phthiriinae, or even in a new genus. For this study, our cladistic analysis included species of all biogeographic regions with known records of *Phthiria*, and also representatives of other Phthiriini genera. The cladistic analysis was based on 36 taxa and 39 morphological characters, resulting, after simple heuristic search, in six most parsimonious trees, whose strict consensus has 128 steps, CI: 37 and RI: 75, and also another topology from implied weighted, with three most parsimonious trees. *Phthiria* does not have a supported monophyly: the Neotropical species group in a distinct clade, are monophyletic, and are transferred to a new genus, which is the putative sister-group of the Australian clade *Acreotrichus + Australiphthiria* + *Pygocona*.

The complete mitochondrial genome sequence of *Gasterophilus pecorum* (Fabricius) with a comparative mitogenomic analysis of Oestroidea

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Keywords: *Gasterophilus pecorum,* mitochondrial genome, Oestroidea

Gasterophilus larvae are obligate parasites of equids and live on the mucosa of various regions of the equid gastrointestinal tract as horse gastrointestinal myiasis. *Gasterophilus pecorum* (Fabricius, 1794) (Diptera: Oestridae) is the most damaging parasite of equids in Kalamaili, Xinjiang, China, as opposed to other regions of the world, where *G*. *intestinalis* always predominates. mtDNA has been extensively used for studying evolutionary relationships among animal species, due to its maternal inheritance, rapid evolutionary rate, and lack of genetic recombination. The aim of this study is to describe the complete mtDNA sequence of *G*. *pecorum*, the most important species of the genus and the subfamily Gasterophilinae, to enhance basic knowledge of oestrid mtDNA, and to evaluate the evolutionary pattern of mtDNA within the Oestroidea. The results found that the *G*. *pecorum* mtDNA genome is very similar, both in genes order and orientation, to all known oestrids. It is a circular molecule of 15750 bp, which contains all 37 genes usually present in bilaterians: 13 protein-coding genes, 22 tRNA genes, and 2 rRNA genes. The complete set of 22 tRNAs typical of metazoan mitochondrial genomes is present in *G*. *pecorum*. tRNASer and tRNALeu occur twice. All tRNAs possess the typical clover-leaf secondary structure, except tRNASer(AGN), where the DHU-arm is entirely absent, as observed in other insects. Twenty-two mismatched base pairs are observed in the tRNA genes. Differently from other oestrids, the TΨC loop of tRNA ARG is only 2 bp. In addition, the nucleotide composition of *G. pecorum*, with a low A+T content (70.7%), compares with other known oestrids. Within the superfamily Oestroidea, the A+T content has a higher trend from vertebrate parasitic flies to invertebrate parasitic flies. The possible relationship between characters of the *G. pecorum* mtDNA genome and its special biology is also discussed.

Culicomorpha [poster]

Mitochondrial phylogeography of *Culicoides oxystoma* in East and Southeast Asia, and Australia

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Keywords: *Culicoides* biting midge, vector, arbovirus, phylogeography, gene flow

Culicoides oxystoma Kieffer (Diptera: Ceratopogonidae), a suspected vector of Akabane, Aino, Chuzan and epizootic hemorrhagic disease viruses, is widely distributed across Asia, Africa, and Oceania. Epidemics of diseases in ruminants caused by these arboviruses induced serious economic losses to livestock industries in East Asia and these may be due to seasonal movements of infected vectors from endemic regions in southern Asia.

To investigate this hypothesis, we examined the phylogeographic distribution of *C. oxystoma* in East and Southeast Asia, and Australia. Mitochondrial DNA sequences up to 1,948 bp length (cox1-trnL2-cox2) were analysed from more than 200 specimens of *C. oxystoma* sampled across East and Southeast Asia, Australia and Israel.

Diversity of haplotypes was high within and among sample locations. Maximum sequence difference among specimens in East and Southeast Asia, and Australia was less than 3%, suggesting a recent shared origin for the species in the region. The Middle East fauna differed to those from East and Southeast Asia, and Australia by over 3%.

Maximum likelihood analyses revealed numerous clades in East and Southeast Asia, and Australia, but relationships among these clades were poorly resolved or supported. Haplotype clades from Australia/Indonesia were totally absent from tropical or temperate locations throughout the other regions. In contrast, marginal

haplotype sharing was evident between temperate (Japan, Korea, Taiwan) and tropical locations (Cambodia, Lao PDR, the Philippines, Thailand, Vietnam) in East and Southeast Asia. This may have resulted from historical gene flow and/or infrequent long distance dispersal events between the two regions and indicates some propensity for gene flow by this species. The genetic separation of the Australian/Indonesian populations, however, indicates contemporary barriers to dispersal exist. The relevance of these findings for evaluating arbovirus dispersal in the region will be discussed.

Discovery of the subgenus *Neoilliesiella* in the Oriental region (Diptera: Empidoidea: Empididae: Trichopezinae)

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Keywords: Empidoidea, Empididae, Trichopezinae, *Neoilliesiella*, Oriental region

The genus *Heleodromia* Haliday, 1833 belongs to the subfamily Trichopezinae with 26 known species distributed in the Holarctic and Oriental regions. It contains two subgenera, *Heleodromia* and *Neoillliesiella*.

Recently we found 5 species of the subgenus *Heleodromia* in China, which are distributed in Inner Mongolia (Northwest China) and Southern Tibet (Southwest China).

Hitherto, the subgenus *Neoilliesiella* Wagner *et* Özdikmen, 2006 has been considered very rare and known to occur only in Eastern Europe with the following two known species: *Heleodromia* (*Neoilliesiella*) *banatica* Wagner, 1985 reported from Romania, and *Heleodromia* (*Neoilliesiella*) *pectinulata* (Strobl, 1898) from Bosnia and Herzegovina, Croatia. Tibet is a plateau region in Asia, north east of the Himalayas. Most of this region belongs to the Palaearctic region except for southern Tibet which is considered Oriental. The dance fly fauna of Tibet is poorly known. We found this rare subgenus in the Oriental region for the first time, with one undescribed species collected by the second author in a subtropical forest in Southern Tibet in 2013. This undescribed species may be easily separated from two European species by the absence of acr and epandrial dorsal process.

The two European species, *H.* (*N.*) *banatica* and *H.* (*N.*) *pectinulata,* seem to be sister species in having 3–4 paired acrostichal bristles and an epandrium with a well developed dorsal basal process.

Austral Biogeography – goodbye Gondwana and the Moa Buoyancy Hypothesis

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Keywords: Austral taxa, biogeography, Gondwanaland, Mecoptera, vicariance

Our understanding of the biogeography of the southern end of the world has been revolutionized in recent years. The comfortable assumption that austral distributions can be explained by Gondwanan ancestry followed by vicariance has been overturned by evidence from studies estimating divergence times of key austral taxa, using molecular data. A number of iconic Gondwanan groups have diverged too young to be explained by Gondwanan vicariance, and suggest that long distance, over-ocean dispersal has been an important process in shaping austral distributions. Also, there is compelling geological evidence that most of New Zealand was submerged in the Oligocene, and much of its biota has been assembled since then. Our knowledge of these distributions and the processes that shape them will improve as we gain further insights into the distribution of extant and extinct austral lineages and improve divergence time estimation methods. A number of processes are likely to have affected the distribution of each austral lineage, and ecological factors will influence the probability of these processes. We discuss these issues using recent evidence from Diptera and Mecoptera.

Inferring the phylogenetic relationships of early dipteran lineages based on transcriptomic data

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Keywords: Lower Brachycera, phylogenomics, 1KITE, transcriptomes

While the Brachycera are undoubtedly monophyletic, the relationships between the earliest evolving lineages of this megaradiation are not resolved. A recent molecular analysis inferred a monophyletic clade of Lower Brachycera (excluding the Empidoidea) (Wiegmann et al. 2011), but most morphological phylogenetic analyses have inferred a paraphyletic grade of infraorders, with the Asiloidea being more closely related to the Eremoneura than the remainder. Recent published analyses have disagreed on the placement and monophyly of Nemestrinoidea (Nemestrinidae and Acroceridae). Previous studies have been based on a relatively small number of genes have been hampered by short branch lengths and low support levels at critical nodes. By including much larger samples of the genome, phylogenomic approaches may address these challenges. We present the results of our Orthorrhapha phylogenomic analysis using ~2,000 orthologous single copy genes for phylogenetic inference derived from transcriptome data from the 1KITE project.

Comparative study of the structure of male terminalia of the genus *Lispe* Latreille (Diptera: Muscidae)

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Keywords: House fly, male terminalia, morphology

The genus *Lispe* Latreille is distributed worldwide and consists of approximately 150 species. Since some species have hook or pad like protuberance on the tarsomeres of the male legs, the leg morphology has been well used for identification. In contrast, the male terminalia have not been examined for most of the species of *Lispe* despite the fact that their features are useful for phylogenetic reconstruction. In particular, the pregonite, postgonite and phallus are little studied.

We investigated the homology of the male terminalia in order to infer the phylogenetic relationships within the genus. We redefine different morphological characters of the male terminalia. In the species with a hook-like protuberance on the first tarsomere of the male fore leg, the male terminalia have a small pregonite and a very long postgonite. In contrast, the pregonite is long and the postgonite is bifid in the species with modifications on the first tarsomere of the male hind leg. Additionally, in these species, the phallus has a pair of peculiar projections at the base.

Species-area relationship (SAR) in Muscidae with uniform and proportional sampling

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Keywords: Conservation, diversity, fragmentation, power model, species richness

The species-area relationship (SAR) is one of the few laws in ecology. One of the problems in testing it is the effect of the different types of sampling used. To avoid unequal sampling efforts and to capture the largest possible heterogeneity of environments, we used an uniform and proportional sampling method to test the effect of area size in the richness and diversity of Muscidae species in coastal plains of southern Brazil. The area size was represented by the distance between Malaise traps. We installed 108 Malaise traps in 27 forest fragments of different sizes and they were divided into five collection regions. We considered the ecological guilds of Muscidae and collection region as covariates within the power model used to test the SAR. As response variables we used the species richness of each trap (local richness), each forest remnant (set of four traps that we call gamma diversity), and the average number of species of each forest remnant (alpha diversity). Species richness of each trap, alpha and gamma diversities increased with increasing the area size of remaining forest, featuring a common pattern of SAR. There was no change in the SARs due to ecological guilds of Muscidae and interestingly the regions of sampling influenced the type of curve in the SAR between the species richness of each trap and area size. The value of the z slope of the power model varied between positive and negative values depending on the collection region in the coastal plains of southern Brazil. We demonstrate in this paper that the uniform sampling with proportional distance between traps in the fragments efficiently detected SAR in Muscidae.

Gene expression profiling of *Calliphora vicina* (Calliphoridae) pupae basing on MACE (Massive Analysis of cDNA Ends) derived data

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Keywords: MACE, gene expression, forensic entomology

The determination of a minimum post mortem interval by determining the age of juvenile blow flies is the key task of forensic entomology. Determining their age using the weight or length of blowfly larvae is well established. But to date there are only a handful of studies dealing with age estimation of pupae. As the metamorphosis can last up to 50% of the total juvenile development time of a blowfly, it is of immense importance to understand its mechanisms and to develop a method for a robust age estimation of blowfly pupae. Recent studies have shown that the analysis of gene expression patterns can be such a tool. Therefore, we have analysed the transcriptome of one of the most abundant blowfly species in Europe – *Calliphora vicina*. Analysis was carried out using MACE. MACE is a deep sequencing method for high-resolution gene expression analysis. Only cDNA-ends of transcripts are sequenced which leads to increased coverage. Each cDNA molecule is represented by one highly specific tag. This achieves ultra-deep analyses to include the rare transcripts at about a 20-times lower sequencing depth as RNAseq. A typical transcriptome consists mainly of a few transcripts in high copy number, which can make up 40–80% and many of them in low copy number. These are often important for the understanding of crucial functions. MACE captures these low-level transcripts and provides quantification. This facilitates the choice and increases the success of newly designed gene expression assays for pupal age estimation. 53538 different transcripts were identified, 7548 were annotated to known insect genes. Genes of Interest (GOIs) showing a highly specific increase of gene expression at a particular time during metamorphosis were identified. Based on this study gene expression assays of new identified GOIs are being designed and tested.

Biodiversity surveys [poster]

A Checklist of the subfamily Dexiinae (Diptera: Tachinidae) from China

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Keywords: Tachinidae, Dexiinae, China, collections, checklist

In this study, about 4,000 specimens of Dexiinae collected from 32 Provinces, Autonomous regions and Municipalities of China were classified and diagnosed, and are preserved in the Insect Collection of Shenyang Normal University (SNUC), National Zoological Museum, Institute of Zoology, Chinese Academy of Sciences, Beijing, China (IZCAS), and the Shanghai Entomological Museum (SECAS), China Agricultural University (CAU), and other universities and institutes. A checklist was built and includes 132 species in 28 genera (*Campylocheta, Elfriedella, Billaea, Dexia, Dinera, Estheria, Prosena, Pseudodexilla, Trixa, Redtenbacheria, Riedelia, Rutilia, Actinochaetopteryx, Athrycia, Crytophleba, Dexiomimops, Eriothrix, Halydaia, Hyleorus, Hypovoria, Leptothelaira, Periscepsia, Peteina, Phyllomya, Stomina, Thelaira, Voria, Wagneria*) of 6 tribes (Campylochetini, Dexiini, Eutherini, Imitomyiini, Rutiliini, Voriini). Four species are reported from China for the first time: *Phyllomya artistalis* Mesnil & Shima, 1978 (Liaoning), *Stomina caliendrata* Rondani, 1862 (Sichuan), *Voria edentata* Baranov, 1932 (Yunnan), and *Wagneria gagatea* Robineau-Desvoidy, 1830 (Liaoning, Shanxi). New provincial distributions of species of Dexiinae of China and diagnostic drawings of Chinese species are given. In addition, a key to Chinese genera of Dexiinae and keys to dexiine species are also provided.

Phylogenetic relationships of the genus *Sarcophaga* Meigen (sensu lato) (Diptera: Sarcophagidae) based on the complete cytochrome oxidase I (COI) gene sequences: a preliminary study

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Keywords: Sarcophagidae, *Sarcophaga* (sensu lato), cytochrome oxidase I (COI) gene, genetic variation, phylogeny

Currently, there are approximately 850 known species of *Sarcophaga* Meigen (sensu lato), the largest genus of the subfamily Sarcophaginae (Diptera: Sarcophagidae), with about 160 subgenera. However, the validity, phylogenetic relationships and the inter/intra subgeneric genetic distance within *Sarcophaga* s.l. are not very clear. The most commonly used molecular fragment, cytochrome oxidase I (COI) gene, was used to separate species at specific- and subgeneric-level, to reconstruct the phylogeny and to test existing phylogenetic hypotheses in Diptera. In this preliminary study, we proposed a subgeneric-level phylogenetic hypothesis for *Sarcophaga* s.l. based on complete COI sequences (1534 bp) for five out-group species and 102 in-group species representing 36 valid subgenera. The sequences were available from GenBank or obtained by sequencing. Nucleotide sequence divergences were calculated using the Kimura two-parameter distance model and phylogenetic relationships were inferred using Bayesian Inference and Maximum Likelihood methods. Intra-subgeneric and inter-subgeneric variation ranged from 3.3% to 10.4% (average =5.8%) and 5.0% to 12.4% (average =9.2%), the analysis indicated that the complete COI gene fragment can be utilized to distinguish different *Sarcophaga* s.l. subgenera. Our phylogenetic analysis based on complete mitochondrial COI fragments provided strong support for the monophyly of the subgenera *Boettcherisca* Rohdendorf, *Heteronychia* Brauer & Bergenstamm, *Wohlfahrtiopsis* Townsend and *Sarcophaga* Meigen (sensu stricto). The subgenus *Discachaeta* Enderlein was recently synonymized with *Heteronychia* Brauer & Bergenstamm mainly according to male morphological characters, and this was strongly supported in our study, indicating that molecular and morphological data are in agreement. The subgenera *Liosarcophaga* Enderlein, *Parasarcophaga* Johnston & Tiegs, *Lioproctia* Enderlein, *Pandelleisca* Rohdendorf, and *Helicophagella* Enderlein were not monophyletic. Notably, *Liosarcophaga* and *Parasarcophaga* were divided into five and four clades, respectively, in spite of being supported by the male terminalia morphological characters. Future phylogenetic studies on the genus *Sarcophaga* s.l. should use combined datasets for analyses.

What is a rhinophorid fly? A new perspective on an old question – based on DNA sequences

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Keywords: Oestroidea, Rhinophoridae, *Stevenia*, phylogenetics, DNA

It all began with the idea of revising the rhinophorid genus *Stevenia* and describing the numerous recently discovered species. This is sometimes a difficult task because of their morphological similarity combined with a high level of infraspecific variation. For this reason the DNA of *Stevenia* species and of other Rhinophoridae was examined in order to obtain additional information at the species level and also to elucidate the systematic position of the genus. We amplified six mitochondrial (12S, 16S, COIa, COIb, COII, CytB) and two nuclear (28S, ITS2) gene fragments. The final concatenated dataset was used to reconstruct the phylogenetic relationships.

The results confirmed the validity of the new species and the monophyly of *Stevenia*. The probable sister-group is *Acompomintho* and the sister-group of these two is *Tricogena*. The genera *Azaisa, Oplisa, Rhinomorinia* and *Ventrops* form the sister-group of this monophylum. *Rhinophora* emerges as the basal branch of this grouping which is similar with that of Bedding, who established possession of apomorphic fleshy protuberances of their larvae. Tschorsnig too has placed these genera (without *Rhinophora*) together in one clade on the basis of their apomorphic acrophallus with three sperm openings. All the other genera, such as *Baniassa, Melanophora, Paykullia, Phyto, Tromodesia*, and a few undescribed ones, form a second group which does not have the mentioned larval and genital characters. Also in this group are *Angioneura, Melanomyia*, and (partly) *Morinia* which has recently been assigned to the Calliphoridae on the basis of the structure of its metathoracic spiracle. Surprisingly, these two branches of the traditional Rhinophoridae are not in a sister-group relationship with each other. But both clades of the Rhinophoridae together with the Rhiniidae are a monophyletic unit. This forms the sister-group of the Tachinidae together with the Helicoboscinae, Mesembrinellinae, and Polleniinae.

Ochlerotatus japonicus japonicus (Diptera: Culicidae) in Europe: population genetics of an invasive mosquito species

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Keywords: Invasive mosquito, population genetics, microsatellites, Asian bush mosquito, *Ochlerotatus japonicus japonicus, Hulecoeteomyia japonica japonica*

The Asian bush mosquito *Ochlerotatus japonicus japonicus* (Theobald 1901) [= *Hulecoeteomyia japonica japonica* sensu Reinert et al., 2009], native to temperate East Asia, has recently become established in the United States of America and in Europe. To find out how often introductions led to founder populations in Europe and to study the patterns of expansion of the species, samples from five collection sites of a West German population were genetically compared to formerly analysed material from other European populations in Belgium, Switzerland and Austria/Slovenia. Specimens were genotyped at seven pre-existing microsatellite loci, and part of their *nad*4 mitochondrial locus was sequenced. Thus, various mitochondrial haplotypes were found, which are associated with two different genotypic signatures, leading to the conclusion that *Oc. j. japonicus* must have been introduced to Europe at least two times. Predominantly, West German specimens have a unique genotype, which clearly isolates them from all other European populations. However, the West German population also shows traces of mixing with the second European genotype indicating that mosquitoes resulting from the two separate introductions are passively transported within the continent instead of expanding and merging actively. Therefore, human-driven transportation must be considered to play a decisive role in the expansion of invasive mosquitoes. The resulting mixed populations are more adaptive and successful due to higher genetic diversity.

Review of the Eurasian *Polietes* Rondani, 1866 (Diptera, Muscidae)

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Keywords: Muscidae, Muscini, *Polietes*, review

Polietes is a small genus of flies in the family Muscidae subfamily Muscinae, represented in the Eurasian region by 9 species. The genus includes medium-sized flies characterized by a long plumose arista, scutum with 3+4 dorsocentral setae and 3+3 acrostichal setae, M1 vein straight, and narrow thoracic calypter. Larvae are coprophagous and facultative predators, prefering the dung of large herbivores.

This study is based on *Polietes* specimens from the Zoological museum of Moscow State University, Institute of Biology and Soil Science FEB RAS, Museum für Naturkunde in Berlin. The studied specimens belong to 8 species: *P. lardarius* (Fabricius, 1781), *P. meridionalis* (Peris & Llorente, 1963), *Polietes domitor* (Harris, 1780), *P. steinii* (Ringdahl, 1913), *P. nigrolimbata* (Bonsdorff, 1866), *P. hirticrura* (Meade, 1887), *P. major* (Ringdahl, 1926), and *P. fuscisquamosa* Emden, 1965.

The first two species have a disputed status; some scientists consider them as different species, and some classify them as one species – *P. meridionalis*. Characters that distinguish these species are uncertain. For example, the number of anteroventral setae on the hind tibia (which is used as one of the main distinguishing characters) may be the same in both species.

The only reliable difference is the color of the anterior spiracle: *P. meridionalis* has a yellow-brown anterior spiracle, whereas that of *P. lardarius* varies from greyish brown to brownish black. In my opinion, it is not sufficient to recognize these as separate species. For reliable separation of these two species I conducted a morphological analysis of the male terminalia. Reliable differences were found in the form of the epiphallus, surstylus, and cercal plates. I have likewise processed and illustrated the terminalia of all other Eurasian species of this genus, and prepred the first. Identification key for *Polietes* species of the Eurasian region.

Author Index

Keyword Index


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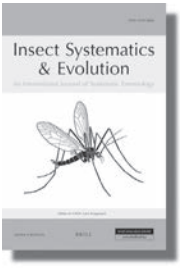
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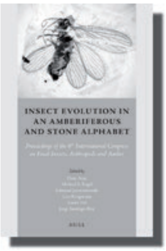
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