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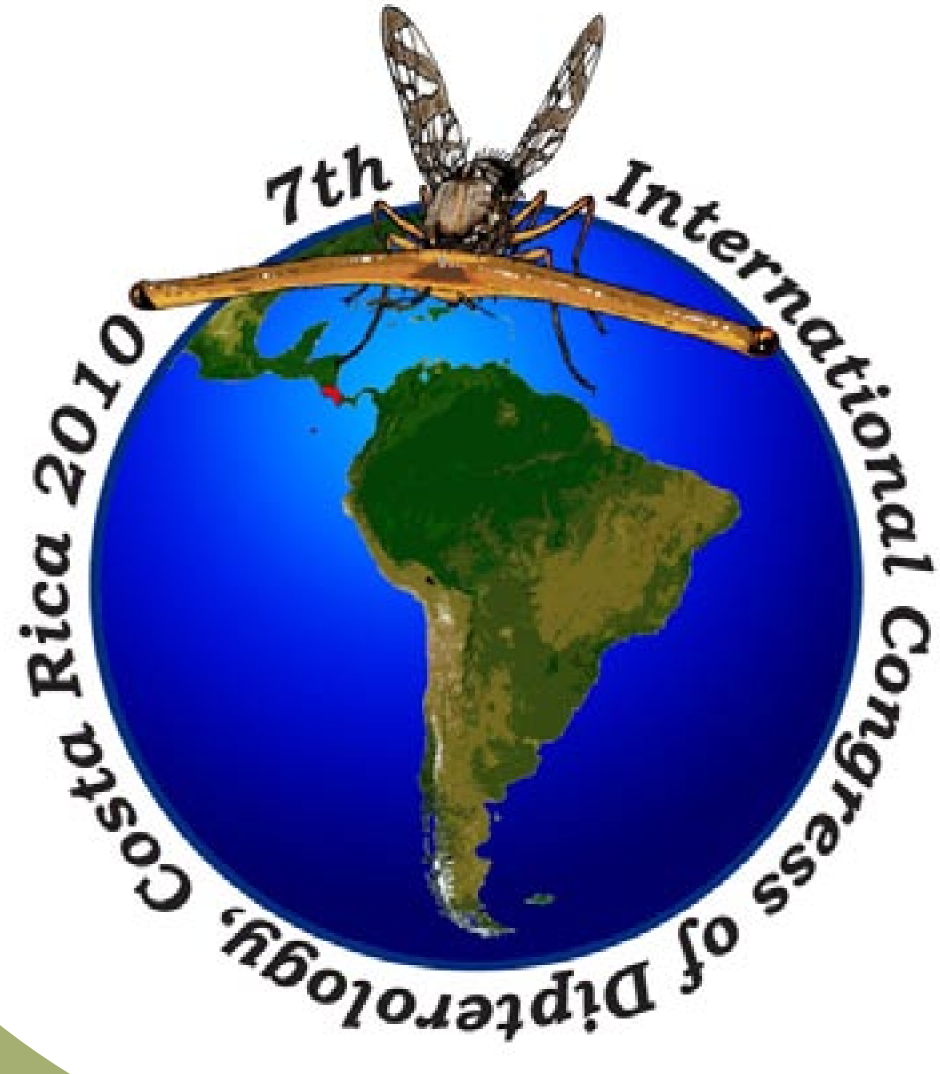
7th INTERNATIONAL CONGRESS OF DIPTEROLOGY

ABSTRACTS VOLUME



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8-13 August 2010, San José, Costa Rica
Ramada-Herradura International Conference Center

SEVENTH INTERNATIONAL CONGRESS OF DIPTEROLOGY
8-13 August 2010
San José, Costa Rica

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Preface

This, the Seventh International Congress of Dipterology, follows six previous congresses held every four years since the First International Congress of Dipterology was held in Budapest, Hungary, in 1986.

At each congress, dipterists from all of the world have met and shared their work and their findings. On this occasion, held here in San José, Costa Rica from August 8 to 13, 2010, a group of 240 dipterists from more than 34 countries on five continents have registered.

This volume contains the abstracts of 280 oral and poster presentations submitted to the Organizing Committee of the Seventh International Congress of Dipterology, ICD7. This publication summarizes the many impressive recent advances in the field of dipterology.

Although a number of names of new taxa are included in this volume, this is not intended to be regarded as validation of new taxa. The Organizing Committee encourages that the proper publication of those scientific names must appear in scientific journals to comply with ICZN rules. It is here stated that any new scientific name mentioned in this volume is disclaimed for nomenclatural purposes.

The abstracts are arranged in alphabetical order by each first author´s family name. For oral presentations the presenting author´s name is underlined.

A General Index includes all key words, while the Author Index lists all the authors.

Most abstracts published here have been edited to some degree to improve typographical errors and to clarify the text.

Several colleagues contributed to the preparation of this volume and I am very grateful for their imput. My special thanks to Monty Wood, Grace Wood, Jeff Skevington, Brad Sinclair, Scott Brooks, Annia Picado and Carlos Hernández.

Manuel A. Zumbado
Editor

08 August, 2010

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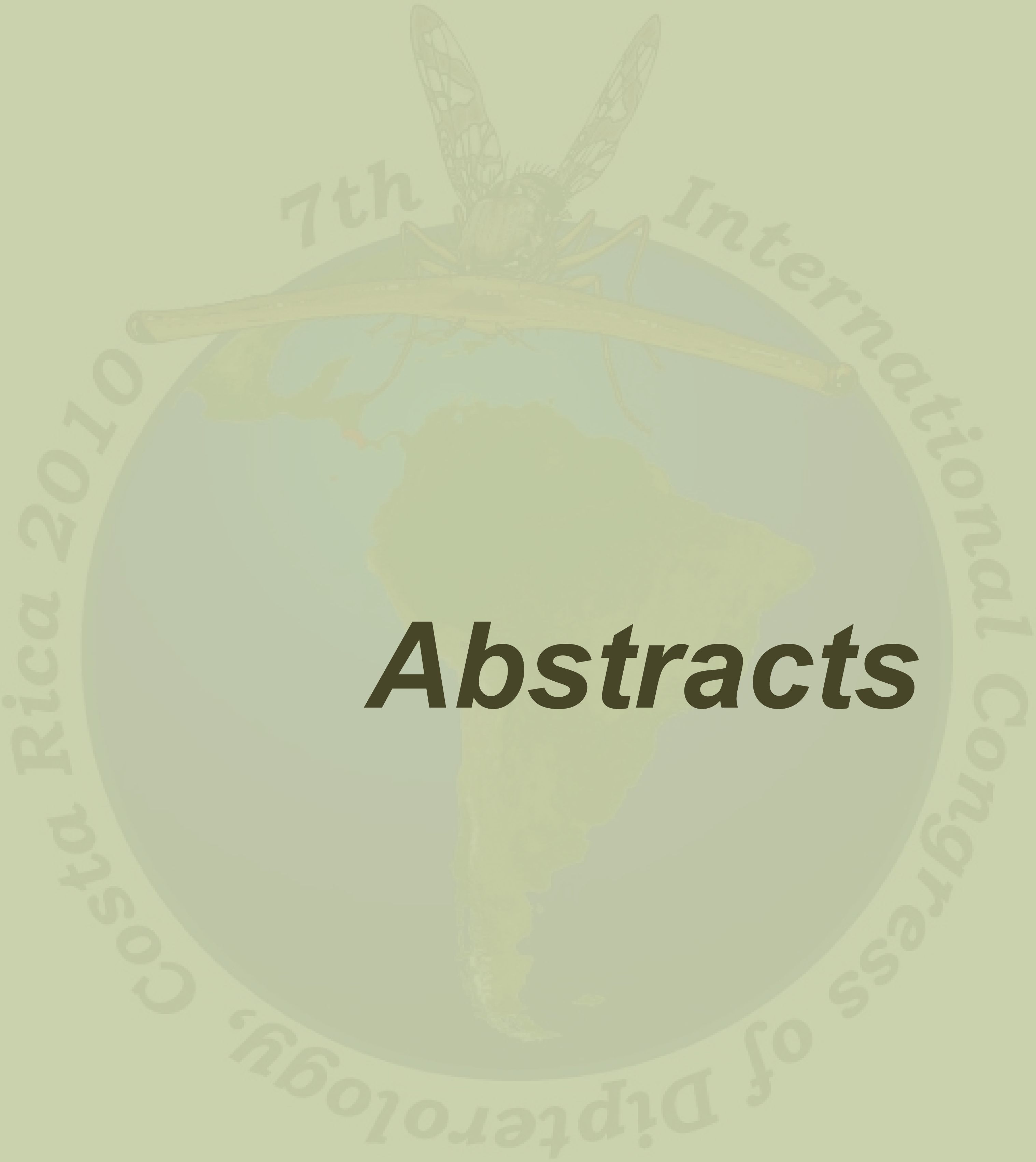

Abstracts

Phylogenetic relationships within the Mydinae (Diptera: Mydidae)

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Mydidae (Diptera, Asiloidea) are a widely distributed group of flies, comprising of 11 subfamilies and approximately 460 species. Mydinae, the main focus of this research, are restricted to the New World, and includes the largest known flies. This taxon comprises 12 genera, 4 tribes and about 90 species. This study aims to test the monophyly of Mydinae and its supraspecific taxa, as well as to infer the relationships among them. So far, we have preliminary results based on a cladistic analysis of 32 species of Mydinae, plus 10 from other subfamilies of Mydidae and Apioceridae, sampled as outgroups. All 100 characters used in this analysis were obtained by means of a comparative study of the external morphology of adults and terminalia of the specimens. As a relevant result, the monophyly of Mydinae is not recovered. A clade composed of *Paramydas igniticornis* (Apiophorinae) and all the Mydinae except *Messiasia wilcoxi*, on the other hand, is evidenced by our results. This unnamed clade is supported by a closed cell r_4 and by the presence of hairs instead of spines on tergite 10 of female. The relationships among the majority of species of *Messiasia* (Messiasiini) remain uncertain, but it is clear that they do not constitute a monophyletic group. *Dolichogaster brevicornis* (Dolichogastrini) and *Phyllomydas bruesii* (Phyllomydini) are sister-groups, and they are nested among species of *Messiasia*. The tribe Mydini is supported as monophyletic, possessing a crested aedeagus as one of its synapomorphies. Within the Mydini, two of the three subtribes are non-monophyletic: Mydina and Stratiomydina. *Mydas* is shown to be polyphyletic, and *Gauromydas* (Mydina) is paraphyletic in relation to *Protomydina*. *Stratiomydas lividus* (Stratiomydina) is found as the sister-group of all other studied Mydini. The classification of Mydinae thereby will require extensive re-evaluation, since this group and supraspecific taxa were not supported as natural.

KEY WORDS: cladistics, Asiloidea, morphology, classification

The genus *Dorylomorpha* Aczél (Diptera: Pipunculidae) in South America

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The South American species of the genus *Dorylomorpha* Aczél, one of the genera classified in the tribe Tomosvaryellini of the subfamily Pipunculinae (Diptera: Pipunculidae) is revised. Two new subgenera of D*orylomorpha*, *Paramuna* subg. n and *Montinicola* subg. n., are described. Eleven new species in the two new subgenera are described and illustrated. Three previously known species are re-described, namely *D*.(*Pipunculina*) *lenkoi* Hardy, 1965, *D*.(*Pipunculina*) *reveloi* Hardy, 1963 and *D*. (*Montinicola*) *laeta* (Becker, 1900). A phylogeny of the genus based on thirty-two morphological characters is proposed; the current subgeneric classification is corroborated and phylogenetics relationships are discussed. The geographical distributions of each are also discussed based on map distributions and modeling species distribution maps suggested by environmental variables. Finally, comments on a biogeographical analysis for Andean species are presented.

KEY WORDS: *Dorylomorpha*, Pipunculidae, identification, classification, distribution

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Hypopygial characters and phylogenetic relationships between species of *Coniceromyia* (Diptera: Phoridae)

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Hypopygium morphology has an important role in species diagnoses of pterygote insects. The use of this kind of information in cladistic analyses, however, has been questioned, on the grounds that structures associated with reproduction supposedly would evolve too quickly, loosing phylogenetic signal. In a study of the morphology of the male terminalia in the genus *Coniceromyia* we found a profound departure from the phorid ground plan, in particular the presence of surstyli fused and shifted to the left side, creating a left epandrial process, probably associated with grasping. Intermediate modifications are present in other genera of Phorinae, presenting an interesting transformation series in the subfamily. Most of the relationships between genera of Phorinae were proposed based mainly on hypopygial character states. *Coniceromyia* hypopygial morphology has received scarcely any attention in the literature, used only recently in species diagnoses, so there is little information available in the literature for phylogenetic reconstruction. Homologies are proposed for sclerites in the hypopygium of species of *Coniceromyia, Plethysmochaeta, Neopleurophora, Chaetocnemistoptera, Chaetopleurophora,* and *Phora*. A cladistic analysis of 30 species of *Coniceromyia* and 10 other species chosen as outgroups has hown that changes in hypopygial morphology have revealed homologies and have provided sufficient character states to interpret the phylogeny within the genus. The main clades within *Coniceromyia* can be recognized, showing considerable support. Congruence with other sources of morphological information is considered, especially modifications on the front leg and features of the wing.

KEY WORDS: Phoridae, *Coniceromyia*, phylogeny, hypopygium.

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A large scale survey of the Diptera of the Atlantic Forest

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The results of a large scale survey of the Diptera of the Atlantic Forest, involving over 400,000 specimens, most sorted to family revealed a total of 61 families. Some of this material was identified to higher levels, with 304 genera recognized and nearly 700 species, of which about 400 were undescribed. Many particularly speciose families have not yet been processed, so an estimate of 1,000 new species among this material is probably an underestimation, so it seems an underestimation accepting 1,000 new species in the material analyzed, with more than 50% of the specimens corresponding to new species. These numbers vary according to taxa and geography. Families more intensively studied have smaller rates of new species, but for many genera 100% of the fauna is undescribed. Also, the southern range of the Atlantic Forest has rates of about 30% for new species of all families, while the northern range has about 95% undescribed species. Mapping these distributions has revealed well defined areas of endemism. Instead of using geographical coordinates we used small topographical units based on rivers and altitude. [Some conservative groups in their distribution quite strictly

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follow patterns of endemism, while others frequently have species with large distribution. Four main areas of endemism are well corroborated: (1) temperate and subtropical forests in southern and areas of higher altitude in southeastern Brazil; (2) ombrophylous forests along the coast, between Santa Catarina and northern Rio de Janeiro; (3) the northern range of the Atlantic Forest, from Bahia to Paraíba; (4) the seasonal semideciduous forest in the west range of the Atlantic Forest. A couple of small possible additional areas of endemism in the State of Espírito Santo need further study. Seasonal semideciduous forests have almost no relevant biological reserves and must be considered under high risk of destruction due to the expansion of ethanol production,

KEY WORDS: Diptera, biogeography, endemism, Atlantic Forest, taxonomy, biodiversity

Fossils, biogeography and evolution of flies

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Assigning a time scale to phylogenies has always been a difficult task. As new data have accumulated, the postulated origins of animal and plant taxa have been gradually pushed back in time. But there is still conflict between authors as to how to interpret the evidence. Sources of information to assign age to given taxa are fossils, molecular clocks and biogeographical disjunctions. Each of these, however, have their own constraints—fossils indicate only minimum age and are absent from many clades, molecular clocks are affected by calibration protocols, and there are strong disagreements about biogeographical reconstructions. The oldest fossils of flies come from the Lower/Middle Triassic of Alsace, France. These fossils already show some diversification of the Diptera, from the extinct Grauvogeliomorpha to early stems of Brachycera. The sister clade of Diptera, the Mecoptera, has fossils known from the Permian (which is the age of the stem group of Diptera), but there is disagreement about the origin of the crown-group of dipterans including fossils or including only recent clades. A more difficult problem, however, concerns the extent of diversification before the division of Pangaea into its two main subcontinents, Laurasia and Gondwana, and its effect on explanations for intercontinental disjunction. It is widely accepted that Upper Jurassic fossils of Platypezidae and Lower Cretaceous fossils of Sciadoceridae would indicate that the oldest lineages of the Cyclorrhapha could have been in Pangaea or at least in Gondwana or Laurasia, but that Schizophora would not be diversified at that time. There are no known fossil Schizophora from the Mesozoic. This means that all cases of intercontinental disjunction in schizophoran families originated by large scale dispersal between the continents. This seems acceptable because of secondary contact or proximity between South America/North America, Africa/Eurasia, and between Australia/Southeast Asia, but also the lasting connection between Antarctica, South America, and Australia. This, however, does not explain the wide distribution of most of the large families of Calyptratae and Acalyptrata. And there is still the need to explain the extent of the diversification of dipteran lineages originated before the Late Jurassic, i.e., which subgroups of Tipulomorpha, Bibionomorpha, Culicomorpha, Psychodomorpha, Stratiomyiomorpha, Tabanomorpha, Asiloidea, Empidoidea, and Platypezoidea were differentiated at that time. For some groups, such as the Bibionomorpha, there is more detailed information on the phylogeny and precise position in time of Jurassic/Lower

Cretaceous fossils, which allows an estimate of the composition of the Gondwanan fauna. In the family Mycetophilidae, the genera of Mycetophilinae are absent in the Mesozoic fossil record, so their present wide distribution may be due to post-Cretaceous dispersal, while genera of Sciophilinae and Leiinae are present in the Lower Cretaceous and may have undergone diversification prior to the Gondwanan break-up. The presence of quite large number of early clades of Diptera in the fossil record of the Triassic and Jurassic implies the need for an explanation of their distribution, but the necessary phylogenetic and palaeontological information (in the sense of the precise position of the fossils in the phylogeny) is still not available.

KEY WORDS: Diptera, phylogeny, biogeography, evolution, age, Mesozoic, intercontinental

Arthropods associated with a human corpse found in a natural forest area of Valinhos Municipality, Sâo Paulo State, Southern Brazil

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In this study we analyzed the occurrence and frequency of arthropods collected from a human corpse in order to determine the abundance and diversity of arthropods that are attracted to human corpses. This fact has forensic importance and therefore can be used as a tool to help in investigations of death. One corpse was examined in July, a cool and dry month of the year, during the necropsy performed by a forensic expert in the coroner's office, in the city of Campinas, SP (-22°54'20»N, 47°03'39»W, elevation 854m). The subject had suffered a violent death approximately 10 days before, and was found lying in a recreational fishing pond in the city of Valinhos, SP (22°58'14»N, 46°59'45»W, elevation 660m) near the shore in the vicinity of a natural forest. The subject had sustained skull fractures in the occipital region caused by gun shot, and otherwise also presented other characteristics such as advanced stage of autolysis. Adult and immature arthropods were collected on the body and taken to the laboratory of Entomology, State University of Campinas where they were kept until adult emergence. The reared adults were pinned and identified using identification keys. The abundance of the specimens was presented as percentages. Diptera were the most abundant, followed by Coleoptera and Hymenoptera. This result showed that the arthropod fauna that had visited and colonized the corpse was very diverse, probably due to the fact that the area was in the vicinity of a natural forest.

KEY WORDS: forensic entomology, cadaver, arthropods, Brazil

The identity of three Neotropical genera of Sarcophaginae (Diptera: Sarcophagidae)

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The subfamily Sarcophaginae comprises approximately 70% of known flesh flies. Although with worldwide distribution, its species richness is remarkable in the Neotropics. External morphology of the Sarcophaginae is fairly uniform, while phallic morphology is very complex and distinctive, causing different interpretations of the generic and subgeneric limits. Its Neotropical species are assigned to 51 genera, with some of them not well-defined, many are monotypic, and in others only the type specimen is known. While the monophyly of the subfamily is well-supported, that of some genera and subgenera is not, and therefore revisionary studies are needed to clarify generic concepts. In such a way, *Microplagia* Townsend, *Weyrauchimyia* Bequaert and *Malacophagula* Lopes are poorly known and their classification has been discrepant among previous authors. *Microplagia* is monotypic and only the female holotype from Peru is known. *Malacophagula*, with only one nominal species from Brazil, was considered either a subgenus of *Microplagia* or senior synonym of *Weyrauchimyia* (with four South American, mainly Peruvian, species). After having access to the type material, these six taxa were revised and to clarify the relationships among them, a cladistic analysis was carried out with 29 morphological characters and 10 terminal taxa. The six taxa are indeed very closely related in a well-supported monophyletic clade, with the following topology (*Ma. neotropica* +((*Mi. nitens* + ((*W. peruviana* + *W. bicoloricauda*) + *W. schlingeri*)) + *W. andina*))))). Preliminary evidence of their sister-group relationship with *Rafaelia* Townsend and the classification resulting from this study is discussed.

KEY WORDS: flesh flies, Neotropics, morphology, phylogeny

Increased sampling of taxa, genes, and morphological data leads to the dissolution of Diachlorini (Tabanidae: Tabaninae)

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The cosmopolitan but predominantly Neotropical and Australasian horse fly tribe Diachlorini (Tabanidae: Tabaninae) contains many exceptional species. Included in this group are some of the only horse flies known to exhibit host specificity or nocturnal feeding behavior as adults, mimic wasps, or whose larvae are phytophagous. The horse flies with the longest proboscides outside of Pangoniinae are diachlorines in the genus *Dasychela*. Recent advances in horse fly phylogenetics have shown that this morphologically diverse assemblage is a progression of relationships which includes the extremely species rich genera, *Tabanus*, *Haematopota* and related genera. This study examines the phylogenetic relationships of these flies by sampling half of the described genera for regions of mitochondrial cytochrome oxidase 1, ribosomal 28S, and three nuclear protein coding genes, and 50 external adult morphological characters. Ten genus groups in the Tabaninae are strongly supported, though the relationships between some of these clades do not receive strong support. Several genera are not placed with confidence, including the wasp mimicking type genus *Diachlorus* and the ostensibly phytophagous *Lepiselaga*. A more stable classification based on natural groups identified by this study is presented. Members of 'Diachlorini' exhibit several clear examples of convergence and homoplasy such as multiple independent origins or losses of long proboscides, mimicry, nocturnal behavior, phytophagy, and adult host specificity. However, including morphological data increases overall support for the phylogeny. Divergence time estimates and distribution data provide some evidence for the hypothesis that early diversification in the group is correlated with the fragmentation of Gondwana.

KEY WORDS: Tabanidae, Diachlorini, systematics, long-tongued pollinators, biogeography

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A phylogenetic study of the relationships of the genera of Xylophagidae

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Xylophagidae, the sole family in the Xylophagomorpha, is a small family of flies with highly derived larval morphology and a rich fossil record. Members of the family are a distinctive component of most wet temperate forests, and many species found in the tropics await description. Xylophagidae may be characterized by a range of morphologies; *Dialysis* has stylate to nearly aristate antennae while some species of *Rachicerus* have more antennal annulations than any other brachyceran fly. Several studies have investigated the relationships of xylophagids to other flies, and while this question is not fully resolved, xylophagids are most likely the sister group of most Brachycera or of a few other 'orthorrhaphous' infraorders. Phylogenetic hypotheses of the subfamilies and genera within this presumably ancient family, however, have never been rigorously tested. This study samples all the genera of Xylophagidae, excluding two small Eastern Palaearctic genera *Anacanthaspis* and *Odontosabula*, for 28S ribosomal DNA and two nuclear protein coding genes. The two subfamilies are supported as monophyletic, but groups defined by large-scale distribution patterns, wing or antennal characters, or larval habitats, are not so clearly defined.

KEY WORDS: Xylophagidae, systematics, larval morphology, biogeography

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Dispersal and behaviour of *Myzus persicae* (Hemiptera: Aphididae) in the presence of *Sphaerophoria rueppellii* (Diptera: Syrphidae): consequences for transmission of *Broad bean wilt virus* 1 in pepper

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Aphidophagous hoverflies (Diptera: Syrphidae) are potentially important agents in aphid biological control (Gilbert, 1993). *Sphaerophoria rueppellii* is a predacious hoverfly that usually occur in Mediterranean crops (Speight, 2005). Several studies in the Southeast of the Iberian Peninsula show the importance of this hoverfly in outdoor crops and greenhouses. For thsis reason, it has been suggested that this syrphid be made commercially available (Pineda & Marcos-García, 2008) and its rearing method is in the process of being patented. The high potential of *S. rueppellii* for reducing aphid pest populations on pepper (*Capsicum annuum* L.) has been reported (Pineda & Marcos-García, 2008). However, aphids are also vectors of several plant viruses. Natural enemies might induce antipredator behaviour that affects feeding and dispersal of aphids, and therefore virus spread. *Myzus persicae*, an aphid fequently found on pepper, is vector of several plant viruses. *Broad bean wilt virus* 1 (BBWV-1) is a Fabavirus non-persistently transmitted by aphids to several greenhouse crops. Here we studied the effect of larvae of *S. rueppellii* on behaviour and dispersal of *M. persicae* and, therefore, on transmission of BBWV-1 in pepper. Aphids showed a higher dispersal rate to uninfested plants in the presence of syrphid larvae rather than in their absence. Antipredator behaviour of aphids in the presence of syrphids was described. Consequences of behaviour and dispersal of *M. persicae* in the presence of *S. rueppellii* on transmission of BBWV-1 are discussed.

KEY WORDS: Syrphidae, *Sphaerophoria rueppellii*, biological control, aphids, pepper, virus transmission, BBWV-1

Diptera.info, the dipterist' site

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The Diptera.info site has been online since May 2004. A general Content Management System (CMS) is used to create and maintain this dynamic site. Storing the content in a database also facilitates searching the sites for particular types of content and creating custom pages with mixed content.

The initial intent was to create a portal to information on Diptera but the CMS also allowed for addition of a forum. Before they could contribute to the forum visitors needed to register, and registration also opened the door for them to contribute other content. Though some of the traditional portal features are still present (weblinks, gallery), the forum has become the eye-catcher and centrepiece of the site. As a result, the site has become more of a community site than a true portal. It brings together both specialists and non-specialists, experienced workers as well as novices, in posting and answering queries. Other features, some specifically or initially coded for the site, are the Diptera Gallery, a glossary, a marketplace, etc. A user-group feature makes it possible to restrict access of some content to certain users. For example, there is a user-group for communication between dipterists involved in the Kerkini Wetland Survey run by Gordon Ramel in Greece.

A general misconception is that **Diptera.info** is aimed at Europe. Entomologists from all continents have registered and have visited the site but because of the size of the entomological community in Europe the majority of users are European.

A few statistics: registered members, almost 1600; gallery images, almost 6000; fórum, nearly 30,000 threads with 130,000+ posts.

KEY WORDS: Diptera, website, forum, identification, community

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A collective empidoid worker site?

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A survey was conducted amongst workers on Empidoidea to establish if the need exists to start a collective empidoid worker site. The results of the survey will be presented and can be discussed among those present in the Empidoidea worshop.

KEY WORDS: Empidoidea, specialists, community site

The subfamily Medeterinae (Dolichopodidae): an overview of genera and characters

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The dolichopodid subfamily Medeterinae is defined (more or less) by the following suite of characters: posterior mesonotum strongly flattened and slightly depressed, dorsal postcranium concave, absence of anterior preapical seta on femur I and II, and legs mostly bare of major setae. As well, many genera have a predilection for resting on vertical surfaces especially tree trunks, accounting for the abundance and diversity of medeterines in Baltic amber. The subfamily centers around the speciose type-genus *Medetera*, known for its Holarctic association with bark beetles (Scolytidae). However, its supposedly diagnostic venation is actually so plastic that generic limits are unclear. Of particular interest is the diversity in the female oviscapt, especially the development in genus *Thrypticus* of a sclerotised plant-piercing oviscapt in parallel with the Tephritoidea. This has allowed radiation into a new adaptive zone, larval mining in monocots, the only example in the lower Brachycera. The male poststabdomen is highly variable in structure, with the hyopopygium variably reduced or enlarged, and ranging from being encapsulated within the postabdomen to being permanently exserted on a peduncle formed by abdominal segment 7. The inclusion of Robinson's "microdolichopodid" genera and new genera being discovered from fossil amber and recent sticky traps have only served to make what one might loosely call "subfamily Medeterinae" more intractable.

KEY WORDS: Dolichopodidae, Medeterinae, generic definition, character plasticity, Thrypticus

The Baltic amber Dolichopodidae (Diptera): an abundant and diverse fauna

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Although there are no reliable records of Dolichopodidae from the Cretaceous, the family displays a notable diversity and abundance in Baltic amber. Further, a recent molecular phylogeny suggested the family underwent rapid radiation in the early Tertiary, which lends additional support to its putative absence in the Mesozoic. The Dolichopodidae are one of the most abundant families in Baltic amber, and some 3000 inclusions, both institutional holdings and the outstanding personal collection of Hans Ulrich, are being used in a current taxonomic revision. The fauna comprises some 120 species, 75% to be newly described. Although a range of recent subfamilies and genera are present, there are many new and often enigmatic taxa. A review of the taxonomic composition shows a rich diversity of Medeterinae, reflecting that subfamily's predilection for resting on tree trunks and increased likelihood to be trapped in exuded resin. In this regard, a recent tree trunk sticky trap study in Australia demonstrated the abundance of Dolichopodidae, and sticky traps might be regarded as taphonomic analogues of sticky tree resin. Other topics include a summary of major collections, especially Meunier's work and the interpretation of his types. Of particular biogeographic interest is the distinctive genus *Atlatlia*, currently known only from Australia & New Caledonia. Its presence and demonstrable origin in Baltic amber inclusions makes its true distribution pseudo-Gondwanic. This talk will be illustrated with photographs of many striking dolichopodid inclusions.

KEY WORDS: Dolichopodidae, Baltic amber, collections, faunal richness, sticky traps, biogeography

Internet or paper: a possible solution

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The ubiquity of the internet and a plethora of biodiversity informatics initiatives in recent years have caused taxonomists to consider problems related to publication of nomenclatural decisions online. Proposed amendments to the International Code of Zoological Nomenclature (ICZN) allowing e-only publications have been published and were widely discussed. Two main objections were expressed: uncertainty of date of publication/registration and the ephemeral nature of web-pages compared to paper-based publications. We demonstrate how collaboration between online data providers and traditional publishers (represented by Scratchpads and ZooKeys) could eliminate these problems.

KEY WORDS: e-taxonomy, digitisation, nomenclature, publication, web

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Large-scale collection imaging

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At the beginning of the twenty-first century, large and varied entomological collections had been built up in museums and universities throughout the world. Taxonomists today do not have enough time or resources to study all of these by employing only traditional methods of requesting material from different collections. Digital images of specimens may reduce this necessity to loan this material and may even replace loans in many cases. Traditionally, photography (both film and digital) was usually applied to individual specimens. In this study we investigated the feasibility of photographing a larger collection unit such as a drawer of specimens. To be scalable (digitising an entire collection or a significant part of the collection) there is a need to ensure speed, usability and accessibility. This new system enables fast data capture by bulk imaging the collection units, drawers, etc. In order to be usable, specimen images are associated with metadata (unique IDs, collection labels, identifications, etc.). These can then be made accessible over the web and allow user input (identifications or comments). Following standards like Darwin core will ensure data exchange and interoperability. A combination of SatScan for data capture, and Scratchpads for data publication and annotations, were used to prove the concept.

KEY WORDS: e-taxonomy, digitisation

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Chironomidae are the sister group of all remaining Culicomorpha (Diptera)

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There are numerous competing hypotheses regarding the phylogenetic relationships between the families of Culicomorpha. Although there is general agreement about the monophyly of the Culicoidea and the arrangement of the families within that superfamily, the relationships between families traditionally placed in the Chironomoidea is a muddle of conflicting conclusions. Molecular studies have provided inconsistent results and morphologically based matrices have generally rehashed previously known features, with what strong synapomorphies there are, buried in a field of more questionably interpreted character states.

My study of the pupae of the Culicomorpha provides fresh evidence regarding interfamilial relationships and incorporates morphological features from all life stages. Chironomidae are the sister group of all remaining families, based on several character states including the position of the palpus, plesiomorphically directed laterally in Chironomidae and synapomorphically directed posteriorly or medially in remaining families of Culicomorpha. Further characters indicate that Simuliidae and Thaumaleidae are sister groups, that Ceratopogonidae are the sister group of these two, and that all three are the sister group of the Culicoidea.

To interpret the morphology of the pupae, a single set of terms is proposed for the various families. Previously, each of the following had independently developed their own modern terms: Chironomidae, Simuliidae, Thaumaleidae, Ceratopogonidae and the Culicoidea.

The pupae of Diptera are far more poorly understood than the larval and adult stages. It is clear that for the nematocerous Diptera and the Orthorrhaphous Brachycera the pupal stage will provide further characters of phylogenetic importance.

KEY WORDS: Diptera, Chironomidae, Ceratopogonidae, Simuliidae, Thaumaleidae, Dixidae, Corethrellidae, Chaoboridae, Culicidae, Culicomorpha, phylogeny, pupa

Systematics of *Leptomorphus* (Mycetophilidae)

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The Mycetophilidae, or fungus gnats, is a diverse and dominant family of Diptera in moist habitats, especially in forests, where they play a major role in decomposition of fungi and wood. The Mycetophilidae are divided into two subfamilies, Mycetophilinae and Sciophilinae, containing two and four tribes respectively. One of the five largest genera in the tribe Sciophilini is *Leptomorphus* Curtis, which is known from all biogeographic regions except Australasia and Antarctica, with current centers of diversity in central Africa and northeastern North America. At present the genus contains 28 extant species placed in four subgenera. No phylogenetic hypothesis of the relationships between the species and subgenera has been proposed to date, as a revision of the genus was first believed necessary. Here we report the results of a worldwide revision of this genus, along with the first phylogeny of the species relationships. More than 700 specimens were examined for the revision and compared with all types that could be obtained. Sixteen new species were discovered and the resulting change to the biogeographic distribution of the genus is discussed. A dataset of adult morphological characters was analysed, using parsimony, to reconstruct a phylogeny of the species relationships. This yielded a number of monophyletic species-groups. The validity of the proposed subgenera, along with questionable species synonymizations, is determined in light of this new phylogenetic information. The placement of *Leptomorphus* with respect to other genera in the tribe Sciophilini is also discussed.

KEY WORDS: Mycetophilidae, taxonomy, phylogeny, morphology

CDM portals and taxonomic editor – the Milichiidae portal

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The Common Data Model (CDM) portals (http://dev.e-taxonomy.eu/dataportal/diptera) are being developed as part of the European Distributed Institute of Taxonomy (EDIT). The Diptera portal aims to provide nomenclatural and taxonomic information on flies in combination with species pages. As an exemplar group the family Milichiidae was chosen and for this family webpages are available for all taxa including nomenclature, taxonomy, a distribution map and a list of all citations with keywords.

All data are stored in the CDM and edited using the EDIT Desktop Taxonomic Editor. The editor uses an on-the-fly parser to put free text into structured fields, so there is no need for the user to know the details of the data model. Both, portal and editor are part of the EDIT Platform for Cybertaxonomy (http://wp5.e-taxonomy.eu), a collection of tools and services, which together cover all aspects of the taxonomic workflow.

KEY WORDS: biodiversity informatics, species pages, Milichiidae

Contents

Scratchpads – A social networking tool to build, share and publish taxonomic information

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Scratchpads (www.scratchpads.eu) is a social networking application that enables communities of researchers to manage, share and publish taxonomic data online. Sites are hosted at the Natural History Museum London, and offered free to scientists. Key features of the Scratchpads include tools to manage classifications, bibliographies, images, specimen records and custom data. Data added to a Scratchpad are automatically classified and grouped around a taxonomy that is supplied by the users or imported from EOL. This is optionally supplemented with information from high quality web accessible databases, to automatically construct content rich web pages about any documented taxon. Currently these sources include Genbank, GBIF, Biodiversity Heritage Library, Morphbank, and Flickr.

There are several Scratchpads on Diptera and I will demonstrate various features by using the Milichiidae Scratchpad at www.milichiidae.info.

KEY WORDS: biodiversity informatics, Web 2.0, species pages, Milichiidae

Contents

The effect of Ivermectin on the developmental rate of *Chrysomya putoria* (Diptera: Calliphoridae)

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With the expanding use of ivermectin, a veterinary parasiticide, and lack of control on its commercialization, the number of deaths caused by intoxication has substantially increased. Cases associated with the death of animals that have a high economic value can be of a great concern for both owners and insurers. Thus, studies on the developmental rate of carrion flies can contribute information regarding the cause of death or can assist in estimating the postmortem interval (PMI). This study aims to assess the effect of different concentrations of ivermectin on the developmental rate of *Chrysomya putoria* (Wiedemann), a blowfly of forensic importance in Brazil. Five experimental groups were used: 4 of them contained the following concentrations; 200 mcg/kg, 50 mcg/kg, 25 mcg/kg, 12.5 mcg/kg, and a control group – where no drug was added. Ten larvae from each group were individually weighed at intervals of 12 h from hatching to pupation. Larval viability and the emergence rate of adults were also measured. One-way ANOVA was performed to compare the effect of the different concentrations of ivermectin on larval development. The drug interfered with weight gains of the immatures ($F=20.83$; $p<0.0001$) and Duncan's multiple comparisons test showed significant differences between the higher concentration groups (200 mcg/kg; 50 mcg/kg; 25 mcg/kg), and the lower concentration group (12.5 mcg/kg) and the control. Furthermore, the control group showed differences in adult emergence ($F=108.14$; $p<0.05$) and larval viability ($F=64.22$; $p<0.05$), when compared to the low dose (12.5 mcg/kg) group. It was also observed that the 12.5 mcg/kg group took 24 h longer to form the puparium compared to the control group. In conclusion, the effect of ivermectin should be taken into consideration when investigating animal deaths, and to expand our experiments to other insects of forensic importance.

KEY WORDS: blow flies, postmortem interval, entomotoxicology

Contents

Species-specific behavioral differences in male tsetse fly genitalia revealed by X-ray videos

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A long-standing question in morphological evolution is why male genitalia often diverge more rapidly than other structures. One possible explanation of this trend is that male genitalia function as “internal courtship devices”, and are under sexual selection by cryptic female choice to induce female responses that favor the male’s chances of fathering her offspring. Males of closely related species are thought to provide divergent stimulation. Testing this hypothesis has been difficult because the presumed genital courtship behavior is hidden from view inside the female, and because studies of how the male’s genitalia interact with those of the female are nearly always limited to a single species in a given group, thus limiting opportunities for comparison. We use new X-ray technology and morphological and behavioral data from five species in the tsetse fly genus *Glossina* to deal with these limitations. Male genitalia perform dramatic, stereotyped, rhythmic movements deep within the female. As predicted by theory, these movements differ among closely related species. In addition, at least some other male genital structures that are apparently designed to stimulate the female also move with different rhythms against different portions of the female’s body in different species. In no case does female morphology show signs of counter-adaptations to avoid or reduce male stimulation or fit mechanically with male structures, as predicted by alternative hypotheses to explain rapid divergent evolution of genitalia.

KEY WORDS: sexual selection, signals, genitalia, display traits

Contents

What's new in New World Parathalassiinae (Diptera: Dolichopodidae)

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The Parathalassiinae are a subfamily of basal dolichopodids that includes over 30 described extant species in seven genera. Parathalassiines are tiny non-metallic, grayish to dark coloured flies generally found along sea coasts and river banks. Presently, two genera of Parathalassiinae are known to occur in the New World, i.e. *Parathalassius* Mik and *Microphorella* Becker. Here we report on some recently discovered additions to the New World parathalassiine fauna, including a new species of the genus *Thalassophorus* from the western Nearctic, a new species of the genus *Chimerothalassius* from the Caribbean island of Dominica, and two as yet unplaced species from coastal Chile that appear to represent a new genus. Some preliminary remarks on phylogenetic relationships and generic limits within the Parathalassiinae are provided in light of these new discoveries.

KEY WORDS: Empidoidea, Dolichopodidae, Parathalassiinae, *Thalassophorus*, *Chimerothalassius*, new taxa

Monophyletic groups in the Phoridae, and the evolution of termitophily

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Phoridae are a large group of small flies with varied life histories. Some have extreme modifications of their bodies, especially those associated with social insects. Many of these associates have wingless or brachypterous females that are either limuloid or bizarrely physogastric in body form. In this study, the phylogeny of the family Phoridae is re-assessed using combined morphological and molecular characters, and termitophily is examined in a phylogenetic context. The resulting analysis is a novel arrangement, differing from both the "traditional" phylogeny of Schmitz (1929) and that of Brown (1992), although with elements of both. Three subfamilies are recognized: Sciadocerinae, Metopininae and Phorinae. Within the Phorinae, the various termitophiles previously classified in subfamilies Aenigmatiinae, Thaumatoxeninae and Termitoxeniinae, all appear to belong in a single lineage.

KEY WORDS: Phoridae, phylogeny, termites

Contents

Phylogeny of the genus *Peckia* Robineau-Desvoidy (Diptera: Sarcophagidae)

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A phylogenetic analysis of the genus *Peckia* designed to test its monophyly and the status and relationship of its subgenera is conducted. Male genitalic characters combined with other morphological characters systematized in the DELTA program were used to perform a Ratchet search under the parsimony criterion using NONA of the WinClada package. Partitioned analyses on 'terminalia' and 'non-terminalia' datasets were compared with a total evidence analysis. Strategies of implied weighting of characters were explored too. All analyses were performed on a taxon sample including 58 exemplar species representing the four currently recognized subgenera of *Peckia* (*Euboettcheria, Peckia, Pattonella* and *Squamatodes*), and *Engelimyia inops*, *Oxysarcodexia intona*, *Peckiamyia minutipenis*, *Ravinia rufipes*, *Retrocitomyia retrocita,* and *Sarcodexia lambens* were used as outgroups. The mainly Neotropical genus *Peckia* is recognized as monophyletic with the exclusion of *Peckia adolenda* and the inclusion of *Sarcodexia lambens*. The subgenera of *Peckia* were grouped in two clades: one composed of *Pattonella* + *Squamatodes*, and the other of (*Sarcodexia* (*Peckia* + *Euboettcheria*)). Each subgenus emerged as monophyletic, and its synapomorphies were drawn from characters of both datasets. Characters of both terminalia and non-terminalia were informative at the generic and subgeneric levels, but overall terminalia provided higher support values. Our results highlight the fact that that the combination of external characters with character states of the terminalia provides greater phylogenetic resolution and higher branch support for the tree obtained with all characters, agreeing with the total evidence approach. Equally weighted and weighted analyses of total evidence provided the same relationships between the taxa studied, and although the tree from the weighted analysis had greater resolution at the species level, its support values were lower.

KEY WORDS: Diptera, *Sarcodexia*, genitalia, systematics

Revision of the genus *Lyroneurus* and comments on the Diaphorinae phylogeny (Diptera: Dolichopodidae)

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The Dolichopodidae correspond to the largest empidoid lineage with more than 7,000 described species. Current classifications recognize 15 subfamilies, the Diaphorinae being one of the most diverse. The boundaries of the subfamily are poorly defined, but two main groups are recognized: one comprising *Diaphorus* Meigen and related genera (sometimes referred to as Diaphorini), the other comprising *Argyra* Macquart and related genera (occasionally named Argyrini). There are doubts if these groups fit into a clade, the Argyrini sometimes being associated wirh the Raphiinae. A detailed understanding of the genera of the subfamily is necessary for overall analyses of the group, still lacking for the Diaphorinae. A study of the Neotropical genus *Lyroneurus* Loew is therefore worthwhile in this context. The genus has been synonymized both with *Diaphorus* and *Chrysotus* Meigen, the two largest and most problematic Diaphorinae genera. *Lyroneurus* is revised and 14 of the 17 known species are redescribed. The diagnostic sigmoid curve of vein R4+5 on the male wing shows intraspecific variation throughout the genus, but it is an apomorphic condition not seen elsewhere. Seven synonyms and two new combinations are proposed; the fossil *Lyroneurus venustus* Meunier is considered *incertae sedis* for Dolichopodidae. *Lyroneurus* is actually far from the strict definition of *Diaphorus* and probably corresponds to a subclade of the paraphyletic "*Chrysotus* s. lat.". However, synonymizing *Lyroneurus* wirh *Chrysotus* is not enough to solve the paraphyly of *Chrysotus*, since it is probably paraphyletic in relation to other genera in the subfamily. Furthermore, synonymizing *Lyroneurus* reduces the information about the relationships within "*Chrysotus* s. lat." without significant improvement of our understanding of *Chrysotus*. A solution depends on a worldwide revision of *Chrysotus*, in the context of the phylogeny of the Diaphorinae, splitting it into smaller clades (which will require the use of names such as *Lyroneurus*).

KEY WORDS: Dolichopodidae, Diaphorinae, *Lyroneurus*, revision

Altitudinal patterns in horse fly activity in a tropical cloud forest

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We studied the effect of altitude and its related variables on the flight behaviour of a horse fly species along a 1-km altitudinal gradient on the north-western slopes of the Ecuadorian Andes. We predicted that (1) flight activity patterns would differ among altitudes, and (2) highland individuals would present greater anatomical modifications of flight structures as a physiological response to elevation. The study area was located between 1100–2200 m in elevation at "Los Cedros", a Chocoan 6000ha primary forest. Horse flies were collected using Malaise traps during the dry season (July–October 2005) at three different stations of elevation, 1180, 1680 and 2180 m above sea level. Traps and six environmental variables were checked every hour between 06h00–18h30 for 20 days at each station. Flight activity was inferred from relative abundances/hour in traps. GLM analyses were used to test the correlation of species activity and climatic factors along the gradient. Flies´ body structures were measured and means compared with one-way ANOVAs to test for differences among altitudes.

Two different unimodal distributions and one bimodal distribution were found along the gradient. GLM analyses showed that temperature and rainfall were the best predictors of flies´ activity ($P \leq 0.05$). ANOVAs showed that morphological features such as body size, wing loading and body and thorax volumes increased with increasing altitude. Differences were found between asynchronous groups of flies at mid-altitude, but similarities of synchronous groups of flies were found between low-mid and mid-high altitudes, suggesting that flies may migrate from highlands to lowlands at defined hours of the day. This, along with additional field observations of mist presence/absence, suggests that horse flies´ dynamics are strictly driven by environmental conditions. Our results may have important insights on cloud forest ecosystem ecology such as disease dissemination between mammals and/or genes fluxes between pollinated plants, especially in the present global climate-change context.

KEY WORDS: behaviour, climate factors, elevation, migration, *Stypommisa* sp. *pequeniensis* group, Tabanidae

Contents

Advances in Neotropical dipterology: rediscovering the New World Diptera and dipterist diversity in South America

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The New World tropics has an extremely rich and unique fauna, including the order Diptera. While the Diptera may be most diverse in the New World tropics, most species are still unknown. Today, a few countries, including Brazil, Argentina and Colombia, have very qualified dipterists that are able to describe these new taxa as well as to train the many new students interested in this fascinating task. Soon, the number of qualified fly taxonomists will be much greater and will contribute to this ongoing challenge of finding and describing the unknown species. Indeed, the number of fly taxonomists is on the increase in South America, in contrast to the rest of the world where the number of taxonomists is decreasing. Also, in all of South America, more than 80% of the fly taxonomists are Brazilian. In this study, using data from world databases (e.g. BDWD, Web of Science), I will examine correlations between fly diversity, number of fly taxonomists and publications about flies. Although taxonomy is growing and improving in South America, today still few or no taxonomists study some key families, e.g., the Chironomidae and Phoridae, and they are poorly understood as a consequence. Some taxa have a reasonable number of taxonomists working on them, including Sciaroidea, Tabanomorpha, Empidoidea, Syrphoidea, Muscoidea and even Tachinidae. Yet, there is still much to be done, such as answering questions of phylogenetic and biogeographical patterns in South America. To illustrate groups with good or incipient understanding of their species I will describe diversity in the Muscidae and Richardiidae. To understand the growing knowledge of Dipteran diversity we must foster the growth in Dipterist diversity.

KEY WORDS: Brazil, fly taxonomy, megadiversity, Neotropical endemism

Contents

Over 200 genera and counting – the megadiverse fauna of Afrotropical Tachinidae

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Tachinids are arthropod parasitoids that play an important role in regulating host populations. Despite this ecological importance, most dipterists have been deterred from studying Afrotropical Tachinidae because of the large fauna and difficulty in identifying specimens to generic and species levels. The Tachinidae are the largest family of Afrotropical Brachycera with more than 1010 described species and 215 described genera, yet are poorly studied in comparison with other well-known and less species-rich regions; e.g., the Nearctic with 303 genera and 1345 species and the Palaearctic with some 410 genera and more than 1700 species. It is not possible to estimate reliably the diversity of Afrotropical Tachinidae but an important clue jumps to the eye of a specialist: about half of the unidentified specimens housed in examined collections are not attributable to any known species. Another topic requiring attention is the systematic arrangement of Afrotropical Tachinidae proposed by Crosskey in the 1980s and still in use but badly outdated. The classification needs revision along the lines of the more recent regional catalogues, and also many 'artificial' genera and tribes require careful revision. The development of modern and accurate keys to dipteran genera is one of the main goals of the Manual of Afrotropical Diptera. In preparing such a key for Afrotropical tachinids it would be useful to better define, albeit empirically, at least the more speciose genera. We therefore plan to re-describe all genera following a strict protocol based on 100 characters and 420 states. The resulting data matrix will be used to comparatively evaluate diagnostic features, and to eventually develop an online and open access illustrated interactive key. This approach is expected to improve communication among specialists and may result in more interest in tachinids and greater global taxonomic expertise in the family.

KEY WORDS: Africa, Tachinidae, diversity, interactive key

MOSCHWEB - An open access interactive key to the Palaearctic genera of Diptera: Tachinidae

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The main purpose of an analytical key is specimen identification. In other words, placing a specimen, after close examination, within a pre-existing classification. Thus, identification is undoubtedly the main and ineluctable problem of taxonomy ever since its origins. With more than 1,500 valid genera, the Tachinidae represent an excellent model to which diagnostic systems alternative to the traditional, dichotomic one, can be applied. Hence the idea of working out an original software that fulfilled the double function of a) helping a beginner to familiarize with a very complex and diverse group and b) assist the taxonomic activity of even a well established specialist, by giving immediate access to an enormous amount of information about the genera of the whole Palaearctic fauna. MOSCHWEB is an original interactive key based on a morphological (made up of 421 terminal taxa, 98 characters and 416 states), biological, faunistic and iconographic database. In MOSCHWEB, characters and states appear simultaneously and can be consulted and used in any order: no character is propaedeutic to others and the states can be selected or deselected in any possible order. A character of difficult interpretation or missing due to a damage or lack of entire body parts can be ignored, since many others will compensate its absence. The possibility to proceed in spite of the incompleteness of a specimen is due to the high redundancy of the data in the matrix, and can be of aid, for instance, wherever faecal or stomachal material need identifying, in nutrition studies or in the case of sub-fossil material from archaeological excavations. We think that tools of this type can increase the reliability of identifications thanks to the traceability of the selected characters.

KEY WORDS: Interactive key, Palaearctic Region, Tachinidae, database

Contents

Cladistic analysis of *Oidardis* (Asilidae: Laphriinae)

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Oidardis is a Neotropical genus of small robber flies, distributed from Costa Rica to Argentina. At present the genus includes seven species, *O. gibbosa, O. aenescens, O. triangularis, O. gibba, O. nigra, O. aveledoi* and *O. curopaoensis.* Other species are in the process of being described. In this study, we attempted to test the monophyly of the genus *Oidardis*, to test its relationship to the seemingly close genus *Eumecosoma* Schiner, and to discover the phylogenetic relationship between the known species of *Oidardis*. A parsimony analysis was performed on 14 ingroup taxa (six valid species, except *O. nigra* which is unrecognized, and six undescribed species including *O. signaseta* Fisher MS, *Eumecosoma tarsalis* and *E. shropshirei*), and two outgroup taxa (*Dissmeryngodes* sp. and *Strombocodia* sp.) using 69 morphological characters, including those of the male genitalia. Specimens used for the study were obtained from museums and collections worldwide. The analysis produced a single most parsimonious hypothesis (L=250, Ci=41, Ri=42). Monophyly of *Oidardis* was demonstrated, based on three synapomorphies (eye margin in lateral view smoothly curved posteriorly, scutellum with only regular setae, and longest marginal scutellar seta as long as scutellum). Preliminary results show *Eumecosoma* as being paraphyletic in relation to *Oidardis*, but a better sampling of it is necessary before any nomenclatural changes are made. Within *Oidardis*, some well-supported groups were demonstrated, in particular, *O. signaseta* and *O*. sp. 2 share a distinctive morphology of facial swelling and macrosetae of the mystax and are thus considered sister taxa. Their closest relative is *O. aenescens*, based on the very short marginal scutellar setae. The two Venezuelan species, *O. aveledoi* and *O. curopaoensis*, are shown to be sister-taxa. *O*. sp. 1 and *O*. sp. 4 shared a similar color pattern of the thorax and were regarded as sister taxa. When color was omitted from the analysis only one group (*O. signaseta* and *O*. sp. 2) was retained, indicating that color is an important attribute in the interpretation of the phylogeny of the genus.

KEY WORDS: Atomosiini, robber flies, phylogeny, Neotropical

Contents

Biodiversity of mosquitoes (Diptera: Culicidae) in relation to its larval habitats in México and Central America

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In México and Central America 412 described species of Culicidae distributed in 25 larval habitats have been recorded. Ground pools contain 32% of this diversity followed by tree holes and swamps with 24% and 18% respectively. Phytotelmata represent the habitat for 43% of the species and some habits are specific for certain species of *Aedes*, *Anopheles, Culex, Shannoniana* and *Wyeomyia*. The larval habitats of 12% of the species of this region are not known. The larval habitats of epidemiologically important species are restricted to ground pools, artificial containers, fallen coconuts, rice fields, ditches, lakes and swamps. In Costa Rica 51 new habitat records have been found and some species previously considered "rare" are now known to be abundant in specific habitats. Various species of native bamboo as well as bromeliads have been shown to be good habitats for finding new species.

KEY WORDS: Culicidae, larval habitats, phytotelmata

Molecular tests of a chomosome based speciation model in black flies (Diptera: Simuliidae)

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Cytological analyses reveal that black fly morphospecies are often composites of chromosomally distinct populations. Whether these entities are considered reproductively isolated depends on their stage of chromosome evolution. Focusing on the diverse *Simulium arcticum* species complex, containing nine 'cytospecies' and 21 'cytotypes', we aim to understand the molecular basis of chromosomally induced speciation. Specifically, we test whether cytologically defined taxa reflect underlying genetic structure by estimating population differentiation, gene flow, and phylogenetic history with a suite of molecular markers. Preliminary results of such studies will be presented and future plans discussed.

KEY WORDS: cryptic species, cytogenetics, microsatellites, mitochondrial DNA

New species of *Psychoda* Latreille (Psychodidae) from Brazil

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The genus *Psychoda* is one of the most speciose in the family Psychodidae. This poorly studied genus has a worldwide distribution, comprising more than 330 known species, 58 of which are from Latin America and the Caribbean. Brazil, with many plant formations, has been neglected with respect to this genus, hence only six species are known. Four of these were originally described in Brazil: *Psychoda divaricata* Duckhouse, from the state of Santa Catarina, *Psychoda dantilandensis* Bravo, Cordeiro & Chagas and *P. serraorobonensis* Bravo, Cordeiro & Chagas both from the state of Bahia and *P. amazonensis* Cordeiro & Bravo from the state of Amazonas. Two additional species, found in Bahia, are the cosmopolitan *P. alternata* and *P. zetoscota* from Panama and Trinidad. Here, we examined 420 specimens of *Psychoda* and type specimens from the British Museum of Natural History, the Smithsonian Institution and the United States National Museum are also analyzed. We identified 25 species, six are first records for Brazil and 13 are newly described. Illustrations and redescriptions of nine species and the description of the female *Psychoda dantilandensis* Bravo, Cordeiro & Chagas are also included. Identification keys (for males and for females) for Brazilian species are also provided. While both males and females were examined, the new species are described based only on females.

KEY WORDS: Psychodidae, biodiversity, new species, taxonomy

A once-unique character of *Psychoda* Latreille found in *Philosepedon* Eaton (Psychodidae, Psychodinae)

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Taxonomy of the genera *Psychoda* and *Philosepedon* is controversial. These two diverse (> 330 and > 90 species, respectively) and cosmopolitan genera are under study with proposals to separate them into smaller genera. While no cladistic analyses test the relationships of their species, morphological studies of adults and larvae suggest that they comprise additional genera. Nevertheless, consensus has not been reached for their internal relationships as well as their relationships with other genera in the Psychodini sensu Duckhouse. Here, we examined four recently collected females that fit all characteristics of *Philosepedon*, yet also have a subgenital plate typical of *Psychoda* (bilobed and with digitiform internal structure). This digit-like structure (the genital digit in *Psychoda*) was thought to be unique to some species in this genus. Although most genital digits are relatively thin with an acute apex (e.g. *Psychoda trinodulosa* Tonnoir, *Psychoda talamanca* Quate), some species can have a wide subtriangular digit (e.g. *Psychoda pusilla* Tonnoir, *Psychoda grisesces* Tonnoir), as well as additional possible variations. The "genital digit" of the new species described herein is broad, short, very similar to that in *Psychoda satchelli* Quate, and has four, not apical, microsetae. As is common in descriptions of species of *Philosepedon*, often female genitalia are neither illustated nor described. Therefore, it is uncertain whether this apparent homoplasy is found in other species of *Philosepedon*. We suggest that not only should the presence, but also variations and modifications, of the genital digit be included in future descriptions based on females.

KEY WORDS: Psychodidae, taxonomy

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Attributing sex to species with mtND4 in two species of *Psychoda* Latreille (Psychodidae)

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Attributing individuals of different sexes to the appropriate species is difficult in the genus *Psychoda*. Currently, descriptions of > 130 species are based on only one sex, mostly female. The difficulty is because closely related species of *Psychoda* are identified by genitalia and often several related species occur at the same location. Here we use mtDNA fragments from 18 specimens (6 male, 12 female) in an attempt to attribute sex to species. Samples are from the southern Brazilian state of São Paulo. Maximum parsimony joined two males and a female of *P. serraorobonensis* Bravo, Cordeiro & Chagas as well as confirmed the association of sexes of a new species. Interestingly, the analysis also suggested the identification of an additional two species, one in each genus, *Psychoda* and *Philosepedon*. The male *P. serraorobonensis* is described here for the first time. Molecular analysis can help resolve taxonomical problems of this group, by correctly attributing sexes to species and thereby avoiding the creation of new names for species that have already been described. Additional analyses will be carried out to unite the sexes in their correct species and to insure a more accurate description of the species in these complicated genera.

KEY WORDS: Psychodidae, mitochondrial gene, taxonomy

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Occurrence of Calliphoridae (Diptera: Insecta) throughout the process of decomposition of a swine corpse (*Sus scrofa* Linnaeus, 1758) exposed in an Atlantic Forest fragment at Salvador, Bahia City, Brazil.

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Forensic entomology is the science which deals with issues related to the biology of insects and their relation to criminal investigations.In forensic medicine, especially, the science becomes an important tool for obtaining estimates of the interval of postoperative death (IPM). Members of the family Calliphoridae (Diptera) are among the main families of forensic interest since they are the first to locate the body and to develop in it, and are found throughout the process of decomposition. This study aimed to verify the occurrence of species of this family in a swine carcass exposed in a fragment of Atlantic Forest. Flies caught in traps specifically designed for adults were collected daily. Immature stages were collected from the carcass and reared at the Forensic Laboratory of Entomology, Department of Technical Police of Bahia, for post-emergence identification. Also, we tried to correlate the species of adults that visited the carcass with those that developed in it, linking both to the stages of decomposition. We collected 11,589 adults but of the total number of immatures collected only 369 emerged in the laboratory. Among adults caught were the following species: Cochliomyia macellaria (1.5%), Chrysomya megacephala (11.3%), Chrysomya albiceps (83.3%), Chrysomya putoria (2.1%), Lucilia eximia (0.9 %), Mesembrinella bellardiana (0.7%) and Hemiluciliasegmentaria (0.2%). The immatures collected and reared in the laboratory were identified after emergence as Cochliomyia macellaria (0.3%), Chrysomyamegacephala (0.3%), Chrysomya albiceps (95.9%), and Lucilia eximia (3.5%). This work will contribute essential information for implementing this kind of expertise at the Laboratory of Forensic Entomology in DPT-BA.

KEY WORDS: forensic entomology, decomposition of cadavers, Calliphoridae, cadaver fauna.

Contents

Brazilian Dipterology: History and research

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This presentation offers a resumé of the historical development of dipterology in Brazil. During the 19th century, the study of Neotropical Diptera was developed almost exclusively by European and North American taxonomists, working outside Brazil, with the exception of Fritz Müller (1821-1897), a German biologist living in Santa Catarina who studied the biology of the Blephariceridae. Müller (for whom Müllerian mimicry is named) also authored the first paper on Diptera to be published in a Brazilian scientific periodical ("Arquivos do Museu Nacional", 1879). It was only after him, during the first decades of the 20th century, that the first Brazilian dipterists began their researches, collections, and the training of the next generations of dipterists, and among those who were active in the early part of the 20th century were such celebrated scientists as Arthur Neiva, Carlos Chagas, Oswaldo Cruz and Adolpho Lutz from the "Fundação Instituto Oswaldo Cruz" in Rio de Janeiro, and Emilio Goeldi from the "Museu Emilio Goeldi" in Pará. Because of the serious problems with public health, especially with yellow fever, these scientists began to study the Brazilian species of Diptera that were suspected vectors of diseases. This first generation was followed by important researchers such as Costa Lima, Messias Carreira, and Lauro Travassos who, although he did not work directly with Diptera, encouraged many young students to undertake research into various zoological groups. Hugo de Souza Lopes and Sebastião José de Oliveira were students of Travassos. Dalcy Albuquerque, Nelson Papavero, Ângelo P. do Prado, Nelson Bernardi, José Henrique Guimarães, and many others who were active throughout the decades of the 20th century, were responsible for the training of a much more numerous generation of dipterists. Although the number of dipterists has been increasing, there are still too few, and too few families are covered.

KEY WORDS: Diptera, Brazil, history

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Stability in a phylogenetic morass: monophyly and interfamilial relationships of the Culicomorpha

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The Culicomorpha, which contains mosquitoes, black flies, midges and other well known flies, is one of the most diverse clades of Diptera. With nearly 19,000 described species, culicomorphs comprise 36% of lower Diptera and >12% of all Diptera. Because of their diversity, ubiquitous distribution, trophic significance, and role as disease vectors, the Culicomorpha is one of the most important lineages of flies. Their diversity in species, habitat, and life style translates into extreme structural diversity, particularly in immature stages. Despite this structural diversity, morphological characters have provided a robust phylogenetic signal across taxa. The landmark studies of Hennig (1973) and Wood & Borkent (1989) and later quantitative studies (e.g., Oosterbroek & Courtney, 1995; FLYTREE, in preparation) have identified consistent and compelling synapomorphies from nearly every life stage. All of these investigations, as well as those based on molecular characters (e.g., Bertone et al., 2008; Wiegmann et al., in review), provide strong support for monophyly of Culicomorpha. This is in contrast to most lower Diptera, where conflicting data generally provide poor resolution of phylogenetic relationships among major clades, including those between Culicomorpha and other subgroups. Although relationships within Culicomorpha remain somewhat contentious, most morphological studies have supported monophyletic superfamilies Culicoidea (Dixidae, Corethrellidae, Chaoboridae, Culicidae) and Chironomoidea (Thaumaleidae, Simuliidae, Chironomidae, Ceratopogonidae). Certain relationships within these superfamilies and potential inclusion of Nymphomyiidae at the base of Culicomorpha (Courtney, 1994; Saether, 2000) remain matters of debate. The goals of this presentation are to review the phylogeny of Culicomorpha, comment on both consistent and conflicting characters and tree topology, and provide a prospectus for future research.

KEY WORDS: Culicomorpha, Culicoidea, Chironomoidea, phylogeny, cladistics

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Twigs around the trunk: Phylogenetic relationships of Neotropical Blephariceridae

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Net-winged midges (Blephariceridae), which comprise approximately 320 described species in 29 genera, are morphologically distinct and ecologically important inhabitants of lotic habitats. The group contains two subfamilies, the Edwardsininae (southern hemisphere) and Blepharicerinae (both hemispheres). Relationships within the Blepharicerinae remain problematic, especially between and within the currently recognized tribes Blepharicerini, Apistomyiini, and Paltostomatini. The latter contains five described genera, including four from the Neotropical Region — *Aposonalco* Hogue (1 species), *Kelloggina* Williston (34 species), *Limonicola* Lutz (8 species), and *Paltostoma* Schiner (20 species) — and *Elporia* Edwards (19 species) from southern Africa. Previous phylogenetic hypotheses have provided relatively robust support for monophyly of the subfamily Edwardsininae, the subfamily Blepharicerinae, and, to a lesser extent, the tribe Apistomyiini and various generic groupings. However, the monophyly of and relationships within the Paltostomatini, and their relationship to apistomyiines, have been much more contentious. In order to test hypotheses on relationships between subfamilies, tribes, and genera of Blephariceridae, I evaluated >60 morphological characters in exemplars of nearly all genera of Blephariceridae and several "species groups" in the widespread and poorly defined Neotropical genus *Paltostoma*. The analysis provided strong support for both subfamilies, a combined Paltostomatini + Apistomyiini, the Apistomyiini, and various subgroups within these clades. However, monophyly of the Paltostomatini was not supported and relationships within this group remain poorly resolved. Results are also compared to a previous molecular phylogenetic study of a subset of blephariceridgenera. Despite poor resolution within paltostomatines, data provide compelling evidence for two new genera from southern South America.

KEY WORDS: Blephariceridae, phylogenetics, morphology, net-winged midges, Neotropical, *Paltostoma*

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Up-date on revision of New Zealand *Austrosimulium* (Simuliidae)

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Austrosimulium is a small segregate of simuliids in Australia, New Zealand and some outlying islands. It was Edwards (1931) who noted the relationship to a simuliid of South America, now recognized as the monotypic *Paraustrosimulium*. This latter genus is aberrant in some aspects, but there are convincing apomorphies shared with *Austrosimulium*. Molecular work by Moulton also strongly substantiates this relationship. My focus is an ongoing taxonomic revision of the New Zealand *Austrosimulium*. Some 20 species are now recognized. Dumbleton's (1973) species groupings are still maintained and are fully supported by molecular analysis. While the genus as a whole is of Gonadwanan origin, lack of divergence in the 16S gene indicates that the New Zealand *Austrosimulium* are of relatively recent origin. They no doubt arrived from Australia at some point following the Oligocene Epoch (25 mya), in keeping with recent evidence for major inundation of New Zealand at that time. This is congruent with biogeographical patterns reported for other elements of NZ's flora and fauna. The CO1 gene, however, has good divergence for some species and shows evidence of the original separation of the North and South Islands (3 mya) and formation of the modern Cook Strait.

KEY WORDS: Simuliidae, Gondwana, New Zealand, *Austrosimulium*, taxonomy, DNA

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A tritrophic geographic mosaic of coevolution and local adaptation

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Coevolution is potentially a major force in speciation. Geographic variation in interactions between species can be used to measure the influence of divergent coevolutionary forces on the evolution of reproductive isolation. We are studying coevolution and speciation in the community centered on *Eurosta solidaginis*, a gall-inducing tephritid fly. Geographic variation in both its host plant, *Solidago altissima*, and its natural enemies, including avian predators, a parasitoid, *Eurytoma gigantea*, and an inquiline *Mordellestina convicta*, create divergent selection on parapatric populations of *E. solidaginis*. The *E. solidaginis* populations in the prairie and forest biomes in Minnesota, USA, have higher survival on their local populations of *S. altissima* than on those goldenrods from other biomes indicating that there is divergent selection for host adaptation. Natural enemies also create geographically divergent selection on gall morphology and experiments have demonstrated that gall morphology is a heritable trait of *E. solidaginis*. In the forest biome birds cause higher predation on larvae in larger galls, while parasitoids cause higher mortality of larvae in smaller galls resulting in stabilizing selection on gall size. In the prairie biome bird predation is rare while there is high mortality on larvae in small galls due to both the parasitoid and the inquiline resulting in the evolution of large galls. Hybrid larvae produced by crossing the prairie and forest fly populations have low survival rates indicating that there is post-reproductive isolation between the geographical populations. We hypothesize that the prairie and forest *E. solidaginis* populations are in an intermediate stage in speciation due to tritrophic geographic divergent selection.

KEY WORDS: Speciation, tritrophic interactions, coevolution, Teprhitidae, *Eurosta solidaginis*

What advances have been made in the last decade in Afrotropical Dipterology?

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The first decade of the 21st century saw the deaths of Botha de Meillon, Brian Stuckenberg, David Greathead and Arthur Harrison, and the retirements of the cohort of colonial and newly post-independence entomologists interested in the Afrotropical Diptera Fauna. What effects can be seen on the study of African flies? Are there new students of Diptera, based within Africa, or outside, and what are their interests, as evidenced by publications? Google Scholar and ISI allow data retrieval and show clearly most studies in this decade concern disease vectors, as in the last century (noted by Crosskey in the introduction to the Catalogue of the Diptera of the Afrotropical Region). Molecular tools have been applied to tsetse, Simulium, Anopheles, Aedes, Culicoides imicola and Phlebotomus and also to forensically-important blow flies, to provide diagnostic probes. Molecular tools have been applied to studies of certain Cape Diptera: Tabanidae and Blephariceridae have revealed interesting spatial patterns. In aquatics, palaeo-studies involving Africa have been advanced by studies of chironomid head capsules in equatorial East African lakes (Uganda, Kenya, Tanzania). The extant chironomids are known better through studies including those by Arthur Harrison, and the Bergen group including several Ghanaian students funded to study in Norway. Revisionary taxonomic studies in the Tephritidae, Tabanidae, Bombylioidea, Empididae, Lauxaneidae, Curtonotidae and Muscidae have increased our understanding of the biodiversity of these groups. Diptera fossils are present in the (Botswanan) Orapa *insect fossil* assemblage, and perhaps of greater value, in newly-revealed Cretaceous amber from Ethiopia, the first such find in a 'Gondwanan' area. Sadly there has been no advance in the numbers of Dipterists residing on the continent, with South Africa (host of the 2008 ICE) the residence of most publishing African-based scientists. The Norwegian-funded Ghanaian chironomid students epitomise some of the problems.

KEY WORDS: Africa, Diptera, advances, fossils

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A molecular phylogeny for the Chironomidae

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Hennigian phylogenies have been estimated within the family Chironomidae using morphology, including on addition of each new subfamily since Prodiamesinae (in 1976). We provide the first highly sampled phylogeny estimate using molecular data from fragments of two ribosomal genes (*18S* and *28S*), one nuclear protein-coding gene (*CAD*), and one mitochondrial protein-coding gene (*COI*), analysed using mixed model Bayesian and maximum likelihood inference methods. We lack most-recently described, elusive, subfamilies Chilenomyiinae and Usumbaromyiinae, but confirm monophyly of all those sampled, excepting Prodiamesinae which contains *Propsilocerus*. Chironomoinea is confirmed only with Telmatogetoninae included, as sister group to Diamesinae (Prodiamesinae (Orthocladiinae+Chironominae)) closer to Brundin's original suggestion. Buchonomyiinae is excluded: it is sister to all remaining Chironomidae, conforming more to Murray and Ashe's argumentation. Tanypodoinea is a grade and is unsupported: the austral Aphroteniinae is sister to all Chironominae (less Buchonomyiinae), Podonominae is weakly supported as next sister, rather than sister to Tanypodinae alone in earlier analyses.

In Diamesinae, austral tribes Heptagiini and Harrisonini are confirmed, as is the undersampled Diamesini. Tribe Pentaneurini and the 'non-Pentaneurini' are monophyletic in Tanypodinae. Recent molecular findings concerning Podonominae are substantiated with monophyletic Podonomini, Boreochlini a grade and *Lasiodiamesa* uncertainly placed. In Orthocladiinae, postulated tribes Orthocladiini and Metriocnemini are unsupported: a *Corynoneura* group is recovered, a *Brillia*-group is revealed as sister to *Stictocladius* and the marine *Clunio* and *Thalassosmittia* (given high rank in the past) clearly are embedded deeply within the Orthocladiinae as proposed by Strenzke a half-century ago based on Hennigian argumentation. In Chironominae the finding of *Shangomyia* + *Xyiaomyia* as sister to all others justifies the high rank proposed by Sæther. Tribe Tanytarsiini is monophyletic, Pseudochironomini is untested (by sampling shortfall) but, with a weakly supported inclusion of enigmatic *Nandeva*, is sister to Tanytarsiini. The tribe Chironominae can be supported only by excluding early-branching *Beardius* and the clade comprising the so-called '*connectens*' group.

KEY WORDS: Chironomidae, molecular phylogeny, subfamily, tribe

Revision of the *Hesperempis* genus group (Diptera: Empididae)

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The Hesperempis genus group currently contains Dryodromia Rondani (with one western Palaearctic species), Hesperempis Melander (with two western Nearctic species and one eastern Palaearctic species) and Melanderalus Özdikem & Başar (= Toreus Melander) (with one western Nearctic species). Revision of the group indicates that it should now include only two genera, Dryodromia (with a new Chinese species) and Hesperempis (with a new eastern Nearctic species, a new western Nearctic species, and two new Japanese species). Melanderalus should be synonymized with Hesperempis. Phylogeny and zoogeography of this essentially Holarctic genus group will be discussed, including its probable relationship within the Empididae.

KEY WORDS: Empidoidea, Empididae, *Hesperempis*, *Dryodromia*, *Toreus*, *Melanderalus*, new species, phylogeny

Cladistic Analysis of Toxophorini Schiner (Diptera, Bombyliidae)

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Toxophorini includes only the genus *Toxophora*, with 51 species distributed all over the world: 10 NT, seven NA, 18 AF, 15 PA, one OR and one AU. Traditionally, species actually placed in *Toxophora* have been included, by different authors, in two distinct genera (*Toxophora* and *Eniconevra*), which were synonymized in a catalog without justification. Toxophorini are characterized by a stout body with humped thorax, enlarged pronotum, elongated antenna with a thin, flattened flagellum, and a long style, three posterior cells, anal cell always closed and two or three submarginal cells, abdomen strongly convex, wider than thorax at base and covered by dark brown, yellow or white scales forming different patterns of spots or stripes. According to the most recent classification based on cladistic analysis, the tribe is the most basal in the Toxophorinae. Its monophyly is sustained by the following synapomorphies: ocellar tubercle with two large, anteriorly directed setae; prothorax developed with long setae; male epandrium fused to the posterior region of the gonocoxite; and female furca with an anterior spine. This study aims to test the monophyly of *Toxophora* and *Eniconevra* and to infer the relationships among their species. The analysis was accomplished with PAUP*, using a heuristic search. A total of 46 taxa (including three species sampled as outgroups and four new species) were analyzed using 92 morphological characters of adults of both genders. The analysis resulted in 101 most parsimonious cladograms. After applying successive weighting, a single cladogram was obtained. The monophyly of *Toxophora* plus *Eniconevra* is confirmed and supported by 27 synapomorphies. The species that were once included in Eniconevra, however, are dispersed in the cladogram forming a polyphyletic group. These results therefore support the synonymy of *Toxophora* and *Eniconevra*, as presented in previous papers without justification.

KEY WORDS: *Toxophora*, *Eniconevra*, systematics, morphology

Origin and evolution of the *Disneyempis* lineage, a phylogenetic and biogeographic approach

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The *Disneyempis* lineage is mainly distributed in Africa and most of the Afrotropical Empidini belong to this lineage. However two members of the lineage are found elsewhere: the *Empis atra* group is entirely Neotropical, and the *Empis poecilosoma* group has representatives both in Africa and in the Oriental Region. We discuss the diversity of the *Disneyempis* lineage, and we propose a biogeographic study based on a morphological phylogeny in order to elucidate the origin and evolution of the group.

KEY WORDS: Afrotropical Empidinae, phylogeny, biogeography

An exemplar approach of the morphological phylogeny of the subfamily Empidinae

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A phylogeny of the Empidinae was obtained from a worldwide sampling of about 200 examplar species (10 % of the total number of known empidine dance flies) using more than 100 morphological characters. For the first time a morphological analysis of the subfamily includes a large range of Nearctic species of *Empis* and *Rhamphomyia*. The phylogeny corroborates most of the species groups and main lineages found by recent morphological studies. An undescribed new Australian species, the male of which has a pair of wire-like postgonites, could be the "the missing link" between the lineage including the Hilarini + the *Empis macrorrhyncha* group and the remaining Empidinae that lack postgonites. The morphological phylogeny presented here is congruent with initial results obtained from molecular data.

KEY WORDS: *Empis*, *Rhamphomyia*, worldwide sampling, Nearctic species, missing link

LifeDesk: managing and sharing biodiversity research on the Web

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LifeDesk (www.lifedesks.org) is a server-based software which is developed within the Encyclopedia of Life project (EOL, www.eol.org). LifeDesks are dynamic web environments based on the content management system Drupal that make the online management and sharing of biodiversity research easy. It is intended as a tool for taxonomists and systematists to (1) upload, manage, and share a classification, (2) build a team of collaborators from across the planet to exchange research data about a taxon through the platform, (3) import and organise content like diagnoses, descriptions, distributional data, and ecological information about taxa, and (4) help to shape the Encyclopedia of Life by contributing to the ongoing effort to document the world's species in a single web environment. This presentation focuses on the organisation of a LifeDesk and will provide details about the features of the software based on the Leptogastrinae LifeDesk (Asiloidea: Asilidae, http://leptogastrinae.lifedesks.org) that the author is responsible for.

KEY WORDS: LifeDesk, Encyclopedia of Life, biodiversity, Leptogastrinae

An overview of Afrotropical Mydidae – the most diverse mydid fauna worldwide

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With 461 species in 66 genera, the family Mydidae (mydas flies) is one of the less speciose families of Asiloidea. Species are distributed in warmer climates throughout the world, and arid as well as Mediterranean-type environments are particularly species-rich. By far the highest species diversity is found in the Afrotropical Region with 199 species. Southern Africa with 178 species is particularly rich. The predominant Afrotropical taxon is the Syllegomydinae with 182 species, followed by Ectyphinae with 8 species, Rhopaliinae with 3 species, Leptomydinae with 4 species, and Megascelinae with 2 species. The Afrotropical Region has some of the most enigmatic Mydidae species, as shown by its high generic diversity. Of the 31 genera, 25 are restricted to the Afrotropical Region, with 2 of them confined to Madagascar. This presentation introduces some of the enigmatic genera and provides new insights into the species diversity of Mydidae in Africa based on an extensive survey of yet unstudied specimens from numerous museum collections as well as a study of all of the Afrotropical genera.

KEY WORDS: Asiloidea, Mydidae, Afrotropical Region

Phylogenetic relationships within Mydidae based on adult morphology (Diptera: Asiloidea)

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With 461 species in 66 genera, the family Mydidae (mydas flies) isone of the less speciose families of Asiloidea. Species are distributed in warmer climates throughout the world, and arid as well as Mediterranean-type environments are particularly species-rich. The family is currently divided into 11 subfamilies according to studies during the 1970's and 1980's by Nelson Papavero and Joseph Wilcox, as well as an influential paper on Apioceridae, the sister group to Mydidae, by David Yeates and Mike Irwin in 1996. None of the subfamily taxa is distributed world-wide and several taxa are restricted to particular continents or only found in the Southern Hemisphere. This presentation will provide new insights into the phylogenetic relationships of the subfamily taxa based on an analysis of adult morphological characters from 40 genera, constituting a world-wide sample of the diversity of Mydidae. A large scale morphological study including all 11 subfamily taxa with multiple representatives has not been conducted to date. Of particular interest is the phylogenetic position of Apiophorinae, Diochlistinae, and Megascelinae that are entirely restricted to the Southern Hemisphere and the monophyly of the Ectyphinae, which is restricted to western North America and southern Africa. In addition, the largest radiation of Mydidae took place on the African continent by the Syllegomydinae with 201 species in 25 genera and the relationships among its genera will be addressed in detail.

KEY WORDS: Asiloidea, Mydidae, phylogeny, biogeography

The Encyclopedia of Life, the Biodiversity Heritage Library, and Systematic Dipterology

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The Encyclopedia of Life (EOL, www.eol.org) is an online web environment that aims to present a single species page for every described extant or extinct animal, fungus, and plant species. Information is gathered into a single page from several sources either through content partnerships with other biodiversity databases or provided *de novo* through in-house data providers like LifeDesks. Access to the information on a species page is always free to anyone with an internet connection be they scientists, school children, or amateur entomologists. The Biodiversity Heritage Library (BHL, www.biodiversitylibrary.org) is one of the five components of the EOL and aims at digitising all of the natural history literature to provide free access to the vast biodiversity-related literature from the past 250 years. The digitised literature is enhanced so as to allow the search for taxon names, for example, to find every single mention of a species name and a link to its respective EOL species page is provided. This presentation focuses on an introduction to the EOL and BHL and will highlight ways of how all of us can contribute information to the EOL and benefit from the online access to biodiversity literature through the BHL.

KEY WORDS: Encyclopedia of Life, Biodiversity Heritage Library, Species Pages, digitisation of literature, biodiversity

Contents

Afrotropical Flower Flies (Diptera: Syrphidae)

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Flower flies are common and are critical pollinators. Their maggots (immature stages) have diverse habits spanning many niches. So, overall the group is an important indicator of biotic diversity.

Afrotropical flower flies are not well known. Today, we know only 591 species in 64 generic groups, which is only 10 percent of the World species fauna and less than 1/3 of the Neotropical fauna (20 percent of World genus-group fauna).

A conspectus of the Afrotropical flower flies has been developed so as to promote the understanding of these flies in the "dark" continent. This conspectus provides an 1) overview of the family; 2) a key to all the morphologically distinct groups (genera, subgenera and species groups), along with 3) a glossary of terms used; 4) a monographic catalog; and 5) bibliography. Line drawings illustrate critical taxonomic characters and color photographs depict the flies in nature are also included.

This conspectus should serve as a prototype of what should be done for the forthcoming Manual of Afrotropical Diptera.

KEY WORDS: conspectus, generic key, faunistics, pollination

Contents

Malaise traps in biodiversity assessments - II. Evaluating changes in community structure

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In this talk we will present applications of the bivariate Poisson lognormal distribution to evaluate the spatio-temporal dynamics of species abundances. To illustrate this approach we use samples from chironomid communities, caught by Malaise traps, along an alpine-boreal watershed in Central Norway. In the univariate case, a community of S species fits the lognormal distribution if the log of the abundances can be regarded as a sample from the normal distribution. By assuming a Poisson sampling distribution, the species counts can then be described by the Poisson lognormal distribution. When we extend this approach to consider samples from two communities jointly, either from two different locations or sampled at different times from the same location, we can assume that the log abundances in the pair of communities have the binormal distribution. The correlation of this binormal distribution will then serve as a robust measure of the similarity between communities, and can be estimated without any knowledge of the two sampling intensities. With correlation close to 1, e.g. for two parallel samples from the same community, the relative abundances of any species should be approximately the same in both samples although they may differ due to random sampling effects. Sampling methods that yield correlations close to 1 for parallel samples can thereby be expected to give good estimates also for the actual spatial or temporal change in community structure between samples. These correlation structures can then be modeled by either distance in space or time, or by environmental covariates. Using samples from chironomid communities we found correlations between parallel samples ranging from 0.94 to 0.99 for a given week and location, indicating a high consistency in relative species abundances between samples. We will further present models for how the correlations decrease with time between samples from the same location.

KEY WORDS: Bivariate Poisson lognormal species abundance distribution, similarity, spatio-temporal dynamics.

Contents

Two hundred described, thousands more to go – the virtually unstudied fauna of Afrotropical Cecidomyiidae

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With more than 5,700 described species, the Cecidomyiidae constitute one of the largest families of Diptera and are represented on all five continents. However, despite its ubiquity, economic importance, and highly specific association with plants, the family has hardly been studied in many parts of the world, including the Afrotropics, and we estimate that thousands of species are yet to be discovered. Currently, 216 species in 85 genera are known to occur in the Afrotropics, of which small proportions are fungus feeders or predators and the great majority are gall inducers. Almost 70% of these species were described in the early 1900s, many from specimens caught in flight and often from only one sex, and a large proportion of the genera are monotypic. Coupled with the fact that many types are considered lost, numerous species and genera would be impossible to find again and/or be associated with their original descriptions. The big genera *Asphondylia*, *Dasineura* and *Lasioptera*, which are species-rich all over the world, are well represented in the Afrotropical region. The major plant families from which phytophagous gall midges are currently known in the Aftrotropics are the Fabaceae, Poaceae and Chenopodiaceae, but fieldwork during the last few decades revealed scores of undescribed species from diverse plant families. Among these, the Asteraceae and Aizoaceae are expected to yield a particularly high number of undescribed species of gall formers and there is little doubt that many predatory species are likewise awaiting discovery.

KEY WORDS: Cecidomyiidae, gall midges, Afrotropical

Radiation of gall midges (Diptera: Cecidomyiidae) driven by shifts within and between host-plant species of North American goldenrods

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Speciation of plant-feeding insects is typically associated with host-plant shifts, with subsequent divergent selection and adaptation to the ecological conditions associated with the new host plant. However, a few insect groups have undergone speciation while shifting to new plant organs or even on the same plant organ on the same host-plant species. Such within- and between-host radiations may provide novel insights into the causes of adaptive radiation. The rich fauna of galling insects on North American goldenrods (*Solidago* and *Euthamia* species) offers examples of both types of radiation. We used mitochondrial and nuclear DNA data to infer phylogenies for two genera of gall midges (Diptera: Cecidomyiidae) from these plants. The genus *Rhopalomyia* includes a monophyletic group of 15 described species on goldenrods, a radiation that appears to have been driven primarily by host shifts, such that closely related *Rhopalomyia* species induce similar types of galls on related goldenrod species. Conversely, the genus *Asphondylia* proved to consist of numerous cryptic species on goldenrods and exhibits radiation both through between-host shifts, as in *Rhopalomyia*, and within-host shifts. Several of these *Asphondylia* species induce two different types of galls at different times of the year, suggesting a role for phenology in population divergence.

KEY WORDS: Cecidomyiidae, goldenrods, adaptive radiation, speciation, ecological divergence

Contents

Contact courtship devices and sexual selection in Diptera

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Diptera display a wealth of species-specific male morphological traits, including both elaborate genitalia and modifications of many other parts of the male's body. In this talk, I will review studies of the functional morphology of organs in Tipulidae, Sepsidae, Tephritidae, and Glossinidae that contact females directly. In addition to showing species-specific elaborations, they have seemingly excessively elaborate designs compared to their relatively simple mechanical roles (an extreme example is that of convergently evolved proto-appendages on the abdomens of some male sepsids, whose differentiation in one group is controlled by genes that normally control the differentiation of legs). Recent experimental studies in sepsids and glossinids, in which the morphology of the male organs and of the female receptors with which they make contact was altered, indicate that the male structures function as devices that stimulate the female before or during copulation and to induce her to respond in ways that favor the male's reproduction. I will argue that many organs of this sort are "contact courtship" devices, and that their relatively rapid evolutionary divergence into extreme, generally species-specific forms represents adaptations to sexual selection by female choice (both classic, pre-copulatory choice and "cryptic" female choice that occurs after copulation has begun), rather than to selection favoring either species isolation or sexually antagonistic male-female coevolution.

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DNA barcoding of non-biting midges (Diptera: Chironomidae)

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Recent studies have shown that DNA barcoding is very useful for species identification and delimitation in the taxonomically difficult Chironomidae, and that it is an excellent tool for the association of unknown and cryptic life stages. However, DNA barcoding can also be used to pin-point species and species groups that are in need of description or taxonomic revision. This presentation summarizes the current results from our analysis of COI sequences of more than 3000 specimens from northern Europe and Canada, belonging to nearly 100 genera. The result from Neighbour-Joining analysis distinguishes 542 clusters that can be considered species, but we have only been able to identify 318 of these species based on morphology. As the project proceeds and additional reference collections are examined, the number of identified species will undoubtedly increase. Nevertheless, our DNA barcode data currently indicate at least seven cryptic species complexes and numerous new species. Our results also point to a few new cases of synonymy and a rare instance of horizontal gene transfer.

KEY WORDS: DNA barcoding, cryptic species, life stage associations, taxonomy

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Towards a molecular phylogeny of the tribe Tanytarsini (Diptera: Chironomidae): new genera emerge while others disappear

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The chironomid tribe Tanytarsini contains both large, widely distributed collective genera and small species groups with limited geographic distribution. The tribe houses species with peculiar behaviour or unusual habitat choice compared to most Chironomidae, and comprises several species and species groups still unknown to science. A stable phylogenetic hypothesis of the tribe is therefore appealing as it would provide a framework for studying behavioural evolution, character development and zoogeography of this diverse group. Previous phylogenies based on morphology generally are characterised by considerable amount of homoplasy and low branch support, while molecular data have been unavailable until recently for many relevant taxa. Here we present the current knowledge of phylogenetic relationships within Tanytarsini based on nuclear and mitochondrial markers. Our results show that while some taxa new to science require taxonomic placement at the generic level, there is little or no support to keep certain genera as they are understood today. The genera *Micropsectra, Krenopsectra, Parapsectra, Tanytarsus, Corynocera, Caladomyia* and *Virgatanytarsus* all are in need of taxonomic redefinition.

KEY WORDS: CAD, EF-1a, COI, COII, 16s, Bayesian inference

Contents

The Fiji Terrestrial Arthropod Survey – Overview and results of a three-year study

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The Fiji Archipelago is a biological enigma. It consists of over 300 islands and has a complex geological history with islands consisting of Miocene continental rocks, rocks of recent volcanic origin, and smaller low-lying coral atolls or limestone karst islands. With funding from the US National Science Foundation and the Schlinger Foundation, a three-year study was undertaken to survey insects and related groups from as many islands and habitats as possible, to train local students, to provide checklists of taxa, and to publish the results of the terrestrial arthropods occurring there. A brief overview of the study and its results are given in association with incredibly stunning color photographs. Through research conducted during this project, the previous total of some 3000 known Fiji arthropods increased to over 5200. More than 250 new species and over a dozen new genera were described during the study in the journal "Fiji Arthropods", with many of these new species belonging to the Diptera. Knowledge of the arthropod fauna of this biodiverse island archipelago can help us better understand the unusual and complex biogeographical relationships that occur in the South Pacific and point us to other areas needing further study.

KEY WORDS: Fiji, biodiversity, survey, arthropods, Diptera

A new Neotropical ditomyiid genus, with a fossil from Dominican Republic amber and new species

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The Ditomyiidae is a small family of Mycetophiliformia, with approximately 90 species in the world, described in six genera. They are most abundant in the Neotropical and Australasian Regions, but also with Nearctic, Palearctic and Oriental species. The Mycetophiliformia are well represented in the fossil record, first appearing in the Jurassic, but the oldest record for ditomyiids is known only from the Eocene. In the neotropics, species have been described from the genera *Melosymmerus* Munroe, *Nervijuncta* Marshall, *Rhipidita* Edwards, and *Calliceratomyia* Lane. We describe a here new genus for the family, with species known from different areas in South America, as well as of an Oligo-Miocene amber fossil from the Dominican Republic. In a faunistic analysis of the Neotropical Ditomyiidae, we found new species, belonging to this new genus, from the States of Amazonas and São Paulo. Features of the head, thorax, wing and abdomen place the genus into a clade with *Ditomyia*, *Nervijuncta*, *Rhipidita* and *Calliceratomyia*. The species of the genus have a 1-segmented maxillary palpus, a gonostylus with a basal row of strong thorns, and have gonocoxites with a ventrolateral pair of processes and a mid-ventral process projecting distally. These are obviously apomorphic features and clearly define a clade within the family. However, the cylindrical flagellomeres, very much like those of *Nervijuncta* and *Ditomyia*, is a plesiomorphic feature that places the new genus outside the small clade composed of *Calliceratomyia* and *Rhipidita*.

KEY WORDS: Ditomyiidae, amber fossil, systematics

Costa Rican Biodiversity - new species of *Downeshelea* (Diptera: Ceratopogonidae)

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Species of *Downeshelea* Wirth & Grogan are predaceous midges, occurring worldwide even though only 32 species are known. Of these, 19 are described from the Neotropical Region. Fresh sampling of the genus over the past 18 years in Costa Rica resulted in 525 specimens and the discovery of 13 new species and four newly recorded species for this country. These are distributed as follows, according to province: Alajuela [*D*. n. sp. 2, 3, 4, 13, *D. chirusi* (Lane & Wirth)]; Cartago [*D*. n. sp. 3, 5, 13, *D. cebacoi* (Lane & Wirth), *D. chirusi*)]; Guanacaste [*D*. n. sp. 1, 3, 9, 10, 12, 13, *D. chirusi*, *D. panamensis* (Lane & Wirth)]; Heredia (*D*. n. sp. 3, 12, *D. chirusi*); Límon (*D*. n. sp. 3, 6, 7, 9, 11, 12, 13, *D. cebacoi*, *D. chirusi*, *D. panamensis*); Puntarenas [*D*. n. sp. 2, 3, 6, 7, 8, 9, 13, *D. cebacoi*, *D. chiapasi* (Lane & Wirth), *D. chirusi*, *D. panamensis*]; San José (*D*. n. sp. 3, 5, *D. chirusi*). We report for the first time *D. cebacoi*, *D. chiapasi*, *D. chirusi* and *D. panamensis* from Costa Rica. *Downeshelea stonei* (Wirth) has been previously recognized from Costa Rica but we consider the Costa Rican specimens distinct from the type of that species. As such, we recognize 17 species in Costa Rica, a significant increase for both this country (previously with only the misidentified *D. stonei*) and the Neotropical Region (from 19 to 32).

Of the 17 Costa Rican species all but three occur below 860 meters, strongly suggesting that these are more broadly distributed in at least Central America and northern South America. Furthermore, our discovery of so many new species strongly suggests that *Downeshelea* is much more diverse in the Neotropical Region than previously realized, a perspective which appears true for nearly every genus of Ceratopogonidae in this area.

KEY WORDS: Ceratopogonidae, *Downeshelea*, Costa Rica, new species

A new species of gall midge (Diptera, Cecidomyiidae, Lasiopteridi) from Brazil

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A new species of Dasineura Rondani 1840, (Diptera, Cecidomyiidae, Lasiopteridi) is characterized based on material from the restinga of Barra de Maricá, Maricá, Rio de Janeiro, Brazil. Samples of galls were collected in 1987, 1998, 2000 and 2005. Adult flies were reared from galls taken to the laboratory. All slide-mounted material was deposited in the Diptera Collection of Museu Nacional, Rio de Janeiro The new species of Dasineura induces conical greenish galls on leaves of Erythroxylum ovalifolium Peyr. (Erythroxylaceae). Pupation takes place in the soil. The new species was tentatively placed in this genus following the key for Neotropical species. The adult is characterized as follows: occipital process present, antenna with 13 flagellomeres, and palpus with four segments, wing with veins Rs absent, R5 straight at juncture with C, R5 joining C before wing apex, M3 absent, Cu forked and Cup present; legs with tarsal claws curved after midlength, with one tooth, empodia long, extending beyond bend in claws; gonocoxite not splayed with mesobasal lobe, gonostylus elongate and striate, paramere slender, aedeagus truncate at the apex and longer than hypoproct, hypoproct with parallel lobes and cercus with divergent lobes, ovipositor barely protrusible, cerci ovoid and setose, hypoproct bilobed with apical setae, cephalic region of pupa with antennal horn reduced, straight and smooth, cephalic setae long, two pairs of lower facial papillae and three pairs of lateral facial papillae, prothoracic spiracule setiform and abdominal tergites 2-8 with spines, larva with spatula 2-toothed, lateral papillae barely visible and terminal segment with three pairs of setose papillae. This species is unique in having the abdominal tergites 2-8 of the pupa with spines and the female with ovipositor barely protusible.

KEY WORDS: Cecidomyiidae, Dasineura, Erythroxylaceae, gall, taxonomy

Overview of the Neotropical Dexiinae (Tachinidae)

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The cosmopolitan family Tachinidae is one of the largest families of Diptera, with ca. 10,000 species. Currently, the family is catalogued for all biogeographical regions, but the Neotropical catalog is the most outdated, published by J.H. Guimarães in 1971. At the time, he classified Tachinidae in six subfamilies, 69 tribes, 970 genera and 2,827 species. In the last few decades, the status, delimitation and placement of the suprageneric taxa have been frequently modified, and current proposals of classification recognize only four subfamilies: Dexiinae, Exoristinae, Phasiinae, and Tachininae. Furthermore, genera and type-genera of many tribes have been allocated in different taxa by previous authors, but without any phylogenetic support. In this context, the present study aims to update the classification of Neotropical Dexiinae, by discussing the placement and generic composition of the tribes and indicating problematic groups that need to be revised under a phylogenetic perspective. By reconciling the classification in the most recent regional catalogs, a Dexiinae classification is suggested here with 18 tribes of world distribution: Campylochetini, Dexiini, Doleschallini, Dufouriini, Ebeniini, Epigrimyiini, Eutherini, Freraeini, Imitomyiini, Palpostomatini, Rutillini, Sophiini, Telothyriini, Thelairini, Trichodurini, Trichoprosopini, Uramyini and Voriini. Among the 13 Neotropical tribes, only seven (Dexiini, Ebeniini, Sophiini, Telothyriini, Thelairini, Trichodurini and Uramyini) remain valid and allocated in Dexiinae as originally proposed in 1971. In order to propose a classification containing natural groups, a cladistic analysis of the Dexiinae is in progress as a Ph.D. project research by the senior author.

KEY WORDS: systematics, phylogeny, taxonomy

An overview of the taxonomic status of the Afrotropical Tephritidae (Diptera)

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We currently seem to be a little further than half way in the acquisition of taxonomic knowledge of the Afrotropical Tephritidae. While the known fauna has reached 1000 species, and hundreds of undescribed species (probably around 500 are already in collections) remain to be described, the higher classification of this fauna is quite well established and is not expected to be greatly affected by the discovery of new taxa. About 160 genera have been recorded. However, based on undescribed material, about 10-20 new genera will eventually be added (while some existing names might be synonymized). With most world higher taxa (from subfamilies to genus groups) represented, the Afrotropical fauna is not only rich but is also diverse, although some groups are poorly represented, and the overall taxonomic consistency is significantly unique (e.g., very different from both the Palaearctic and Oriental faunas). There are significant gaps in group knowledge regarding the Adramini (8 genera and 35 species known; 2 new genera and about 20 new species are already in collections) and several groups within the Tephritinae: Myopitini (4 genera and 8 species known; unknown number of new genera and about 40 new species are already in collections); Schistopterini (13 genera and 40 species known; about 5 new genera and 140 new species are already in collections). There are numerous geographic gaps, where collecting would be desirable, in particular West Africa, Central Africa (the Congo River basin to Gabon, Angola and Zambia), the south-west corner of the Arabian Peninsula and Madagascar. Based on existing collections, the fauna of Madagascar probably amounts to some 150 species, most of which are endemic to the island and still unrecorded.

KEY WORDS: Tephritidae, Afrotropical, taxonomic status, biology, future work

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Enhanced rate of gene duplicate accumulation in the higher Diptera: potential for phylogeny reconstruction

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Gene duplication is a significant source of evolutionary innovation. Studying the evolution of developmental genes across insect genomes, we discovered an exceptionally high proportion of lineage specific duplicated genes in *Drosophila*. Several lines of evidence suggest that most of these duplications accumulated during the early evolution of the higher Diptera (Brachycera). We are now investigating whether these findings represent a genome-wide trend, how the dynamics of gene duplicate accumulation relate to phylogeny and body plan diversification, and at which level these duplications can be harvested as rare genomic event markers for phylogeny reconstruction.

KEY WORDS: Diptera, systematics, phylogenetics, phylogeny reconstruction, gene duplication

Phylogeny of the adelgid-feeding Leucopini (Diptera: Chamaemyiidae)

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Species in some genera of Leucopini (Diptera: Chamaemyiidae) are among the most important natural enemies regulating species of Adelgidae (Hemiptera: Sternorrhyncha) in their native ranges. Invasive adelgids can be devastating pests of conifers, and chamaemyiids have been used successfully in biological control programs in several parts of the world. With the current problem of hemlock woolly adelgid in eastern North America, several leucopine species are being considered for release as biocontrol agents. This prompted our studies of adelgid-feeding leucopines, first to develop a robust phylogenetic hypothesis to help predict the most effective candidates for biocontrol, and second to develop COI barcodes to aid in their identification to monitor establishment and spread after release. New collections have significantly expanded the known geographical ranges for certain species, as well as the known host associations. The COI barcode region has been sequenced for species within *Neoleucopis, Anchioleucopis, Lipoleucopis, Leucopis* (both adelgid- and aphid-feeding), and several species of *Leucopis* recently placed in new genera. The phylogenetic work began with COI sequences, and is expanding to include additional mitochondrial and nuclear gene regions (e.g., CAD, EF-1alpha, TPI), as well as morphology. Current analyses confirm the monophyly of each of the included genera. In addition to these analyses, in the course of describing the new genera by the first author, a search for morphological character states has resulted in the ability to distinguish the larvae and puparia for certain species, and to identify certain genera by their egg stage. In addition, study of the typically ignored female terminalia has clarified species-level characteristics to identify certain species in this group. To expand on this project, the authors will continue adding taxa to develop a hypothesis of relationships among all genera of the family.

KEY WORDS: Chamaemyiidae, Leucopini, Adelgidae

An overview of Afrotropical Lauxanioidea

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Worldwide, there are about 2400 species of Lauxanioidea: 114 Celyphidae, about 340 Chamaemyiidae and the rest Lauxaniidae. Celyphids, remarkable in their greatly enlarged scutellum, are restricted to the Afrotropical and Oriental regions, with greatest diversity in the latter. Of eight described genera, only two are Afrotropical, with 12 described species. Only *Chamaecelyphus* is endemic to the Afrotropics. Chamaemyiids, known as predators on sternorrhynchous Hemiptera, have slightly fewer than 350 described species in 33 genera worldwide. Of 15 described Afrotropical species, one is in the endemic genus *Melanochthiphila*, while the remainder are in four widespread genera. Interestingly, one subgenus, *Leucopis* (*Leucopella*), occurs in both Africa and South America. Lauxaniids, one of the larger acalyptrate families, have nearly 2000 described species in over 200 genera worldwide, with fewer than 100 Afrotropical species in 22 genera. Of these genera, 10 are endemic (eight of which are monotypic), while seven occur in other Old World regions, and five are more widespread. Two monotypic genera and both species of *Zanjensiella* are known only from Madagascar. Of the remaining genera, only *Neogeomyza* and *Parapachycerina* have species in Madagascar, and several genera have species on the islands (Réunion, Mauritius, Seychelles) north and east of Madagascar. The apparent paucity of Afrotropical lauxanioids only reflects a lack of study. The last celyphid described from the region was in 1963. For chamaemyiids, before new species of *Leucopis* (*Leucopella*) were described in 2002, the last species described was in 1958. For lauxaniids, before new species of *Parapachycerina* were described in 2008, the last species described were in Stuckenberg's monumental 1971 study of Old World lauxaniids. Afrotropical lauxanioid diversity is expected to see a significant boost over the coming years, as many new species are recognized in all three families.

KEY WORDS: Celyphidae, Chamaemyiidae, Lauxaniidae, Afrotropics

A phylogeny of Conopidae based on molecular and morphological character data

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The family Conopidae is a fascinating group of parasitic flies. In their larval stage most species are endoparasitoids of bees and wasps, while members of one subfamily (Stylogasterinae) attack cockroaches and crickets. They are economically and ecologically important as parasitoids of important pollinators. Many species are mimics of bees and wasps, sometimes even of the same species that serve as hosts to their young. Despite the fact that over eight hundred species have been described, there has been very little phylogenetic and higher-level taxonomic work completed on Conopidae. No phylogeny for the family has been attempted and species concepts are based on external features only. Genitalic and molecular characters have not yet been used to test species or generic concepts. While the family has been classified into four extant subfamilies (Conopinae, Dalmanniinae, Myopinae, and Stylogasterinae), no tests of the monophyly of these clades has been performed. We present the first phylogenetic hypothesis for the family based on molecular and morphological characters. DNA was extracted from 68 conopid specimens representing 24 genera. Mitochondrial and nuclear DNA were amplified with PCR and sequenced. Large segments of the 12S ribosomal RNA gene, the cytochrome oxidase I (COI) gene, the 28S ribosomal RNA gene, the cytochrome b gene, and the alanyl-tRNA synthetase (AATS) gene were included in a data matrix of over 5800 bp. To this was added a suite of morphological characters. Parsimony and Bayesian analyses were performed on the complete dataset to produce a preferred phylogenetic hypothesis. All four current subfamilies are recovered as monophyletic with strong support, and to them are added the previously proposed subfamily Zodioninae. Stylogasterinae is recovered as sister to the remaining Conopidae.

KEY WORDS: mtDNA, nrDNA, parasitoid, morphology, phylogeny, Acalyptratae, Schizophora

Hennig's other great, unsolved question: Placement of Conopidae using mtDNA and nrDNA

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Over 800 species of Conopidae, a fascinating family of parasitoid flies, have been described from every part of the world excluding the Pacific islands and Antarctica. In Hennig's approximation, one of the two most pressing issues in Schizophoran systematics was the placement of Conopidae, the other issue was the uncertain monophyly of the two schizophoran subgroupings, Acalyptratae and Calyptratae. Past phylogenetic hypotheses have placed conopids as sister to a number of brachyceran groups including Syrphidae, Schizophora (*s.s.*), and Tephritoidea. The first attempt to phylogenetically place Conopidae using molecular characters, as well as the largest molecular analysis of relationships within Schizophora (Diptera) to date, is presented. Twenty-eight taxa from eleven acalyptrate families and seven acalyptrate superfamilies are represented. Nearly 12,800bp of sequence data from ten genes representing both mitochondrial (cytochrome oxidase I (COI), cytochrome b (cytB), and 12S) and nuclear genes (28S, the carbamoyl phosphate synthetase region of CAD (CAD), elongation factor 1α (EF-1α), white, alanyl-tRNA synthetase (AATS), triose phosphate isomerase (TPI), and phosphogluconate dehydrogenase (PGD)) are analysed. Parsimony and Bayesian analyses strongly support the monophyly of both Conopidae and Schizophora. While in the parsimony analysis, Conopidae are placed as sister to the remaining Schizophora, the Bayesian analysis recovers a Conopidae + Lauxaniidae clade.

KEY WORDS: mtDNA, nrDNA, parasitoid, morphology, phylogeny, Acalyptratae, Schizophora

Phylogeny of black flies based on morphological data (Simuliidae, Culicomorpha)

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The Simuliidae are a well-supported monophyletic family of Culicomorpha, comprising 26 extant genera and about 2,000 species. Black flies are distributed worldwide and are best known for the bloodsucking habits of adult females; the immature stages are confined to running water habitats. We propose the first phylogenetic hypothesis of all the extant genera of Simuliidae using a cladistic approach. Seven exemplars of other culicomorphan families (Thaumaleidae, Ceratopogonidae, Chironomidae and Culicidae) are included as outgroups. The analysis is based on a data matrix of 77 terminal taxa and 203 morphological characters derived from character states of adult, pupal and larval stages. Phylogenetic analysis under equal weights yielded 588 most parsimonious trees of 744 steps (CI = 0.32; RI = 0.76). The analysis corroborates monophyly of the Simuliidae, Parasimuliinae, Simuliinae and Simuliini, but the Prosimuliini are resolved as paraphyletic. At the genus level, *Parasimulium, Gymnopais, Twinnia, Prosimulium, Crozetia, Greniera, Lutzsimulium, Stegopterna, Gigantodax, Cnephia, Ectemnia, Austrosimulium, Metacnephia, Simulium* are all resolved as monophyletic, whereas *Helodon, Tlalocomyia, Paracnephia, Araucnephia* are shown to be polyphyletic. The following monophyletic groups are resolved: *Gigantodax s.l.* + *Cnesia* + *Paracnephia* (in part); *Austrosimulium* + *Paraustrosimulium* + *Cnesiamima* + *Paracnephia* (in part); and *Simulium* + *Metacnephia* + *Sulcicnephia*.

KEY WORDS: Cladistics, morphology, systematics, Insecta, Chironomoidea

Contents

Diversity and systematics of the Neotropical Acroceridae

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The family Acroceridae is distributed worldwide comprising over 500 described species in about 50 genera and three subfamilies - Acrocerinae, Panopinae and Philopotinae. These distinctive small-headed flies may be specialized pollinators bearing conspicuously elongated mouthparts, while the larvae are host-restricted parasitoids of spiders. The Neotropical region comprises more than 120 valid species divided in about 20 genera, although the estimated diversity is much greater. However, no catalog of the Neotropical Acroceridae exists and most genera still need to be revised. Furthermore, comprehensive studies which provide accurate identification keys and detailed descriptions and illustrations of most Neotropical groups are still lacking. To improve this situation, several studies both taxonomic and phylogenetic, concerning the Neotropical species have been conducted. At present, I am working on the revision and phylogeny of *Philopota* (Philopotinae), one of the most specious genera in the Neotropics. So far, after a year of research, several new species have been found and a number of synonymies have been discovered. Future revisions of other Neotropical groups are planned and efforts will be concentrated on the taxonomy and phylogeny of the Neotropical Acroceridae in order to understand the classification of the family and the delimitation of genera and species.

KEY WORDS: evolution, Philopotinae, phylogeny, systematics, taxonomy

Revision of *Philopota* Wiedemann, 1830 (Acroceridae)

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Acroceridae is a small group of flies comprising approximately 520 described species in 51 genera and three subfamilies (Panopinae, Acrocerinae and Philopotinae). Within Philopotinae, *Philopota* Wiedemann is the most diverse genus, consisting of 16 species. The genus is exclusively Neotropical and its distribution ranges from Mexico to south Argentina and Chile. *Philopota* species have a conspicuous morphology, being characterized by a strongly humpbacked appearance, also found in other Philopotinae genera, and a long proboscis used for nectar feeding. This study represents the first taxonomic revision of the genus; its most recently described species is *P. flavolateralis* Brunetti, 1926. The following species were revised: *P. conica* Wiedemann, *P. dolorosa* Williston, *P. flavolateralis* Brunetti, *P. histrio* Erichson, *P. limosa* Walker, *P. liturata* Westwood, *P. lugubris* Williston, *P. maculicollis* Westwood, *P. nitida* Westwood, *P. ovata* Westwood, *P. semicincta* Schiner, *P. sobria* Walker, *P. temperata* Walker, P. *truquii* Bellardi, *P. tuberculata* Westwoodand *P. turbinata* Erichson. The following are provided: a key for identification of the species, a catalog, descriptions and redescriptions of species, illustrations of general morphology, illustrations of male and female terminalia, and maps of species distributions. Five new species are described and three new synonymies are proposed: *Philopota liturata* Westwood, 1848 = *Philopota ovata* Westwood, 1848; *Philopota conica* Wiedemann, 1830 = *Philopota nitida* Westwood, 1848; *Philopota histrio* Erichson, 1840 = *Philopota sobria* Walker, 1852. Furthermore, the female of *P. turbinata* is described for the first time.

KEY WORDS: evolution, phylogeny, Neotropical, systematics, taxonomy

Maggots and mayhem

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In its broadest sense, forensic entomology involves any application of entomology to legal situations. There are three basic subdivisions commonly recognized within the subdiscipline: Stored Product, Structural and Medicolegal. Of these, the most frequently considered “forensic entomology” by the general public and, in reality, most entomologists is Medicolegal Entomology. In this area, the most common applicatioin is to the estimation of a minimum period of insect activity on a dead body as an indicator of the minimum period of time since death or postmortem interval. Additionally, insects may provide valuable information concerning the movement of a body following death, aid in assessment of wounds, provide valuable data on the crime scene at the time of the death, serve as alternate specimens for toxicological analyses, serve as alternate sources of human DNA, and provide insights in cases of abuse or neglect of children and the elderly. During this presentation, these applications will be illustrated using actual cases from Hawaii and other parts of the world and recent advances in techniques will be discussed.

KEY WORDS: decomposition, stages, insects, postmortem changes/artifacts

Patterns of human decomposition

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Decomposition of an exposed cadaver is a continuous process, beginning at the moment of death and ending, for practical purposes, when the body has been reduced to a dried skeleton. Traditional estimations of a period of time since death, or postmortem interval, have been based on a series of grossly observable changes to the body, including livor mortis, algor mortis and rigor mortis. More recently, insects, mites and other arthropods have been increasingly used by law enforcement to provide an estimate of the postmortem interval. Although the process is continuous, it is useful to divide this into a series of five stages: Fresh, Bloated, Decay, Postdecay and Skeletal. In this presentation, these stages will be characterized by physical parameters and arthropod assemblages to provide a framework for consideration of the decomposition process and the roles of the Diptera species involved. The stages will be illustrated using examples from studies conducted at the Anthropological Research Facility of the University of Tennessee at Knoxville, more commonly termed the "Body Farm."

KEY WORDS: decomposition, stages, insects, postmortem changes/artifacts

Bacteria associated with synanthropic flies in an urban area of Medellín, Antioquia, Colombia

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Flies are often found closely coexisting with humans (synanthropy), where they are mechanical vectors of pathogens such as bacteria, mainly enterobacteria, resulting in their being regarded as pests. Microbes involved in diarrhoeic diseases can be located on the flies' cuticle, and disseminated through the fecal-oral route to humans. In this study bacteria from synanthropic flies were isolated, quantified and identified from the urban area of Medellin, Antioquia, Colombia. Flies were collected in area restaurants, residential complexes, a marketplace, and a slaughterhouse. The flies were identified to the highest level possible. Quantification of bacteria was carried out on plate count agar using 0.01 and 0.001 dilutions. MacConkey Agar was used to isolate the bacteria. Identification was carried out using an API E20 kit. A check-list of fly-bacteria associations is presented. We found >100.000 CFU (colony-forming units) on 41% of the specimens at 0.001 dilution. Escherichia coli was the most common bacterium found. The muscid, Ophyra aenescens (Wiedemann, 1830), is reported for the first time in Colombia, associated with Pastereurella pneumotropica. This is the first study of the interaction between flies and bacteria in Colombia.

KEY WORDS: interaction, synanthropy, colony-forming unit, check-list

Diptera from the Atlantic Forest, Brazil: bioindicators for environmental recovery and preservation

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Environmental degradation as a result of human activities can be monitored using biological indicators. Thus, dipterans of the subfamily Mesembrinellinae (Calliphoridae), which are essentially only associated with natural environments, are shown to be important tools for this purpose. This study surveyed these flies as potential bioindicators in an area of Atlantic forest designated for environmental compensation by a private company. The studies were conducted in an area of 847,21 acres in Southeastern Brazil (24º11’S, 48º 25’O) with four distinct vegetational types: forest in the middle stage of retrieval (FMSR); naturally regenerating degraded forest (DF); reforestation with full deployment (RFD) of native plants; and pasture (PT). The flies were collected using Shuey traps exposed for 24 h in each environment, for eight months per year, from April/2006 to April/2009. A total of 1,949 specimens of the family Calliphoridae were collected, with 97.6% belonging to Mesembrinellinae. *Mesembrinella bellardiana* (Séguy, 1925) (n=1,529; 78.4%) and *M. peregrina* (Aldrich, 1922) (n=374; 19.2%) were the most abundant species collected. Mesembrinellinae were most abundant in the FMSR area (65.7%), followed by DF (21.2%), RFD (7.5%) and PT (5.6%), indicating that the studied environment is in a favorable conservation status. The decrease in abundance of *M. bellardiana* from FMSR to PT shows that the recovery process in FMRS areas has been effective and, though still low, also in RFD compared to PT, without any compensative intervention. The presence and relative abundance of *M. bellardiana* in a given area is therefore useful for monitoring environmental changes and for quantifying the level of forest degradation.

KEY WORDS: ecology, tropical forest, South America, *Mesembrinella*

The history of Dipterology in Colombia – the early contributors

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Germ theory and parasitology became paradigms of medicine in the late nineteenth and early twentieth centuries in tropical America. Consequently, an understanding of "alternation of generations" and the "life cycle" concept of 19th century zoology provided new understanding of variation in morphology, habitat, and the relationships of bacteria and parasites with their hosts. This understanding advanced the study of tropical medicine, including tropical diseases and their vectors, which led to publications about insects. In Colombia, naturalists and doctors began to tackle the study of flies, due to their importance in public health and agriculture. One of the earliest publications was in 1881 by Doctor Andres Posada Arango, who described the myiasis produced by "hominivorax flies" in patients with "ozena" (disease characterized by decay of the internal membranes of the nose). The "putrid-smell" in patients led Doctor Arango to examine the possibility of a fly as a cause of this illness. Soon after in 1888, Doctor José Vicente de la Roche observed an endoparasite of the silkworm, which he said was of the family "tachinids." Other important contributors were: J. B. Londoño, Montoya y Florez & Londoño and Santiago Renjifo-Salcedo, all from the end of 19th to the beginning of 20th centuries. New questions of medical interest and concerns about wildlife and conservation arose in the mid 20th century. In 1957, Barreto-Reyes criticized the emphasis on species of medical interest, and the lack of attention on other species. In the 21th century, new interest is arising in insects, stimulated by advances in understanding insect biodiversity. Today, insects receive attention in their own right, rather than as a consequence of their medical importance.

KEY WORDS: Biodiversity, Diptera, history, taxonomy

Neotropical Fanniidae: new species of *Euryomma* and *Fannia* from Colombia

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Fanniidae are a widespread, basal monophyletic group in the Calyptratae, comprising around 400 described species. Currently four genera are recognized: *Fannia* Robineau-Desvoidy; *Piezura* Rondani; *Euryomma* Stein and *Australofannia* Pont, of which two are found in the neotropics: *Fannia* (74 species) and *Euryomma* (10 species). The family is virtually unknown in Colombia partly because detailed taxonomic studies of this family are lacking and only *Fannia* is known in Colombia. We examined five national entomological collections to better understand the distribution and diversity of the Fanniidae in Colombia (and the neotropics). Here we describe three new species of *Euryomma* from Medellín and Copacabana (Antioquia) that are similar to *E. carioca* Albuquerque from Brazil, *E. longicorne* Stein and *E. rufifrons* Stein from Chile. These species are synanthropic and associated with decaying organic matter. Also, we describe 13 new species of *Fannia*, mostly from well-preserved highlands. Species groups included in the *Fannia* were Palearctic and Nearctic (*hirticeps* and *benjamini* groups), Central American (*grandis* group) and southern South American (*anthracina* group). *Fannia grandis* Malloch and *F. pusio* (Wiedemann) are new records for Colombia. Here we include full species descriptions with an identification key for males along with photographs and drawings of male and female terminalia. Distribution maps and observations of their biology are also provided.

KEY WORDS: biodiversity, Colombian Andes, Neotropical Region, new species, taxonomy

Chironomidae and Mycetophilidae from Dominican amber as palaeoecological indicators

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The exploitable fossil-bearing Dominican amber deposits on the Caribbean island of Hispaniola are of Early Miocene to Middle Miocene age (15-20 Ma). Dominican amber is the world's best source for terrestrial invertebrate fossils derived from a tropical forest. Faunistic analyses of key taxa constitute a productive approach for a palaeoecological reconstruction of the ancient Dominican amber-producing forest and reveal potential alterations induced by environmental change. Climate in particular has undergone significant changes in the region, with alternating cool and dry periods. The effects of these climatic changes on the tropical rainforest-ecosystems in the Caribbean are still unclear.

Studies on aquatic Chironomidae in Dominican amber show strong similarities between the fossilized and extant faunas of the Greater Antilles. These studies provide a detailed outline of the ecology of the small mountain streams in the ancient amber forest and establish the stability of this ecosystem from the Middle Miocene until today. In view of these results, it is interesting to examine terrestrial groups, to establish whether terrestrial faunas will exhibit a similar trend. Mycetophilid larvae that live in forest litter constitute particularly suitable models for demonstrating the possible impact of climate change in the Caribbean because cooler and drier conditions should have altered the ecological characteristics of the forest, and thus the composition and availability of organic debris. Drier climate in particular should have had a negative impact on the moisture-dependent mycetophilid fauna. Ongoing studies on fossil and extent Mycetophilidae will help to gain a clearer picture about ecosystem change or stability in the Caribbean since Miocene times.

KEY WORDS: Dominican amber, Chironomidae, Mycetophilidae, palaeoecology, climate change

Identification of larvae of forensically important European Calliphoridae and Muscidae

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Calliphoridae and Muscidae are dipteran families with a worldwide distribution. The presence of these flies on decomposed bodies, both as larvae and adults, has been recorded in hundreds of human legal cases and carrion experiments. The morphology of immature stages of the forensically important blow flies and houseflies of Europe is unequally studied. The quality of published data varies from extensive to superficial. Especially poorly documented is the morphology of the early instars whereas the quality of data concerning mature third instars is reasonably good. However, in some species the immature stages are not described at all. Sometimes even detailed descriptions do not provide the necessary information to enable precise identification according to morphological characters. During an ongoing project the authors plan to revise morphological data concerning the immature stages of all European species of Calliphoridae and Muscidae of forensic importance. To enable a thorough revision a standardized protocol will be used to document larval morphology. Larvae will be treated according to simple methods which can be recommended for use by forensic entomologists even in poorly equipped laboratories. The protocol of morphological analysis will include light and SEM microscope analysis of details of the pseudocephalon, thoracic and abdominal segments and the anal division. Our objective is to prepare keys which can be easily used with standard light microscopy, while SEM will be used as a tool for searching for new characters. Information accumulated in the outlined manner should help in evaluation of previously used characters as well as finding new ones useful for taxonomic purposes. The final step will be to construct well illustrated keys for easy identification of larvae of all forensically important blowflies and houseflies of Europe and make them available online.

KEY WORDS: Muscidae, larva, morphology, forensic entomology, SEM

Contents

Revision of the larval morphology of *Fannia canicularis* (Calyptrata: Fanniidae)

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Fanniidae are a small dipteran family with worldwide distribution. Previously classified as a group within Muscidae family, it is currently treated as a family with well proved status. Among family autapomorphies are also characters of larval morphology. Larvae of Fanniidae are dorsoventrally flattened, usually with branched processes and posterior spiracles on raised stalks. Larvae of the cosmopolitan *Fannia canicularis* (Linnaeaus, 1761) are associated with various types of decomposing organic matter. Among Fanniidae this species is most often involved in myiasis cases, also the forensic importance of this species has been shown.

Larval stages and especially third instar of *F. canicularis* were described by various authors. However available information often varies in accuracy of descriptions. Also some differences were found in these descriptions. The aim of this presentation is to illustrate the morphology of larvae of *F. canicularis* studied recently with use of a combination of light and scanning electron microscopy. Obtained results are compared with existing knowledge on larval morphology of Diptera. Thanks to the information obtained from this study, the earlier descriptions of larval stages of *F. canicularis* are extensively revised.

The following structures are documented for all instars: antenna complex, maxillary palpus, facial mask, cephaloskeleton, ventral organ, anterior spiracles, Keilin's organ, posterior spiracles, pattern of processes and anal pad. Pair of lateral prominences on prothoracic segment, anterior spiracles in first instar, papilla on posterior spiracle stalk, additional ventrolaterals on second thoracic segment and oral teeth in second instar are reported for the first time in *F. canicularis*. For the first time in the Cyclorrhapha, trichoid sensilla are described on the dorsal surface of posterior spiracles in second and third instar larvae.

KEY WORDS: *Fannia canicularis*, larva, morphology, scanning electron microscopy

Sexual selection and viability selection on female ornaments in *Rhamphomyia longicauda* (Empididae)

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Female ornaments, although rare in most animals, are found in a number of empidine dance flies. In all-female mating swarms of *Rhamphomyia longicauda*, each female displays two elaborate sex-specific ornaments, inflated abdominal sacs and pinnate tibial scales. The abdominal sacs appear to increase the size of her abdomen as perceived by choosy males. Sexually selected ornaments are typically regarded as viability costs (going back to Darwin and R.A. Fisher) although recent studies of some avian male ornaments indicate that individuals with larger ornaments actually survive better. We measured sexual and viability selection pressures on the female ornaments of *R. longicauda*. We found significant stabilizing sexual selection (predicted by theory) but for only the tibial scale ornament. Viability selection was assessed using prey of *R. longicauda* taken from two spider species. We provide evidence that large females with large ornaments are better survivors of leg entanglement by a "cob" leaf-covering web. However, results for predation in a sticky orb web are less clear-cut with some evidence for viability selection against females with large abdomens.

A new species of *Djalmabatista* Fittkau from Mato Grosso, Brazil (Chironomidae: Tanypodinae)

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The genus *Djalmabatista* was described by Fittkau in 1968 for five species from the Amazon area in Brazil. Subsequently, three more species have been transferred to the genus, *Prothentes pulchra* Johannson, 1908, from North and South America, *Procladius* (*Calotanypus*) *bifida* Chaudhuri & Debnath, 1983, from India, and *Procladius* (*Psilotanypus*) *reidi* Freeman, 1955, from the Palaearctic, Afrotropical and Oriental Regions. The genus has also been recorded from Australia.

We describe here a new species of *Djalmabatista* from Mato Grosso in Brazil resembling *D. ivanyae* Fittkau, 1968, but distinguished from that species by possession of a comb on the inner margin of the gonocoxite. It can also be readily separated from *D. ivanyae* by the color markings of the abdomen, which is pale in *D. ivanyae* but banded in the new species.

KEY WORDS: Chironomidae, Orthocladiinae, *Lopescladius*, *Cordiella*, new species, Brazil

Three new species of *Lopescladius* (*Cordiella*) Coffman et Roback (Chironomidae) from Brazil

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Lopescladius was described by Oliveira in 1967 based on *L. minutissimus* Oliveira, 1967, from the Amazon in Brazil. The genus is easily recognized by its small size, by the small, protruding, pubescent to hairy eyes, and by the cordiform fourth tarsomere. Two subgenera are recognized; *Lopescladius* s. str. with 4 species distributed in North and South America and *Cordiella* Coffman & Roback based on *L.* (*C.*) *hyporheicus* Coffman & Roback, 1984, from western Pennsylvania, U.S.A. Males of the two subgenera can be separated as follows: *Lopescladius* s. str. has the gonostylus with a long posterior elongation and the inferior volsella is small and spiniform or absent, while in *Cordelia* the gonostylus lacks a posterior elongation and the inferior volsella is broadly digitiform. The immature stages of *Lopescladius* are probably all psammophilic, living in sandy bedded streams and rivers. Here we describe and figure the males of three new species of the subgenus *Cordiella*, all from Brazil. *Lopescladius* (*Cordiella*) sp. A from Santa Catarina State has a wing length of about 1.20 mm, antennal ratio of 0.51 and is dark brown. *Lopescladius* (*Cordiella*) sp. B from Pará State has a wing length of about 0.78 mm, antennal ratio of 0.49 and is pale. *Lopescladius* (*Cordiella*) sp. C from São Paulo State has a wing length of 0.71 mm, antennal ratio of 0.30 and is pale brown. *Lopescladius* (*Cordiella*) sp. A was collected in a Malaise trap close to a small stream at an elevation of about 1.800 m in a fragmented primary cloud forest belonging to the Mata Atlântica forest. *Lopescladius* (*Cordiella*) sp. B was collected in light traps close to high order streams in two localities in the Amazon forest. *Lopescladius* (*Cordiella*) sp. C was collected in a light trap close to a third order stream in a fragment of Mata Atlântica forest.

KEY WORDS: Chironomidae, Orthocladiinae, *Lopescladius*, *Cordiella*, new species, Brazil

Contents

DNA barcording as a routine step toward taxonomic investigation of Korean Tephritoidea

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The superfamily Tephritoidea is a large group of acalyptrate flies including over 7,300 described species arranged in nine families. All the tephritoid families excluding Richardiidae are represented in Korea, but their taxonomy has not been well studied. For example, a total of 80 species of the family Tephritidae are currently known in Korea, but our personal data shows that there actually are at least 150 species. Presence of highly variable or cryptic species has been hampering taxonomic progress involving this group of flies. Some genera such as *Trypeta, Campiglossa, Oxyna,* and *Tephritis* are good examples of taxonomically difficult taxa. We find that DNA barcoding is extremely helpful to clarify such taxonomic problems. We are currently trying to barcode multiple samples for every single Korean tephritoid species. A total of 271 specimens representing 185 species have been barcoded so far. Neighbor-joining analysis of our preliminary data shows many interesting findings that are potentially useful to resolve long standing taxonomic problems. The followings are some of our findings through the DNA barcoding analyses: 1) multiple samples for each included species were almost always clustered together showing utility for specific identification; 2) multiple species per each genus were mostly clustered together; 3) males of two similar new *Acidiella* species were associated with their respective females; 4) strong evidence was obtained to support the synonymy of *Sinacidia* and *Chetostoma*; 5) the possible existence of two cryptic species within *Campiglossa defasciata* was demonstrated; 6) the two genera Dioxyna and Campiglossa were shown to be possibly synonymous; 7) possible synonymy of Herina zojae and H. hennigi was also demonstrated; and 8) two closely similar species of Chaetostomella were resolved.

KEY WORDS: Tephritoidea, Tephritidae, DNA barcode, Korea, taxonomy

Phylogeny and classification of the Tephrellini (Diptera: Tephritidae: Tephritinae)

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The phylogeny of the tribe Tephrellini was reconstructed from mitochondrial 16S ribosomal RNA gene sequences using 43 specimens representing 39 species of the Tephrellini. We analyzed these together with an additional 58 species representing the other tribes of the subfamily Tephritinae, in order to test the monophyly and sister group relationship of the Tephrellini. We used *Plioreocepta, Taomyia* and an undescribed new genus as outgroups. The number of aligned sites was 1572 bps but 1106 bps were used for analyses after excluding sites of ambiguous alignment identified using the Gblocks analysis. Our preliminary results using Bayesian and Neighbor Joining methods suggest the monophyly of the entire Tephrellini (strongly supported except for *Ghentia millepunctata*), biologically characterized by the association with Acanthaceae, Lamiaceae and Verbenaceae (whereas the remaining Tephritinae are all associated with Asteraceae), the monophyly of a clade associated with Lamiaceae and Verbenaceae, and the monophyly of a subclade associated with Verbenaceae. To hone the above results, we are planning to (1) sequence at least 20 additional species of Tephrellini and (2) to add sequences of the 12S rRNA and COI genes (approximately 1500 bps).

KEY WORDS: Tephritidae, Tephritinae, Tephrellini, phylogeny, classification, host plants, 16S gene

Contents

The impact of a mermithid parasite (Nematoda: Mermithidae) on *Neoplasta parahebes*

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During the course of a two-year phenological study (1996-1998) of aquatic dance flies in the subfamily Hemerodromiinae along a mountain stream in Southern California, 20.6% of the *Neoplasta parahebes* population was observed to be patently infected with a nematode parasite (Nematoda: Mermithidae). The parasite filled the abdominal cavity of 21.9% of the male and 20.6% of the female hosts. No evidence of an intersex condition was observed. Subsequent studies involving hundreds of larvae of *Neoplasta* in the area have not produced a single example of nematode infection, demonstrating the parasite to be largely imagicidal. During the initial survey, 13% of adult *N. scapularis* were observed infected with a similar parasite and infections were also seen in *N. hebes*, *Chelifera lovetti* and *Metachela albipes*. A similar parasite also infects *N. paramegorchis* and *M. collusor* in Utah. The morphology of the parasite is consistent with the genus *Strelkovimermis* (Nematoda: Mermithidae) and a bootstrap comparison of an 18S ribosomal DNA sequence places this parasite as a sister group of *S. spiculatus*. Because the parasite develops during the adult stage of the host, early developmental stages of the parasite may be missed by casual observation. Current studies of adult infection rate by dissection of the host suggest that the actual infection rate of *N. parahebes* may be significantly greater than initially observed. Examination of many adult specimens in the genus *Wiedemannia* and *Clinocera* (Empididae; Clinocerinae) from the survey site show no evidence of mermithid infection, suggesting the parasite may be limited to the Hemerodromiinae.

KEY WORDS: Mermithidae, *Strelkovimermis*, *Neoplasta*, Hemerodromiinae, California

Contents

What does *Charadrella* Wulp (Muscidae) tell us about the history of the Neotropical region?

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Charadrella is a small genus of Neotropical Muscidae whose larvae breed in snails. This larval habit is common to other Neotropical (*Cariocamyia*) and Paleotropical (*Alluaudinella* and *Ochromusca*) genera, which are often considered to be closely related despite their disjunct distributions. *Charadrella* comprises three described species: *C. albuquerquei* Carvalho, 1985, *C. macrosoma* Wulp, 1896, and *C. malacophaga* Lopes, 1938. We revise these and describe two additional species from Bolivia and Brazil. A phylogenetic hypothesis for the genus was inferred from morphological characters: (*C. albuquerquei*, (*C. macrosoma* (*C. malacophaga*, (*Charadrella* sp. nov. 1, *Charadrella* sp. nov. 2)))). Additionally, we investigate the relationship of *Charadrella* with closely related genera. The cladistic analysis included 23 species from nine Neotropical and three Paleotropical genera and two outgroups and resulted in two trees. Monophyly of *Charadrella* was supported by six homoplasious and four non-homoplasious characters, as follows: fifth sternite with wedge-shaped projections; surstylus compact, not flattened; surstylus twice as long as cercal plate; gonopods united at base. The strict consensus clade with *Charadrella* was (*Dichaetomyia*, *Alluaudinella, Ochromusca*, (*Itatingamyia*, (*Cariocamyia*, *Charadrella*))), supporting placement of these genera in the Dichaetomyiinae. Implied and successive weighting were also used to find trees. Results varied, but the relationships among the species of *Charadrella* and *Cariocamyia* were the same in all analyses. Intrageneric relationships among species of *Charadrella* are due to vicariance. Intergeneric relationships support a Gondwanan distributional pattern, however dating the clade would be necessary for further conclusions.

KEY WORDS: biogeography, new species, phylogeny, taxonomy

Contents

Aiming towards more resolution - challenges for a phylogeny of Stratiomyidae

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The classification of the subfamily groups of Stratiomyidae has been relatively stable and so far 12 subfamilies are generally accepted: Parhadrestiinae, Chiromyzinae, Beridinae, Antissinae, Pachygasterinae, Clitellariinae, Chrysochlorininae, Hermetiinae, Sarginae, Raphiocerinae, Stratiomyinae, and Nemotelinae. Monophyly of three of these subfamilies (Parhadrestiinae, Chiromyzinae, Beridinae) has never been disputed, while other groups, for example Clitellariinae, have been characterized mainly by plesiomorphic characters and have always been suspected of being paraphyletic. In particular the relationships among certain subfamilies are often unresolved. The only hypothesized molecular phylogeny so far supported several subfamilies (Beridinae, Antissinae) but resulted in a paraphyletic Clitellariinae. To achieve a more resolved phylogeny more taxa as well as additional genes need to be included. The taxonomic gaps and problematic taxa will be discussed, as well as the utility of new genes. Special emphasis has been placed on the inclusion of undescribed fossil taxa and critical re-evaluation of the described fossils.

KEY WORDS: Stratiomyidae, phylogeny

The stratiomyid fauna of Madagascar – is the island richer than the continent?

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The stratiomyid diversities of Madagascar and mainland Africa are compared on a subfamily, genus and species level and possible reasons for the different distribution of taxa are discussed. The taxonomic history of the Afrotropical region is presented, emphasizing the work of Lindner, who described a major part of the fauna. The biogeograhic relationships between the Malagasy fauna and that of the Oriental and Afrotropical regions are discussed. An estimation of the biodiversity loss due to human activities and habitat reduction is made. The specific problems and challenges for the chapter of Afrotropical Stratiomyidae are the large number of undescribed species from Madagascar and the inadequate generic concepts, especially in the subfamilies Pachygasterinae and Sarginae. The subfamily Sarginae is distributed worldwide, but most generic concepts were developed in regional treatises and therefore a worldwide generic revision is necessary to place the African species in their correct genera. Recent collecting efforts in Madagascar have provided much new material for study, amounting to several thousand specimens, compared to the fewer then 200 specimens from which the known Malagasy species were described

KEY WORDS: Stratiomyidae, Afrotropical Region, Madagascar

Review of the net-winged midges (Blephariceridae) of Puerto Rico

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Net-winged midges (Diptera: Blephariceridae) are an unusual lineage of flies whose immature stages show many adaptations to life in torrential streams. The Caribbean blephariceride fauna currently comprises three described species, *Paltostoma palominoi* Hogue & Garces, found in the Sierra Maestra of eastern Cuba, *P. agyrocincta* Curran, widespread in Puerto Rico, and *P. schineri* Williston, which occupies most major islands of the Lesser Antilles. In no previous reports have more than one species been recorded from any single island. Although we are far from knowing the Caribbean fauna with completeness, we have much new material from Puerto Rico, including all life stages of a second (new) species and larvae of what appears to be a third species. Furthermore, these new records come from streams that also contain *P. argyrocincta*, confirming sympatric distributions at several sites. Unfortunately, existing Puerto Rican blephariceride records are limited to few watersheds, most on the northwestern and northeastern side of the island. Many other potentially suitable streams, especially south of the Cordillera Central, remain unsurveyed. Even less collecting has been done on other islands in the Greater Antilles. Our discoveries on Puerto Rico, the smallest of these islands, suggest that future collections in the Greater Antilles should result in the discovery of additional species.

KEY WORDS: Blephariceridae, net-winged midges, Puerto Rico, Caribbean, *Paltostoma*, biodiversity

Contents

Current and future research on the systematics of Neotropical black flies (Diptera: Simuliidae)

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The family Simuliidae (Diptera) contains approximately2072 species world-wide of which nearly 370 are found in the Neotropical Region (Crosskey & Howard, 2004; Adler & Crosskey, 2009). Many species of black flies are considered to be biting pests whilst others are instrumental in the transmission of blood parasites in both humans and other warm blooded animals. They can be also used as potential economic indicators of environmental change, and as a method to monitor freshwater contamination because the immature stages are highly susceptible to both organic and inorganic pollution.

In the last few years the Neotropical Simuliidae has become a research hotspot with a flare of revisions and descriptions of new species. The latter has been compiled in the book "Neotropical Simuliidae (Diptera: Insecta)" by Coscarón & Coscarón-Arias (2007) in the ABLA series at Pensoft. This have been updated in the recent published book in the same series by Shelley et al. (2010) "The Black flies (Diptera: Simuliidae) of Brazil". In this publication the authors have placed the Brazilian simuliid fauna in context with the most up-to-date research in the classification of Simuliidae.

In this talk I will discuss the latest developments on the biosystematics of Neotropical Simuliidae and some of the initiatives/efforts that should take place to probe deeper in the systematics and taxonomy of this family in the Neotropical Region. The use of DNA Barcoding as identification tool on Simuliidae will also be discussed, especially the preliminary results on the use of museum specimens.

KEY WORDS: Simuliidae, systematics, Neotropical Region, black flies

Biodiversity of Costa Rican black flies (Diptera, Simuliidae)

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The family Simuliidae (Diptera) contains about 2072 species worldwide of which nearly 370 are found in the Neotropical Region (Crosskey & Howard, 2004; Adler & Crosskey, 2009). Numerous species of black flies are important as biting pests and several others are involved in the transmission of parasites of the blood and skin in both man and warm-blooded animals. They are also of potential economic importance in terms of indicators for environmental monitoring of freshwater contamination, because their immature stages are highly susceptible to both organic and inorganic pollution.

Early studies on Costa Rican Simuliidae were carried out by M.Vargas and B.V.Travis mainly in the San José Valley during 1968-1970. Due to the increasing development of hydroelectrical projects in Costa Rica and the known damaging impact that this development has on the biodiversity of freshwater organisms together with the proximity of Costa Rica to foci of river blindness (onchocerciasis), we undertook a countrywide survey of Simuliidae in the country. The watercourses flowing from the central mountain range into the Caribbean and Pacific coasts were sampled for Simuliidae and collections housed at the Costa Rican Instituto Nacional de Biodiversidad (INBio), Museum of Zoology of the University of Costa Rica (MZUCR), and the Royal Ontario Museum (ROM) were examined.

In total we have sampled 232 rivers and streams throughout all vegetation zones and different altitudes in Costa Rica. Three genera and 23 species were shown to be present, and seven of these are known to bite humans: *S. callidum*, *S. gonzalezi*, *S. haematopotum*, *S. inaequale*, S. *metallicum s.l.*, *S. ochraceum s.l.*, and *S. quadrivittatum*. The record of *S. panamense* as biting humans in the area of Turrialba is doubtful. The distribution of black flies in relation to geology, precipitation and vegetation, and notes on their basic biology and medical importance is also discussed.

KEY WORDS: biodiversity, Simuliidae, black flies, Costa Rica

Contents

Survey and management of stable flies at the National Zoological Park

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The National Zoological Park is a highly visible facility located in the city of Washington, DC, bounded by densely populated urban areas. For a number of years the zoo has had problems with stable flies, *Stomoxys calcitrans* L., feeding, particularly, on the canids, ungulates, and the great cats. A similar situation has existed at the Smithsonian Conservation Biology Institute (SCBI) located in rural Front Royal, Virginia. In the spring of 2009, a series of alsynite sticky traps and pesticide-treated blue-black cloth targets were placed adjacent to each other in selected locations at the zoo and at the SCBI for monitoring and implementing a management strategy, respectively. Stable flies were present at both locations on May 4, the first collection date. Flies peaked at the zoo on June 8, followed by a similar peak at the SCBI 2 weeks later. Fly populations continued to cycle throughout the remainder of the study but with steadily decreasing peaks. The largest fly populations at the zoo were found at the Kids Farm, followed by the Cheetah-zebra-antelope holding compound. The lowest numbers were at the Przewalski's horses, possibly because traps were placed too high. Traps and targets placed near the great cats proved ineffective because optimal placement was impossible with the cats running free in their open compounds. The study was terminated on November 5. Presently it is difficult to assess the effects of the blue-black targets, because targets placed next to traps increase the numbers of flies captured on the traps. Most flies die within 2 minutes of landing on the targets, but this gives them ample time to get captured on the traps before dying. Feedback from various zoo keepers was positive and a second year of study is underway.

KEY WORDS: Stomoxys calcitrans, alsynite sticky traps, blue-black cloth targets

An overview of Afrotropical endemism in Therevidae

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The Afrotropical stiletto fly fauna includes three of the four recognized subfamilies: Xestomyzinae, Phycinae, and Therevinae. The Xestomyzinae are restricted to the southern part of the African continent and are represented by nine genera and 40 species. The only other xestomyzine is the New World genus *Henicomyia*, the sister taxon to *Arctogephyra*, known from Baltic amber, and the Afrotropical Xestomyzinae. Phycinae is represented by species on all continents except Australia and has its greatest diversity in Africa, with 6 genera and 57 species. Therevinae is distributed worldwide and represented in the Afrotropical Region by nine genera and 66 species, with four Afrotropical endemics and one genus, *Stenopomyia* Lyneborg, endemic to Madagascar. Afrotropical Therevinae has a low diversity with respect to Therevinae in other biogeographic regions that is, however, similar to that of Afrotropical Phycinae and Xestomyzinae. Endemism has been discussed in the context of Gondwanan vicariance but phylogenetic relationships suggest post-Gondwanan dispersal to the Afrotropical Region by ancient stiletto fly lineages.

KEY WORDS: Therevidae, Afrotropical Region

Importance of visual and olfactory cues for foraging in the parasitoid *Exorista japonica*

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Exorista japonica females respond to odours emanating from maize leaves infested with larvae of the common armyworm. We examined the effects of visual stimuli as well as olfactory stimuli for attracting females to host-infested plants. Paper plant models of four colours (blue, green, red or yellow) were separately placed in front of a host-infested plant hidden behind a mesh screen in a wind tunnel. Females landed at significantly higher rates on the green coloured model than on the other coloured models. However, few females landed even on the green coloured model when an infested maize plant was not placed behind the screen. When achromatic plant models of four different grey scales (white, light grey, dark grey or black) were examined in the wind tunnel with an infested plant as described above, the response rate of females was significantly higher toward the white model and decreased as the brightness of the model decreased.

When the four colour models were placed together in a cage filled with odours of host-infested plants, females stayed significantly longer on the green model than on the other three coloured models. These results indicated that *E. japonica* females prefer a green colour when odours of the host-infested plants are present and suggest that flies use visual as well as olfactory cues to locate the host habitat.

KEY WORDS: Herbivore-induced plant volatiles,
insect–plant interaction, \color preference, Tachinidae

Revision of the Neotropical genus *Erythromelana* (Diptera: Tachinidae)

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The Neotropics probably harbor the greatest diversity of tachinids of any biogeographic realm, yet it remains one of the most poorly known faunas. The Exoristine tribe Blondeliini is particularly species rich in this region and is in desperate need of taxonomic attention. Here, I present preliminary results of a revision of the Neotropical genus *Erythromelana* Townsend including the redescription of *E. jaena* Townsend, *E. nigrothorax* (Wulp) and the description of seven new species. In addition, *Myiodoriops marginalis* Townsend and *Hypostena obumbrata* Wulp, which were previously assigned to this genus, are resurrected as distinct genera. Members of this genus are distributed over much of northern South America and Central America, North to Mexico. A collection of 570 museum specimens and 29 specimens reared from Geometridae were used to construct a detailed morphological and morphometric database (n=220), including female (n=40) and male genitalia (n=70). The nine currently known species form two major species groups, which are separated by the presence/absence of a pair of long bristles on the 5th sternite of males. A principal component analysis of 72 characters separates the species of *Erythromelana* from the non-*Erythromelana* species, *M. marginalis* and *H. obumbrata*, and supports the two major species groups. In addition, the tri-trophic associations between *Erythromelana*, their geometrid hosts in the genus *Eois*, and the hosts food plants in the genus *Piper* are described and analyzed.

KEY WORDS: Tachinidae, Blondeliini, *Erytromelana*

Contents

Genetic differentiation of forest and prairie populations of *Eurosta solidaginis*

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Prairie populations of the gall-forming Teprhitid fly, *Eurosta solidaginis* significantly differ from populations in the forest biomes based on allozyme and morphological traits. The differences observed are distinct from the sympatric speciation observed in this species on its two host plant species, *Solidago altissima* and *S. gigantea*. Patterns of genetic variation within fly populations on a single host plant, *S. altissima*, suggest complex interactions between fly genotype, plant genotype and biome. Allozyme variation frequencies vary significantly between the prairie and forest fly populations, with an intermediate cluster in the border. Wing patterns form a cline between the forest and prairie boundary with intermediate forms along border regions. Gall morphology shows a sharp shift at the biome border with galls in the prairie being larger in diameter and more spherical than those in the forest. Not all of the differences can be explained by simple selective differences between the two biomes; exceptions to broad geographic patterns exist when closely examined at a finer scale. The genetic divergence between fly populations at the level of variation within a host plant species, provide insights into the complex mechanisms of speciation.

KEY WORDS: *Eurosta solidaginis*, gall, speciation; Tephritidae

The influence of some biotic and abiotic factors on abundance of aquatic dance flies

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The effect of water velocity and available amount of prey on the abundance of emergent aquatic dance flies was studied at different karstic microhabitat types. Study was performed at nine locations in the National Park Plitvice Lakes, which is situated in a karst region of Croatia. Six pyramid-type emergence traps were placed at each investigated site. Specimens were collected monthly from March 2007 till February 2009. In total 3597 specimens were identified belonging to 20 species; four of them are a new record for the Croatian fauna (*Chelifera pyrenaica* Vaillant, 1981, *Hemerodromia laudatoria* Collin, 1927, *Clinocera wesmaeli* (Macquart, 1835), *Wiedemannia* (*Philolutra*) *aquilex* (Loew, 1869)). Correlation index showed positive correlation between water velocity and abundance of aquatic dance flies; if the water velocity is higher, abundance of dance flies is higher as well. Positive correlation was also observed between amount of prey (Chironomidae and Simuliidae) and dance flies; with more prey the abundance of aquatic dance flies is greater. One-way ANOVA showed significant difference between silt and other type of microhabitats (moss, dead tufa parts with leaf litter and gravel); aquatic dance flies prefer other types much more then silt. In conclusion, aquatic dance flies prefer microhabitats with strong water velocity, high amount of prey and therefore microhabitat types such as moss, gravel and those with organic deposits.

KEY WORDS: aquatic Empididae, water velocity, microhabitat types, prey abundance, emergence traps

The fruit flies of Ontario

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Thirteen species of Tephritidae are newly recorded from Ontario, and alternative format keys are provided to the 31 genera and 72 species of fruit fly now known from, or likely to occur, in the province. Standard dichotomous keys to genera, and simplified field keys to genera and species are provided. Keys are illustrated with approximately 700 colour photographs, and species treatments are supplemented with multiple identification aids, including Ontario distribution maps for each species. To aid in identification of immature stages, we have included sequence data (DNA barcodes) for 41 of the 72 species examined. The project was produced with the intention of publishing in the web-based Canadian Journal of Arthropod Identification and features easy-to-navigate keys with high resolution photos, as well as links between the "paper", the Barcode of Life Data System, and GenBank for increased exposure and connectivity.

KEY WORDS: Tephritidae, CJAI, Ontario, identification keys

Taeniaptera; what is it and who belongs there? (Micropezidae)

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Often conspicuous in Neotropical lowland rainforests displaying on broad leaves, the Taeniapterinae are convincing mimics of ants and ichneumonid wasps. With inconsistent variation in external morphology, a poverty of male genitalic characters, and a lack of distributional or temporal hypotheses, some generic boundaries have been unclear. To understand some of the homoplasy found in the morphological characters, a total evidence tree was produced using 2 mtDNA genes (12S and COI) and 2 nuclear DNA genes (wingless and CAD), against which morphological characters were tested. It was found that the Taeniapterini is paraphyletic with the Grallipezini nested within it, and several genera were found to be paraphyletic, including the genus *Taeniaptera* (Macquart). Genus-level taxonomic changes will also be presented.

KEY WORDS: Micropezidae, *Taeniaptera*, systematics, taxonomy, phylogeny, DNA, morphology

Contents

Visualisation and volumisation of maggot masses using CT technology

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Forensic entomologists estimate post mortem intervals based on the size of the oldest maggots found on a body. Because the developmental time of a maggot is dependent upon the temperature to which the maggot has been exposed, entomologists will usually calculate the average ambient temperature. However, it is likely that the actual temperatures to which maggots are exposed are much greater than ambient if they are involved in massing. The heat produced by these masses correlates strongly with their size, however accurately measuring the size of a maggot mass can be challenging because they are often inside body cavities and thus can only be accessed during autopsy. This disturbs the mass and the maggots disperse.

CT scanning is increasingly finding a place in post mortem practice, and is therefore a promising tool for non-invasive assessment of maggot mass volumes. If maggot masses can be viewed and volumes measured using CT scans, masses will remain intact. The entomologist can therefore be sure that any measurements made are an accurate representation of the mass and not a result of disturbance.

We have shown that maggot masses can indeed be visualised and volumised using CT scans, both in experiments using cups of meat and in human bodies. This could prove an invaluable tool for forensic entomologists, enabling them to account for maggot mass heating much more precisely when estimating minimum post mortem intervals, and hence increase the accuracy of such estimates.

KEY WORDS: forensic entomology, maggot masses, CT, volumisation, temperature production

Mitochondrial genomics in Diptera: the Calliphoridae (Brachycera: Oestroidea) as a case study

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We present the complete mitochondrial DNA (mtDNA) of three species of Calliphoridae of medical, sanitary and forensic importance: *Chloroprocta idioidea, Calliphora vomitoria* and *Phormia regina*, which had 16147, 16143 and 16635 bp, respectively. Each genome was arranged in the same order described for Pancrustacea, with the exception of *P. regina*, which presented a duplication involving the tRNAIle, tRNAGln and a partial sequence of the tRNAMet in the control region. A similar duplication has been described for the blow flies of the gens *Chrysomya* (Diptera: Calliphoridae) and for the stable fly, *Stomoxys calcitrans* (Diptera: Muscidae). The average nucleotide composition was heavily biased toward As and Ts (>70%), mainly in third codon positions and non-coding regions (>90%). The phylogenetic reconstructions were conducted for all available dipteran species, using maximum parsimony, maximum likelihood and Bayesian inference. The use of single genes resulted in topologies with low support, whereas the use of amino-acid data sets with thirteen concatenated protein coding genes provided resolution for intraordinal relationships in Diptera. The monophyly of Muscomorpha was not supported, as well as the monophyly of Acalyptratae, which is a major clade of Schizophora. The Calliphoridae was a monophyletic family, but the superfamily Oestroidea was disrupted by the inclusion of Muscoidea species as a sister group of Calliphoridae. Within Calliphoridae, the subfamilies Luciliinae and Calliphorinae were clustered together, related to the subfamily Chrysomyinae. These results may guide future studies on the evolution of the myiasis habit within Calliphoridae and a revision of the taxonomy of Calliphoridae, including new characters associated with molecular data. The characterization of complete mtDNA sequences provides insights with regard to dipteran relationships and general molecular evolutionary studies of deep-level phylogenies of insects.

KEY WORDS: mtDNA, myiasis-causing flies, phylogeny, long-PCR

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New frontiers in mapping biodiversity specimen data

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Before the internet opened up data retrieval and dynamic presentation to more of the public, tools for georeferencing and mapping our biodiversity data were limited to a few choices: searching printed gazetteers and maps of varying quality, and creating static maps either by hand or a computer-based plotting program. At the first National Science Foundation Partnerships for Enhancing Expertise in Taxonomy meeting in 1996, the most sought after request was for better sources for georeferencing specimen data. In the latter half of the 1990s, researchers began to access through their desktop computers, an increasing number of mapping and georeferencing tools, including Microsoft Encarta Virtual Globe and often cumbersome Internet gazetteers emerging from various governmental organizations. Today, retrospective georeferencing is a finite (if still enormous) task as collectors either take hand-held GPS devices into the field with them or use online mapping programs to pinpoint their collecting locations before labeling their specimens. While retrospective georeferencing is still a challenge in the 21st century, an increasing number of online resources, some specializing in regional or historical place names, help hone in on these collecting localities. New tools can help speed up this process, but how useful are they?

The holy grail of mapping our biodiversity data is to form testable hypotheses derived from our data. Can our maps predict taxon distributions in time and space, backed up by taxon concepts derived from morphological and molecular data? Can we leverage others' data in GBIF, Google Maps/Earth, or Discover Life to provide a more complete picture of the biodiversity and its interrelationships on our planet through geography, time, and space? For this, we must agree to share our data with others through community-supported standards.

KEY WORDS: georeferencing; mapping; specimens

Dedication – the life and career of Brian Roy Stuckenberg (1930–2009)

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The Symposium ‘Advances in Afrotropical Dipterology’ is formerly dedicated to the memory of the late Brian Roy Stuckenberg, who passed away 8th February 2009. With his passing Africa has lost its leading dipterist and doyen of dipterology. Brian was born and raised in the Eastern Cape of South Africa, where he developed a keen interest in zoology from a young age. He studied at Rhodes University, Grahamstown, where he obtained an MSc degree in Entomology with distinction. He was appointed by the Natal Museum in 1953 and was awarded a PhD by the University of Natal in 1972. In 1976 he was appointed Director of the Natal Museum and upon his retirement actively took up the study of his “favourite group”, the Vermileonidae. Brian regarded the Diptera as the most significant insect order and developed an interest in the group from his early career. During his 20 years as Head of the Entomology Department Brian build the largest collection of African Diptera in the world, and actively encouraged its use by specialist researchers. His fieldwork and publications were extensive and over 100 taxa have been named in his honour. Brian’s interests were very broad and his knowledge of geology and biogeography extensive. To the very end of his life Brian was extensively versed in the contemporary literature and lost none of his insightfulness. Brian had a quiet and engaging personality, and was widely known and respected throughout the entomological community worldwide. The quality of his research was given international recognition by the awarding of an honorary membership of the International Congresses of Dipterology in 2002. Brian’s major research interests, discoveries and achievements are outlined and his contribution to the study of dipterology in general are put into a broader context.

KEY WORDS: achievements, Brian Stuckenberg, career, dedication, Diptera, Natal Museum

Official launch of *Manual of Afrotropical Diptera* project

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The *Manual of Afrotropical Diptera* project is the first major initiative on Afrotropical flies since the publication of Roger Crosskey's (1980) *Catalogue of the Diptera of the Afrotropical Region*, and is also the first such initiative for any insect order on the African continent. The project represents a collaboration between the National Museum and the Natal Museum and is, therefore, instigated and driven from within the Region itself. The Mission of the *Manual* project 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*. There are currently only a handful of practising dipterologists on the African continent, so if we are to meet the challenges ahead in the description of the vast array of undescribed Diptera species in the Afrotropical Region (upwards of 30,000 species), it is increasingly important that the international dipterological community focuses its interest on the Afrotropical Region. A first step in this direction is the production in progress of a high-quality, professional *Manual of Afrotropical Diptera*, which will provide information on the Afrotropical fauna at large and identification keys specifically. We have currently secured committed chapter contributions for all 109 systematic chapters and 11 of the 12 introductory chapters. This project is truly an international effort, with contributors from 22 countries (on six continents). We here present the official launch of the *Manual* project, outline progress thus far, illustrate and discuss the now activated website, the timescale for submissions and publication and other issues relevant to contributors and interested parties.

KEY WORDS: Diptera, Afrotropical Manual, official launch

Systematics and biogeography of Afrotropical Quasimodo flies (Curtonotidae)

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The family Curtonotidae is a well-supported monophyletic group in the Ephydroidea and is now known to comprise four extant genera, *Axinota* van der Wulp, *Curtonotum* Macquart, *Cyrtona* Séguy *sensu lato*, and the recently described *Tigrisomyia* Kirk-Spriggs, all of which occur in the Afrotropical Region; the last-named genus exclusively so. Previously under-studied and regarded as a small family, studies of amassed Afrotropical material has now revealed that the family has undergone extensive diversification in both the humid tropical and arid regions of sub-Saharan Africa, and over 50 new species, chiefly in the genera *Cyrtona sensu lato* and *Curtonotum*, have been identified. A molecular phylogenetic analysis of species in all four known genera from the Afrotropical, Nearctic, Neotropical and Palaearctic zoogeographical regions is presented and discussed. Progress with the ongoing revision of the Afrotropical fauna is outlined and examples are drawn from selected genera and species-groups to demonstrate biogeographical patterns. These patterns are related to vicariance and other historical biogeographical processes, specifically topography, past climatic changes and Miocene pan-African forest cover. The curtonotid fauna of Madagascar, with 1 endemic species of *Axinota* (of presumed Oriental origin) and 13 endemic species of *Curtonotum* (6 of which are undescribed), is a special case of interest, given the known minimum Miocene age of the Curtonotidae in the fossil record (20–15 Ma) and the Jurassic separation of Madagascar from Gondwaland, which precludes a Madagascan 'Gondwanan origin' for the family.

KEY WORDS: Curtonotidae, Quasimodo flies, systematics, historical biogeography, Pan-African forest

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Phylogeny of the Archiborborini (Sphaeroceridae) based on combined molecular and morphological data

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The tribe Archiborborini is a clade of approximately 100 Neotropical species of Sphaeroceridae, mostly undescribed. To determine the relationships of species within the tribe and clarify the generic classification, we conducted a phylogenetic analysis of all species based on 56 morphological characters. Based on the results of that analysis, we conducted a further analysis for a subset of 21 ingroup species, representing most of the clades identified in the morphological analysis, based on parts of 5 genes (12S, COI, CytB, AATS, and 28S). Support measures for trees based on individual genes, all genes combined, and morphological data were very low for most internal nodes. Although there is conflict in the data and some taxa remain difficult to place, a combined analysis of morphological and molecular data produces a well-resolved tree which is our best hypothesis for the relationships within the Archiborborini. Based on this tree which shows 3 main clades within the tribe, we revise the generic classification to treat these clades as genera.

KEY WORDS: Sphaeroceridae, Copromyzinae, Archiborborini, phylogeny, generic revision, morphology, DNA

Shine on your crazy diamonds! – Diversity of structural wing colours in Diptera

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A striking visual identification map and potential signalling system, to date overlooked by biologists, lies hidden in the transparent wings of small insects, which are extremely thin and display vivid colour patterns due to thin film interference (see also oral presentation). These hitherto unforeseen Wing Interference Patterns (WIPs) reflect uneven thickness of wing membranes ranging between 100 and 1500 nanometres and appear to be stable, non-iridescent and often taxon-specific down to species level. The sequence of colours produced by WIPs is uniform, very characteristic and identical to the Newton series reflected from a thin film of oil on water. The poster presents a visually stunning taxonomic sweep of this hidden playground for evolution, with examples of WIPs from nearly half of all Diptera families representing all major Diptera sections. The broad taxonomic sampling reveals a huge diversity of a new character universe that might prove to constitute a "morphological barcode" aiding in Diptera identification.

KEY WORDS: Structural wing colours, thin film interference,
taxonomy, barcode, Diptera diversity

Species recognition trade-off between structural wing colours and terminalia in fungus gnats

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Fungus gnat taxonomy is mainly focused on two character systems: wings and terminalia. Their usually elaborate external male terminalia is crucial for species identification in the majority of taxa, while their wings display venation patterns diagnostically important at generic level, sometimes with species-specific venation or pigmentation patterns. Viewed against a light-absorbing background and due to thin film interference fungus gnat wings further display vivid colour patterns. These hitherto unexplored Wing Interference Patterns (WIPs) reflect uneven thickness of the wing membrane and appear to be stable, non-iridescent and often taxon-specific down to species level (see other presentation). A major question is whether fungus gnats, given they are able to see WIPs, use them in visual wing communication for species recognition. Examples from the family Lygistorrhinidae consisting of tiny adults with large eyes reveal striking examples of species-specific WIPs while those from the tribe Exechiini (Mycetophilidae) largely reflect size dependant radial gradients. A wider taxonomic sweep of the different fungus gnat families and subgroups of the major family, Mycetophilidae, indicate a trade-off between species-specific terminalia and species-specific WIPs. Taxa with less species-specific terminalia (often more primitive groups) tend to have elaborate WIPs including pigmentations while taxa with enlarged, elaborate terminalia (often more advanced groups) tend to have less species-specific WIPs.

KEY WORDS: wing patterns, terminalia, taxonomy, evolution, Sciaroidea/Mycetophiliformia

Beyond evolution in black and white – structural colours in transparent Diptera wings

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Colour patterns play central roles in dipteran behaviour, ecology and systematics. Two currently active research fronts, one on the morphogenetic control of black and white wing patterns in *Drosophila*, the other on structural colours and the multiple functions of simple structures in nature, share a common hitherto unexplored potential. Simply by flipping the coin from white to black background a novel hypothesis for visual colour communication in Diptera emerge. Viewed against a light-absorbing background and due to thin film interference, most smaller transparent Diptera wings display vivid colour patterns. These Wing Interference Patterns (WIPs) reflect uneven thickness of the wing membrane and appear to be stable, non-iridescent and often taxon-specific down to species level. WIPs are dioptrically stabilized and reinforced by membrane corrugations, chaetotaxy, pigmentation and venation. The unique Newton series colour sequence, which excludes pure red, fits most insects' colour vision and strongly suggests the significance of WIPs for visual signalling. Some perspectives of these findings are: 1) Calibrated with the Newton colour sequence, WIPs can be used to reciprocally calculate the thickness and map microstructures of wing membranes. 2) WIPs hide an unexplored character universe that might prove to reveal "morphological barcodes" for identification. 3) One of insects' simplest and largest structures, the wing membrane, provides a highly cost-efficient way to create colourful visual signalling "posters". 4) A new visual function emerge for wing veins and pigment patterns where they aid to form distinct colour gradients and unicoloured signalling cells in WIPs. 5) WIPs pose a novel hypothesis for the evolutionary success of Diptera and other winged insects, where evolution may be driven by communication systems involving colour vision and structural wing colours.

KEY WORDS: structural wing colours, taxonomy, barcode, wing signalling, Diptera evolution

Semiochemical based management program for mosquitoes, biting midges and flies for a horse facility

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A semiochemical-based "push-pull" pest management system is being developed for a new horse boarding facility located near Cedar Key, Florida, USA. Currently no horses are permanently boarded at this facility. Target insects include mosquitoes, biting midges, tabanids and stable flies. Various types of traps have been utilized to obtain baseline data on species composition, relative abundance and seasonal incidence. These traps used a variety of physical, visual and chemical attractants. Various models of Mosquito Magnet traps, powered by the combustion of propane, have been used to capture mosquitoes and biting midges. The products of propane combustion, which serve as the main attractants, include heat and carbon dioxide. 1-Octen-3-ol (octenol) is used with these traps as a supplementary attractant. Many species of mosquitoes and biting midges have been captured throughout the year. NZi and Horse Pal traps were used to capture tabanids. Dry ice, octenol and acetone were used as baits. Tabanids were collected from May through September. Sticky alysinite and Captivator traps were used to capture stable flies and some nuisance flies. Stable flies were not very abundant and were restricted to cooler months of the year. Collectively, these traps with their attractants served as the "pull" part of our pest management system. Various compounds are being evaluated as spatial repellents. Effective spatial repellents will serve as the "push" part of the system.

KEY WORDS: mosquitoes, biting midges, tabanids, stable flies

Synanthropy of Calliphoridae (Diptera) of the Distrito Federal, Brazil

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Occurrence of flies in relation to the density of human settlements is termed synanthropy. Flies also exhibit affiliation to different hygienic, climatic and geographical conditions. Investigations on these insects are important for understanding the epidemiology of specific diseases. Considered a biodiversity hotspot, the Cerrado, is one of the most endangered biomes in the world. Brasília, the capital of Brazil, is a planned city and it has experienced a huge demographic growth since 1960, when it was inaugurated. The objective of this study was to determine the synanthropic index (SI) of adult Calliphoridae (Diptera) of the Distrito Federal, Brazil, through simultaneous monthly samplings in different environments (urban, rural, and forest) using van Someren-Rydon traps baited with rotten meat. Three traps were placed in each environment for 72 hours, from September 2009 to May 2010. A total of 2,279 individuals were captured belonging to ten species. *Chrysomya megacephala* (+65.75), the dominant species in urban and rural environment, was followed by *Chrysomya albiceps* (SI = + 49.58), *Cochliomyia macellaria* (+47.55) and *Lucilia eximia* (+39.29), all species showing preference for human settlements. *Chloroprocta idioidea* (SI = - 63.05) was the dominant species in forest environments and, as well as *Hemilucilia semidiaphana* (SI= -100), were characterized as asynanthropic. *Chrysomya putoria*, *Cochliomyia hominivorax*, *Hemilucilia segmentaria* and *Mesembrinella bicolor* were collected in small numbers, and their SI could not be determined. Females were more abundant in all collection sites (59.16 – 82.80%). Six species were collected in all types of environments. Regular monitoring of the synanthropic index of fly species will certainly help in assessing the sanitation and habitat conditions of human settlement. This in turn would help in developing the management strategy of the urban ecosystem.

KEY WORDS: synanthropy, Calliphoridae, Cerrado

How many species of Calliphoridae are there in the Americas south of Mexico?

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Calliphorids are world wide distributed, with over 1000 species and 150 genera hitherto now recognized. Blow flies have high medical and veterinary importance, since they cause myiasis and carry different microorganisms that cause numerous diseases that affect humans and other animals. They are still important in forensic entomology, urban ecology and for the ecology of decomposition. Between 1960-1985, catalogs and partial reviews about Calliphoridae were published in the Neotropical Region contributing to the knowledge of the family. However, they lack recent work on the diversity of blow flies in South and Central America. The most recent works of diversity of Calliphoridae are only from Brazil, Argentina and Colombia. The lack of knowledge plus the different views regarding the family's taxonomy led to a great confusion in which and how many blow flies names are in the Neotropical Region. This misunderstanding is of concern since the group has a significant impact on human society. The main purpose of this work is to provide a taxonomic checklist of the Calliphoridae occurring in the Americas south of Mexico, based on the literature from 1960-2009 and the examination of blow fly specimens deposited in the Instituto Oswaldo Cruz, Rio de Janeiro, Museum of Zoology of Universidade de São Paulo and Entomologic Collection of Universidade de Brasília. At this time, 28 genera and 95 species are recognized, distributed in four subfamilies: Mesembrinellinae (7 genera and 38 species), Chrysomyinae (7 genera and 28 species), Calliphorinae (4 genera and 19 species) and Toxotarsinae (10 genera and 10 species). The subfamilies Mesembrinellinae and Toxotarsinae have many genera defined by unreliable characters, requiring revisions, with the latter composed only of monotypic genera.

KEY WORDS: Calliphoridae, diversity, Americas

Contents

XXL – Giant spermatozoa in *Diasemopsis comoroensis* (Diopsidae)

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Sperm gigantism is a very rare phenomenon in insects, only known from a small number of widely scattered taxa such as some Notonectidae (Heteroptera), Ptiliidae (Coleoptera), Mantispidae (Neuroptera) and Cecidomyiidae (Diptera). The world record for insect spermatozoon length is held by a member of the Drosophilidae (Diptera) at about 58000 microns.

An additional case of sperm gigantism has been reported from the *Diasemopsis*, a genus of stalk-eyed flies (Diopsidae, Diptera). Detailed investigation of the spermatozoa of *D. comoroensis* revealed that they are peculiar in more than one respect. Besides being more than ten times longer than the spermatozoa of other diopsid genera, they also show a remarkable morphological differentiation into five distinct regions: a straight and narrow head region, followed by four tail regions with increasing coiling capacities. The corkscrew-shaped end portion is particularly wide due to highly enlarged mitochondrial derivatives.

The spermatozoa of *D. comoroensis* can be found in two different forms. In the free swimming form, the tail forms a more or less elongate spiral. In the condensed form, the coils of tail sections 2 and 3 are packed extremely tightly to form a cone-shaped cylinder which tapers towards the corkscrew end portion, while the still elongate first tail section with the straight, narrow head protrudes from the other end.

The spiral-shaped giant spermatozoa of *D. comoroensis* seem perfectly adapted to fit tail first into the tubular chambers of the ventral sperm receptacle of the female. The adaptive value of the peculiar morphology of both, spermatozoa and ventral receptacle, is discussed in the functional context of fertilization and sperm competition.

KEY WORDS: Diopsidae, reproduction, morphology, spermatozoa, sperm competition, coevolution.

Contents

Preliminary results on diversity of species of *Clastobasis* in the Afrotropics (Diptera: Mycetophilidae)

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The apparently monophyletic fungus gnat genus *Clastobasis* Skuse, 1890 includes about 20 currently recognised species in the world, including five from the Afrotropical Region (one both from Senegal and Tanzania, one from Comoro Islands and two from Seychelles). Systematically, the genus belongs to the subfamily Leiinae and, besides the wing venation, is primarily diagnosed by the position of ocelli and dark-ringed antennae. The biology of the species is still unknown, but a great part of the studied material was collected by light trapping.

On the basis of the material mostly accumulated in MNHN, altogether 26 species (including 21 undescribed) collected through the tropics in the African mainland (from Senegal to Tanzania), Madagascar and adjacent islands can be distinguished. Today, pending a further molecular analysis, structure of male terminalia is still of utmost importance in species delimitation and identification. Their morphology allows division into two species groups as follows: *C. maculicoxa* group with three described and twelve undescribed species, and *C. tanganyikae* group with two described and nine undescribed species. Species in the *C. maculicoxa* group have the normally developed ventral branch of the gonostylus covered with spine-like setae, or have a comb of similar setae along the internal margin of the branch, while the variably shaped and bare dorsal branch is more or less sclerotized. Otherwise, in the *C. tanganyikae* group, species have a heavily transformed ventral branch of the gonostylus, bearing mostly short, blunt spines which arrangement is species specific, while the dorsal branch is similar to that in the *C. maculicoxa* group: sclerotized and lacking setae.

KEY WORDS: Mycetophilidae, *Clastobasis*, biodiversity, systematics, new species, Afrotropical Region

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Diptera and the long-proboscid pollination mode of the Mid Mesozoic

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An iconic event in the history of terrestrial ecosystems was the diversification of angiosperms that commenced in the middle of the Early Cretaceous. Numerous clades of pollinating insects codiversified with angiosperms and established intricate pollinator associations. Flies became pollen and nectar feeders, developing elongate mouthparts to extract nectar from their deep-throated flower hosts. These associations still survive today. However, the fossil record of insects with long proboscises and deep-throated flowers of seed plants other than angiosperms extends back much earlier, minimally to the late Middle Jurassic at 165 Ma. During this interval, floras harbored lineages of gymnosperms such as cycads, cheirolepidiaceous conifers, seed ferns, bennettitaleans and gnetophytes, all which had members displaying anomalous reproductive structures inconsistent with wind-pollination, that have perplexed paleobotanists. Instead, these reproductive structures, and the unisexual nature, suggest insect pollination. For instance, the nutritional quality of nectar and pollen rewards in extant insect-pollinated cycads and gnetaleans approach values similar in carbohydrate, lipid and protein levels to that of angiosperm nectar. Most striking are a variety of diverse and structurally convergent elongate tubular femalere productive structures that consisted of extended micropylar tubules (*Problematospermum*), elongate integumental openings leading to inner pollen chambers (*Caytonia*, *Leptostrobus*), catchment funnels surrounded by trichomes and nectary-like structures (*Alvinia*), and flower-like bennettitalean strobili whose access along closely adpressed bracts formed a channel to inner ovulate rewards. Many Eurasian, mid Mesozoic compression biotas preserve both extinct and extant insect clades with long proboscises, for example, members of Nemestrinidae, Apioceridae and Tabanidae (Diptera). During the mid Cretaceous, concurrent with the extinction of clades with long proboscises from the Jurassic, morphologically convergent, siphon-bearing clades appeared, notably the Glossata (Lepidoptera), some Apoidea (Hymenoptera), and possibly Trichoptera and nemognathine Meloidae (Coleoptera). Evidently, mecopteran, neuropteran and dipteran clades with long proboscises were earlier pollinators of gymnosperms, whereas their morphoecological

equivalents among the Lepidoptera, Hymenoptera, and others later became pollinators of angiosperms. The only clade to participate in both phases of pollination, of gymnosperms as well as of angiosperms, were Diptera.

KEY WORDS: pollination, fossil Diptera, long-proboscid pollination

Recent advances on the taxonomy of Neotropical Phthiriinae (Diptera, Bombyliidae)

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Bee flies include ca 4700 species worldwide with 480 from the Neotropical region. Current work on the subfamily Phthiriinae in the Neotropics shows that the fauna of this biogeographic region is still poorly known and that the numbers are far from reality. Phthiriinae presents an interesting distribution pattern, with three genera (*Acreotrichus*, *Australiphthiria* and *Pygocona*) endemic to Australia, one (*Phthiria*) present in the Old World (excluding Australia) and South America, and other six (*Acreophthiria*, *Neacreotrichus*, *Euryphthiria*, *Poecilognathus*, *Relictiphthiria* and *Tmemophlebia*) restricted to the New World. Currently, out of 115 total species, only 16 species are known from the Neotropical Region, and only 11 from South America. These 11 South American species are distributed in three genera: *Phthiria*(6); *Poecilognathus*(3) and *Tmemophlebia*(2). Study of over 1,000 South American specimens from museums worldwide shows the following main results: 1. *Poecilognathus*, restricted in South America to three known species (*P. philippiana, P. stictopennis and P. xanthobasis*), all endemic to Chile, is shown to be much more diverse and also to have an enlarged distribution throughout the continent. Thus far, 24 new species have been found, including the first records of the genus from Argentina, Brazil, Paraguay and Venezuela. 2. *Tmemophlebia*, previously known from only two Brazilian species (*T. albida* and *T. testacea*) has more diversity and a larger distribution, but still restricted to Brazil. Six new species have been found in this study from a number of different localities in Brazil. 3. The otherwise Old World genus *Phthiria*, seems to be, in South America, restricted to just Chile, as new species or records from other countries have not yet been found. Detailed descriptions of both sexes and illustrations will be given for all the included species and an identification key to the South American species will be presented.

KEY WORDS: *Poecilognathus*, *Phthiria*, Tmemophlebia, taxonomy, new species, Neotropical

Nocturnal activity and oviposition in carrion-breeding flies from south-eastern Australia

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The incidence of nocturnal activity and oviposition in carrion-breeding blowflies is unclear. Limited studies, so far restricted to the northern hemisphere, have produced contradictory results, with some researchers confirming that nocturnal oviposition occurs, while others dismiss this possibility entirely. Thorough investigation of this phenomenon is critical as it is usually assumed in forensic entomological casework that blowflies remain inactive at night and thus do not oviposit. Estimates of minimum time since death could be substantially affected in cases where such an assumption is incorrect. Nocturnal oviposition was investigated in south-eastern Australia using piglet carcasses placed in the field. Experiments were carried out at night, coinciding with a new moon, full moon, and under artificial lighting. Nocturnal oviposition did not occur on any carcass. The diurnal and nocturnal activity of blow flies was also monitored in the laboratory under differing light intensities. A significant association was found between the time of day and degree of activity for all light intensities, as well as between activity and light intensity irrespective of time of day. An association was also evident between oviposition and the time of day and light intensity. Overall, our results support the general assumption that nocturnal oviposition is unlikely to occur in the field under typical circumstances in south-eastern Australia. However, laboratory data suggest that this may still be possible under certain circumstances.

KEY WORDS: Forensic entomology, PMI, nocturnal ovipostion, activity, blow flies

Contemporary systematics of the southern hemisphere horse fly genus *Scaptia* (Diptera: Tabanidae)

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Horse flies (Diptera: Tabanidae) have a worldwide distribution and are one of the most notorious groups of Diptera, often considered to be a major pest of both humans and livestock. Ironically, it is also one of the least studied, as interest in the family has faded over the last 50 years. Recent interest in the taxonomy of horse flies has been generated by the National Science Foundation, through funding from the Partnerships for Enhancing Expertise in Taxonomy (PEET) program. The large genus *Scaptia* (Tabanidae: Pangoniinae: Scionini) is comprised of seven subgenera with an exclusively southern distribution, being found in Australia, New Zealand, New Guinea and South America. Evolutionary studies on *Scaptia* are extremely limited and have utilized only morphological characters. The first molecular phylogenetic hypothesis for *Scaptia* is presented here, using a Bayesian analysis of a concatenated COI (mtDNA) and CAD (nucDNA) gene dataset. Most of the subgenera are recovered as robust monophyletic groups and largely confirm the traditional morphology-based classification. However, other Scionini genera including *Fidena* and the *Pityocera* group within *Scaptia*, indicate that the Scionini are likely to be paraphyletic and that a tribal revision may be required. Using divergence time estimation and fossil calibration, the influence of the breakup of Gondwana on the speciation of *Scaptia* was also investigated. Overall, molecular techniques have proven useful in providing a sound phylogenetic hypothesis for *Scaptia*.

KEY WORDS: Tabanidae, horse flies, Scaptia, systematics, taxonomy

Standardization of histological procedures for entomotoxicology

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Entomotoxicology, a branch of forensic entomology, applies toxicological analyses to insects feeding on decomposing tissues to identify drugs and toxins present in this type of substrate, and also investigates the effects of these substances on the development of these necrophagous insects, to minimize errors in postmortem interval estimates. Immunohistochemistry (IHC) is one of the techniques that can be used for this purpose. To improve IHC analyses, the aim of this study was to standardize the histological procedures by choosing the best fixative protocol. The fixatives paraformaldehyde 4% (PFA) and Carnoy´s fluid (CF) were tested on *Sarcophaga* (*Lyopigia*) *ruficornis* (Fabricius, 1794) (Diptera: Sarcophagidae) maggots, a flesh fly of forensic importance in Brazil, as follows: I- larvae fixed for 2 h in 70% alcohol and transferred to CF for 3 h; II- larvae fixed for 3 h in CF; III- larvae fixed for 2 h in 70% alcohol and transferred to PFA for 12 h; IV- larvae fixed for 2 h in 70% alcohol and transferred to PFA for 24 h; V- larvae fixed for 12 h in PFA; and VI- larvae fixed for 24 h in PFA. After these procedures, the samples were embedding in parafin and sectioned at 5 µm. Sections were stained with Ehrlich's hematoxylin and made into slides. In tests I, III, IV and V, larval tissues were fragmented while in II and VI the sections were more preserved. Because preserved tissues are necessary for IHC analyses, our findings suggest that fixation in Carnoy´s fluid for 3 hours or in 4% paraformaldehyde for 24 h are most recommended for preparing the samples that will be used in qualitative toxicological analyses.

KEY WORDS: flies, immunohistochemistry, postmortem interval, entomotoxicology

Coleopteran parasitoids in Dipteran hosts: Implications for forensic entomology

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The estimation of postmortem interval (PMI) is always one of the most important issues in forensic entomology, and estimating the developmental time of the immature stages of necrophagous flies has been the main tool to estimate PMI. There are a large number of parasitic insects that may parasitize and alter the development of immature stages of flies, and thus affecting the PMI estimation. For most species of the rove beetle genus *Aleochara* which have been studied, their larvae are believed to be the ectoparasitoids of the puparia of Cyclorrhaphan flies; and some species that parasitize necrophagous flies may have forensic importance. Two species of *Aleochara* that visit carrion site, *A. nigra* and *A. formosanorum*, have been studied for their life histories, potential host ranges, and distribution in northern Taiwan. The effects of several factors of the hosts that may influence the acceptance, suitability, and developmental time of these parasitoids have also been tested. According to the results, all tested hosts, including the puparia of *Chrysomya megacephala*, *Chrysomya rufifacies*, *Lucilia cuprina*, *Hemipyrellia ligurriens*, *Bactrocera dorsalis*, and one Sarcophagid species was accepted at least by some individuals of these two species of *Aleochara* under optimal host finding conditions. This result suggested that these *Aleochara* larvae have potentially wider host ranges, but varied degrees of host acceptance and suitability also indicated that larvae may have their preference for specific host species. The larval stage together with the pupal stage of *A. nigra* and *A. formosanorum* are both longer than the pupal stages of their hosts, implying their potential usage of elongating the PMI estimation in forensic investigation. In addition, the host weight and the duration of the larval stage of *A. formosanorum* are positively correlated. This should be considered while applying the flies and their parasitoids for PMI estimation.

KEY WORDS: ectoparasitoid, PMI estimation, Staphylinidae, Calliphoridae, forensic entomology

To split or not to split: Is integrative taxonomy leading us to more robust species concepts in Nearctic *Dasysyrphus* (Diptera: Syrphidae)?

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The genus Dasysyrphus Enderlein (Diptera: Syrphidae) is taxonomically challenging. There are 43 described species, ten of which are currently recognized as occurring in the Nearctic Region. There is no key to the species of the entire region. Keys exist only for Canada and eastern North America, with the western and southwestern United States currently not represented. As well, no major phylogenetic revision has been done for the group before. Recent morphological work by Doczkal, supported by the genetic work of Ståhls, on the venustus group in Europe has illustrated many new characters. Findings from the Palaearctic Region suggest that many cryptic species exist, especially within the venustus group. Preliminary data from COI analysis suggest that there are at least 26 Nearctic species of Dasysyrphus. Data from the nuclear gene ITS2 will be added to the COI and morphological data to corroborate the species concepts. Our work will be linked with ongoing work in the Old World to develop global species concepts for Dasysyrphus.

KEY WORDS: *Dasysyrphus*, Syrphidae, phylogenetics, revision, integrated taxonomy

Contents

Comparison and selection of saprophagous Diptera species for the conversion of poultry manure

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Disposal and management of manure produced by agricultural practices is an ongoing process which must be handled responsibly to reduce potential environmental contamination. Current methods of processing the large volume of manure produced daily by commercial farms are often time-consuming and costly, and can still harm the environment. In nature, manure is broken down into smaller compounds that can be taken up and used by plants, continuing the nutrient cycle. This is accomplished by a variety of saprophagous organisms that use the slowly decomposing material, or the bacteria it contains, as food. Several families of Diptera have larvae that develop in manure, increasing the rate of decomposition. Species often have very narrow environmental tolerances which can limit the types of manure they can inhabit and break down. Other species, such as *Musca domestica*, are able to tolerate broader environmental conditions and can utilize a variety of manure. These differences in habitat selection and biological limitations (size, population density, lifespan etc.) may affect the usefulness of the species as a manure-converter at an industrial scale. Fly species naturally found in chicken manure were selected and reared in the laboratory. One generalist species (*M. domestica*) and two species that specialize in chicken manure (*Fannia pusio* and *Coproica hirtula*) were assessed for ease of rearing and mass production of eggs. Fresh chicken manure was inoculated with fly eggs and a response surface analysis was conducted to determine the ideal environmental conditions (egg to manure ratio, depth, etc) for that species. The ideal species must be easily reared in large, high density populations, and convert manure efficiently. We here summarize the results of our species comparison thus far. Evaluation of the above species is an initial step in selecting the optimal fly species for poultry manure conversion.

KEY WORDS: larvae, saprophagus, manure managment

Advances in the taxonomy of Afrotropical Asilidae

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Since the description of the first Afrotropical robber fly, *Apoclea algira*, by Linnaeus in 1767 there has been a steady and sustained interest in the taxonomy of this the most speciose family of Afrotropical Diptera. Our growth in knowledge continues to show an almost linear progression suggesting that many more species still await discovery and description.

Nine subfamilies are represented as follows (percentage of fauna in brackets): Apocleinae (28%), Stenopogoninae (26%), Laphriinae (12%), Leptogastrinae (10%), Ommatiinae (8%), Asilinae (6%), Trigonomiminae (4%), Dasypogoninae (3%), Stichopogoninae (1%). 2% of the fauna remains unplaced. Growth in knowledge since the 1980 Catalogue is greatest for the more speciose groups. Eleven people have contributed to the taxonomic literature over the last 30 years, perhaps the main authors being Dikow, Geller-Grimm, Londt, Scarbrough and Tomasovic.

A 20% increase in the number of genera has occurred between 1980 and 2010, while the number of species has increased by 31% (1980 – 1114 species in 104 genera, 2010 – 1604 species in 130 genera). Much of the growth in knowledge has probably been due to the presence of a specialist working in the region. Being resident in South Africa it is not surprising that southern African countries are best represented, the South African figures being the most impressive – 1980: 380 species in 61 genera, 2010: 700 species in 91 genera (a 33% increase in genera, 54% increase in species). Clearly one of the greatest limitations to the growth of knowledge has been adequate sampling. As Asilidae are not generally effectively sampled using Malaise traps, hand netting, especially by specialists, remains the most effective means of accumulating material.

Current research priorities are revisions of the following genera (in order of priority): *Microstylum*, *Ancylorrhynchus*, *Promachus*, *Alcimus*, *Ommatius*, *Laphria* (*Choerades*), *Laxenecera*, *Oligopogon*.

KEY WORDS: taxonomy, Afrotropical, Asilidae

The Snow collection of Gambian Asilidae: advantages of a sustained sampling programme

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William Snow sampled Gambian Asilidae between 1974–1977. His collection of 298 specimens was donated to the Oxford University Museum of Natural History in 1996. Although 12 localities, spread out across the country, are represented, most of the specimens came from Keneba. Localities represented are: Bansang, Brufut, Burrong, Fajara, Hela Kunda, Karantaba, Keneba, Kubuni, Sapu, Tendab, Tuba, and Wallikunda.

Until recently the following Gambian genera were represented (number of species in brackets) – Apocleinae: *Alcimus* (1), *Philodicus* (2). Asilinae: *Heligmonevra* (1). Laphriinae: *Choerades* (1), *Hoplistomerus* (1), *Lamyra* (1), *Storthyngomerus* (1), *Trichardis* (1). Leptogastrinae: *Euscelidia* (3). Ommatiinae: *Afroestricus* (2), *Pygommatius* (1), *Thalosia* (1). Stenopogoninae: *Hynirhynchus* (1), *Sisyrnodytes* (1). Trigonomiminae: *Rhipidocephala* (1) – i.e. 19 species, 15 genera, 7 subfamilies.

Snow's collection contains the following taxa – Apocleinae: *Alcimus* (1), *Hippomachus* (1), *Philodicus* (1), *Promachus* (4), *Robertomyia* (1). Asilinae: *Heligmonevra* (1). Dasypogoninae: P*egesimallus* (1). Laphriinae: *Choerades* (1), *Hoplistomerus* (1), *Lamyra* (1), *Laxenecera* (5), *Nusa* (1), *Storthyngomerus* (2), *Trichardis* (3). Leptogastrinae: *Euscelidia* (2), *Leptogaster* (2). Ommatiinae: *Afroestricus* (1), *Emphysomera* (1), *Ommatius* (3), *Pygommatius* (2), *Thalosia* (1). Stenopogoninae: *Ancylorhynchus* (1), *Connomyia* (1), *Gonioscelis* (1), *Habropogon* (2), *Hynirhynchus* (1), *Microstylum* (3), *Oligopogon* (2), *Rhabdogaster* (1), *Scylaticus* (1), *Sisyrnodytes* (1) new genus (1). Stichopogoninae: *Stichopogon* (2). Trigonomiminae: *Rhipidocephala* (2) – i.e. 55 species, 34 genera, 9 subfamilies.

Snow's collection includes - 3 genera newly reported for West Africa (*Hippomachus*, Robertomyia, and *Scylaticus*) and 8 newly reported Gambian genera. Descriptions of 5 new species and a new genus are in press and more will follow when revisions of some genera are undertaken.

KEY WORDS: Afrotropical, Asilidae, Gambia, new discoveries

Contents

Occurrence and seasonable variation of *Hermetia illucens* (Diptera: Stratiomydae) (Linnaeus, 1758) on swine corpse (*Sus scrofa*) exposed at an Atlantic rainforest fragment at Salvador-Ba/Brazil

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Stratiomyidae is a fly family that colonize carcasses. The present work on *Hermetia illucens* a very common species in Brazil, which may be important in estimating postmortem interval (PMI) calculation. This paper aims to verify the seasonality influence on the abundance of *H. illucens* and observe its occurrence along each decomposition phase. The experiment was divided into four stages, corresponding to the seasons: spring, summer, autumn and winter. To capture the insect four pigs (*Sus scrofa*) (one per stage) were placed on appropriate traps. Adults and immatures were collected daily at each stage. The decomposition stages between the seasons are presented with similar aspects, but the duration of the stage was shorter in summer and longer in winter and autumn. The immatures of *H. illucens* develop on carcasses only in spring and autumn, and 237 maggots were collected, with 97 specimens emerging in the laboratory. Winter showed the highest prevalence of females, and the relationship was direct. Corroborating with other authors, the occurrence of this species was only recorded in the final stages. Participating in the decomposition process, *H. illucens* can be a useful forensic indicator to calculate PMI.

KEY WORDS: decomposition, forensic entomology, entomologic succession, seasonality

Diversity of gall midges (Cecidomyiidae, Diptera) from “restinga” areas of Rio de Janeiro State

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“Restinga”, a typical ecosystem of the Brazilian coast, is part of the Atlantic Forest, considered to be one of the hot spots of world biodiversity. This ecosystem supports a great diversity of gall midges of the family Cecidomyiidae (Diptera). In the restinga areas of Rio de Janeiro State (southern Brazil), 170 morphotypes of cecidomyiid galls have been recorded from 35 families, 56 genera and 79 species of plants. Myrtaceae, Fabaceae, and Asteraceae are the plant families which show the greatest richness of galls, with 46, 10 and 9 cecidomyiid morphotypes, respectively. Most (64%) of the galls occur on leaves. Nevertheless, bud, stem, tendril, flower and fruit galls have also been recorded. About 45% of the gall midges are identified to the species level; the others are in suprageneric categories. The Cecidomyiidi are better represented than the Lasiopteridi, with 92 and 32 species, respectively. Asphondylini, Clinodiplosini, and Lopesiini are the most diversified tribes, and Lopesia, Dasineura, Asphondylia, Clinodiplosis, and Stephomyia are the genera with the greatest number of species (11, 7, 6, 6, and 6, respectively). In addition to the gall makers, 18 inquilines, 4 predators and 3 free-living species of gall midges have been recorded. Data on the diversity of gall midges, from restinga areas of other southern Brazilian states, such as São Paulo and Espírito Santo, also exist. The number of gall midge species and/or gall morphotypes that Rio de Janeiro State has in common with both other states is very low: 15 and 10, respectively, suggesting that each area has its own faunal composition.

KEY WORDS: Cecidomyiidae, taxonomy, restinga, Brazil

Contents

A new gall midge (Diptera, Cecidomyiidae) associated with *Microgramma vacciniifolia*

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Galls on ferns are poorly known in Brazil, where nine morphotypes are recorded on eight plant species. Stem galls on Microgramma vacciniifolia (Polypodiaceae) induced by a new genus and species of Cecidomyiidae were found in Maricá, Rio de Janeiro State (RJ). It is the first record of a gall midge on ferns in Brazil. Field work was carried out from June to August, 2009. Stem galls were collected and transported to the laboratory, where part of the sample was packed in plastic bags with moist cotton and checked daily for adult emergence. The remaining galls were dissected to obtain larvae and pupae. All specimens were mounted on slides and are deposited at the Diptera collection of Museu Nacional, Rio de Janeiro.

The gall-forming species belongs to a new genus of Cecidomyiidi which does not fit into any known tribe. It is characterized by having the following characters: a three-segmented palpus, male flagellomeres binodal with three circumfila irregular in length, R5 joining C beyond wing apex, tarsal claws one-toothed and bowed near basal third, gonocoxite with mesobasal lobes, gonostylus cylindrical, slightly tapered from base to apex, hypoproct concave apically, conspicuously longer and thinner than cerci, ovipositor barely protrusible, cerci separate, and spatula absent. The new genus appears to be more similar to *Clusiamyia* Maia, 1996, based mainly on characters of the male terminalia, especially the proportions of the cerci, hypoproct, and aedeagus and shape of cerci and hypoproct. Both genera differ in the shape and chaetotaxy of female cerci, shape of circumfila, tarsal claw and female hypoproct, number of segments of the palpi, length of male circumfilar loops, shape of antennal bases, presence of superior frontal horn, length of prothoracic spiracle, and degree of body sclerotization of the pupa.

KEY WORDS: Gall, Polypodiaceae, Cecidomyiidi, restinga, Brazil

Knowing the immature stages of Costa Rican hoverflies

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Among phytophagous Diptera, hover flies of the family Syrphidae are one of the groups most dependent on plants, both as adults and as larvae. Adults depend for food on nectar and pollen, while larvae of many species also show close relationships with plants, including phytophagy and saprophagy, as well as living in phytotelmata and other less specialized aquatic habitats, feeding on decomposing vegetation therein. Previous knowledge of syrphids comes mainly from studies of adults collected using different techniques and traps, while studies of syrphid larvae, their life cycles, and other aspects of their natural history, have generated interesting and probably more useful information about the biology of various species, thus providing valuable understanding of the processes of diversification and specialization, all of which may prove useful in biodiversity conservation. In this paper we present some results of a study of Costa Rican syrphids collected as larvae from different vegetal microhabitats over the last seven years. These studies: i) have increased our knowledge of various genera, revealing many previously unknown undescribed species, immature stages and life cycles, particularly in the megadiverse neotropical genus *Copestylum*; ii) have provided diagnostic morphological characters of immature states of various species and species groups; and iii) have revealed patterns of endemism and geograhical distributions of Costa Rican species as well as their relationships with their larval microhabitats.

KEY WORDS: saprophagous syrphids, tropical breeding habitats

Molecular phylogenetics of Calliphoridae flies (Diptera: Brachycera) based on ITS2 and COI

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The Calliphoridae (Diptera: Brachycera: Oestroidea) is a family of great economic, veterinary, medical and forensic importance since it includes myiasis-causing species. Until now, molecular phylogenetic analyses in this group have focused mainly on synanthropic species of economic or forensic significance, especially those from the subfamilies Calliphorinae, Chrysomyinae and Luciliinae. Mitochondrial DNA has been by far the most used marker for phylogenetic reconstruction in this family, with few exceptions (e.g. 28S rDNA). In this context, we PCR-amplified, cloned and sequenced the ITS2 (300-350bp) and COI (848bp) regions from 34 species of 20 genera of Calliphoridae, 3 species of 2 genera of Sarcophagidae and 1 other species of Oestroidea. Species of Muscidae were used as outgroups. Sequences available at GenBank were also included in the analyses. Preliminary phylogenetic analyses using Bayesian and maximum likelihood inference methods support the following relationships: (Muscidae, (Oestridae, (Rhiniinae [Rhiniidae], (Mesembrinellinae [Mesembrinellidae], Sarcophagidae), (Bengaliinae [Bengaliidae], (Chrysomyinae, (Auchmeromyinae, (Luciliinae, Calliphorinae))))))). These results corroborate the non-monophyletic status of the Calliphoridae family observed in phylogenetic trees inferred from morphological data, although some relationships may be due to poor sampling of some taxa (e.g. Oestridae). The numbers of molecular markers and taxon sampling are being improved. Future analyses will include more molecular markers and more refined analyses based on secondary structure of ITS2 sequences. The results will contribute to phylogenetic and systematic studies of the Calliphoridae, including the controversial elevation of some subfamilies to family status.

KEY WORDS: Calliphoridae, molecular phylogenetics, COI, ITS2, secondary structure

Fly dispersed dung mosses: manipulating insect behaviour through odour and visual cues

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The use of sensory attractants is central to most animal-mediated pollination and seed dispersal interactions. Approximately half the 73 species of mosses in the family Splachnaceae are entomophilous and grow on feces and carrion. When mature, entomophilous species often produce brightly coloured, scented sporophytes which, for several species, have been shown to attract Diptera. In a number of cases, sporophyte colours and odours, as well as the flies that visit them, have been shown to be species-specific. Analyses of scent chemistry identified that sporophyte odours of North and South American species sampled were both complex and diverse, with an apparent inverse relationship between the size and showiness of the apophysis and its odour complexity. Field experiments exploring differences between the fly faunas attracted to two locally sympatric North American species (*Splachnum ampullaceum* and *S. pensylvanicum*) and exploring the relative importance of visual and odour cues in attracting flies to these species suggest that although each species attract an overlapping fly fauna, they differ in the relative numbers of flies of different genera that each attracts and that odour cues alone relative to both odour and visual cues decrease the visitation rates by flies to each of the moss species.

KEY WORDS: directed dispersal, Diptera, moss, sensory signals, Splachnaceae, spore dispersal

Syrphidae in Brazil: The last ten years and perspectives

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Since 2000 research on Syrphidae in Brazil has increased. This presentation is an overview on those studies and also provides perspectives for the future. Most studies are taxonomic or ecological. The taxonomic studies have taken place mainly at the Federal University of Paraná, Curitiba, and the following taxa have been studied: Revision of Toxomerus (Zuleica M. Borges & Marcia S. Couri; Museu Nacional do Rio de Janeiro); Cladistics analysis of the tribe Eristaliini (Mírian Nunes Morales, UFPR – doctoral degree); Phylogeny of Toxomerus (Amanda Ciprandi Pires, UFPR – doctoral degree); Phylogeny of Leucopodella (Alberto Carvalho, UFPR – masters degree); Taxonomy and Phylogeny of Ocyptamus (Gil Felipe G. Miranda, Steve Marshall UFPR and University of Guelph). The diversity of Syrphidae collected in two surveys in the State of Paraná has been evaluated – Survey of Entomological Fauna in Paraná (PROFAUPAR) and Project "Vila Velha" (PROVIVE). During two years of the project (1986 to 1988) PROFAUPAR, carried out in eight localities of Paraná, 3,316 specimens of Syrphidae were collected, 1,607 in the first year and 1,709 in the second. Five species were most commonly collected for a total of 1,554 specimens and their seasonality was evaluated: Toxomerus procrastinatus Metz, T. tibicen (Wiedemann), Microdon mitis Curran, Leucopodella gracilis (Williston) and Paramicrodon flukei (Curran). For PROVIVE, the diversity of Syrphidae in five areas with distinct vegetational composition in Vila Velha State Park, Ponta Grossa, Paraná, southern Brazil has been evaluated. In 2008 we started research on the syrphids of Bromeliads - a project to survey the species and to describe their immature stages was submitted for funding. Information on these specimens is deposited in the Entomological Collection Padre Jesus Santiago Moure in a database and is available online (Project Network of Biological Collections www.taxonline.ufpr.br.)

KEY WORDS: Syrphidae, Brazil, taxonomy

Digital Diptera revisited: new tools for the identification of flies

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The “taxonomic impediment” and the resultant “identification bottleneck” are serious issues for entomologists, ecologists, biodiversity researchers and other biologists throughout the world ... if you can’t identify the players it is hard to understand the play. Dipterists have long been leaders in addressing these issues, notably through the production of the “Manuals”, and we can now build on that lead by encapsulating our taxonomic expertise into freely accessible and user-friendly web products including reviews, galleries, and keys. Some revolutionary and supposedly revolutionary new identification tools will be discussed, with an emphasis on the way that a potent combination of digital photography, taxonomic expertise and the World Wide Web is providing unprecedented opportunities for dipterists to publish synthetic reviews and new identification tools for groups with a sound revisionary framework. These points are illustrated using recent or pending dipterological contributions to the Canadian Journal of Arthropod Identification.

KEY WORDS: Diptera identification, keys, digital taxonomy

Contents

A case of alpha diversity of blow flies (Calliphoridae) in the Colombian Andes

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The Calliphoridae family is currently represented approximately by 126 species in the neotropics. They have different feeding habits; some are generally scavengers, while others are parasitoids or predators. Their habits are of importance to human health, as vectors of pathogens, and as causative agents of myiasis in mammals and birds. As such, they can be implemented in forensic investigations. All of these attributes led to the need to study the α diversity of a community of Calliphoridae at Salto de Tequendama, Cundinamarca, Colombia, in the Andean Forest, for that were performed 24 traps in three collecting events, using traps made of plastic bottle inverted funnel visors, baited with fish and chicken in putrefaction.

A total of 352 individuals were collected, with only a few species showing a marked predominance in abundance.

The study of the diversity of Calliphoridae can provide information for future criminal investigation and pest management so that allows us to understand the behavior of communities in particular areas.

KEY WORDS: Calliphoridae, alpha diversity, Andes, Colombia

Saprophagous syrphid-cactus network

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We analyzed the community structure of a cacti-saprophagus syrphid using network analysis. We analyzed whether the exploitation of decaying cacti resources exhibited a nested topology as a structural pattern, or whether it was temporally random (between seasons). We hypothesized that if the availability of cactus resources was predictable during the rainy season, then it would be exploited by a more structured community (nested). Otherwise, as resource availability would be unpredictable during the dry season, it then would be exploited by a random community. The resulting networks show that the community of saprophagous *Copestylum* in the rainy season is not randomly assembled but highly nested, revealing a highly structured pattern of resource use by saprophagous larvae of *Copestylum*. The opposite was found for the dry season, where community structure presented a random organization. The factors structuring nested subsets in the cactus-saprophagous hoverfly communities can be viewed as filters that restrict the occurrence at decayed cacti of some species via characteristics of both groups (flies and cacti). The wide spectrum of cactus resource types, especially in relation to their temporal availability, and the gradient in cactus use by saprophages, determined by the different adaptations and trophic needs of the species, may generate nestedness.

KEY WORDS: Saprophagous hoverflies, *Copestylum*,
mutualistic networks, consumer-resource interactions, nestedness

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Molecular phylogeny of the tribe Aphrosylini (Diptera: Dolichopodidae)

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The family Dolichopodidae contains about 250 genera and 7,000 nominal species, which are distributed in all zoogeographical regions. Adult dolichopodid flies mostly live near water (freshwater), such as streams, brooks, marshes, and wet fallen leaves, but there is a unique group, the tribe Aphrosylini in the subfamily Hydrophorinae (classified by some as a separate subfamily), that exclusively inhabits rocky seashores. This group contains 13 genera and 102 described species occurring widely on sea coasts of the temperate and tropical zones of the world. The phylogenetic relationships of the Aphrosylinae, and thus their proper taxonomic placement, remain to be clarified. In this study, I tried to elucidate their relationships within the Hydrophorinae using sequence data of the mtDNA ND5 gene for 57 species from Australia, New Zealand, Africa, Europe, Asia, and North America. At this stage, it is apparent that the genera inhabiting rocky beaches form a monophyletic group, supported by a high bootstrap score in the ND5 tree. Sequence data of the 28S gene is now being obtained for most of these species in order to confirm and raise the reliability of these results.

KEY WORDS: Dolichopodidae, Hydrophorinae, Aphrosylini, ND5, 28S

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The discovery of shore flies (Diptera: Ephydridae) in the New World with an emphasis on the Neotropical fauna: Status, recent progress and process

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The Neotropical fauna of shore flies (Diptera: Ephydridae) is rich and diverse with over 450 described species in nearly 70 genera. Growth since publication of Wirth's 1968 Neotropical catalog is documented with more specific and comparative data from Argentina, Bolivia, Brazil, Costa Rica, and Guyana. The results of a recent six-month sabbatical in southern Brazil are highlighted, providing more specific examples and details. These combined data clearly indicate that the whole biogeographic Region is under sampled, sometimes dramatically so, and largely undocumented. What is now needed are: (1) training (more postgraduate students and short courses, producing more knowledgeable "minds and hands"); (2) improved tools (catalogs, keys, faunal studies, revisions); (3) much improved sampling: coordinated field work, especially to areas of high priority; (4) more and improved depositories; (5) laws, regulations, and protocols (such as Material Transfer Agreements) favorable to research on biodiversity (need for more regional perspective and responsibility and less national parochialism); and (6) fewer wars and diversion of their funding to biodiversity studies.

DNA-based identification of forensically important Australian Sarcophagidae (Diptera)

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Reliable identification of the immatures and many adults of Australian Sarcophagidae (flesh flies) is currently very difficult due to limited relevant taxonomic data. Moreover, species display great morphological similarity. However, sarcophagid maggots are often among the first on dead bodies, and thus valuable for estimating the minimum time since death. Due to the morphological impediments, molecular methods may be the only means of reliably identifying larval and adult flesh fly specimens. Studies to date on sarcophagid species have shown that the mitochondrial cytochrome oxidase subunit I (COI) gene is reliable for species level resolution. Meiklejohn et al. (2009) showed that the COI ‘barcode’ sequence was suitable for the molecular identification of 16 species of Australian Sarcophagidae: 96.5% of the examined specimens were assigned to the correct species. In the current work, the ‘barcoding’ approach has been further evaluated with sequence data from an additional 120 specimens. These comprise 10 newly represented species and 7 newly represented subgenera of the genus *Sarcophaga*. The results of the ‘barcoding’ analyses with the expanded taxon set will be presented, along with a revised evaluation of this approach for the molecular identification of Australian Sarcophagidae.

KEY WORDS: Sarcophagidae, Diptera, identification, DNA barcoding

Contents

Interspecific interactions between larvae of carrion-breeding blow flies (Calliphoridae)

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Developing a better understanding of the factors that influence the development of blow fly larvae is crucial for refining estimates of post mortem interval in forensic entomology. Currently, intraspecific resource competition among blowfly larvae is the only biotic factor that has been thoroughly investigated as an influence on larval growth and development. However, the larvae of many blowfly species coexist on carrion and interspecific interactions must therefore also be considered. This project investigated the effect of interspecific interactions among the larvae of six forensically important carrion blowfly species at low densities. Larvae were divided into two seasonal cohorts consisting of three species each. The size and/or development of most species were significantly affected by their interspecific interaction. A second part of this study was designed to investigate how blowfly larvae might interact with one another using chemoreception, using the response of larvae to conspecific and heterospecific chemical cues. The same species and seasonal cohorts were used as for the previous experiment. The responses of each species to the cues varied; there was no consistent preference among species for the conspecific cue. This project challenges the assumption that interspecific interaction only affects the growth and development of blowfly larvae when it is in the form of exploitative resource competition resulting from high larval densities. Furthermore, it shows that chemical-based interactions may play important roles in the behaviour of, and the interactions among, species of carrion blow fly larvae.

KEY WORDS: forensic entomology, interspecific, interactions, maggots, development, chemical cues

Contents

Revision of the South American species of Teretrurinae (Diptera: Pyrgotidae)

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Pyrgotidae is a small family of Tephritoidea composed of approximately 360 species with worldwide distribution. Two subfamilies are recognized: Pyrgotinae and Teretrurinae. Teretrurinae is composed of 11 species distributed in the following genera: *Frontalia* Malloch (five species from Australia), *Maenomenus* Bezzi (one species from Australia), *Prodalmannia* Bezzi (one species from Australia), *Pyrgotosoma* Malloch (one species from Argentina and Chile), and *Teretrura* Bigot (three species from Argentina and Chile). The subfamily has an Austral Kingdom distribution in the Andean and temperate Australian regions. The species from South America are endemics to the Andean region which correspond to Central Chile and Patagonia. This distribution corroborates the hypothesis that South America is a composite area in which the biota from the southern part is closely related to the southern temperate areas, that comprises the Austral Kingdom, and the tropical biota is more related with the African and North American biota. The main morphological features that characterize the subfamily are sternite 1 well developed, full sclerotized and separated from sternite 2. The two South American genera *Pyrgotosoma* and *Teretrura* are redescribed. The monotypic genus *Pyrgotosoma* erected to host *P. flavida* can be recognized by the presence of ocellar and postvertical setae; longitudinal vein R_1 ending distal from to the level of crossvein r-m; and females with two lateral processes on sternite 6. *Teretrura*, comprising *T. flaveola* Bigot, *T. shannoni* Malloch and *T. tinctipennis* Malloch is characterized by the lack of ocellar and postvertical setae; longitudinal vein R_1 ending nearly the level of crossvein r-m; female sternite 6 without lateral processes. Besides the redescriptions, distributional map and an identification key to all genera and species of the subfamily, including the Australian ones are presented.

KEY WORDS: Tephritoidea, South America, Australia, Austral Kingdom

Phylogenetic relationships of Neotropical Empidinae lineages with regard to the entire subfamily

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The subfamily Empidinae is a large, heterogeneous group that is very diverse in the Neotropical region and, eventually, many species will be described. This group is interesting because males transfer nuptial gifts to females during mating, and phylogenetic study can help to understand the evolution of this behaviour. Empidinae includes 30 genera in two tribes, Empidini and Hilarini. In the Neotropical region there are 20 genera, however *Empis*, *Lamprempis, Macrostomus, Porphyrochroa* and *Rhamphomyia* (Empidini) and *Hilara* and *Hilarempis* (Hilarini) are the genera that best represent this subfamily in this region. In the present work, portions of two genes (the nuclear gene CAD and mtCOI) were sequenced from a worldwide sample of Empidinae, with emphasis on the Neotropical region. The aim of the analysis was to analyse the relationships between the Neotropical lineages in relation to the rest of the subfamily. The data show that Hilarini is monophyletic, while Empidini is paraphyletic, which corroborates previous studies. Many genera were recognized to be non-monophyletic, and because of this the classification of the whole subfamily needs revision. The clade of *Macrostomus* + *Porphyrochroa* has good support and the sister group of this is found to be *Lamprempis* and not species of *Rhamphomyia*, as previously thought.

Contents

New insights into molecular phylogenetics of Syrphinae (Diptera: Syrphidae)

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The family Syrphidae (Diptera: Cyclorrapha) is traditionally divided into three subfamilies: Microdontinae, Eristalinae and Syrphinae. The subfamily Syrphinae includes the majority of predatory syrphids. The current classification of this subfamily basically follows Vockeroth (1969; Mem. Ent. Soc. Can. 62: 1-176) and, on the basis of adult characters, four tribes are typically recognized: Bacchini, Paragini, Syrphini and Toxomerini. Rotheray & Gilbert (1989; Zool. J. Linn. Soc. 95: 29-70), using larval characters, recognized five tribes including Pipizini in Syrphinae. Mengual et al. (2008; Cladistics 23: 1-20) addressed the monophyly of the tribes and their relationships using mitochondrial COI and nuclear 28S rRNA genes.

The aim of the present study is to reanalyze molecular data of the subfamily Syrphinae for exploring new phylogenetic relationships of tribes and to infer the phylogenetic placement of recently analyzed genera. The total number of ingroup taxa went up to 122 species and a short fragment of the nuclear 18S rRNA gene was added to previous molecular data: a large fragment of the mitochondrial COI gene and the D2-3 region of nuclear 28S rRNA gene. Four Eristalinae species were used as outgroups and eight species of Pipizini were also included. Genera such as *Doros*, *Talahua, Betasyrphus*, and *Notosyrphus* were analyzed for the first time, and genera not studied by Mengual et al. (2008), such as *Exallandra* and *Salpingogaster*, were also included. The inclusion of subgenera not studied in 2008: *Carposcalis, Pelecinobaccha, Pipunculosyrphus, Antillus, Costarica, Rhinoprosopa, Pseudodoros,* and *Austrosyrphus*, is also significant. Direct optimization, a parsimony algorithm as implemented in the computer program POY, Bayesian inference (MrBayes) and maximum likelihood (PAUP*) were used for analyses using parallel computing when possible. Results using different methodologies were similar. The tribe Pipizini was shown to be monophyletic.

KEY WORDS: molecular systematics, phylogeny, predatory flower flies, classification

Attractive pictures of [fly] genitalia: an easy and affordable solution for illustrating genitalic structures

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Drawing genitalia can be a very time consuming task in any taxonomic study. An alternative is photographic imaging. With an appropriate set-up one can obtain high quality informative illustrations, but which take less time and talent to produce. The Insect Systematics Laboratory of the University of Guelph uses a Nikon D70 camera set on a Zeiss triocular microscope equipped with a Nikon vertical camera tube. The freeware program Camera Control 4.1 is used to remotely control settings, take photos, and automatically download images to the computer. The images from different foci are combined into a single image using the freeware program CombineZ5. The advantages and disadvantages of this method of illustration will be discussed, and comparisons to hand illustrations will be made. There is no doubt that it is much faster than traditional genitalia depiction using a camera lucida and ink. Furthermore, the results provide a more accurate depiction of the specimen and a basic set-up can be very affordable. This presentation will also cover the steps taken from specimen preparation to the final combined image.

Contents

Ocyptamus (Diptera, Syrphidae, Syrphinae) systematics improved through the addition of DNA and female genitalia data

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With about 300 described species, *Ocyptamus* Macquart is the second most speciose genus of Syrphidae in the New World, and the most diverse genus of Syrphinae. This group was last revised as a whole by Hull (1949) in his classic work "The genus *Baccha* of the New World". A new overview of the genus is now under way, starting with the division of *Ocyptamus* into recognizable monophyletic subgroups. This work involves a review of the entire genus and a revision of the *tristis* group. The study of the *tristis* species group provided significant novel female genitalic characters which haven't been used previously. Such characters include the shape of the 7th tergite and its basal extensions, and the structure of the 8th tergite. Parts of the mitochondrial genes 12S, COI and CytB, and the nuclear genes AATS, CAD and 28S were sequenced and used for the phylogenetic analysis. We here present preliminary results from this study, with a new diagnosis and a tentative phylogeny for the genus and closely related taxa.

Contents

Flower fly (Diptera, Syrphidae) identification made easy: a photographic key to the North American syrphids

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Representatives of the conspicuous and diverse family Syrphidae are found worldwide, and adults of many species are of considerable economic importance as pollinators. Due to their relatively large size, frequently colorful appearance and conspicuous habits, many (if not most) syrphid genera are readily identifiable in the field with the help of proper identification tools. This project aims to provide such a tool by taking advantage of the opportunities provided to taxonomists by the combination of newly available techniques and equipment for digital macrophotography and new opportunities for publishing photo-rich products on the web. By drawing from a database of over 10,000 images ranging from live field shots to high magnification photographs of specific morphological characters, we have developed a photographic key which is intuitive to use yet comprehensive, covering all genera of Syrphidae in the Nearctic Region. Every page is fully illustrated, with accompanying text designed to highlight important characters. The completed key will be submitted to the CJAI (Canadian Journal of Arthropod Identification), an online, open-access and peer reviewed journal. Publication in CJAI will guarantee that the key will be available anywhere in the world where internet access is possible and that the scientific content will be reviewed by relevant specialists.

Contents

Application of geographic information system in the study of the distribution of Syrphidae (Diptera) Antioquia-Colombia

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Syrphidae are one of the most diverse families of Diptera. Adults are pollinators, associated with a variety of plants, whereas the larvae exhibit a wide spectrum of feeding habits. Since adults are generalists the presence of syrphid species in an ecosystem depends on the availability of different resources for larval development. Antioquia is located in northern Colombia and presents a mosaic of altitudinal ranges and life zones. In order to understand the relationship between distributions and a series of key environmental variables, we reviewed and identified 1100 syrphid specimens housed in various entomological collections. Geographic information was databased, and maps of environmental variables (e.g. altitude, temperature, life zones and rainfall; IGAC, 2007) were digitized using ArcGIS tools. Distribution maps and Canonical Correspondence Analysis were produced in order to link environmental variables to the distribution of each genus. A total of 28 genera and 125 species were identified, of which 2 genera and 79 species (*Scaeva* Fabricius and *Lycastrirhyncha* Bigot) are reported for the first time in Colombia. There are also 14 new reports for páramo-inhabiting species and 12 species that are likely new to science. The results show that elevation and temperature are broadly correlated with the distribution of syrphid taxa, possibly mediated by larval feeding habits. Field work in additional and underexplored areas will help expand and substantiate these observations.

Contents

Phylogeny of the Eristaliini tribe (Syrphidae, Eristalinae) based on morphological characters

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The family Syrphidae is traditionally divided into three subfamilies: Eristalinae, Syrphinae and Microdontine. Eristalinae currently comprises ~3000 described species in 114 genera, which is half of the known species diversity in the family. Among recognized tribes of Eristalinae, Eristaliini is the second largest regarding number of genera (32), with ~820 described species and with a world-wide distribution. Eristaliini comprises species with 'rat-tailed' larvae and is traditionally divided into three subtribes: Eristaliina (characterized by adults with cell r_1 closed, vein R_{4+5} strongly sinuate and hind femora with basal setal patch), Helophiilina (with the same character combination as the Eristaliina except for cell r_1 open) and Sericomyiina (characterized by adults with cell r_1 open, vein R_{4+5} straight or slightly sinuate and hind femora without basal setal patch). Recent research supports Eristaliini as a monophyletic group, but there are no available inferences about internal relationships. In this study, the phylogenetic relationships among Eristaliini taxa are being reconstructed using parsimony and based on adult morphology. A total of 150 taxa around the world are being studied, totaling 30 Eristaliini genera and four outgroup taxa. Phylogenetic relationships among included taxa and the concordance of placement of taxa with traditional subtribal classification are discussed in light of these results.

KEY WORDS: cladistic analysis, flower flies

Contents

Morphology of the immature stages of *Microdon biluminiferus* Hull, 1944 (Diptera, Syrphidae)

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Specimens of Microdon biluminiferus were found in ant nests residing in bromeliad rosettes. Field work was carried out between December 2005 and January 2009 at a mountainside in Santo Antônio de Lisboa (in the following called "Santo Antônio"; 27°30' S, 48°30' W) within the district of Florianópolis, on Santa Catarina Island, southern Brazil. All larvae, pupae and adults of M. biluminiferus were obtained from nests of ants belonging to the species Crematogaster limata. Their nests were usually found in rosettes with broad, short, erect leaves, forming hollow cavities between each other; frequently carton-like structures closed the upper opening of the cavity. Sometimes rosettes with slender, far-projecting leaves were also found to form such cavities at their bases, making those plants suitable nest sites, too. Ten out of 33 (30%) systematically examined Crematogaster nests contained M. bilumineferus brood. Twenty-three colonies of other ant genera were found, one of them (Brachymyrmex coactus) with remains of puparia of Microdon, the others without evidence of Microdon infestation. Almost all ant nests were found in rosettes of the bromeliad species Aechmea nudicaulis and A. lindenii. Larvae and pupae were conserved in Kahle's solution; voucher specimens of larvae and imagines of Microdon as well as associated ants were deposited in the collection of the Native Bee Laboratory of the Federal University of Santa Catarina [LANUFSC] and Entomological Collection Father Jesus S. Moure, Federal University of Paraná [DZUP]. The first, second and third instar larvae were differentiated, the third instar larva was described. The adult male genitalia were described and illustrations presented.

KEY WORDS: Bromeliads, Microdontinae, Neotropical Region

Molecular phylogeny of the horse flies: a framework for renewing tabanid taxonomy

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Introduction: Horse flies (Diptera: Tabanidae) are an economically, medically, and ecologically interesting group containing bloodfeeding pests and long-proboscis pollinators. This group, with over 4,300 described species and difficult, simplistic morphology, has experienced an almost complete loss of taxonomic expertise in the last decade. The Tabanid PEET project will fill this gap by training at least four postgraduate students. As a framework for student taxonomic revisions, we present here a new, higher level molecular phylogeny of the horse flies. This molecular work will guide the choice of informative, morphological characters, and help focus student projects on evolutionary units. We also use this phylogeny to ask the following questions: 1) Are the three, current subfamilies monophyletic? 2) Is long-proboscis morphology ancestral in Tabanidae?

Methods: Using multiple exemplars from all currently described tribes (9) and widely accepted subfamilies (3 + Scepsidinae), we sampled two nuclear (CAD, ATTS), and one mitochondrial (COI) gene from alcohol preserved material. Phylogenetic inference was performed using Parsimony and Maximum Likelihood in Paup*, and using Bayesian Inference in Beast. Character reconstruction was optimized using BayesTraits and MacClade.

Results: Our resulting phylogenetic hypothesis for Tabanidae is largely similar to the classical systematic hierarchy with a few exceptions. Chrysopsinae is paraphyletic with respect to the Tabaninae. Also, the three tribes of Pangoniinae do not form monophyletic groups. The long-proboscis habit is strongly supported as ancestral.

Conclusions: The current taxonomy of Tabanidae at the subfamily and tribal level needs to be revised based on new, molecular evidence. Additionally, long-proboscides appear to be ancestral suggesting tabanids are ancient pollinators.

KEY WORDS: Tabanidae, Tabanomorpha, molecular phylogenetics, PEET

Contents

Floral niche models best explain proboscis length evolution in long-tongued, bloodsucking pollinators (Diptera: Tabanidae)

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The relationship between plants and their pollinators has often been upheld as the best example of bioticaly mediated speciation, specialization and co-divergence. Hypotheses regarding the mechanism of trait evolution in these relationships are focused on plants. They include two main hypotheses 1) plants and pollinators are in a coevolutionary race and 2) pollinators are relatively constant and plants evolve in response to pollinator shifts. Here I address the adaptive significance of pollinator morphology in a species complex of long-tongued horse flies by asking: 1) Have long proboscides evolved multiple times? 2) Is their evolution consistent with a coevolutionary arms race (always increasing)? 3) Is pollinator morphology adapted to floral niches?

Methods: I sampled nuclear and mitochondrial genes from 9 of the 11 tabanid tribes with multiple geographic exemplars within the *Philoliche aethiopica* species complex. Twenty trees were randomly sampled from a Bayesian posterior distribution of 20 million generations, representing 13 unique topologies and branch lengths variation. For each tree, branch lengths in terms of time were estimated in r8s, character reconstruction was optimized using BayesTraits (Maximum Likelihood) and Mesquite (Max-Min Squared Changes Parsimony). Floral association models were tested using OUCH.

Results: Ancestral reconstruction supports multiple, independent evolutions of long proboscis morphology. Max-Min coding shows evolution of both longer and shorter proboscides. OUCH models strongly support the adaptive significance of Floristic Region and Wastonia floral morphology.

Conclusions: Proboscis length evolution seems labile and non-directional, incongruent with a coevolutionary arms race. However, proboscis length appears to evolve in response to floral niches.

KEY WORDS: Tabanidae, coevolution, pollination

Contents

Modelling the zoogeography of South African Atherigona s. str. (Diptera: Muscidae)

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Distributional data of approximately 2000 specimens from all nine provinces within South Africa were recorded from various natural history museums and research collections and used to determine the zoogeography of the species of Atherigona s. str. found in South Africa. Due to the biology and close association of larval instars of this subgenus with gramineous plants, it is possible to do predictive modeling of the flies' distribution throughout South Africa, using various environmental variables, including the vegetation map of South Africa and rainfall patterns. All calculations and analyses were done in MAXENT. A probability model was created and the feasibility of the model tested by comparison to current distribution data. This knowledge will be used to plan future collection trips, ensuring that the distribution and richness of the species of Atherigona s. str. is more accurate and complete for South Africa. This information will lead to numerous outputs, one of which will be the complete revision of the group in South Africa. This information can ultimately be applied to not only current and future Integrated Pest Management practices, but also in ecological evaluations throughout South Africa.

KEY WORDS: *Atherigona*, zoogeography, modelling,
Geographic Information Systems, Integrated Pest Management

Contents

Cross-shifting of the clasping components of the epandrium of *Plethysmochaeta nobilis* Schmitz (Diptera: Phoridae)

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The male genitalia of *Plethysmochaeta nobilis* show asymmetric features, mainly due to the presence of a surstylus situated only on the left side. This unique feature is interpreted by Brown (1992) as the right surstylus shifted to the left side and completely fused to the left surstylus. In this study, further detailed structure of the asymmetric male genitalia in *P. nobilis* is investigated. In *P. nobilis*, the bacilliform sclerites of the epandrium extend from the small subepandrial sclerite to two claspers, the left surstylus (the fused surstyli) on the left side and the small clasping lobe on the right side of the epandrium. Interestingly midway along the bacilliform sclerite to the clasping lobe on the right side of the epandrium, an extra clasping lobe is observed. The extra lobe appears to be equivalent to the clasping lobe on the right side of the epandrium. The extra lobe must have originally been situated on the left side of the epandrium, and is shifted to the right side. It is considered that relative to the derived state in *P. nobilis*, the plesiomorphic state of the clasping components of the epandrium is comprised of two pairs (the left and right surstyli, and the left and right clasping lobes). In *P. nobilis*, the left clasping lobe is shifted to the right side and its bacilliform sclerite is completely fused to the one for the right clasping lobe, while the right surstylus is shifted to the left side and completely fused to the left surstylus. The current feature of the epandrium in *P. nobilis* is due to the cross-shifting of the clasping components.

KEY WORDS: asymmetry, bacilliform sclerites, male genitalia, subepandrial sclerite, surstylus

Phylogenetic analysis of entire mitochondrial genomes recovers Dipteran relationships

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Use of the entire mitochondrial genome is a promising new source of genetic evidence for insect phylogeny, but these have rarely been used to establish intraordinal relationships. We tested the utility of mitochondrial genome data for the resolution of relationships within Diptera, the insect order for which the most data are available. Mitochondrial genomes were sequenced by the FLYTREE consortium for the 42 First Tier species, and we complemented these with fly mitochondrial genomes available for other species. Phylogenetic analyses of these sequences produced trees that were largely consistent with previous phylogenetic hypotheses of the Order. The implications of this study for dipteran systematics and effective approaches to using mitochondrial genome data are discussed. Mitochondrial genomes resolve many expected nodes within Diptera and are useful over wide time scales and genetic distances. The addition of ribosomal and transfer RNA genes to the protein coding genes traditionally used in mitochondrial genome phylogenies improve resolution and support.

KEY WORDS: Diptera, mitochondrial DNA, phylogeny, relationships, evolution

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The dance flies (Diptera: Empidoidea) of Western Mongolia and the Selenge River Basin

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Dance flies of the superfamily Empidoidea (Diptera: Empididae, Hybotidae, and others excluding Dolichopodidae) were collected from northern and western Mongolia from 2006 to 2009. Historical published records of Empidoidea, of similar taxonomic scope, in Mongolia along with unpublished, more recently collected records from the Selenge River Basin were compared with the samples from extreme western Mongolia. Thirteen genera were identified from western Mongolia in 2009, with eight of these as new records for the country. Although 23 genera of Empidoidea are now recorded in Mongolia, only five were found in both the Selenge River drainage and the 2009 collection from western Mongolia, suggesting distinct differences in faunal composition between the two areas. Future work will fill in gaps of distribution, with a trip planned to the Uvs region in summer 2010. The generic faunas of the aimags (provinces) of Mongolia will be compared to those of other, similarly sampled geographic regions.

KEY WORDS: survey, expedition, biomonitoring, diversity

Native parasitoids (Hymenoptera) in larvae of frugivorous Tephritoidea (Diptera) in South Pantanal, Brazil

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The frugivorous larvae of Tephritidae and Lonchaeidae are key pests of fruits and vegetables in Brazil and many other countries of South America. Their most important natural enemies for biological control are parasitoids in the families Braconidae and Figitidae. The aim of this study was to evaluate the incidence of parasitoids (Hymenoptera) on larvae of fruit flies (Tephritidae) and frugivorous Lonchaeidae infesting several species of native and exotic fruits in the South Pantanal Region, Mato Grosso do Sul, Brazil. Ninety-one species of fruits from 36 families and 21 orders were sampled. A total of 89,593 fruits were collected (1,141.55 kg of biomass), resulting in 28,680 frugivorous larvae, including 22,254 larvae of Tephritidae from which emerged 10,845 adult fruit flies, and 6,426 larvae of Lonchaeidae, resulting in the mergence of 3,792 adults. In 13 species of host fruits, larvae of Tephritoidea were parasitized by species of Braconidae, Figitidae, or Pteromalidae (729 parasitoids). Among these parasitoids, 99.45% were Braconidae but only 0.55% were Figitidae or Pteromalidae. The following species of Braconidae were obtained: *Doryctobracon areolatus* (Szépligeti) (92.78%), *Utetes anastrephae* (Viereck) (6.17%), and *Opius* sp. aff. *bellus* Gahan (0.82%). The figitid, *Lopheucoila anastrephae* (Rohwer) comprised 0.27% of the non-braconids,and 2 adults of *Spalangia* sp. (Pteromalidae) emerged from puparia of *Neosilba* spp. (Lonchaeidae) in pods of *Inga laurina* (Swartz) (Mimosaceae). *Doryctobracon areolatus* was the predominant species (92.47% of total number of parasitoids), attacking larvae of *Anastrepha* spp. (Tephritidae). This species was associated with third instars of *Anastrepha alveatoides* Blanchard feeding on fruits of *Ximenia americana* L. (Olacaceae). The braconids were specific to Tephritidae, and the figitids were associated only with larvae of frugivorous Lonchaeidae.

KEY WORDS: frugivory, Braconidae, Tephritidae, Lonchaeidae, tritrophic interactions, taxonomy

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Taxonomy and phylogeny of Ormiini (Tachinidae): diversity and evolution of cricket parasitoid flies

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Members of Ormiini are characterized by a prosternum strongly inflated, bilobed and anteriorly projected as the prothorax is internally modified as an auditory organ. This unusual acoustic system allows female flies to locate singing male hosts (crickets, mole-crickets and katydids; Grylloidea and Tettigonioidea) and then deposit endoparasitoid planidia larvae, which will penetrate and develop inside the host until pupation. Therefore, the adults have preferably crepuscular and nocturnal habits. The tribe Ormiini comprises 64 species in 7 genera: *Aulacephala* Macquart, 1851 (2 spp; Afrotropical/Palaearctic/Oriental); *Homotrixa* Villeneuve, 1914 (3 spp; Australasian/Oriental); *Mediosetiger* Barraclough, 1983 (1 species; Afrotropical); *Ormia* Robineau-Desvoidy, 1830 (27 spp; Nearctic/Neotropical); *Ormiophasia* Townsend, 1919 (9 spp; Neotropical); *Phasioormia* Townsend, 1933 (2 spp; Oriental); *Therobia* Brauer, 1862 (20 spp; Afrotropical/Australasian/Oriental/Palaearctic). The systematic position of Ormiini is controversial. Previous authors placed it within Dexiinae (as 'Proseninae'), Phasiinae, or even in Oestridae, although recent classifications are consensual about Ormiini within Tachininae. The present research project is composed by two parts. First, a phylogenetic study includes a cladistic analysis based on morphological characters in order to: 1) examine the monophyly of the tribe and genera, 2) generate an hypothesis of the phylogenetic relationships among the seven genera and other supraspecific taxa, and 3) to support a systematic placement of Ormiini. Members of Glaurocarini are included in the analysis to test its close relationship with Ormiini as suggested by some authors. And, finally, a taxonomic study includes: 1) revision of all 34 Neotropical species in *Ormia* (25 spp) and *Ormiophasia* (9 spp), 2) an identification key to species of *Ormia* and *Ormiophasia*, and 3) a key to world genera of Ormiini.

KEY WORDS: systematics, cladistics, biogeography

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Swedish insect diversity and the family of Phoridae (Diptera)

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Biodiversity is an important topic in biology, conservation, and politics. In Sweden, the government decided in 2002 to launch a project with the goal to provide keys to all multi-cellular organisms in Sweden, the Swedish Taxonomy Initiative. One project that received funding by this initiative is the Swedish Malaise Trap Project. Over the course of three consecutive years (2003-2006) 75 Malaise Traps were placed all over Sweden. This resulted in an estimated 40 million insects being collected. The material is being sorted to orders and, in the case of Hymenoptera and Diptera, even further to families or subfamilies and made available for taxonomists to study. One family of Diptera that is found in virtually all of the more than 2,000 samples is Phoridae.

Phoridae is one of the largest families of Diptera, with about 3,000 species described at present. However, possibly as much as 90% of the species are not described yet and even in a well-sampled and well-described region as the Palaearctic, new species are described every year.

The project presented here deals with systematics and taxonomy of the largest genus of Phoridae, the genus of *Megaselia*. Almost half of all currently described species of Phoridae belong to this genus. Although a number of morphologically distinct groups within *Megaselia* were described by Schmitz in the middle of the last century, these groups have not been used by other researchers.

One part of the project is to investigate with molecular methods if these groups hold and may be used to split up *Megaselia*. Preliminary results show that at least some of these groups appear to be monophyletic. A revision of one of these groups, the *Kryophila* group, is planned with new species being described. This will be a first step towards an easier taxonomy of *Megaselia*.

KEY WORDS: Phoridae, biodiversity, new species

The fruit fly genus *Parastenopa* Hendel (Diptera: Tephritidae)

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Parastenopa Hendel is a New World, mostly Neotropical, genus of fruit flies associated mainly with the plant genus *Ilex* (Aquifoliaceae). It includes one described eastern Nearctic species and nine described and at least 28 undescribed Neotropical species. The bulk of material we examined is from Costa Rica and Panama where at least 18 species, only one of them described, occur. Four of the five species for which host records are known were reared from species of *Ilex*, including one from fruit, two mining twigs, and one feeding in leaf galls of a psyllid. Three species breed in *I. paraguariensis* (yerba-mate). Another species reportedly was reared from bud galls caused by a species of Cecidomyiidae on a *Marcetia* sp. (Melastomataceae). *Parastenopa* is one of the basal-most lineages of the subtribe Chetostomatina of the tribe Trypetini. Preliminary phylogenetic analysis based on morphological characters indicates that most of the species, except for one interesting species from Costa Rica with a bifurcate aculeus tip, belong to two well-defined clades.

KEY WORDS: Tephritidae, fruit flies, taxonomy, biology

Building a unified classification of the Tachinidae (Diptera) of the world

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The Tachinidae are among the largest families of Diptera with almost 10,000 described species. These species are currently assigned to an unmanageable and oversplit 1500+ genera. The existing and in some cases disparate classifications of the Tachinidae are delimited by biogeographic region and were established between 1971 and 2009, with the classification of the huge Neotropical fauna being the oldest and most in need of revision. Two major initiatives are underway to address problems in tachinid systematics: 1) morphological and molecular studies to investigate tachinid relationships at the generic, tribal and subfamilial levels, and 2) a world catalogue of the Tachinidae to reflect the state of knowledge about tachinid relationships and to establish a unified global classification scheme. The latter involves an authoritative re-appraisal of all names in Tachinidae to provide the most accurate and Code-compliant information possible about original names, name-bearing types (as reinterpreted to comply with Recommendation 73F, "Avoidance of assumption of holotype"), type depositories, type localities (in original and modern forms), and distributions. Original descriptions of 15,000+ generic and specific names, as published in ca. 3000 works, form the basis for the name and type data. All name, type and distributional data are managed in a custom-designed FileMaker Pro database and references are managed in a separate EndNote library. Distributions are recorded first by biogeographic region and then by finer divisions at or below the country level according to the best fit of available data. Distributions based on the old triangulation system formerly used for the tachinids of America north of Mexico have been converted into a databasable format that recognizes 18 divisions in Canada, United States, Greenland, and Bermuda. The division between the Palaearctic and Oriental Regions in China has been studied in particular detail in light of the topographical and ecological complexities involved.

KEY WORDS: Tachinidae, classification, catalogue

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Taxonomic revision of the Neotropical species of genus *Ablabesmyia* Johannsen (Diptera: Chironomidae)

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The genus *Ablabesmyia* was erected by Johannsen (1905) based on *Tipula monilis* (Linnaeus). This genus, which belongs to the subfamily Tanypodinae, shows large geographic distribution and is commonly cited in ecological studies, most of which at a generic level, since there are few studies relating adults to immatures. Up to now 11 species have been recorded or described in the Neotropical Region: *A. monilis*, *A. peleensis* (Walley), *A. cinctipes* (Johannsen), *A. costarricensis* Picado, *A. punctulata* (Philippi), *A. infumata* (Edwards), *A. bianulata* Paggi, *A. reissi* Paggi et Suarez, *A. metica* Roback, *A. oliveirai* Oliveira et Gessner and *A. platensis* Siri et Paggi. Based on the re-examination of the holotypes, these species are revised, re-described, figured and keys to known larvae, pupae and male adults are presented. Eleven new species from Brazil, with their respective immature stages, are diagnosed and described. The generic diagnosis given by Murray and Fittkau (1989) is emended. The partial results of cytocrome oxidase subunit I (COI) gene sequences (DNA barcodes) of nine species are presented. The main characteristics to distinguish the species are: in the adult stage, the complex aedeagal structures; in the pupal stage, the shape of thoracic horn and anal lobe; and in the larval stage, the characteristics of posterior parapod claws.

KEY WORDS: Brazil, DNA barcodes, keys, new species, non-biting midges

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Evolution of Mycetophilidae Leiinae: limits, diversity, phylogeny, and biogeographical relationships

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The dipteran family Mycetophilidae presently includes about 135 extant genera and 4,100 species worldwide, with a well supported hypothesis of monophyly. Seven subfamilies are currently recognized: Sciophilinae, Gnoristinae, Mycomyiinae, Leiinae, Manotinae, Allactoneurinae, and Mycetophilinae. The Leiinae comprises 32 recent genera and about 550 species. The fossil record includes 54 species in 8 genera, the oldest ones from the Cretaceous. Problems with subfamily delimitation point to doubts about its monophyly. There is no agreement about *Tetragoneura*, *Docosia*, and *Ectrepesthoneura*, e.g., belonging to Leiinae or Gnoristinae. Moreover, *Allactoneura* is either treated as a subfamily, a genus of Manotinae or Leiinae. A phylogenetic analysis of Leiinae shows sets of apomorphies in the wing venation that define inclusive clades of genera at different levels: (1) displacement of the separation between R_1 and Rs to the apex, reduction of the extension of R_5, perfectly transverse position of the first sector of Rs, and more or less longitudinal r-m; (2) basal interruption of M_4; (3) fusion of A_1 to a sigmoid CuA, resulting in a secondary close cell. The first group of features helps to include in Leiinae *Tetragoneura*, *Docosia*, *Aphrastomyia*, *Novakia* and other closely related genera with relatively plesiomorphic features, so they would be close to the base, but already belonging to the subfamily. The second group of features gathers *Leiella*, *Rondaniella*, *Cycloneura* and related genera. The third group includes basically genera around *Cycloneura*. The evolution of some features is complex, with obvious reversions along the evolution of Leiinae. Some of Neotropical species of *Leia*, better fits in *Clastobasis*, so the genus is paraphyletic. One of these smaller clades of Leiinae displays a typical austral distribution, known from southern South America, Australia, New Zealand and related southern temperate areas.

KEY WORDS: Mycetophilidae, Leiinae, phylogeny, taxonomy, biogeography

An overview of Afrotropical Oestroidea

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The Afrotropical Oestroidea comprise a rich fauna of the families Calliphoridae, Oestridae, Rhiniidae, Rhinophoridae, Sarcophagidae and Tachinidae. The Rhinophoridae seem to have their greatest species richness in the southern part of the continent, but this may be at least partly due to lack of collecting and/or attention to this family in other parts of the region. New taxa are continuously being discovered, including records from Madagascar, and generic definitions are improving but still needs to take full advantage of phylogenetic methodology. The Oestridae have their center of diversity in the Afrotropics, and the origin and early evolution of stomach bot flies probably took place in humid African forests. The Afrotropical Rhiniidae have diversified considerably and are in many ways comparable to those of the Oriental Region. In the Calliphoridae, there is a marked lack of several subfamilies (Ameniinae, Aphyssurinae, Helicoboscinae, Melanomyiinae, Mesembrinellinae, Polleniinae, Toxotarsinae), but the subfamily Bengaliinae seems to have undergone a significant diversification, probably taking advantage of the rich termite fauna with which many species are associated. In the Sarcophagidae, the Miltogramminae are richly diversified in the semi-desert and savanna biomes, and the particularly diverse phylloteline clade would be a promising target for biological studies as they are expected to show numerous examples of associations with termites, ants, and buried carrion. The Afrotropical Tachinidae are diverse, although apparently less so than those of the Oriental and Australasian regions, and far less diverse than those of the Neotropical Region.

KEY WORDS: Calliphoridae, Oestridae, Sarcophagidae, Rhiniidae, Rhinophoridae, Tachinidae

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Rhinophoridae here, there and everywhere: evidence of ancient origin?

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The Rhinophoridae are a small family with about 150 described species, all of which are known or suspected to be parasitoids of wood-lice. Previously, the family was considered to be largely European-Afrotropical, but this picture is now changing dramatically. While Rhinophoridae still appear to have their peak of species-diversity around the Mediterranean, which is a biome well-known for its rich fauna of terrestrial isopods, this distributional skewness may now be considered as partly due to lack of collecting and/or attention to this family in other parts of the world. Species that are best placed in the Rhinophoridae are being discovered from the warmer parts of all continents, and records are now at hand from the large islands Madagascar, New Guinea and New Caledonia, which were previously without any known representative of this family. Even the European fauna continues to bring surprising discoveries, which have implications much beyond simple faunistics. Our knowledge of immature stages and breeding biology is still very fragmentary, which is unfortunate as in particular first instar morphology would seem to contain by far the strongest evidence for an unambiguous definition of the family. As of today, no reliable unique autapomorphies have been found in the adult morphology. Phylogenetic groupings are very tentative, but there is growing evidence that the family dates from the early Tertiary and shows some ancient distributional patterns.

KEY WORDS: Calyptratae, Rhinophoridae, phylogeny, diversity, origin

Systema Dipterorum – the new portal for information about Diptera

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Names are crucial for precise communication. And names are the critical components from which we build our classifications, which in turn are the key indexing and organizing structures for information about life on earth. The BioSystematic Database of World Diptera grew out of various initiatives proposed by USDA dipterists a quarter of a century ago. Today, the dipterist community can be proud of being in charge of the most comprehensive and authoritative nomenclatural portal for a major group of animals. With more than 156,000 valid species, Diptera alone contains about 10% of all named, multicellular lifeforms on this planet. While the current dataset is far from finalised, we realise the considerable benefits in integrating a comprehensive nomenclator with a species interface to satisfy user needs for taxonomic authority data. And as a logical extension to that, we will be providing a model for accessing species by attributes of biological significance, such as distribution and associations. This new, more comprehensive and more elaborate portal, which will be deployed under the name 'Systema Dipterorum', will be demonstrated along with our progress report and global and regional statistics.

KEY WORDS: nomenclature, taxonomic authority files, progress report

Calyptrate family-level phylogeny – has the dust settled yet?

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The Calyptratae is one of the largest and most diverse clades of two-winged insects, and with some 18,000 described species the calyptrates represent 12% of Diptera diversity. Recent research has intensified the focus on family-level relationships within the calyptrates, utilising mainly molecular data. Calyptrate monophyly remains uncontroversial, although only few unique autapomorphies are known. The Hippoboscoidea are firmly established as the sister taxon of the remaining calyptrates, but growing evidence points to the Nycteribiinae being paraphyletic with regard to the Streblinae. The muscoid grade is paraphyletic, with the Fanniidae being the most probable sister taxon of the remaining non-hippoboscoid calyptrates, and Anthomyiidae-Scathophagidae possibly being the sister clade of a well-supported Oestroidea. Family-level phylogeny within the Oestroidea is still largely obscure, but some important advances have been made. With the notable exception of the traditional Calliphoridae, the monophyly of the constituent oestroid families is well-corroborated from morphology, while molecular data are still ambiguous for the Oestridae and Rhinophoridae and inconclusive for the Tachinidae. The family Rhiniidae – recently raised from its status as a calliphorid subfamily – seems well justified. The morphologically and biologically highly derived *Mystacinobia zelandica* appears to be cladistically near McAlpine's Fly, and both of these seem to have a position close to the base of the Oestroidea, although with some differences between molecular and morphological data.

KEY WORDS: Calyptratae, Hippoboscoidea, Muscoidea, Oestroidea, phylogeny, family-level

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The Neomuscina Townsend (Muscidae) in Brazil: a review

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The genus *Neomuscina* Townsend, 1919, comprises 38, mostly neotropical, species. The genus was last revised in 1949, with the addition of a few new species. An addendum in 1954 provided new synonyms for the known species. Subsequently, the genus has been mostly ignored. Here we review the genus and describe three new species. We identified 24 known species, of which three are new for Brazil. We provide an identification key based on morphological characters of both males and females. Because of this first morphological analysis, including male and female genitalia, monophyly of the genus is now questioned. Today, *Neomuscina* and *Spilopteromyia* Malloch, 1921 are synonyms. Interestingly, we found differences in genitalia of species previously included in *Spilopteromyia* from those in *Neomuscina*. For example, the genitalia of *Neomuscina atincticosta* are similar to those in *Cyrtoneurina*, while genitalia of *N. currani* are different from all other species of *Neomuscina*. These differences suggest that *Spilopteromyia* should be reinstated as a valid genus. Additionally, we updated the distributions of some species. We continue reviewing the remaining species and are carrying out a phylogenetic analysis of all the *Neomuscina*, to resolve the major problems associated with this genus.

KEY WORDS: Brazil, Neomuscina, review, taxonomy

A historical narrative of the Neriidae: the taxonomic abandonment and the new perspectives

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After the first description of a species in the Neriidae (*Nerius pilifer*, by Johann Fabricius in 1805) the family has received very little attention. Few species were described until the early 1900s, when a taxonomic boom occurred. Here we examine this history of taxonomy of the family, starting with Günter Enderlein, who, in 1922, was the first to attempt to clarify the obscure taxonomy of the family. Willi Hennig, in 1937, comprehensively reviewed the family. This was followed by arguably the greatest contribution due to Martin Aczél, between 1949 and 1961, who elucidated morphology and taxonomy. The taxonomic revival, however, ended with the death of Aczél, after which only five species have been described. Today, 19 genera with around 111 species are recognized. Here, we begin a new revival of the family with a thorough, detailed taxonomic revision of all species, with a phylogenetic analysis. The information is being used to update the global catalog of the Neriidae, as well as a list of family-group names applied to the family. Through these initiatives, we will augment the continued revival of the Neriidae in an attempt to fill the gap of the last 50 years.

KEY WORDS: historical review, Neriidae, taxonomy

Taxonomy, phylogeny and biogeography of the genus *Apsil* (Muscidae) with description of a new Colombian species

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Previously, the muscid genus *Apsil* Malloch was known to be endemic to Patagonia and southern Chile, with 12 species found in mountainous regions of the southern Andes. *Apsil* is in the tribe Coenosiini, the most derived of the subfamily Coenosiinae, which includes ~40% of the known species of Muscidae. *Apsil* is considered to be monophyletic based on three synapomorphies: head flattened, gena high, and four frontal setae present. *Reynoldsia* Malloch is a sympatric sister-genus of *Apsil*. Here, we describe a new species based on a male that was found at 4700 m at El Nevado de Santa Isabel, in the central range of the Andes in Colombia. Presence of this species in Colombia extends the distribution of the genus to now include the northern Andes. Such discoveries are not uncommon in the Muscidae. Phylogenetic analysis of the 11 species, using 22 morphological characters, produced only one tree. We used Brooks parsimony analysis (BPA) and NONA in WinClade. Through this analysis we find an Andean distribution for the genus. The Andean region is considered by many to be the key for understanding the hybrid origin of the South American biota.

KEY WORDS: Andes, Colombia, South American Transition Zone, taxonomy

Contents

Cladistic analysis of *Toxomerus* Macquart, 1855 (Syrphidae: Syrphinae): preliminary results

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Toxomerus belongs to the monotypic tribe Toxomerini. It is one of the most specious genera within Syrphidae, currently comprising approximately 150 described species that are found in the New World. Despite available taxonomic studies of species groups, *Toxomerus* is notable for its lack of internal taxonomic resolution. Thus, a cladistic study, including comprehensive taxon sampling, has been undertaken to further clarify phylogenetic relationships within this genus. Currently, 65 species are being used in the analysis, in addition to two outgroups, *Ocyptamus fuscipennis* and *Salpingogaster nigra*, which are species in genera possibly related to *Toxomerus*. In spite of the likely inclusion of other terminals in the future, a preliminary analysis has been undertaken, using the program TNT. The initial analysis of 46 phylogenetically informative morphological characters has produced a strict consensus tree that confirms the monophyly of the genus and the existence of historical species clusters involving some of the included species. Important synapomorphies for the genus thus far are: (1) face produced anteriorly, (2) eyes with distinct posterior triangular emargination at or dorsal to level of antennal insertions and (3) wings without dark markings. Most of the larger species of this genus grouped together as previously indicated in the literature. Some other expected close relationships have also been indicated, such as: the sister-relationship between *T. marginatus* and *T. rohri* as well as between *T. occidentalis* and *T. geminatus*; and *T. vertebratus* and *T. calceolatus*. Another distinct clade is formed by the darker species: *T. funestus*, *T. ovatus*, *T. flaviplurus*, *T. anthrax*, *T. dispar* and *T. laenas*. The results obtained thus far show positive prospects for continued analysis.

KEY WORDS: flower flies, historical relationships, New World

Diversity and phylogeny of Hemerodromiinae (Diptera: Empididae)

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Phylogenetic relationships in Hemerodromiinae (Diptera: Empididae) were investigated by cladistic analysis of 69 adult morphological characters. *Afrodromia*, *Drymodromia* and an undescribed Chilean genus were recovered basally to a sister-group relationship between the tribes Hemerodromiini and Chelipodini. Although *Chelipodozus* and an undescribed Australian genus were weakly supported in Hemerodromiini they were considered incertae sedis within Hemerodromiinae. *Anaclastoctedon* and an undescribed Australian genus were resolved basally in Chelipodini below two sister-group clades:- (1) A Widespread *Chelipoda*-like group comprising *Achelipoda*, *Ptilophyllodromia*, *Chelipoda* s.str. and *Phyllodromia* s.str. with world-wide distribution excepting the Afrotropics, considered to be of early origin dating from before the later fragmentation of Gondwana. *Phyllodromia* s.str. is a Northern Hemisphere genus of doubtful validity to which Southern Hemisphere forms have been incorrectly assigned. *Ptilophyllodromia* is shown to be based on male secondary characters and should be reassigned to *Chelipoda*. (2) An Austral *Chelipoda*-like group confined to New Zealand, New Caledonia, Lord Howe Is. and Vanuatu included *Monodromia* and species currently incorrectly assigned to *Chelipoda* and *Phyllodromia*. This group is hypothesised as a relictual Gondwanan element which has survived Oligocene drowning as metapopulations persisting in situ on ephemeral islands along arcs, ridges and buoyant crustal blocks overlying hot spots. Many Southern Hemisphere Hemerodromiini species currently assigned to *Hemerodromia*, *Cladodromia* and *Neoplasta* require reassignment. The basal sister-group relationship between the southern African endemic *Afrodromia* and other Hemerodromiinae is viewed as evidence of early divergence of Hemerodromiinae and Empidinae by the early Cretaceous, before major Gondwanan fragmentation.

KEY WORDS: Diptera, Empididae, Hemerodromiinae, phylogeny, diversity, biogeography

Contents

Evidence for mimicry in the pollination of *Dracula* orchids

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The orchid genus *Dracula* Luer was segregated from *Masdevallia* Ruiz & Pav. based in part on the unique mushroom-like morphology of the lower labellum shared by species in this genus. This morphology has led to long-held hypotheses that these flowers mimic mushrooms to attract fungus gnat pollinators. Recently it has been shown that at least some members of the genus are in fact pollinated by fungus-visiting flies in the family Drosophilidae. Our project examines in greater detail the pollination biology and the ecology and evolution of mushroom mimicry in these enigmatic plants. We are using field experiments, genetic analysis, and scent chemistry to elucidate the causes and consequences of pollination by fungus-seeking drosophilid flies. Our preliminary results show congruence between the fragrance chemistry of *Dracula* orchids and co-occurring mushrooms. While fragrance seems to be important, field experiments suggest it is not sufficient on its own to elicit insect visitation. Our observations confirm that *Dracula* orchids and co-occurring fungi attract the same types of flies, and individual flies have been observed travelling between flowers and mushrooms. We have also documented similar behaviors by the flies on both the orchids and the mushrooms, including displays of territoriality and mating. Rearing insect larvae from older flower and mushroom specimens is in the preliminary phases, but suggests that at least some visitors are using these flowers are brood sites.

KEY WORDS: pollination, mimicry, orchids, Drosophilidae

Contents

Dolichopodid diversity assessment in Neotropical montane forest habitats (Dolichopodidae)

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Trapping techniques such as Malaise traps, pan traps and sweep nets are considered highly complementary with respect to their use in biodiversity assessments. Hence, in order to get a representative picture of present species diversity it is generally recommended to employ them in combination. This integrated approach was applied during a three-week survey (February – March 2009) in and near Podocarpus National Park in the southern Ecuadorian Andes. At three altitudes (Bombuscaro, 1000 m; Estación Científica San Francisco, 2000 m; Cajanuma, 3000 m), at least three sampling sites were selected. In the principal sampling site, one Malaise trap and a series of ten yellow, white, blue, and red pan traps were installed. One series of ten yellow pan traps was in operation in each of the two or more supplementary sites. In each sampling site, long-legged flies (Diptera, Dolichopodidae) were also collected by sweep-netting at least during trap servicing events. Traps were serviced after sampling periods of approx. 6–7 days and yields were pooled per five traps. Dolichopodidae and all other invertebrates were extracted from the samples, and most Diptera were stored separately per taxonomic group. The results of this sampling campaign should enable us to achieve the following five objectives of this study: (1) to assess the alpha and beta diversity of dolichopodid faunas in the southern Ecuadorian Andes; (2) to investigate the impact of altitude – habitat type on species diversity and community structure; (3) to establish the ecological characteristics; and (4) the vagility of the different species in the field. By comparing these yields with those obtained during similar surveys in Costa Rica, it will be investigated if the observed biodiversity patterns are of a general nature. The usefulness of pan traps as devices for short-term dipteran surveys is discussed.

KEY WORDS: biodiversity, trap, Dolichopodidae, Ecuador, Costa Rica, montane

Molecular data yield new insights in the phylogeny of long-legged flies (Diptera, Dolichopodidae)

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With over 7100 species in 17 subfamilies, long-legged flies or Dolichopodidae represent one of the most speciose families in the order Diptera. At present, knowledge on the internal structure of the family and relationships is still mainly based on morphological characters and often poor, whereas recent molecular phylogenetic research generally has a limited zoogeographical and taxonomic scope. Here we present the results of a first comprehensive molecular analysis of the family with an ingroup of 157 dolichopodid species representing 68 genera and 15 subfamilies retrieved from the Palaearctic and Oriental realms, and the New World. Seven Hybotidae and Empididae were used as outgroups. Phylogenetic relationships were inferred from three mitochondrial (COI, 12S, 16S) and one nuclear (18S) markers using Bayesian and Maximum Likelihood analyses. Trees of both analyses featured a very similar topology with well supported and clearly structured clades in the centers and at the top of the tree. The monophyly of Dolichopodidae sensu lato was confirmed, and Microphorinae occupied a sister clade position to the remaining Dolichopodidae. In contrast, Parathalassiinae were not confirmed as sister clade of Dolichopodidae sensu stricto. Achalcinae, Dolichopodinae and Sciapodinae proved monophyletic, whereas Diaphorinae, Medeterinae, Neurigoninae, Rhaphiinae and Sympycninae appeared paraphyletic. Stolidosomatinae is retrieved as strongly supported clade within Sympycninae. Two and three strongly supported but seemingly unrelated lineages are distinguished within the Peloropeodinae and Hydrophorinae sensu Robinson (1970) respectively. Short branches between higher taxonomic entities and longer branches at lower taxonomic levels suggest an early and rapid radiation of the family during the lower Cretaceous.

KEY WORDS: molecular phylogeny, markers, COI, 12S, 16S, 18S, morphology, Dolichopodidae

Contents

Diverse females: Rapid evolution of the internal female genitalia in Sepsidae (Diptera)

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The species-specificity of male genitalia has been well documented in many insect groups. The internal female genitalia, in sharp contrast, are commonly believed to be indistinct among close relatives and remain poorly studied. Here, we present the first comparative study of the internal reproductive system of Sepsidae with a description of the tract for 41 species, representing 21 of the 37 described genera, and we test the species specificity of the female genitalia by comparing recently diverged sister taxa. The female reproductive tract comprises the following components, which are lined by cuticle: a tubular vagina, a ventral receptacle, a ventral evagination, paired dorsal spermathecae, accessory glands, and a tubular ovipositor. The latter, together with sternite VIII, is invaginated between sternite VII and the terminalia. In addition, all sepsids, except *Orygma luctuosum* and *Ortalischema albitarse*, have a dorsal sclerite associated with the opening of the spermathecal ducts. Using a well-resolved molecular phylogeny based on 10 genes, we reconstruct the evolution of female reproductive structures across the family. The ventral receptacle accounts for more than half of all the evolutionary changes observed and it is morphologically diverse across genera, but usually similar in close relatives, can be bi-lobed or multi-chambered (up to 80 chambers), and is strongly sclerotized in one clade. The dorsal sclerite is often distinct even among sister species. Overall, we find the internal female genitalia are diverse in Sepsidae and suggest that fast-evolving structures like the ventral receptacle and dorsal sclerite are likely involved in post-copulatory sexual selection.

KEY WORDS: female genitalia, fast evolution, post-copulatory sexual selection

Population fluctuation of tabanids (Diptera: Tabanidae) in a cattle ranch in the Venezuelan plains

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Females of the family Tabanidae are considered important vectors of various pathogenic parasites, due to their haematophagus habits. They are able to generate serious disease as damaging effects due to their bite and creating economic losses in cattle farms. The main objective was to study the population fluctuation of Tabanidae in a farm in Muñoz County, Apure State, Venezuela. Monthly captures were carried out from November 2009 until May 2010, period in which we comprised the seasonal transition of rain-drought and drought-rain respectively. Six Canopy traps were installed (Hribar et al., 1991) distributed at random in an area of 9 km^2, which is between gallery forests and a savanna occupied by cows, buffaloes and horses. The traps were placed with an approximate distance of 25 m between them. The precipitation data was obtained from a weather station, located on the farm and compared with the data of the weather station of the National Institute for Agricultural Investigations in Mantecal in the Apure State, Venezuela.

After completing seven samples, the results show a total of 1299 captured specimens, belonging to 11 species. We observe that the peak of highest activity was in the month of December (n = 532), during the transition rain-drought, followed by a progressive decrease during the drought period and then a gradual increase of activity in the transition drought-rain. These results allow us to conclude in a partial way that the seasonal transitions have a very important effect over the population fluctuation of these insects. Additionally, we observed that *Tabanus pungens* (n = 522) and *T. claripennis* (n = 491) were the most numerous species (RA = 40.18% and 37.80%, respectively).

KEY WORDS: haematophagy, seasonality, seasonal transition, population fluctuation, relative abundance (RA)

Survival of submersed blow fly species and their parasitoids: Implications for PMSI

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Pupal survival of three blow fly species, *Chrysomya albiceps*, *Chrysomya megacephala,* and *Chrysomya putoria* (Diptera: Calliphoridae) and the parasitoid species *Nasonia vitripennis* (Hymenoptera: Pteromalidae) were studied after experimental submersion in water. Non-parasitised pupae at different developmental stages, 0, 24, 48, and 72 h, and parasitised pupae after 3, 8, 10, and 12 days of development were submersed for 6, 24, 48, or 72 h. Control groups for each pupal developmental stage (parasitised or not), which were not submersed, were used as controls in order to compare the adult emergence rates. The survival of white pupae (0 h/age) decreased with time of submersion for all three blowfly species, showing the lowest rates compared with other experimental pupal groups. For the three blowfly species, non-parasitised pupae at 24 and 48 h of age showed survival rates above 60%. However, for pupae at 72 h of age, the survival rates decreased with increased underwater time, with less than 30% survival after 72 h in *C. putoria* and *C. albiceps.* The survival of parasitoids inside blowfly pupae that were submersed during their larval stage (3 days/age) decreased with the increase of submersion time. After the parasitoids reached the pre-pupal stage, the survival was higher for all periods of submersion. These observations can be useful in investigations of the decomposition of partially submersed bodies, or in cases of pupae found adhering to decaying flesh, hair, or clothes of corpses that were submersed after the larvae had developed and pupated.

KEY WORDS: Calliphoridae, Nasonia vitripennis, forensic entomology, water submersion

Contents

A second survey of Surinam Syrphidae (Diptera)

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Surinam is a small country on the Guyana shield in the northern part of South America. More than 80% of the area is covered by primary rainforest. Compared with other South American countries, the syrphid fauna of Surinam is relatively well known. In the 1960's, around 130 species were recorded by P.H. van Doesburg Sr. In 2006, a second survey of the Syrphidae of Surinam was carried out. Again around 130 species were found, 40 of which had not been found by Van Doesburg. So, the number of Syrphidae species currently known from Surinam is approximately 170. An estimated number of 20 species is undescribed, belonging to; e.g., *Lepidomyia*, *Meromacrus*, *Microdon* and *Palpada*. New biological knowledge is gained from the rearing of larvae of species of *Ceriogaster*, *Copestylum*, *Lepidomyia*, *Ocyptamus*, *Quichuana* and *Toxomerus*, some of which appeared to have an unusual feeding mode. This poster presentation reveals some results of the survey.

KEY WORDS: Neotropics, Guyana shield, Syrphidae, faunistics, taxonomy, ecology

Contents

Taxonomy and phylogeny of Microdontinae (Diptera: Syrphidae)

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As the American entomologist W.M. Wheeler put it in 1908: “Few insects have occasioned more perplexity in the minds of entomologists than the species of *Microdon*”. The ant-associated larvae of *Microdon* were described as molluscs several times, while the adults of certain tropical taxa rank among the most bizarre of all Syrphidae. With over 400 species names considered valid, the Microdontinae constitute the smallest of the three subfamilies of Syrphidae. Paradoxically, this subfamily is taxonomically the least organized of the three: more than 300 species are currently classified in a single genus, *Microdon*. This apparent taxonomic indecisiveness seems to result not so much from a lack of morphological variation, but rather from an excess of it. A long overdue phylogenetic classification of Microdontinae is now being prepared, based on both morphology and DNA (COI, 18S, 28S).

Microdontinae are most diverse in the tropics and a large proportion of the species is only known from the primary types. As a consequence, DNA data could (so far) be included for only approximately 80 species. The morphological matrix contains around 200 characters and 150 species, representing all recognized genera and species groups. More than 300 type specimens were examined, in order to be able to classify all species into higher taxonomic groups. Many additional specimens from various regions were studied, including many undescribed taxa.

This presentation will show some preliminary phylogenetic results, as well as some considerations on what these results may imply for classification, biogeography and evolution of host specialization.

KEY WORDS: taxonomy, phylogeny, Syrphidae, Microdontinae, morphology, COI, 18S, 28S

Contents

Patterns in spatial and temporal changes in muscid flies from Churchill (MB)

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A number of studies have shown that some organisms are affected by recent environmental changes occurring in the Arctic. However, the responses of insects to these changes have not been well studied in the Nearctic Region. In Churchill (MB), the ever-increasing human-related activities combined with the effects of climate warming have disturbed arctic habitats and potentially affected the biodiversity of local insects. Therefore, the study of historical changes in the distribution and abundance of some important northern taxa, such as the Muscidae, may allow us to better understand the impacts of recent environmental changes on the biodiversity of northern insects. The objectives of this study were to: 1) establish past (pre-1965) and current muscid diversity and species composition in Churchill in order to detect repeated patterns in distribution changes and 2) test current species limits and resolve taxonomic issues in the Muscidae using DNA Barcoding. Preliminary results indicate that the species composition of Muscidae in Churchill has changed. Forty-three new species records have been confirmed for the area but 14 previously recorded species were not collected in 2007. While improved sampling techniques seem to account for many of the new records, repeated patterns of distribution changes (mostly northern range expansions) were identified for 14 species. Preliminary barcoding results are also discussed.

KEY WORDS: Muscidae, arctic, distribution changes, DNA barcoding

Revised overview of the species of the Neotropical-endemic genus *Quichuana* (Diptera: Syrphidae)

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Since Hull published a revision of the species of the genus Quichuana in 1946, no other revisionary studies have been published for this genus. After 1946, descriptions of particular species of Quichuana have been provided. Recent revision of specimens, including types, deposited in several public collections (AMNH, CEUA, CNC, HM, INBio, MCSN, NHM, NMS, SNSD, USNM) has provided an updated overview of the taxonomy of the genus and its species. Some of these specimens were collected, frequently as larva, as a result of field work during the last decade in countries such as Costa Rica, México, Trinidad & Tobago and Venezuela, performed by the following researchers: Hancock, G.; Marcos-García, M.A.; Pérez-Bañón, C.; Rotheray, D.E.; Thompson, F.C.; Zumbado, M.A. This taxonomic study has resulted in a new characterisation of the genus Quichuana that has been here compared with other close genera. A total of 52 taxa have been studied, of which 31 are new to science. Some of the new taxa have been described on the base of few specimens. Quichuana chamiponi has been synonymised with Quichuana cincta, and Quichuana inca var. brevicera has stat. nov. as species brevicera. The male of Quichuana picadoi has been described. Further studies on early stages and molecular analyses will help to complete this study on adult morphology and to construct a well-supported phylogeny.

KEY WORDS: adult morphology, genitalia, new species, synonymy, species accounts, neotropics

A taxonomic review of the Neotropical genus *Psilochlorops* Duda (Diptera: Chloropidae: Chloropinae)

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The genus Psilochlorops Duda is monobasic and its only known species, Psilochlorops clavitibia, was collected from Bolivia in the Neotropical Region. This genus has been associated to Bricelochlorops Paganelli to comprise a small clade within the Chloropinae. These flies are 3.5-5.5 mm long, with an elongated body, long pilosity, and surstylus partially fused to the epandrium. A gena with transversal rugosity and a swollen postgena are most probably synapomorphies of Psilochlorops. Material from different parts of South America in the collection of the Museu de Zoologia da Universidade de São Paulo includes specimens belonging to five new species in the genus. The pattern of black or brownish spots over the yellow pleural sclerites and mesonotum corresponds to clearly diagnostic features for the species. Features of the male terminalia and, in some cases, in the shape of the frontal triangle also help to discriminate between the species of the genus. Three of these species are known from the southern Atlantic Forest in Brazil (States of Santa Catarina, São Paulo, and Rio de Janeiro), one is from Peru, and one is from Ecuador. All these species are from areas with rather temperate climate in the Andes and in southern Brazil. In this study, we review the genus Psilochlorops, presenting descriptions and illustration of the new species, and a key to species of the genus.

KEY WORDS: *Psilochlorops*, taxonomy, Neotropics, Chloropidae

Contents

Morphological phylogeny of *Stylogaster* Macquart (Conopidae, Stylogasterinae)

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The family Conopidae comprises parasitoid flies that mimic hymenopterans. The genus *Stylogaster* Macquart is very different from the others in this family with several synapomorphies associated with host switching (from Hymenoptera to Orthoptera) and oviposition mode (from active perforation of the host cuticle to insertion of spine-bearing eggs by impact oviposition). It has 93 recognized species, of which 68 are Neotropical, 15 are Afrotropical, five Australasian, three Oriental and two Nearctic. Relationships among the species are still unknown, but four species-groups have been proposed for New World *Stylogaster*. A cladistic analysis was performed based on 109 morphological characters from male, female and egg. The ingroup is composed of 23 species, 20 from of New World species-groups and three non-American species (Afrotropical and Australasian); the outgroup consists of species from three other genera of Conopidae. The resulting topology, with length of 358 steps, is: ((((((((((*S. stylata* + *S. stylosa*) + (*S. longispina* + ((*S. leonum* + *S. westwoodi*) + *S. frauci*))) + *S. brasilia*) + *S. dispar*) + (((*S. alvarengai* + ((*S. ornatipes* + *S. lopesi*) + *S. peruviana*)) + ((*S. neglecta* + ((*S. nigrifrons* + *S. souzalopesi*) + *S. longicornis*)) + *S. macrura*)) + *S. tarsata*)) + *S. breviventris*) + (*S. hirtinervis* + (*S. shannoni* + *S. pilosa*))) + *S. rectinervis*)). Thirteen synapomorphies support the monophyly of the genus (100% bootstrap and 22 Bremer support). From the four previously proposed species-groups only *neglecta* is recovered, inside a major clade with *ornatipes*-group. The three non-American species appear as a highly supported clade inside the *stylata*-group. This fact could provide an interesting argument for biogeographic considerations, but without Oriental species in the analysis, any conclusion on distribution must be considered preliminary.

KEY WORDS: Conopidae, *Stylogaster*, morphology, phylogeny

Two new species of *Lopesia* Rübsaamen (Diptera, Cecidomyiidae) from Brazil

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Lopesia Rübsaamen, 1908 is known from 20 described species associated with 11 plant families. Two new species are characterized; *L. erythroxyli* and *L. maricaensis*, inducing conical bud galls on *Erythroxylum ovalifolium* Peyr (Erythroxylaceae) and leave galls on *Protium brasiliense* (Spr.) Engl. (Burseraceae), respectively, at restinga of Barra de Maricá (RJ). Both host plants occur only in Brazil. The material was mounted on slides following the methods of Gagné (1994) and is part of the Diptera collection of Museu Nacional/UFRJ.

Both species have binodal and tricircumfilar male flagellomeres; cylindrical female flagellomeres; four-segmented palpi; toothed tarsal claws; pupa: elongate prothoracic spiracle; larva: prothoracic spatula with two elongate triangular teeth; six lateral papillae per side; terminal segment with eight corniform papillae.

Lopesia erythroxyli can be recognized by having male circumfilar loops distal and basal bigger than median; sinuous female circumfila; ovoid cerci; pupa: reduced antennal horns; curved prothoracic spiracle; complex spines abdominal. *Lopesia erythroxyli* is morphologically close to *L. caulinaris* by setulose male flagellomeres necks, four-segmented palpus, rudimentary empodium, well-developed mesobasal lobe of gonocoxite; pupa: prothoracic spiracle slightly sclerotized, complex abdominal spines; larva: prothoracic spatula two-toothed.

Lopesia maricaensis have linear male circumfila; X-connected female circumfila; gonostyli as long as gonocoxites; elongated female cerci; pupa: antennal horns less-developed, prothoracic spiracle sclerotized and almost straight; abdominal segments without spines; larva: terminal segment with two terminal lobes. *Lopesia maricaensis* is morphologically close to *L. similis* by shape of male mesal circumfilum; pupa: prothoracic spiracle sclerotized, abdominal spines absent. And, both induce the same gall morphotype on the same plant genus.

KEY WORDS: *Lopesia*, Burseraceae, Erythroxylaceae, galling insect, restinga, taxonomy

Contents

A new genus and species of Lasiopteridi associated with *Myrciaria delicatula* (Myrtaceae) from Brazil

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The Myrtaceae in the Neotropics are hosts to an extremely rich fauna of galling species, especially Cecidomyiidae. *Myrciaria* is a genus of shrubs and small trees; the flora of Brazil is estimated to include at least 30 species. In Rio Grande do Sul, there are 5 reported species of this genus. In the present work, a new genus and new species of gall midge - *Acornatamyia meridionalis*, gen. nov., sp. nov., galling leaves on *Myrciaria delicatula* – is characterized. Samples were taken from the National Forest of São Francisco de Paula, Rio Grande do Sul State. Vegetation is mixed broadleaf-Araucaria forest. The material was mounted on slides following the methods of Gagné (1994) and is part of the Diptera collection of Museu Nacional/UFRJ.

Acornatamyia may be recognized by the following character states: male flagellomere necks striated, palpi four-segmented, vein R5 straight and shorter than wing, Sc and Rs absent, M3 present, CuA forked, tarsal claws one-toothed, male cercus, hypoproct, and aedeagus shorter than gonocoxites, bilobed hypoproct, well-developed parameres, barely protrusible ovipositor, and fused female cerci; pupal character states are as follows: reduced antennal horns, elongate prothoracic spiracle, abdominal segments without dorsal spines, bilobed terminal segment; larval character states as follows: well-developed prothoracic spatula with two apical teeth, five lateral papillae per side, eight terminal papillae, and bilobed terminal segment. This genus does not fit into any known tribe, and is considered closely related to *Guareamyia* Tavares, 1909, *Guarephila* Maia, 2007 and *Sphaeramyia* Maia, 2007, because of the fused female cerci, short and barely protrusible ovipositor, and toothed tarsal claws.

Acornatamyia meridionalis can be recognized as follows: male flagellomeres with sinuous circumfila, female flagellomeres with variable circumfila, ovoid male cerci and gonocoxites, gonostylus slender, female cerci ovoid; the pupa may be recognized as follows: reduced antennal horn, elongate and slightly curved prothoracic spiracle, and absence of abdominal dorsal spines; larvae may be recognized by their corniform terminal papillae.

KEY WORDS: Cecidomyiidae, Diptera, gall midges, *Myrciaria*, taxonomy

Contents

Characterization of mtDNA sequences in Sarcophagidae species (Diptera: Oestroidea) for DNA-based id

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The family Sarcophagidae has about 622 species in the Neotropical region. Identification to species is a complex issue in this family, especially for larvae, considering the morphological similarities among different species. The aim of this study is to characterize levels of intraspecific and interspecific variability of Sarcophagidae using COI sequences and to evaluate its usefulness to identify larvae. Each adult was photographed, the aedeagus was preserved as a voucher and the thorax was removed and stored in absolute ethanol or -70°C prior to use in molecular analysis. Identification was based on digital images of male genitalia. DNA extraction was performed by Invisorb Spin Tissue Mini Kit (Invitek) and the samples stored at -70ºC. PCR analyses were performed in a range of annealing temperatures varying from 42ºC up to 52ºC. From a total of 165 specimens sampled using rotten fish as bait, *Oxysarcodexia thornax* (Walker, 1849) was the most abundant (~64%). A ~800pb region of the COI gene was successfully amplified, using the primers L2-N-3014 and C1-J-2195, for the species *O. thornax*, *O. admixta* (Lopes, 1993), *O. culmiforceps* (Dodge, 1966), *O. parva* (Lopes, 1949), *Peckia* (*Peckia*) *pexata* (Wulp, 1895), *P.* (*Euboettcheria*) *australis* (Townsend, 1927), *P.* (*Euboettcheria*) *anguilla* (Curran & Walley, 1934), *Sarcodexia lambens* (Wiedemann, 1861) and *Ravinia advena* (Walker, 1852). PCR reactions for *P.* (*Squamatodes*) *ingens*, *P.* (*Euboettcheria*) *collusor* and *P*. (*Pattonella*) *intermutans* samples are being optimized using newly designed primers for the COI/COII region. In addition, Long-PCR amplification recovered a ~9.6 Kb product from the mitochondrial DNA of *O. thornax* and *R. advena* species, which could be informative for the characterization of other molecular markers in species of Sarcophagidae.

KEY WORDS: COI; Sarcophagidae, molecular marker, Brazil

Near infrared spectroscopy: the bridge between the phenotype and the genotype in Diptera

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Hennig's holomorphology concept defines taxonomy as the process that synthesizes evidence from all relevant comparative sources. One of these sources is possibly metabolomics, in which the global metabolic profile is analyzed. An integral metabolic profile can be quickly obtained, nondestructively, through near infrared spectroscopy (NIRS). We use NIRS to quantify ecological and evolutive patterns of populations, species, genus, tribes, subfamilies and families of many specimens of Neotropical Muscoidea. All spectra were analyzed by combined methods of multivariate analysis using the technique of crossed validation for the multivariate models. Populations of the same species isolated geographically and without apparent morphological differences were discriminated successfully. Simultaneous separation of many species of the same genus was possible without superposition between the species. Taxonomic correspondence to display the genus, tribe or family by NIRS was possible. The correspondence between the phylogeny of many clades was relatively congruent with the correspondence by NIRS.

We feel that this technique promises to be very important to propose and test simultaneous hypotheses about species delimitation and will soon become a new source of characters that may be used in phylogenetic systematics, ecology and biogeography of Muscoidea and Diptera. A philosophical comparison with DNA barcoding displays the relevance of the NIRS as an alternative tool.

KEY WORDS: DNA barcoding, infrared spectroscopy, metabolomics, phenotype, species identification, taxonomy

Contents

Monophyly and subtribal classification of Eristalini is not supported by molecular data (Syrphidae)

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Immature stages of syrphids exhibit a wide range of trophic modes, such as phytophagy, mycophagy, predation, and saprophagy in diverse range of media. Eristalines, in addition to some other saprophagous species, live immersed in fluids, and show a characteristically extended breathing tube in the anal segment; i.e., the “long-tailed” larvae. The current classification of Eristalini recognises three subtribes with long-tailed larvae: Sericomyiina, Eristalina and Helophilina. The subtribe Sericomyiina is however frequently treated as an independent tribe.

The previous studies on phylogenetic relationships of Eristalini have shed little light on this particular question of monophyly of tribe Eristalini. A first attempt to elucidate the phylogenetic relationships among the taxa of the tribe Eristalini included DNA sequences of the nuclear 28S and mitochondrial COI gene regions for more than 60 taxa (approx 24 genera/subgenera) around the world, with the Holarctic and Neotropical regions particularly well represented. The first molecular study did not aim to address the placement of Sericomyiini, but representatives of the tribe were included as additional taxa because the similarity in larval morphology. The present study is performed with a more comprehensive sampling of taxa for phylogenetic analysis of Eristalini (sensu lato) species-groups and includes 82 taxa for the same gene regions. Nine outgroup genera were included, and the tree was rooted using *Merodon* (Eumerini). The data was analysed using dynamic homology with the direct optimization method as implemented in the computer program POY4. The results do not agree with the current subtribal classification. Sericomyiini was not resolved as sister group of Eristalini (sensu stricto) in the present analysis. Subtribe Helophilina is resolved as monophyletic group, but *Quichuana*, *Mallota*, and *Meromacrus* were resolved within subtribe Eristalina.

KEY WORDS: Eristalini, molecular phylogeny

A conspectus of the Dolichopodidae of the Lesser Antilles

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The Lesser Antilles, an arc of rather small islands at the eastern edge of the Caribbean, are recognized as a biodiversity hotspot that contain an exceptionally high level of endemic and threatened animal and plant species. With the exception of the island of Dominica, relatively little is known about dipteran diversity in the Lesser Antilles. Focusing on Dolichopodidae, I review the history of collecting in this region and discuss our current state of knowledge about the dolichopodid fauna. Material from recent surveys of Montserrat and St. Lucia have increased our understanding of dolichopodid diversity and distribution. At least 150 species from 31 genera are known to occur in the Lesser Antilles, but many more species await discovery. The rate of endemism appears to be very high with many species restricted to a single island or several adjacent islands. The genus *Cryptopygiella* has only been found there, and may be endemic. A notable element of the dolichopodid fauna consists of the so-called 'micro-dolichopodids', minute species that belong to several genera (e.g., *Enlinia, Harmstonia*) that have speciated extensively in the region. Other well-represented genera include *Chrysotus*, *Diaphorus, Medetera, Thrypticus, Paraclius,* and *Xanthina*. More intensive sampling is needed to better document Lesser Antillean dolichopodid diversity and endemism – something that should provide insights into the factors affecting the distribution and evolution of species, and to encourage and guide the preservation of the habitats in which these unique species occur.

KEY WORDS: long-legged flies, Dolichopodidae, biodiversity, islands, endemism

Flies at risk: Overview of the Blephariceridae of Madagascar

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Net-winged midges (Blephariceridae) are an unusual group of lower Diptera that is uniquely adapted for life in torrential streams. Within this family, the subfamily Edwardsininae is restricted to south temperate regions — eastern Australia, southern South America, and Madagascar — whereas the subfamily Blephariceridae occurs in both hemispheres. The Malagasy fauna contains both subfamilies, with the Blepharicerinae represented by an undescribed member of the tribe Apistomyiini. The remaining species belong to the edwardsinine genus *Paulianina* Alexander, which historically has been subdivided into the subgenera *Paulianina* (sensu stricto) and *Eupaulianina* Stuckenberg. All members of the Malagasy fauna are endemic to the island country, where their habitat is endangered due to massive deforestation. Recent examination of historical material and collection of new specimens has required that the group be fully revised. Our objectives included testing the monophyly of all Edwardsininae and various Malagasy subgroups (genera and subgenera), as well as reconstructing the evolutionary relationships of species within *Paulianina*. Morphological studies included many novel characters discovered through scanning electron microscopy. Molecular characters were based on a single nuclear gene and single mitochondrial gene. Cladistic analyses of both data sets support monophyly of the subfamily Edwardsininae and the genus *Paulianina*, and provide justification for raising the subgenera *Paulianina* (sensu stricto) and *Eupaulianina* to generic status. Relationships within *Eupaulianina* remain less resolved, due partly to lack of associated adult material for several species. We also provide an overview of the natural history of Malagasy net-winged midges and discuss primary threats to the survival of these unusual flies.

KEY WORDS: Blephariceridae, net-winged midges,
Madagascar, *Paulianina*, *Eupaulianina*, biodiversity

Diversity of *Culicoides* (Ceratopogonidae) in PPBio plot of research – Caxiuanã, Melgaço, PA, Brazil

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The genus *Culicoides* includes 1311 extant species worldwide (Borkent, 2009). Borkent & Spinelli (2007) listed 266 species from the Neotropical Region, and nearly 82 were recorded in the Brazilian Amazonia. This work provides a survey of the species of *Culicoides* in the research plot of the Caxiuanã National Forest, a typical floodplain ecosystem in the PPBIO program in the Brazilian Amazon Region. From 30 sites of the plot, collections were made with CDC light traps in five terrestrial sites (1, 4, 7, 8 and 9) from 9 to 13 February 2007 on ground and subcanopy. After identification, the frequency of species in each stratus and the Simpson's diversity index were calculated. A total of 542 specimens were collected. Site 1: 50 females (ground: 15 *Culicoides fusipalpis* Wirth & Blanton; subcanopy: 31 *C. fusipalpis*, 1 *C. foxi* Ortiz, 3 *C. hylas* Macfiei). Site 4: 55 females of *C. fusipalpis* on ground; 88 females (86 *C. fusipalpis*, 1 *C. foxi*, 1 *C. glabrior* Macfie) and 1 male of *C. vernoni* Wirth & Blanton in subcanopy. Site 7: 101 females on ground (99 *C. fusipalpis*, 2 *C. foxi*); 109 females (106 *C. fusipalpis*, 1 *C. guerrai* Wirth & Blanton, 2 *C. foxi*) and 1 male of *C. foxi* in subcanopy. Site 8: 84 females (ground: 40 *C. fusipalpis*, 5 *C. hylas*; subcanopy: 35 *C. fusipalpis*, 1 *C. foxi*, 3 *C. hylas*). Site 9: 52 females (ground: 35 *C. fusipalpis*, 1 *C. foxi*, 3 *C. hylas*; subcanopy: 12 *C. fusipalpis*, 1 *C. foxi*). The diversity of species was low in both stratus (λ= 0.91 on ground; λ= 0.89 in subcanopy). *Culicoides fusipalpis* was the most frequent species in all sites and stratus (95.3% on ground; 94.4% in subcanopy). Previously works cited that *C. fusipalpis* is abundant in floodplain ecosystem in Amazon region and can be also found in modified areas such as hydroelectric, feeding on humans. This species is not incriminated as a vector of none tropical diseases.

KEY WORDS: hematofagous ceratopogonidae, PPBio, Culicoides

Aedeagus variation in *Drosophila*/Cactus interaction between sympatric and allopatric populations

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The aedeagus of insects present rapid and divergent evolution in relation to other morphological traits and it is used as a taxonomic character and morphological evolution studies. In the *Drosophila repleta* group (genus *Drosophila*), the *Drosophila buzzatii* cluster radiation is composed by seven cactophilic and sibling species and the aedeagus morphology is a diagnostic character for their identification. In this study we analyzed phenotypic plasticity and genetic variation related to aedeagus size and shape in the closely related species *D. serido* and *D. antonietae* (*D. buzzatii* cluster) from sympatric (without hybrids) and allopatric populations to understand the factors involved in the evolution of this structure. Phenotypic plasticity in aedeagus morphology was estimated by geometric morphometric using the outline method to evaluate the responses in cactus/species/strains interaction with flies being reared in a medium prepared with each species natural hosts cacti: *Cereus hildmaniannus* and *Opuntia monacantha*. Our results show that *D. serido* has larger aedeagi than *D. antonietae*, regardless of cactus breeding. This result was also observed in the cactus/strains interaction, suggesting that size phenotype has genetic basis. The aedeagus shape differed significantly among species and also it is related to the different breeding cactus, showing host-dependent phenotypic plasticity. Shape variation was observed considering Lineages and lines/cacti interactions. The shape changes associated with line/cactus interaction suggest genotype-environment interaction. These results indicate a potential role of environmental heterogeneity (represented by different cacti hosts) in the maintenance of interespecific and intraspecific variation of the aedeagus morphology. This *Drosophila*/cactus interaction seems to be important by playing a significant role in the history of their species.

KEY WORDS: aedeagus evolution, host plant, phenotypic plasticity, repleta group.

Systematics and historical biogeography of Tabanomorpha (Diptera, Brachycera)

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The taxonomic group under inquiry is the infraorder Tabanomorpha (Brachycera), which traditionally includes the families Rhagionidae, Athericidae, Tabanidae, Vermileonidae, Pelecorhynchidae and Oreoleptidae. A phylogenetic analysis of Tabanomorpha was performed using 82 morphological characters of adults in a taxonomic sampling of 72 terminal taxa. Analyses using implied weighting with k values from 1 to 10 were executed. The proposed definition of Tabanomorpha sensu stricto matches some previous non-phylogenetic classifications, excluding the family Vermileonidae and the genera previously positioned among the "Xylophagomorpha". In Tabanomorpha s.s. are included the families Austroleptidae, Rhagionidae, Oreoleptidae, Athericidae and Tabanidae. *Pelecorhynchus* is positioned among the monophyletic Rhagionidae, in a clade with genera distributed in the Neotropics. The support for the monophyly of Rhagionidae is high. A pangeic origin for the Tabanomorpha is supported, with a subsequent radiation after the break-up of Pangea in Laurasia and Gondwana during the Jurassic. Nevertheless, neither the biogeographical evolution of the infraorder nor their phylogenetic relationships are completely understood. Phylogenetic systems are human constructs based on attempts to discover the evolutionary patterns.

A parameter of reality should be searched to validate the taxonomic groups presented in the cladograms. The proposal is to use consilient biogeographical hypotheses to measure the robustness of phylogenies. Consilience was raised to designate situations in which a causal explanatory theory, constructed to explain a particular set of phenomena, provides an equally successful causal explanation to other kinds of phenomena. The congruence of a phylogenetic hypothesis with consilient biogeographical hypotheses can suggest that the patterndepicts a meaningful evolutionary scenario.

KEY WORDS: Athericidae, biogeography, Rhagionidae, systematics, Tabanidae, Tabanomorpha

Contents

Efficacies of the permethrin-impregnated resin net in controlling the blood sucking tabanid flies

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The efficacies of the permethrin-impregnated resin net (Olyset net) in controlling Tabanidae were examined in Japan. The adjusted knock-down rate against Tabanus nipponicus was very high, even in the 1-minute contact group. The knock-down effect was observed even 24 hr after contact in each treatment. An NZI trap made with an Olyset net, instead of Nylon Organdy for the screen of the trap, captured almost the same number of T. nipponicus as the standard NZI trap. However, the locations where the flies were captured were distinctly different amongst treatments. There was no inhibiting effect in capturing flies of the Olyset net trap. As a result of the 45 hr trapping (one hour trapping repeated 45 times) against T. nipponicus, a total of 2,255 individuals were captured. 53.8% of flies were captured in the top cage, while 37.7% were captured at the bottom of the trap. 332 Tabanus trigonus were captured and 67.2% of those were captured in the top cage and 9.0% were at the bottom. 2,882 Hirosia iyoensis were captured by the 32 hr trapping, and 50.5% of those were captured in the top cage and 40.2% were at the bottom of the traps. A total of 840 flies of Hirosia humilis were captured by the 32 hr trapping, and those in the top cage were 54.2%, while those at the bottom of the traps were 33.9%. 753 Tabanus rufidens were captured by the 32 hr trapping, and 68.9% were captured in the top cage and 23.5% were at the bottom of the traps. All the captured flies at the top cage were knocked down within one hour. These results indicate the efficacies of the Olyset net NZI trap in controlling medium or small sized species of Tabanidae such as T. nipponicus, H. iyoensis, and H. humilis.

KEY WORDS: tabanid fly, control, trap, permethrin-impregnated risin net

Contents

An undescribed species of the genus *Phthiridium* (Nycteribiidae, Diptera) from Iriomote Island, southern Japan, with a key of Japanese nycteribiid bat flies

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The genus Phthiridium contains 35 species, which are distributed throughout the Old World (Graciolli & Dick, 2008). Among them, only two species have a peculiar serrated process on the phallobase; they are P. szechuanum (Theodor, 1954) and P. ornata (Theodor, 1954) from Central and East Asia. Each of them contains two subspecies; both parasitize bats belonging to several genera, especially to the genus Rhinolophus, species of which roost in caves. The authors found an undescribed species from the endemic bat species of the Ryukyu Islands, Rhinolophus perditus, in Iriomote Island, Okinawa, southern Japan. This fly belongs to the above mentioned group and has some unique characteristics in both male and female genitalia. We will discuss the relationship among them based on morphological observations, distributions, and host information.

The old Japanese faunal records of Nycteribiidae still present difficult problems, e.g., lost types, possibilities of misidentification, and specimen contamination from other countries. With the finding of an undescribed species from Iriomote Island, the Japanese nycteribiid bat flies now number eleven species, exclusive of above-mentioned uncertain records. We also present a preliminary key to all eleven of the Japanese nycteribiid flies.

KEY WORDS: undescribed species, *Phthiridium*, Japanese Nycteribiidae, key

Contents

Griffiths' legacy: current status and future directions in Nearctic Anthomyiidae systematics

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In North America, the family Anthomyiidae is represented by more than 700 species, several of which are important agricultural pests. Over the last decades, Nearctic anthomyiids have been extensively revised by Graham Griffiths (with the exception of *Botanophila* and *Fucellia*). Regrettably, the unfortunate death of Dr. Griffiths in 2009 came before an updated key to genera was published, therefore making the generic identification of Nearctic material by non-specialists virtually impossible. The current status of Nearctic Anthomyiidae taxonomy is reviewed and a plan is proposed to resolve the most pressing taxonomic issues. An hypothesis of relationships proposed by Kutty et al. (2008) in the context of a larger study on the Muscoidea, presented scathophagids as a derived branch nested within the anthomyiids. However, none of the nodes supporting a paraphyletic Anthomyiidae were well supported by the data, and taxon sampling was inadequate for the family (proportionally too few exemplars and no representatives of *Anthomyia*, *Egle* and *Fucellia*). A detailed proposal to test the hypothesis of Kutty et al. (2008) using a much wider range of examplar species and a combination of molecular and morphological data will be presented.

KEY WORDS: Anthomyiidae, taxonomy, phylogenetics, Nearctic fauna, Muscoidea

Cospeciation and cophylogeography in Fergusoninid galling flies and their nematode mutualists

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All fergusoninid flies have an obligate mutualistic association with nematode worms in which the fly-worm partners together form galls on plants of the eucalypt family (Myrtaceae). This unique association appears to be restricted to Australasia (>200 species pairs in Australia, 1 in New Zealand, 1 in the Philippines, 1 in India); one Australian species has been introduced to the U.S. as a biological control agent against the invasive paperbark tree in Florida. Fly-worm species pairs are generally monophagous on a single plant species, although a given plant species may serve as host to as many as five, often sympatric, fly-worm species pairs. Phylogenetic analyses of multilocus sequence data from several datasets involving the flies and their worms (separately) results in somewhat concordent but moderately unresolved trees, a common finding in cospeciation studies. In the phylogenetic trees, gall shape and peculiar fly larval “dorsal shield” morphology is highly conserved; individual plant hosts appear to have been colonized multiple times independently. Phylogeographic analysis within one broadly distributed fly-worm species pair provides additional insights on speciation and coevolution in these plant-feeding mutualists.

KEY WORDS: *Fergusonina*, Fergusoninidae, Myrtaceae, phytophagous insects, speciation

Contents

Oriental Sciaroidea: current state of knowledge and interesting new taxa

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The Oriental fauna of fungus gnats (Diptera: Sciaroidea) is still insufficiently known. Current numbers of valid species and expected numbers of undescribed taxa from the Oriental and adjacent parts of the Australasian Region (Sulawesi, New Guinea) are presented for each family of the Sciaroidea (excl. Sciaridae). The author has been studying extensive Malaise trap collections from various parts of this region and the analysis of the species spectrum found in those samples is given in this contribution. Special attention is devoted to some recently described and phylogenetically important genera of Keroplatidae, such as *Sciarokeroplatus* Papp & Ševčík, 2005, *Microkeroplatus* Ševčík & Papp, 2009, *Langkawiana* Ševčík, 2009, and several yet undescribed taxa. Recent discoveries in the traditional tribes Gnoristini, Metanepsini and Sciophilini of the species-rich family Mycetophilidae and their implications to the delimitation of those taxa are also discussed, suggesting that a new intrafamilial classification of the family is much needed.

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Dismemberment of a murder victim and forensic entomology: a case study of PMI estimation using blow fly larvae

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Dismemberment or defensive mutilation of a dead body is usually intended to remove the body from the place of homicide or render identification of the victim impossible. The operation of dead body mutilation is generally carried out immediately after the crime, although more rarely a long time may pass between the two events. In May, 2006, two men were found dead in the mountain area of Ilan county, northeastern Taiwan; their bodies were dismembered and packed into two plastic bags. The suspect claimed he did not murder these two men, but only mutilated the bodies several days after they died. In other words, he admitted an involuntary manslaughter for fighting with the victims and the crime of insulting corpses instead of an intentional dismemberment murder. During the autopsy, two different sized blow fly larvae of the same species were collected, and the younger ones obviously found only on the cutting face of bodies. So, it is necessary to clarify the time interval between the death of victims and the body mutilation. We believed this time lag could somehow reflect the crime motivation. The objective of this study is to try to connect the larval thermal history to the time interval of these two crime events. To understand the oviposition and feeding behavior of blow flies in this dismemberment case, 300 g pork was used in a simulation experiment; fresh pork was exposed in shade and open land for 24 h. After 24 h, eggs and larvae on it were recorded. Then, the pork was equally cut into two parts and exposed again for 24 h, 48 h, and 60 h. The secondary occupied fly eggs and larvae were then recorded. Our results indicated the newly cut area of pork is suitable for providing new laying and feeding habit for the secondary arrival of blow flies; furthermore, the age difference of larvae between firstly and secondary occupied individuals could be observed with potential use in estimating time interval.

KEY WORDS: dismemberment, postmortem interval, Calliphoridae, Taiwan

Contents

The status of *Labrundinia maculata* Roback, 1971, a junior synonym of *L. longipalpis* Fittkau, 1962 (Diptera: Chironomidae: Tanypodinae)

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The Pentaneurini genus Labrundinia (Diptera: Chironomidae: Tanypodinae) was described by Fittkau in 1962 based on Tanypus longipalpis Goetghebuer, 1921. Currently the genus comprises 14 species distributed in the Nearctic, Palaearctic and Neotropical regions. The species Labrundinia maculata was described from California, USA by Roback in 1971 and adult males were separated from other known Labrundinia only on the coloration pattern of the abdominal tergites and gonocoxites. As additional North American specimens of L. maculata were analyzed and compared with the holotype and original description of L. longipalpis, they were found to fall within the range of morphological variation of L. longipalpis. Labrundinia maculata thus is regarded as a junior synonym of Labrundinia longipalpis. In this study, we argue for the synonymy of the two species and present new descriptions of the male, female, pupa, and larva of L. longipalpis. The available information on the distribution of the species extends the species range to cover large parts of the Holarctic.

KEY WORDS: Chironomidae, Tanypodinae, *Labrundinia*, new synonym

Contents

Phylogeny of *Oxyvinia* (Sarcophagidae) with descriptions of three new species from Brazil

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The genus *Oxyvinia* Dodge is exclusively Neotropical and comprises of 13 species, of which three are new from Brazil and recognized herein. Few phylogenetic analyses exist for the genera or species of Sarcophagidae. Therefore, a phylogenetic hypothesis of the relationships among species of *Oxyvinia* is proposed, based on parsimony analysis using 33 morphological characters mostly of male terminalia, and 15 terminal taxa including two outgroups, *Dexosarcophaga bermudezi* Silva & Mello-Patiu and *Oxysarcodexia parva* Lopes, genera related to *Oxyvinia* by previous authors. The monophyly of *Oxyvinia* is strongly supported by four unique synapomorphies (98% bootstrap) but within-species relationships are defined mainly by homoplastic characters. The basal position of *O. panamensis* is not well-established due to missing data. A strict consensus tree recovered the following relationships: ((((*O. angolensis* + (((*O. grata* + (*O. grisea* + *O. piliventris*)) + *O. vitatta*) + ((*O. tridentata* + (*O. uraricoera* + *O. xanthophora*)) + *O. wicharti*))) + (*O. excisa* + *O. spinulosa*)) + *O. zenioi*) + *O. panamensis*). Male genitalia furnished the most effective characters for establishing the monophyly and interspecific relationships in *Oxyvinia*, and consequently should be exhaustively analyzed in all genera in future comprehensive studies of flesh fly evolution.

KEY WORDS: flesh flies, Neotropics, cladistic, morphology

Contents

Phylogeny of *Lepidodexia* (*Notochaetisca*) (Diptera: Sarcophagidae)

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Notochaetisca, recognized as a subgenus of *Lepidodexia*, comprises six species, five from Brazil (*L. (N.) oliveirai*, *L. (N.) rosaliae, L. (N.) malacophaga*, *L. (N.) travassosi* and *L. (N.) santista)* and one from Dominica (*L. (N.) dominicensis*). These species were revised and a morphological cladistic analysis was performed to test the monophyly of this subgenus and generate a phylogenetic hypothesis on the interspecific relationships. *Oxysarcodexia avuncula* (a basal genus in the Sarcophaginae) was used as an outgroup. Due to the morphological similarity with the studied taxa, three species of *Lepidodexia* (*Johnsonia*) were included in the ingroup. The analysis yielded a single most parsimonious tree (length = 70 steps, CI = 0.83, RI = 0.85), which did not support the monophyly of L. (*Notochaetisca*). L. (*Notochaetisca*) *dominicensis* shares more synapomorphies with L. (*Johnsonia*) than it does with the other species of L. (*Notochaetisca*). Therefore, we provisionally consider it as *incertae sedis*. The remaining five species, however, form a well-supported clade. In addition, morphological and phylogenetic analyses have shown that L. (*N.*) *rosaliae* is a junior synonym of L. (*N.*) *oliveirai*.

KEY WORDS: Neotropical, flesh flies, morphology, cladistics

Contents

Selection of biting sites on anuran hosts by frog-biting midges (*Corethrella* spp.)

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A critical challenge of obtaining a blood meal resides in locating an appropriate host. Once haematophagous insects reach their host, however, there is a still another vital step ahead, selecting a biting site. Optimal foraging theory predicts that biting insects should feed on their host on those areas that maximize blood intake while minimizing the costs and risks. Here we investigate the biting sites of *Corethrella* species on three species of frog: túngara frogs, *Physalaemus pustulosus*, and two species of treefrogs, *Dendropsophus ebraccatus* and *D. microcephalus*, that are attacked by the midges. The midges bite the small tree frogs on a variety of body areas including their back and legs, but they exclusively bite túngara frogs on their nostril. We explore the reasons behind such differences in biting sites examining the properties of the skin of these species of frogs. For each frog species, we prepared histological samples of the dorsum and the area around the nostril. We also collected frog-biting midges by playing advertisement calls of the frogs studied here. Microscopic slides of the mouth parts of midges were prepared to measure the length of their proboscis. Preliminary results indicate that the skin of túngara frogs on their dorsum consists of a thickened epidermis followed by a dense dermis with multiple layers of connective tissue and glands while it is thinner in the treefrogs. In all species there is a high density of small blood vessels around the nostrils with the highest density towards the proximal end of the nostril. Although there is variation in the length of the proboscis of the midges, preliminary results suggest that it may not have implications on site bite selection. Our preliminary results suggest that biting site preference of *Corethrella* midges is highly influenced by the properties of the skin in different areas of the frogs.

KEY WORDS: biting behavior, frog-biting midges, skin characteristics, tungara frog, treefrogs

Contents

Neotropical Sepsidae: overview and perspectives

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Sepsidae are an acalyptrate Diptera family with 37 recent genera and 318 species in the world, with ten genera and 43 species described in the Neotropical Region. The monophyly of the family is widely accepted. Phylogenies have been proposed for most of the family, entirely or mostly based on larval characters, but also based on morphology and molecular data. These analyses confirm the monophyly of Sepsidae, with Ropalomeridae as its sister group. The proposed phylogenies show that some genera with representatives in the Neotropical Region are monophyletic, among them, *Meroplius* Rondani, *Microsepsis* Silva and *Themira* Robineau-Desvoidy. Two of the genera in the Neotropics, however, do not appear as monophyletic: *Archisepsis* Silva, which would be paraphyletic with regard to *Palaeosepsis* Duda and *Sepsis* Fallén, the largest genus in the family. *Archisepsis* has been proposed as a synonym of *Palaeosepsis*. The only species of *Palaeosepsis* included in these analyses was unfortunately *P. pusio*, which is now a species of *Archisepsis*. A phylogenetic hypothesis for the relationships between the species of *Archisepsis* point to the monophyly of genus and allows the reconstruction of its groundplan, contributing to the discussion of its position within the system of the Sepsidae. In this hypothesis, *Lasiosepsis* Ozerov, used as an outgroup, appeared either nested inside *Archisepsis* or outside it, leaving an open question about its monophyly. There are pending questions about the monophyly of the Neotropical genera not covered in previous analyses, that is, *Mepliosepsis* Duda, *Palaeosepsis*, *Palaeosepsioides* Ozerov and *Pseudopalaeosepsis* Ozerov.

KEY WORDS: Sepsidae, Neotropical region, phylogeny, Archisepsis

Pseudogriphoneura Hendel, 1907 (Lauxaniidae) in the Brazilian Atlantic Forest

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Pseudogriphoneura Hendel was described for a Neotropical species of lauxaniid. The genus is now composed of 30 species, one of which with Nearctic distribution. Pseudogriphoneura may be distinguished from other lauxaniid genera by the convex frons, a fronto-facial with an obtuse angle, eye strongly constrict below, with posterior margin concave, arista plumose, 0+2 dorso-central setae well developed, intra-alar seta absent, 1 katepisternal seta, veins R4+5 and M not parallel. Most species are known from Central and Northern South America. Six species are known to occur in Brazil: P. cormoptera Hendel (also Venezuela and Bolivia), P. elegantula Frey (RJ), P. micans Hendel (PA), P. testacea Hendel (SP), P. tristis Hendel (PA, RJ) and P. willistoni Curran (MG). In a large survey of the Diptera diversity in the Brazilian Atlantic Forest, five species of Pseudogriphoneura have been found: P. elegantula Frey (Espírito Santo, Rio de Janeiro), P. tristis (Bahia, Minas Gerais), P. willistoni (Minas Gerais, São Paulo), and two undescribed species (from Minas Gerais and São Paulo). One of the new species is distinct due to the dark brown scutum, with thick yellow medial pruinosity, base of scutellum blackish, with grayish pruinosity, pale legs, and abdomen yellow with lateral brownish black spots on tergites. The other species is black, with brownish wings with black costal apical area, scutum black, with no vitae and covered with cupreous polinosity, legs mostly black, fore first three tarsomeres white. The Brazilian Atlantic Forest is composed of two major vegetation types, the ombrophylous forest along the coast and the semi-deciduous forest to the west. The known distribution of the new species of Pseudogriphoneura seems to corroborate the hypothesis that the dipteran elements in semi-deciduous forests correspond to endemic elements, separate from the ombrophylous forest in the east margin. This research was supported by grants from FAPESP (2009/54497-8)

KEY WORDS: Lauxaniidae, new species, Brazilian Atlantic Forest, Neotropical Region, endemism

An overview of Afrotropical Empidoidea (exclusive of Dolichopodidae sensu lato)

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Empidoidea (exclusive of Dolichocopodidae) comprise four families and 512 described species. Afrotropical Atelestidae include two described species and one genus, Brachystomatidae 12 species and two genera, Empididae 216 species and 17 genera and Hybotidae 146 species and 19 genera. More than half of the described species are from South Africa, due in part to the monograph of Ken Smith (1969) and the collecting efforts of Brain Stuckenberg. Generic diversity is centred in southern Africa, with nine described and two undescribed endemic genera.

KEY WORDS: Empidoidea, Afrotropics, South Africa, Atelestidae, Brachystomatidae, Empididae, Hybotidae

Seepage midges: current knowledge and future direction (Culicomorpha: Thaumaleidae)

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Thaumaleidae are a small family of some 182 described species in 7-8 recognized genera. Immature stages are confined to madicolous (= hygropetric) habitats and are known worldwide. Very few characters of the immature stages are known for distinguishing the genera, and species identification remains dependent solely upon the adult male. Diversity of thaumaleids in South America and eastern Asia remain poorly known. An US National Science Foundation grant (MIDGEPEET) will focus on western Nearctic species and monophyly of the Northern Hemisphere genus *Androprosopa*, and make hypotheses concerning evolution and biogeography of the Holarctic lineage of Thaumaleidae. A DNA fingerprinting method implementing portions of rapidly evolving nuclearly encoded genes will be used also to discriminate all western Nearctic *Androprosopa*, enabling bionomic and distributional data for all Nearctic species in the family to be elucidated using collections of the most often encountered life stage, the larva.

KEY WORDS: Culicomorpha, Thaumaleidae, madicolous habitats, immatures

Taxonomy and biogeography of Neotropical Ceratomerinae (Empidoidea)

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Thirteen Neotropical species of *Ceratomerus* Philippi, including nine recently described species are recorded from South America. One of these species, *C. apterus*, from Ecuadorian páramo above 4000 m, lacks wings and has reduced halteres. A preliminary phylogeny of the genera and species groups of the Ceratomerinae is presented, with a discussion of the generic concept of *Ceratomerus*. A provisional biogeographic hypothesis of this Gondwanan lineage is discussed. Significant relationships include the Southern Gondwana Pattern, the Inverted Southern Pattern and the Neotropical *C. paradoxus* group evolved within the Australian *C. campbelli* group, illustrating both an intra-generic and intercontinental pattern.

KEY WORDS: Empidoidea, Brachystomatidae, *Ceratomerus*,
Neotropics, Chile, Ecuador, Argentina, Bolivia

Correlation between age, body length and dry weight of larvae belonging to two species of forensically important blow flies (Diptera: Calliphoridae)

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Various species of blow flies lay their eggs on exposed corpses and the hatched larvae feed vigorously upon the latter. Fly larvae found in association with decaying human cadavers are often used for the estimation of minimum postmortem interval (PMI). *Chrysomya megacephala* (Fabricius) and *Chrysomya rufifacies* (Macquart) are the forensically important blow flies distributed in many parts of the world and larvae of both the species have been used for forensic investigations in several cases. Although development rate investigations have previously been undertaken for these species, no studies have been undertaken specifically to determine the relationship between larval age, body length and dry weight. These flies can withstand considerable temperature fluctuations and the present study was conducted in the laboratory at different temperatures (22˚C, 25˚C, 29˚C, 31˚C) so that the data could be useful under varied environmental conditions. Graphs have been drawn between larval age and body length as well as dry weight which are typical sigmoid curves as has also been reported by earlier workers. The pattern reiterates the fact that the third instar grows rapidly and the growth stops suddenly thereafter. The mean larval length increased steadily from 1.4 mm to 17.4 mm and from 1.8 mm to 15.9 mm for *C. megacephala* and *C. rufifacies*, respectively. Shrinkage in length began soon afterwards which is indicative of the larva reaching the post-feeding stage. Similar trend has been observed with respect to the larval dry weight.

The generated data would be helpful to estimate the age of these fly larvae collected from decaying corpses giving indication of the period of insect activity and then the minimum PMI.

KEY WORDS: Calliphoridae, larvae, forensic entomology

Contents

Taxonomy of Indian Satellite flies (Sarcophagidae: Miltogramminae) in eastern India

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The kleptoparasitic Miltogramminae are very superficially covered in India. A small number of species was reported by earlier workers, and a detailed field survey has not been done before in India. The present work aims to fulfill the scarcity. The eastern part of India was selected to prepare a taxonomic database of Miltogramminae. Extensive field work and a thorough survey was done followed by Malaise trapping and hand collecting with sweep net to hills, deep forests including National Parks and Sanctuaries, local forest patches, plain areas and sea beaches. Different fly specimens were collected from different habitats viz. termite nests, tree bark, flowering plants, sandy earth surfaces, and rocks and bushes. All five states were visited repeatedly for two years. Miltogramminae specimens were identified taxonomically from the large collection of fly specimens. A number of species are new to science and will be described.

KEY WORDS: taxonomy, Miltogramminae, eastern India

Contents

Canpolin – Current Canadian research on pollinators

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Pollination research in Canada recently received a substantial boost in the form of a 5 million dollar NSERC Strategic Network grant, in addition to more than 5 million dollars in matching funds (2009-2013). Researchers at 26 universities across the country are working with government agencies, NGO's and industry to deliver critical insights and sustainable solutions to problems related to pollination. Leading experts in entomology, ecology, plant reproductive biology, genomics, prediction, and economics have joined forces to explore the full scope of theseproblems – from pollinator health and conservation to gene flow in plants, the impact of climate change on pollinators, and the economics of pollination. As is usually the case, bees are receiving a major share of the grant and most of the network attention. However, unlike many of these projects, the Diptera are included and their study is receiving substantial funding. We will discuss several of the projects that are being supported by this new funding. Projects include a revision of Nearctic Dasysyrphus (Syrphidae), a review of Nearctic Platycheirus (Syrphidae), a databasing initiative on Syrphidae in Canadian collections, new online keys to Syrphidae, a course in syrphid taxonomy, and building a COI DNA database for Syrphidae. The last is being developed to facilitate association of sexes, identification of larvae, and to act as an additional dataset for difficult taxonomic problems.

KEY WORDS: Diptera pollinators, Syrphidae

Contents

The high altitude distribution of Muscidae (Diptera) in the South-East Altai Mountains of Siberia

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Adult Muscidae occur in most habitats, except for the most dry. They seem to be most typical inhabitants of the broad-leafed and coniferous forest zones, but at high altitude and in subarctic areas they form a very high proportion of the fauna, both in species and in individuals. At present there is very little information on muscid flies in Russia, and in particular the specific composition, taxonomy, distribution and zoogeographic affinities of the mountain muscids are almost unknown.

Our research activities are based on a series of expeditions over the last five years to the Altai Mountains. Previous records of Altai muscids total 50 species in 19 genera, but we now know 171 species in 31 genera and the list continues to grow year-by-year.

Most of our collections have been made in the South-East Altai, where 115 species in 23 genera have been found. The high altitude distribution of these species was studied in three localities: 1) forest zone of the Chulyshman plateau (1500-2000 m); 2) tundra-steppe of the Ukok plateau (2200-2400 m); 3) high mountain tundra of the Ukok plateau (2500-3000 m). *Drymeia* was excluded from our analysis, but flies of this genus are typical inhabitants of high mountain habitats.

Our analysis has shown that the number of genera decreases with increasing altitude. Twenty-three genera were found in the forest zone, 16 genera (70%) in the tundra-steppe, but only 10 genera (43%) in the high-mountain tundra.

The number of species, on the other hand, increases with increasing altitude. Seventy-nine species were found in the tundra-steppe, compared with 48 species in the forest zone and 44 species in the high-mountain tundra. Some species occur in more than one zone, but 15 species were found only in the high-mountain tundra, and this includes several endemics.

KEY WORDS: Muscidae, Altai, mountains, Siberia

Effect of steroids on the developmental rates of *Chrysomya* species (Diptera: Calliphoridae).

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Because of the increase in deaths related to drug abuse, knowledge of the effect of these substances on the development of certain necrophagous insect species can be very important, especially when estimates of postmortem intervals (PMI) are based on the age of the necrophagous insects. The presence of drugs in decomposing tissues that the larvae are feeding on may interfere with their developmental rate, thus potentially altering the PMI. Using *Chrysomya putoria* (Wiedemann) and *C. albiceps* (Wiedemann) (Diptera: Calliphoridae) as test organisms, this study aimed to determine the effects of different concentrations of the association of Deca-Durabolin™ (nandrolone decanoate) (DE) and Durateston™ (testosterone esters) (DU), anabolic-androgenic steroids (AAS) commonly used to increase muscle mass, on their developmental rates. Four experimental groups were used: 3 of them contained the following associated concentrations of ASS: 2.25 mg/kg DE + 3.57 mg/kg DU; 11.25 mg/kg DE + 35.7 mg/kg DU; 22.5 mg/kg DE + 357 mg/kg DU; the fourth was a control group without any drugs. Individual weights were recorded for groups of 10 larvae at each 12-h interval from hatching until the pupae stage. A one-way ANOVA was performed to compare the effect of the treatments on larval development, using weight as a measure of response. Despite the heterogeneity of the developmental curves, the AAS did not interfere with the developmental time (F=0.550; p=0.647 and F=0.680; p=0.564) nor the emergence interval for *C. albiceps* or *C. putoria*, respectively. However, larval viability and emergence rate (F=5.830; p=0.005) of *C. putoria* were affected by higher concentration of AAS. For both species, at almost all ages, the mass weight gain of the groups exposed to AAS was different from that of the control group. Extrapolating to actual human cases, these results point to a possible error in estimates of PMI if the effect of these drugs is ignored.

KEY WORDS: blow flies, hormones, Postmortem Interval, entomotoxicology

Contents

Barcoding of *Merodon* hoverflies (Diptera, Syrphidae) in the Eastern Aegean Islands, Greece

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DNA barcoding has become a useful system for linking different biological life stages, and for identification of species within a known taxonomic framework. We generated mtDNA COI barcodes using adult specimens of all species of the hoverfly genus *Merodon* (Diptera, Syrphidae) occurring on Lesvos and Chios Islands (Greece), and also for some samples from additional Eastern Aegean islands. The generated COI barcodes could discriminate well between all taxa of *Merodon* on Lesvos and Chios, except for the species *M. loewi* and *M. papillus* that shared the same COI haplotype, despite their clear morphological differences. The Eastern Aegean islands of Greece have habitats with a rich geophyte flora facilitating life history studies of this insect taxon. Recent studies showed that the number of species of *Merodon* on the Lesvos and Chios were 25 and 16, respectively, or 20% and 26% of the total hoverfly fauna. High diversity in the Mediterranean species of *Merodon* may be linked to narrow host specificity, but tests are complicated by incomplete taxonomy of the flies and unknown food sources. Larvae of *Merodon* are phytophagous and develop in underground parts of bulb plants (e.g. Liliaceae, Amaryllidaceae), but the specific larval host plants remain unknown for the majority of the taxa.

We were interested in testing the phylogeographic propensity of the taxon and to estimate the COI haplotype diversity of the species of *Merodon* in the Eastern Aegean region. We thus compare and discuss the faunal composition of *Merodon* of the Eastern Aegean islands and present recent results of phylogeographic studies for the *Merodon* species based on COI sequences and evaluate the utility of COI barcodes in discovering morphologically cryptic species of the taxon. We were particularly interested to elucidate whether island size was reflected in the observed levels of genetic diversity of the species.

KEY WORDS: barcoding, COI, *Merodon*, Eastern Aegean

Contents

Progress towards an understanding of flesh fly evolution. New phylogenetic information from mtDNA

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Generic relationships within the Sarcophaginae are poorly understood. In an effort to provide greater understanding of the phylogenetic relationships between recognized genera of Sarcophaginae and to confirm the monophyly of these genera, we analyzed and compared four mitochondrial gene sequences. Cytochrome oxidase I (COI), cytochrome oxidase II (COII), dehydrogenase subunit 4 (ND4) and dehydrogenase subunit six (ND6) mtDNA genes were amplified from a variety of species of Sarcophaginae representing many of the New World genera. We compare and contrast the phylogenies derived from this mtDNA work with classical and cladistic phylogenies based on morphology proposed by sarcophagid experts of the past and present.

KEY WORDS: Sarcophagidae, mitochondrial DNA, systematics

Host-associated differentiation in Diptera: Contrasting plant parasites and insect parasitoids

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There is growing realization of the importance of ecological interactions in fostering population divergence and speciation. These affects are most evident when populations diverge in resource use, such as in host-parasite systems, where parasites experience strong selective pressures associated with host use. Here, I contrast host ranges and host associated genetic differentiation in two groups of dipteran parasites, plant galling Cecidomyiidae (*Asteromyia*) and insect attacking Tachinidae. The gall midge genus *Asteromyia* exhibits striking levels of morphologically cryptic host-associated differentiation in an apparent adaptive radiation onto their goldenrod (*Solidago* sp.) hosts. Host-associations in this group are remarkably conserved with few shifts to unrelated host groups and significant phylogenetic signal, suggesting strong physiological constraints. There is also mounting evidence of cryptic host-associated lineages in Tachinidae, revealing finer levels of host-specialization than previously appreciated. However, shifts among unrelated host taxa are frequent, and physiological constraints appear to be weak or absent. Contrasting host-associated selective pressures and differing models of evolutionary divergence for these two taxa are compared.

KEY WORDS: Cecidomyiidae, Tachinidae, speciation, specialization, host range, cryptic species

Diversity and host use patterns of Lepidoptera-attacking Tachinidae in the Ecuadorian Andes

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The family Tachinidae is the most diverse and ecologically important group of parasitoid insects outside of the parasitoid Hymenoptera. They are also among the most species rich families of flies, with the Neotropics likely harboring more species than any other geographic region. Here we describe and analyze the richness of Tachinidae reared from Lepidoptera as part of a biological survey of Lepidoptera and their parasitoids in a mid-elevation (~2000 m) tropical montane forest in the Ecuadorian Andes. Two hundred and five separable tachinid "morpho-species" were reared from approximately 230 species of Lepidoptera in 16 families. Tachinid species accumulation and rarefaction curves exhibit little sign of reaching an asymptote and richness estimators indicate that the community likely consists of at least twice this number of species. Most tachinid species were reared infrequently, with about 50% of species represented by a single rearing event. In contrast to previous studies of temperate Tachinidae, most species appeared to be relatively specialized on one or a few related hosts, but sampling remains insufficient to make strong conclusions regarding host range. The fauna is dominated by the tribes Blondeliini and Goniini, known to primarily attack Lepidoptera, but other Lepidoptera attacking groups such as Tachinini and Winthemiini were poorly represented. The estimates of tachinid species richness derived here support the hypothesis that the Northern Andes of the Neotropics is a geographic epicenter of tachinid species richness and a cradle for their diversification.

KEY WORDS: Tachinidae, diversity, host-association, parasitoid, Neotropical, Ecuador

Contents

Black soldier fly larvae (*Hermetia illucens*) as an option for municipal organic waste management in Costa Rica

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In developing countries, effective waste management strategies are constrained by high collection costs and lack of adequate treatment and disposal options. The organic fraction in particular, which accounts for more than 50% of the waste production, constitutes a great, yet mostly neglected, reuse potential. Concomitantly, livestock farmers demand alternative protein sources as prices of livestock feed are increasing sharply. The larvae of the non-pest Black Soldier fly (*Hermetia illucens*) not only feed voraciously on a large range of organic waste, thus reducing the dry matter content by up to 70%, but transform it into high value insect protein, offering the opportunity to develop a source of income for small entrepreneurs. In the adult stage, the fly no longer feeds and will therefore not become a pest in agriculture or spread diseases. Furthermore, its larvae act as a biological control agent for the common house fly and other fly species.

In Costa Rica, medium-scale field experiments proved municipal organic waste (MOW) to be a good feeding source for soldier fly larvae. The yields obtained were superior to those found in systems using pig manure as a food source and MOW was reduced by 60–70% of its dry mass. In regard to the reuse of the residue in agriculture as a soil amendment, treatment beds have to be adapted with drainage systems and waste has to be chopped before feeding to ensure a homogenous product.

We conclude that the use of black soldier fly larvae has a great potential in organic waste treatment while also enhancing income generation in low and middle-income countries.

KEY WORDS: Stratiomyidae, black soldier fly, *Hermetia illucens*, municipal organic waste, animal feed

Malaise traps in biodiversity assessments – I. A spatio-temporal comparison of Chironomidae (Diptera) documents community change in a mountain stream

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The family Chironomidae is the most species rich group of insects in freshwater ecosystems of temperate regions and chironomid communities are well suited to characterise past and present environmental conditions. We used Malaise traps emptied regularly through the 1986 and the 2008 seasons to document possible changes in species composition along an alpine-boreal watershed in Central Norway. To test the comparability and the reliability of the sampling method, five parallel traps were placed along the main stream at elevations of 1105 to 1119 m with trap-distances of about 40 to 230 m. The similarity of the parallel collections is very high with correlations of 0.94 to 0.99 for a given week and location. The correlations between parallel samples are obtained by a bivariate Poisson lognormal species abundance distribution. Thus, within a small area, two Malaise traps collect approximately the same species in about the same frequency when positioned in the same way relative to water flow. In comparison, correlation of the samples from 1986 with samples from the same locality in 2008 and taken at the same time of the season is below 0.75 (between 0.56 and 0.75). The observed change in species composition includes both introduction of new species and alterations in abundance patterns. In addition, a shift of species towards higher altitude points to a community response to a warmer climate. This hypothesis is supported by a distinct increase in water temperature over the last 20 years.

KEY WORDS: Freshwater monitoring, Atna River, Norway, Poisson lognormal species distribution

Contents

Anthomyiid fauna of Sakhalin and adjacent territories

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Based on a collection of flies made in 2002 and information in literature, 59 species of Anthomyiidae are recorded from Sakhalin. In adjacent territories, 53 species of Anthomyiidae have been known to occur in Kamchatka, 165 species in Hokkaido, and 222 species in the whole of Japan. These are grouped into the following four categories based on their distribution:

1. East Palaearctic. No records from Europe or North America up to the present. In Kamchatka: 5 of 53 spp. (9.4 %); Sakhalin: 12 of 59 spp. (20.3 %); Hokkaido: 58 of 165 spp. (35.2 %); whole of Japan: 87 of 222 spp. (39.2 %).

2. Transpalaearctic. Found in Europe, but not in North America. In Kamchatka: 7 spp. (13.2 %); Sakhalin: 6 spp. (10.2 %); Hokkaido: 43 spp. (26.1 %); whole of Japan: 55 spp. (24.8 %).

3. Holarctic. Widely distributed from Europe to North America. In Kamchatka: 35 spp. (66.0 %); Sakhalin: 39 spp. (66.1 %); Hokkaido: 58 spp. (35.2 %); whole of Japan: 71 spp. (32.0 %).

4. East Palaearctic - Nearctic. Found in North America, but not in Europe. In Kamchatka: 6 spp. (11.3 %); Sakhalin: 2 spp. (3.4 %); Hokkaido: 6 spp. (3.6 %); whole of Japan: 9 spp. (4.1 %).

In the fauna of Sakhalin the percentage of species common to Europe (Categories 2+3) is 76.3 % (45 of 59 spp.). This numerical value is larger than that of species common to Hokkaido (66.1 %, 39 of 59 spp.), though Sakhalin is far distant from Europe and has a history of land connection with Hokkaido during the most recent period of Warm glaciation (ca. 12000 years BP).

Some discussion will be given on what is to be deduced from these faunal data.

KEY WORDS: Anthomyiidae, fauna, Sakhalin, Kamchatka, Japan

Morphological and molecular phylogenetics of *Culicoides* (Diptera: Ceratopogonidae) with notes on phylogenetic patterns of ecology

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Culicoides is the major pest genus in the family Ceratopogonidae, but despite their economic importance, the phylogenetic relationships among the various subgenera, species groups, and species are poorly understood. The genus is divided into numerous subgenera (ca. 30 depending on author) and unplaced species groups, but these groupings are largely based on phenetic methodologies. Here cladistic analyses using morphological and molecular techniques are performed to assess the relationships of the subgenera and species groups of the *Culicoides* of North America north of Mexico. Morphological analysis indicates that some subgenera and species groups are monophyletic, with some species warranting elevation to subgeneric rank, while other assemblages do not represent natural groups. Molecular data are currently being analyzed for comparison to the morphological data. A preliminary assessment of phylogenetic patterns of midge ecology is also presented.

KEY WORDS: Ceratopogonidae, *Culicoides*, systematics, ecology, North America

Miltogramminae (Diptera: Sarcophagidae) as a new forensic indicator for buried bodies

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Flesh flies are rarely used for PMI-estimations because of their secondary role in decomposition of larger carcasses, their fast larval development, and problems with precise species identification. However, in dry habitats the participation of Sarcophagidae in decomposition seems to be significantly higher. The most frequently recorded species of flesh flies reared from larvae collected in actual cases and from experiments with animal models belong to the subfamily Sarcophaginae or more rarely to the Paramacronychiinae. The present studies have discovered a possible importance as forensic indicators also for species of the third subfamily of flesh flies, the Miltogramminae. The first breeding records of miltogrammine fleshflies from buried vertebrate carrion are presented. First instars of *Eumacronychia persolla* Reinhard (Nearctic) and *Phylloteles pictipennis* Loew (Palaearctic) are able to penetrate dry, loose soil and reach deeply buried animal remains, an ability unique among necrophagous Calyptrata. Fully grown third instars of *E. persolla* and *P. pictipennis* were found on the experimental carrion already 20–21 days after burial at a depth of more than 40 cm. In the laboratory experiments, newly deposited first instars of *P. pictipennis* successfully reached and completed their development on pig liver hidden under dry sand at depths of 5 cm and 33 cm. Broad geographical distribution, fast location and colonization of the carrion, development exclusively on buried food resources, and easy identification make *E. persolla* and *P. pictipennis* useful forensic indicators for buried bodies in dry habitats. Similarities in larval morphology of many species of other Miltogramminae to larvae of *E. persolla* and *P. pictipennis* point to the possibility of discovering several other species with similar breeding behavior in western and southern USA, Mexico, dry parts of Africa, the Middle East, and Central Asia.

KEY WORDS: Sarcophagidae, Miltogramminae, buried carrion, forensic entomology

First instars of European Miltogramminae (Diptera: Sarcophagidae) – an excess of missing links

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The subfamily Miltogramminae is a relatively diverse group with more than 600 described species. During recent work extensive documentation concerning morphology of the first instars of 72 European species of Miltogramminae was completed. Material was obtained by keeping wild-caught females under laboratory conditions or by dissecting dry specimens from museum collections. Larvae were subsequently prepared for analysis by light and scanning electron (SEM) microscopy. Results showed an unusual morphological variation of first instars among Miltogramminae in most of the analyzed features. Several structures, unique among Oestroidea, are described for the first time. Cuticular sculpture and elongation of the first sensillum basiconicum of the maxillary palpus mentioned in previous literature as possible autapomorphies of the subfamily are present in almost all of the described larvae. Comparison of this data with descriptions in earlier literature for 20 species revealed several discrepancies, mainly in interpretation of shape of particular elements of the cephaloskeleton and presence of cuticular structures. Morphological characters of the first instars of Miltogramminae may carry phylogenetic information, but their coding for analysis is difficult because of the existence of many transitional stages. According to general evolutionary trends in higher Diptera from saprophagy to parasitism or predation, a set of seven general plesiomorphic larval characters is defined. Among Miltogramminae the first instars of Phyllotelini bear the highest number of these characters. In contrast to earlier hypotheses, saprophagy of various buried resources is suggested as the ancestral life habit of the whole subfamily. First instar morphological data are in conflict with current systematics in many points, suggesting the necessity of further research on the systematics and phylogeny of Miltogramminae.

KEY WORDS: Sarcophagidae, Miltogramminae, first instar, morphology, SEM, evolutionary trends

Contents

Homology of metathoracic pleura in the family Syrphidae (Cyclorrhapha: Aschiza)

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The metathoracic segment of flies is atrophied and is accompanied by a reduction of the hind wings into halteres, as compared with the mesothoracic segment that bears a pair of well-developed fore wings and internally has large and powerful flight muscles. The pleura of the pterothorax comprise important mechanical elements, and hence are considered to contain significant phylogenetic information (Snodgrass, 1935; Hennig, 1973). Here I investigate the characteristics of the metathoracic segment in brachyceran Diptera, particularly the pleura of the segment in the family Syrphidae. The homologies of the metepisternal and metepimeral pleura are redefined based on the metapleural suture, which is projected as an internal apophysis. My new interpretation of the homology of the metathoracic segment in the Syrphidae indicates: 1) monophyly of the Syrphidae is supported; 2) the family Pipunculidae is sister to the section Schizophora, supported by having an articulated structure between the thoracic and abdominal segments; and 3) members of the Schizophora have a suture on the first abdominal tergum at its articulation point, as mentioned by Young (1921).

KEY WORDS: homology, comparative morphology, metathoracic segment, metepisternal pleura (= metepisternum)

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Response of the uzi fly *Exorista sorbillans* to silkworm-infested mulberry in a wind tunnel

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Host-foraging behavior of the female uzi fly *Exorista sorbillans* (Diptera: Tachinidae) in response to a herbivore-damaged mulberry plant was examined in a wind tunnel bioassay. *Bombyx mori* was used as the host for this fly and as the herbivore to infest mulberry plants. Mated female flies (58%) took off from a release site and 23% landed on infested mulberry without hosts, whereas 10-20% took off from a release site and <5% landed on artificially damaged or intact mulberry. When a filter paper treated with a solution of headspace volatiles collected from infested mulberry was attached to intact mulberry, 57% of the flies took off from a release site. Analysis of headspace volatiles from infested and intact mulberry revealed that some chemicals ((E)-β-ocimene, (E)-2-hexenal, (E)-4,8-dimethyl-1,3,7- nonatriene, α-farnesene) were emitted in greater amounts from infested mulberry. These results indicate that *E. sorbillans* responds to and is attracted to volatiles from infested mulberry.

KEY WORDS: Herbivore-induced plant volatiles, insect–plant interaction, silkworm, mulberry, Tachinidae

Contents

Flower flies: Where have we been recently and where should we be going next

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The Modern classification of flower flies (Diptera: Syrphidae) begins with the work of Hull and Shiraki, published in 1949. With those as a baseline, changes in our knowledge of flies are reviewed and suggestions made for what needs to be urgently investigated to fill in the lacunae and expand our understanding of these critical flies.

Phylogeny of flat-footed flies (Diptera, Platypezidae) based on mitochondrial gene analyses

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The family Platypezidae is a small brachycerous family of forest-dwelling flies that develop in fungi, mostly in sporocarps of typical mushrooms. Immature stages are known only for some of the species; although recently more detailed information became known forthe genus *Callomyia*, as well as its association with mycelium-infested rotten wood. The current phylogeny of the family is based on earlier morphological cladistic studies, with Opetiidae as the putative sister family of Platypezidae. In this study we focused on the intrafamiliar relationships of Platypezidae using *Opetia* as an outgroup. Based on a multigene analysis (20 spp., 2696 bp, 4 mitochondrial markers), we tried to reconstruct the relationships within the family using representatives of all major West Palaearctic genera. *Microsania pectipennis*, the only member of the subfamily Microsaniinae studied, is a sister group of the monophyletic Platypezinae. It consists of strongly supported clades ((*Platypeza, Kesselimyia* (*Paraplatypeza, Lindneromyia*)) (*Protoclythia* (*Seri, Polyporivora*))), which is in agreement with recent cladistics of the family. Callomyiinae is not resolved as a monophyletic clade. Part of the genus *Agathomyia* (*falleni* group) forms a clade in a polytomy together with the Microsaniinae/Platypezinae and the remaining Callomyiinae, rendering the Callomyiinae paraphyletic. The remaining Callomyiinae form a polytomy; relationships between the *Agathomyia viduella*group, the *A. elegantula* group, *Callomyia* (a well-supported monophyletic clade), and *Platypezina,*remain unresolved. The genus *Agathomyia* is not resolved as a monophyletic clade, but its recently considered subgroups, the *A. falleni* group and the *A. elegantula* group, form monophyletic clades. The presence of *Agathomyia* makes the subfamily Callomyiinae paraphyletic and therefore needs further study by inclusion of additional species.

This study was supported by the grant of the Ministry of Education of CR No. MSM 0021622416.

KEY WORDS: phylogeny, Microsaniinae, Callomyiinae, Platypezinae,
CO I, Cyt b, 12S, 16S, platypezids

Contents

Factors affecting abundance and distribution of *Pseudasphondylia neolitseae* (Diptera: Cecidomyiidae)

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The abundance and distributional ranges of various organisms have been affected by global warming. To predict future shifts in distributional range by organisms, the investigation of factors affecting population densities is important, especially around their northern and southern limits. In 2009 and 2010, we investigated the geographical distribution, population density, and survival rate of Pseudasphondyia neolitseae (Diptera: Cecidomyiidae) in the Izu District of Japan. Special attention was paid to synchronization of adult emergence with budburst phenology of the host plant, Neolitsea sericea (Lauraceae). The population density was highest at localities where latitudinal equivalent was around 35˚ or annual mean temperature was 15˚C. In northern localities, galls were induced only on trees with late budburst phenology, indicating that adult emergence was relatively later than budburst. In these localities, frost damage to host buds was observed in the spring of 2010, which was probably caused by extremely low temperatures in late March. Such phenological asynchrony and occasional frost damage to host buds seemed to be important mortality factors operating on P. neolitseae around their northern limit of distribution. In southern localities such as Miyake, Mikura, and Hachijo Islands, many suitable buds for oviposition existed on host trees during the adult emergence season of P. neolitseae. However, galls by P.neolitseae were not found at low elevation sites (<300 m) on these islands, suggesting that factors other than phenological asynchrony restricted the existence of P. neolitseae. The population density of P. neolitseae was very high in the late 1970's at high elevation sites of Miyake Island. However, it declined remarkably in 2000 as a result of the eruptions of Mount Oyama on Miyake and has since been kept at a low level probably due to subsequent volcanic activities including volcanic ash fall and volcanic gas emission.

KEY WORDS: distribution, gall midge, host phenology, mortality factor, population density

A molecular analysis of Sciomyzidae (Diptera)

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The Sciomyzidae as a family of Acalyptrata includes 540 species in 61 genera distributed over all the main biogeographic regions. The monophyly of Sciomyzidae is based primarily on their malacophagy (though some recently discovered larvae also attack aquatic Oligochaeta).The Phaeomyiidae (treated originally as a subfamily of Sciomyzidae) is considered as a sister-group of Sciomyzidae along with 9 families treated recently in the Sciomyzoidea. Members of Coelopidae, Dryomyzidae, Helcomyzidae, Heterocheilidae and Huttoninidae were analyzed and used as outgroups. In this study, we tried to reconstruct the intrafamiliar relationships based on 7 gene markers (5 mitochondrial, 2 nuclear). The resulting alignment contained 8234 bp of 60 analysed species and the resulting tree enables a basic discussion on relationships among the examined taxa. The suitability of the outgroup families was proved. The examined genera of Sciomyzinae are grouped into two phyletic lines which do not correspond with the current system of the family (Salticellinae and Sciomyzinae with tribes Sciomyzini and Tetanocerini). *Salticella fasciata* is apparently more closely related to the Tetanocerini. Within the tribe Sciomyzini, some interesting results were found (the position of *Pherbellianana*, the isolation of *Sciomyza*, the position of *Colobaea*, etc). In the framework of Tetanocerini, *Anticheta* and *Renocera* form a clade of primitive genera. The rest of this tribe is arranged in three phyletic lines, the first of them including *Dichetophora*, *Ectinocera, Euthycera* and *Coremacera*, the second comprising *Tetanocera* spp. and the third with the remaining genera of the Tetanocerini.

This study was supported by the grant of the Ministry of Education of the Czech Republic No. MSM 0021622416.

KEY WORDS: Sciomyzidae, phylogeny, mitochondrial, nuclear markers

New insights into the origin and evolution of Diptera from phylogenomics

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Phylogenetic relationships among the 11 extant orders of holometabolous insects are important as a context for understanding the origin and evolution of Diptera. Here we present evidence from nucleotide sequences and microRNAs, in addition to reviewing recent hypotheses from other phylogenomic and morphological studies, regarding Holometabola and the closest relatives of Diptera. Our DNA analyses support the monophyly of the extant orders, a sister-group relationship for Hymenoptera and all other Holometabola, and the monophyly of traditionally recognized groupings of Neuropterida, Amphiesmenoptera, Antliophora and Mecopterida. Most significantly, we find a sister-group relationship between Diptera and Mecoptera + Siphonaptera, with Strepsiptera as the sister group to the Coleoptera, thus refuting speculation that the parasite order is the closest relative to the flies. Analyses of the phylogenetic distribution of miRNAs from holometabolan model organisms returns a topology congruent to our DNA analyses, supporting our findings and the phylogenetic utility of miRNAs. Additional phylogenomic and morphological studies show congruence and conflict with our results, particularly regarding the sister group to Diptera. Together, these results provide the most complete evolutionary framework for future comparative studies on model organisms and contribute strong evidence for the resolution of the 'Strepsiptera problem,' a long-standing and hotly debated issue in insect phylogenetics.

KEY WORDS: phylogeny, Diptera, molecular systematics, genomics

Contents

Molecular phylogenetics of the bee flies: overcoming the effects of rogue taxa

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Bombyliidae, or bee flies, are a lower brachyceran family of flower-visiting flies that, as larvae, act as parasitoids of other insects. Including almost 5000 spp., the bee flies are both species-rich and extremely morphologically diverse. The subfamily relationships are primarily known from a single, previous morphological analysis that yielded minimal support for higher-level groupings. We use the protein-coding gene CAD and 28S rDNA in combination with existing morphological data to test the monophyly of the existing subfamilies, the higher-level divisions Tomophthlamae and 'the sand chamber subfamilies', and to determine the intersubfamilial relationships. We explore the topological incongruence between analysis methods and the effects of the exclusion of conflict-inducing taxa. We find eight subfamilies to be monophyletic and the interrelationships of most subfamilies to be represented by short branches with low support. Our data do not support the monophyly of Tomophthalmae or the 'sand chamber subfamilies'.

KEY WORDS: Phylogeny, Diptera, bee flies, Bombyliidae, molecular systematics, rogue taxa

Phylogeny and sexual selection in the dance fly species group *Enoplempis* (*Empis*, Empidini)

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Sexual selection is an evolutionary process that can result in the evolution of complex behavioural, morphological and physiological traits in many groups of organisms. It is thought to be a key driving force in the evolution and diversification of hyperdiverse groups. An example of a group where sexual selection may have a significant effect on phylogenetic diversity are Dipterans in the family Empididae. The evolution of mating behaviour in the subgenus *Enoplempis* of the genus *Empis* is one such interesting system of study. This group exhibits a variety of stages of nuptial feeding behaviours culminating in ballooning behaviour. Kessel (1955) hypothesized that this species group has evolved in stages from offering large prey items with much nutritional benefit to frothy balloons which contain crushed fragments of prey with little nutritional benefit. Members of this species group also exhibit morphological ornamentations whose evolution may also be driven by sexual selection. Species of *Enoplemis* offer an ideal opportunity to study the possible effects of sexually selected traits on the evolution of diversity in the wider Empidini in a phylogenetic context. Here are presented the initial findings of the phylogeny of *Enoplempis* and their implications for the evolution of ballooning behaviour.

KEY WORDS: sexual selection, empidid flies

Ecotone effect on trapping of fruit flies (Tephritidae) in natural environments in central Brazil

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Populational patterns of fruit flies (Diptera: Tephritidae) were evaluated in a fragment of semideciduous forest and in a commercial orchard in Central Brazil. This survey was carried out in a fragment of forest (22º 12’ S, 54º 55’W, at an elevation of 430 m) and in a commercial orchard (22º 13’ S, 54º 43’ W, elevation 411 m) in Dourados-MS, Brazil. The aim of this study was to compare the abundance and species richness of fruit flies caught in McPhail traps installed along the border (ecotone) and in the middle of a native forest (Reserva Florestal Fazenda Coqueiro, Dourados-MS), as well as along the border and in the middle of a commercial orchard (Pomar Sindicato Rural de Dourados). *Ceratitis capitata* (Wiedemann 1824) was the most abundant species in both places, representing more than 80% of the all captured fruit flies. From the genus *Anastrepha* Schiner, 292 females from 12 different species were caught, as follows: *Anastrepha amita* Zucchi 1979, *A. barnesi* Aldrich 1925, *A. daciformis* Bezzi 1909, *A. elegans* Blanchard 1961, *A. fraterculus* (Wiedemann 1830), *A. montei* Lima 1934, *A. obliqua* (Macquart 1835), *A. pseudoparallela* (Loew 1873), *A. sororcula* Zucchi 1979, *A. striata* Schiner 1868, *A. turpiniae* Stone 1942, and *A. zenildae* Zucchi 1979). *A. sororcula* was the most abundant species (50.68%) of *Anastrepha*. There were no significant differences in the abundance of fruit flies caught along the border or in the middle of the forest, nor along the border or in the middle of the commercial orchard. However, there were significant differences in species richness and diversity. The traps installed along the border of the forest captured a higher diversity (Shannon index H’ = 2.13) in comparison with those intalled in the center (H’ = 1.67) of the forest. The results from this study corroborate the prediction that in ecotones species richness and diversity are higher compared with the middle of each of the adjacent ecosystems in natural environments.

KEY WORDS: Rapid Survey, frugivorous flies, species richness, diversity, taxonomy

Contents

Species of fruit flies (Diptera: Tepritidae) in the southeast of Mato Grosso, Brazil

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Mato Grosso is the third largest state in Brazil (906,806.9 km^2), surpassed only by Amazonas (1,567,953 km^2) and Para (1,246,833 km^2) states, and it is connected with the Amazon Forest complex. However, before this study, only eight species of fruit flies were recorded from Mato Grosso. The aim of this paper is to provide the first systematic survey on fruit flies (Tephritidae) species richness in the southwestern region of Mato Grosso. Twenty-eight mcphail traps baited with hydrolyzed corn protein diluted to 10% (vol./vol.), and stabilized with borax (ph between 8.5 and 9.0) were used monthly. The traps were installed in branches of native trees (1.8 to 2.0 m height) in six different municipalities of southeastern Mato Grosso, from February 1st, 2005 to July 14th, 2005. A total 16 species of fruit flies were caught: 15 species of *Anastrepha* Schiner (*Anastrepha* sp. n.1, *Anastrepha* sp. n.2 aff. Montei Lima, *A. coronilli* Carrejo & Gonzalez, *A. distincta* Greene, *A. dissimilis* Stone, *A. fraterculus* (Wiedemann), *A. obliqua* (Macquart), *A. matertela* Zucchi, *A. pickeli* Lima, *A. pseudoparallela* (Loew), *A. serpentina* (Wiedemann), *A. sororcula* Zucchi, *A. striata* Schiner, *A. turpiniae* Stone, *A. zenildae* Zucchi), and *Ceratitis capitata* (Wiedemann). The species of fruit flies previously reported in Mato Grosso were: *Anastrepha daciformis* Bezzi, *A. dissimilis*, *A. grandis* (Macquart), *A. leptozona* Hendel, *A. mixta* Zucchi, *A. oblique*, *A. puntacta* Hendel (as *A. minor*), and *A. sororcula* Zucchi. This work adds 12 new records of species of fruit flies to Mato Grosso, updating to 21 the number of species of fruit flies recorded in that Brazilian state.

KEY WORDS: diversity, frugivorous insects, fruit flies, taxonomy

Larval structures in the forensically useful flesh fly, *Sarcodexia lambens* (Wiedemann, 1830)

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Forensic entomology, the study of the relationship between insects and corpses, often includes flies in the family Sarcophagidae. These flies are found on all stages of decomposition of animal carcasses, including those of humans. The age of the larvae is an important tool used to estimate time since death or displacement of the corpse after death. Sarcodexia lambens, a species often found on corpses, is widely distributed in the Neotropics, including Brazil. Because larval form and age are important for both forensics and taxonomy, we used scanning electron microscopy to illustrate the most important characters for those purposes. Larvae were from a culture derived from wild S. lambens at the Oswaldo Cruz Foundation, Rio de Janeiro, Brazil. Larvae were prepared and fixed using standard scanning electron microscopy techniques. First, second and third instars were described from the micrographs. First instars have 12 segments with spines of various shapes and sizes at the edges of all segments, as follows: ventrally, the thoracic segments have trichoid sensilla and large spines, the abdominal segments have long, slender spines, and the posterior spiracle is located in a terminal cavity. Second instars are similar to the first, but differ as follows: the antennae, and maxillary palpus with its 5 papillae, are more apparent, the anterior spiracles have 12 branches, the mouthhook has scars, the abdominal and thoracic segments have larger and flattened spines, and the posterior spiracle has two openings. The larger, third, instar has conspicuous ornamentation on the cephalic segment, a smooth mouthhook and simple thoracic spines are mixed with clumped spines. Often characters are not easily visible in optical microscopy and this study adds complementary characters for the use of S. lambens in forensics.

KEY WORDS: Brazil, forensic entomology, Sarcophagidae

Pictorial key of species of Sarcophagidae of potential forensic importance found in Southern Brazil

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Forensic entomology, the study of the relationship between insects and corpses, often includes flies in the family Sarcophagidae. These flies are found during all stages of decomposition in carcasses, including those of humans. An analysis of the fly larvae and pupae, permits an estimate of the time since death and movement of the corpse can be inferred. Pictorial keys are essential for these studies because correct identification of the flies is of fundamental importance for forensics – such keys are lacking in Brazil for the Sarcophagidae of forensic importance. To fill this lacuna, the main goal here is to provide such a key that shows specific diagnostic characters. Flies were collected in the year 2009 in the city of Curitiba, Paraná, in southern Brazil. Flies were collected daily by direct capture on pig and rabbit carcasses that were protected from other scavengers within cages. Male flies were subsequently prepared for identification and photography by exposing the terminalia. Twenty two species were captured and are included, as follows: *Boettcheria aurifera, Helicobia aurescens, Microcerella halli, M. analis*, *Nephochaetopteryx cyaneiventris, Oxysarcodexia admixta, O. culmiforceps, O. parva, O. paulistanensis, O. riograndensis, O. thornax, O. xanthosoma, Peckia (Euboettcheria) australis, P. (E.) collusor, P. (E.) florencioi, P. (Pattonella) intermutans, P. (P.) resona, Sarcophaga (Bercaea) africa, S. (Lipoptilocnema) lanei, Sarcodexia lambens, Titanogrypa (Sarconeiva) fimbriata* and *Udamopyga percita.* The main characters used in the key were: plumosity of arista, presence of proclinate fronto-orbital setae, setosity of wing veins R1 and R4+R5, presence of ctenidium of mid-femur, presence of dense spine-pad on hind trochanter, color of epandrium and syntergosternite 7+8, shape of the cercus, phallus and vesica, relative size of the basiphallus and distiphallus, presence of setae on the postgonite and pregonite, and number of scutellar setae.

KEY WORDS: flesh flies, forensic entomology, identification key

Contents

Biology of snail-killing Sciomyzidae flies

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We present the essentials of a 550-page book (including 101 tables, 228 figures, 4 color plates) on all aspects of the Sciomyzidae by Knutson and Vala. The book, published by Cambridge University Press, will be released at the end of August, 2010. A pageproof of the book will be available for inspection at the poster presentation. The world literature is reviewed and analyzed in the book, with 1055 publications cited there-in. Life-cycle information in the book concerns the 240 biologically known species from among the 538 described species (about 580 undescribed species are included), 40 of the 61 genera of Sciomyzidae. Larvae of all reared Sciomyzidae are malacophagous except for one obligate and one facultative predator of freshwater oligochaetes in Africa. Most other reared species are obligate natural enemies of non-operculate freshwater, semi-terrestrial, or terrestrial snails. A few are restricted to slugs, eggs of snails, or freshwater finger-nail clams. Behaviorally, the larvae range from a few highly specialized, semi-terrestrial parasitoids (one snail per larva, one larva per snail), to predator-parasitoid-saprophages of shoreline or otherwise exposed snails, to many overt predators of snails in water or on land. The value of Sciomyzidae for potential biological control of snails that are transmitting agents of flatworm parasites of man and animals –and of snails and slugs as agricultural pests - is reviewed. Also explored are the potential of Sciomyzidae to be used as bio-indicators of endangered habitats and as ecosystem providers for the natural control of snails. Information for a paradigm of the evolution of predatory/parasitoid behavior of Sciomyzidae is also included. Notably, a CD of Clifford Berg's classical, 1978, 20-minute film on Sciomyzidae is included in the book as well as at the poster presentation. The book also features keys to the genera of adults, larvae, and puparia by major zoogeographical regions, and a tabular, expanded checklist of species of world Sciomyzidae.

An overview of Afrotropical Sciomyzidae

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The Sciomyzidae comprise of 539 species in 61 genera, most in the Northern Hemisphere. The Afrotropical (AFT) fauna includes 63 species in 12 genera and at least 17 undescribed species. Six AFT genera and subgenera, with 21 species, are endemic. Three Holarctic genera (*Colobaea*, *Ditaeniella*, *Pteromicra*) with six undescribed species are newly reported here for AFT. Two widespread Palearctic species of *Hydromya* and *Colobaea* are marginally adventive into AFT. Two genera (*Ditaeniella* and *Pherbellia*) are shared with the Neotropical Region. Interesting zoogeographical relationships are *Sepedoninus* (2 AFT endemic, 1 Oriental (O) endemic), *Salticella* (1 AFT, 1 P), and the subgenus *Parasepedon* (34 AFT, 6 O). The cosmopolitan *Sepedon* (94 species) has speciated explosively in AFT, with 42 + species in 3 endemic subgenera. Complexes of many closely related AFT *Sepedon* require molecular analyses. Biologies of 240 species in 40 genera of Sciomyzidae are known (predators/parasitoids of freshwater and terrestrial snails, slugs, eggs of snails, fingernail clams), but only for six AFT species. Five AFT species of *Sepedon* attack freshwater and terrestrial snails (Succineidae) and freshwater oligochaetes; one species of *Sepedonella* feeds on oligochaetes. The other 19 reared species of *Sepedon* (P, O, N) are predators of freshwater snails. *Sepedon* and four related genera are interesting from behavioral and morphological aspects. In cladistic analyses of sciomyzid genera (Marinoni & Mathis, 2000; Barker et al., 2004) the *Sepedon* lineage appeared as the most derived and best resolved lineage in the Sciomyzidae. An analysis based on molecular characters by Chapman et al. (2006) shows *Sepedon* arising near the base of the Tetanocerini clade. Notably, the *Sepedon* lineage lacks a ptilinum, ptilinal suture, has reduced chaetotaxy and apomorphic labellar hooks, and is the only genus exhibiting trophallaxis. A separate family, subfamily, or tribe has been proposed seven times for one or more genera in the lineage, from Acloque (1897) to Verbeke (1950).

Contents

New views on the taxonomy of *Tachina* spp. (Tachinidae): West Palaearctic species

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The male postabdominal structures of several species of the genus Tachina were described, and identification keys, illustrated with pen drawings and micrographs, were provided. Molecular analyses based on 4 mitochodrial gene markers were done and supervised feed-forward Artificial Neural Networks (ANN) methodology was applied to morphometric and qualitative characters. This parallel application of three alternative methods based on genotypic and phenotypic inputs used in parallel has enabled the principle of "Polyphasic Taxonomy" to solve some taxonomic discrepancies (see references to*Novotná et al. 2009, and **Muráriková et al. 2010, below). All approaches resolved taxonomic doubts with identical results: 1) the four presently recognized subgenera of the genus Tachina were confirmed and the description of a new subgenus was recommended; 2) the validity of a new boreo-alpine species (sp.n.) was confirmed; 3) the previously supposed presence of T. casta in central Europe was not supported; 4) West Palaearctic T. nupta was contrasted with East Palaearctic specimens from Japan, but the latter seems to represent a valid species not conspecific with central European specimens, therefore T. nupta needs detailed further study; and 5) T. nigrohirta, resurrected recently from the synonymy of T. ursina, was confirmed as a valid species. Extending this project to include more of the Eastern Palaearctic fauna of the genus should be a matter of further study.

*Muráriková, N., Vanhara, J., Tóthová, A. & Havel J., 2010: Polyphasic approach applying Artificial Neural Networks, molecular analysis and postabdomen morphology to West Palaearctic *Tachina* spp. (Diptera, Tachinidae). Bull. Ent. Res., accepted.

**Novotná, H., Vanhara, J., Tóthová, A., Muráriková, N., Bejdák, P., Tkoc M. & Rozkošný R., 2009: Identification and taxonomy of the West Palaearctic species of *Tachina* Meigen (Tachinidae, Diptera) based on male terminalia and molecular analyses. Ent. Fenn. 20: 1-31.

KEY WORDS: Artificial Neural Networks-ANN, phylogeny, CO I, Cyt b, 12S, 16S, male postabdomen

Forensic entomology: Analysis of its development ten years after the implementation in Costa Rica

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After ten years of application of forensic entomology in Costa Rica, and under the fact that judicial cases have been given and confirmed by entomologic determinations, we presume to make a review of the results obtained.

The implementation of forensic entomology in Costa Rica took place in 1997 and focuses on five principal pillars of investigation: 1) Review of the diversity of the family Calliphoridae in Costa Rica; 2) Determination of the principal settlers of human bodies; 3) Data generation for the development for the species which are more frequent in decomposition systems , 4) Taxonomic identification of immature forms and 5) Education for crime scene officers, lawyers and judges in the matter of harvest and interpretation of entomological evidence.

The review of the vast collection of specimen of the family Calliphoridae of INBio, as well as the growth of larvae collected directly from putrid bodies, allowed for the determination of following species: Cochliomyia macellaria (Fabricius), Hemilucilia segmentaria (Fabricius), H. semidiaphana (Rondani), Chrysomya megacephala (Fabricius), C. rufifacies (Macquart), Lucilia eximia (Wiedemann), L. purpurescens (Walter), Calliphora irazuana (Townsend) and Choroprocta idioidea (Robineau-Desvoidy), as well as the Peckia intermutans (Walker), of the family Sarcophagidae. These species appear more frequently, developing over the putrid bodies.

This presentation will discuss the analysis of a case with judicial sentence where there is entomological evidence that was very important for the police search, the trial and subsequent processes of legal appeal, showing that the technique has been formally incorporated in judicial debates. It will also be shown that the officials of the process of justice administration know the principals of the interpretation and the use of a scientific opinion as well as the limitations of the technique, for successful implementation in judicial courts.

KEY WORDS: forensic entomology, Calliphoridae, Costa Rican case report.

Taxonomy of *Ommatius* (Diptera, Asilidae) from Brazil

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Ommatius Wiedemann, 1821 is the only genus belonging to the subfamily Ommatiinae in the Neotropical Region. This genus is recognized by setae on the anterior surface of the antennal stylus (subfamily's autapomorphy), and sclerotized postmetacoxal bridge. There are 316 species worldwide, with 116 for the Neotropical Region and 45 for South America. In Brazil 22 species are known: 11 belonging to the *costatus* group, 5 to the *holosericeus* group and 6 to the *normus* group. The Brazilian fauna was revised based on type-material, when available, and specimens loaned from Brazil and other countries. The male and female terminalia were dissected for identification and illustration of the specimens. A total of 1066 Brazilian specimens were examined, 424 males and 642 females. A key to males and females of the Brazilian species, a list including the known and undescribed species, and a distribution with new geographical records of this genus in Brazil are provided.

KEY WORDS: Ommatiinae, new records, distribution

Forensic fly research in Australia: ongoing challenges and recent advances

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Judicial cases continue to highlight shortcomings in the quality and nature of forensic entomology evidence, especially relating to carrion fly identification and biology. These problems emphasise the compelling need for scientific rigour, ethical standards, and appropriately qualified conclusions whenever insect evidence is applied to criminal investigations.

Despite these challenges, forensic entomology has demonstrated value in many cases. It is important that it continue to be accepted by courts to help secure convictions. This can be partly ensured by ongoing, adequately funded research to 1) make identification of forensically important flies easier and more reliable, and 2) improve the application of aspects of fly biology to relevant casework. A main aim is to improve the precision and accuracy of minimum death time estimates.

Fortunately, forensic fly research in Australia is currently flourishing, due largely to the welcome support of national and state law enforcement agencies. This talk will give an overview of recent developments in this field in Australia and what the research priorities should be. The focus will be on work concerned with the identification and systematics of carrion-breeding blow flies (Calliphoridae) and flesh flies (Sarcophagidae) and their behavioural ecology and thermobiology

KEY WORDS: forensic entomology, Calliphoridae, Sarcophagidae, identification, thermobiology

Athericidae and Vermileonidae of the Afrotropical Region

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Worldwide the family Athericidae comprises fewer than 50 species in nine extant genera (*Asuragina, Atherix, Atrichops, Dasyomma, Pachybastes, Suragina, Suraginella, Tricantha, Xeritha*). Four genera and 21 species are known from the Afrotropical region (?*Atherix*, five species; *Pachybates*, two species; *Suragina*, 13 species; and *Tricantha*, one species). The immature stages are aquatic. For many years this family was placed within the Rhagionidae.

Worldwide the family Vermileonidae comprises fewer than 80 species in 11 genera (*Alhajarmyia , Isalomyia, Lampromyia, Leptynoma, Namaquamyia, Perianthomyia, Vermileo, Vermilynx, Vermitigris, Vermiophis,* and *Vermipardus*). Seven genera and 25 species are known from the Afrotropical region (*Isalomyia*, one species; *Lampromyia*, three species; *Leptynoma*, five species; *Namaquamyia*, one species; *Perianthomyia*, three species; *Vermilynx*, two species; and *Vermipardus*, ten species). The immature stages of vermileonids or "worm-lions" have evolved a method of collecting prey similar to those of the neuropteran family Myrmelionidae. For many years this family was also placed within the Rhagionidae.

Morphological differences of metapopulations of *Bactrocera dorsalis* (Diptera: Tephritidae) in Taiwan

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Oriental fruit fly (*Bactrocera dorsalis*) is an important pest of many tropical and subtropical fruits. They are known for their extreme polyphagy; 124 host species from 42 families have been recorded. Due to their economical importance, quarantine restrictions have to be imposed by many countries to limit further spread of oriental fruit flies. Furthermore, more than 70 sibling species are morphologically similar to the *Bactrocera dorsalis* complex and are also almost sympatric with it, thus enormously increasing the quarantine difficulties. Therefore, a more thorough understanding of the Oriental fruit fly, especially of its morphology and identification, is necessary. In this study, two groups of fly samples were studied. First, 160 male specimens, collected in December from Taoyuan and in June at Pingtung were selected, and 14 new morphological characters were discovered. These included the color patterns of the occiput and thoracic brown patterns, the position of intra-alar bristles, and the black patterns on the abdominal tergites. Second, 81 male specimens collected in July, August and December were selected from Taipei, Taichung, Chiayi, Pingtung, and Hualien. Along with the 14 characters mentioned above, characters of the curved and stunted bristles on the tibiae were also included in this study. Both results revealed that, although no geographical variation could be found, some distinct subgroups were clearly detected. We infer that metapopulations exist in Taiwan which are probably the result of some environmental factors rather than geographical isolation. Hopefully, after examining specimens from more localities and some sibling species in the *Bactrocera dorsalis* complex, it will be possible to understand the invasive history of the fly and the possibility of any hybridization within this species complex in Taiwan.

KEY WORDS: Morphological differences, metapopulation, quarantine, Oriental fruit fly, Tephritidae

Antlered flies: new species of *Richardia* R.-D. (Richardiidae) with antler-like genal projections

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Antlers in flies are paired structures formed by cuticular projections, which can be curved, branched, or palmate, arising from the lateral margins of the head without causing displacement of the eyes. These structures are present in five families of flies, three of which belong to the superfamily Tephritoidea: Platystomatidae, Tephritidae, and Richardiidae. Usually the antlers are present only in males. Researches indicate that the presence of these structures is associated with the antagonistic intraspecific interactions in defense of territories; individual males attempt to maintain exclusive possession of oviposition sites along the tree surface to which females will be attracted.

Richardia Robineau-Desvoidy is the largest and the most diverse genus of Richardiidae. Sexual dimorphism is very pronounced in several species. Males may have large modified spines or tubercles on the posterior femur, or may show strong modifications on the head, for example the stalked eyes in *R. telescopica* Gerstaecker or in the only species of the family known for producing antlers - *R. infestans* Hendel. Four news species of *Richardia* with antlers were discovered. The lateral projections of the gena are quite distinctive in *R. elegans* and in each of these four new species, as follows: *Richardia* sp. nov. 1 from Costa Rica has a long, “ribbon-like” extension; *Richardia* sp. nov. 2 from Ecuador has a very long, sinuous and flattened extension; *Richardia* sp. nov. 3 from Panama has the head strongly expanded laterally, the width about five times the height, with a short, tubular and tapering genal extension; and *Richardia* sp. n. 4, also from Panama, has a very short, flatted and ovate extension. The morphological features of these four species are described, illustrated and discussed. A key to *Richardia* with antlers is provided.

KEY WORDS: Acalyptratae, biodiversity, Neotropical Region, Richardiinae

Phylogeny and systematics of *Sarcophaga* (*Heteronychia*) (Diptera: Sarcophagidae)

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Heteronychia Brauer & Bergenstamm, with 88 valid species, is one of the most species-rich subgenera of the large genus *Sarcophaga* Meigen. This paper presents the results of a four-year Ph.D. project consisting of a taxonomic revision and parsimony-based cladistic analysis of *Heteronychia* s.l. and the closely related subgenus *Discachaeta* Enderlein. The taxonomic part of the project includes the re-description of all previously known species and the description of eight species new to science. Almost all species were documented using SEM or ESEM microscopy, with a particular focus on key characters of the male terminalia. A data matrix was constructed for the cladistic analysis, containing 88 species (including two outgroups) and 86 adult male morphological characters. All species of *Discachaeta* were included in the analysis, together with *Sarcophaga* (*Notoecus*) *longestylata* Strobl, suspected to be related to *Heteronychia*. The cladistic analysis resulted in ten most parsimonious trees. The analysis supported the monophyly of *Heteronychia* + *Discachaeta* + *Notoecus* Stein, and the latter two should be included under *Heteronychia*. *Sarcophaga longestylata* was confirmed as a member of the well-supported Centralasiatic-Euro-Mediterranean *filia*-group of *Heteronychia*; few other species-groups were well supported, such as the strictly Mediterranean *minima*-group (10 species) and a group consisting of most former members of *Discachaeta* + *S. ferox* Villeneuve, *S. balanina* Pandellé and *S. desertorum* Salem. The topology of trees changed slightly under implied weighting with different concavity factors, but several clades were retained consistently. Considering the limited phylogenetic resolution and the presence of only a few distinct morphological groupings, the analysed species are included into one subgenus with a number of informal species-groups.

KEY WORDS: flesh flies, *Sarcophaga*, *Heteronychia*, *Discachaeta*, *Notoecus*, phylogeny, taxonomy

Blow flies of the West Indies

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Eleven genera and 21 species of calliphorids were found in the West Indies. Key characters were identified and keys are provided and will be discussed. A possible new species and previously undescribed specimens are described.

KEY WORDS: blow flies, West Indies

Contents

The phylogeny and temporal diversification of mosquitoes: a new combined data hypothesis

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Phylogenetic relationships provide an important comparative framework for mosquito research and are especially valuable for testing and interpreting genetic, ecological and evolutionary evidence. Higher-level relationships within mosquitoes (Diptera: Culicidae) have been difficult to resolve and individual analyses of molecular and morphological data yield conflicting results. We carried out parsimony and model-based phylogenetic analyses on a data set consisting of six nuclear genes and 80 morphological characters to assess their ability to resolve relationships among 25 mosquito genera. We also estimated divergence times based on sequence data and fossil calibration points, using Bayesian relaxed clock methods. Strong support was recovered for the basal position and monophyly of the subfamily Anophelinae and the tribes Aedini and Sabethini of the subfamily Culicinae. Analyses of combined amino acid alignment and morphology showed highest levels of topological agreement across data partitions and analysis strategies. Divergence times for major culicid lineages date to the early Cretaceous. Our results support the notion of rapid radiations early in the diversification of mosquitoes. Despite convincing progress, evidence is still uncertain for deeper relationships in some areas of the tree, especially regarding the composition and placement of Culicinae. Larger studies that include more taxa and more extensive genetic sampling are needed to extend and confirm these findings.

KEY WORDS: Phylogeny, mosquito, molecular systematics, Culicidae

FLYTREE: Collaborative research in Diptera systematics toward a new synthesis of fly phylogeny

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FLYTREE is a collaborative research project funded by the US National Science Foundation Assembling the Tree of Life (AToL) program. During its six-year funding term, this project combined the efforts of over 19 laboratories in 6 countries. We divided data collection and phylogenetic analyses into two main tiers: Tier 1 includes 45 species across the order and several outgroups sampled for approximately 30kb of aligned genetic data from 14 nuclear genes, full mitochondrial genomes and 371 scored morphological features; Tier 2 includes 202 taxa comprising at least one species from 95% (149 / ~157) of recognized families, sampled for 5 nuclear genes. The combined molecular data from the 1st and 2nd Tiers form the largest and most taxonomically broad data matrix completed for Diptera. Tier 3 studies involve detailed phylogenetic analysis within major dipteran clades achieved through a network of interacting research programs and a focus on graduate training and postdoctoral research. Through 3rd Tier studies, the project enabled and produced 30+ published phylogenetic studies that treat over 1000 fly taxa for molecular and/or morphological data. Here, major findings and accomplishments of the FLYTREE project are presented, highlighting specific hypotheses about the origin, age and diversification of fly lineages and emphasizing modern approaches in large dataset construction and analysis. Remaining questions serve to direct, guide, and focus the search for new evidence from genomic data harvests and morphological surveys. The FLYTREE project continues through the shared research activities of the Diptera systematics community and provides a successful model for research collaboration toward resolution of complex and hyperdiverse areas of the tree of life.

KEY WORDS: phylogeny, Diptera, molecular systematics, genomics

Molecular systematics of the sibling species *Lucilia cuprina* and *Lucilia sericata*

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Lucilia cuprina and L. sericata, sister species of greenbottle blowflies, are morphologically very similar and are difficult to identify, even using the available morphology-based keys. They have long been suspected of interbreeding and producing fertile hybrids in South Africa (Ullyett, 1945), where L. sericata is introduced and L. cuprina is indigenous. Additionally, based on preliminary genetic data, several authors have suggested that L. cuprina should be classified as two subspecies or even as two species (Steven & Wall, 1996, Wallman et al., 2005). Lucilia sericata is used for maggot debridement therapy, while L. cuprina is responsible for sheep-strike, and both species are significant in forensic entomology. Natural interbreeding of these two flies therefore has important implications for understanding their biology in several applied settings. To test the hypothesis that they are interbreeding in South Africa, two nuclear genes (28S and Per; 1376 base pairs in total) and one mitochondrial gene (COI; 576 base pairs) were sequenced from 68 South African specimens and 32 specimens from around the globe. Phylograms produced by Bayesian and maximum parsimony analyses showed incongruence between the nuclear and mitochondrial genes: the nuclear genes indicated two monophyletic species and the mitochondrial gene indicated L. cuprina to be paraphyletic, in agreement with previous studies. The results suggest one ancient hybridization event followed by an introgressive selective sweep, and also a low rate of modern hybridization, both distributed at a global scale.

KEY WORDS: *Lucilia sericata*, *Lucilia cuprina*, systematics, mitochondrial DNA, nuclear DNA

Contents

Molecular systematics of schizophoran flies: Can we untangle the tree?

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Resolving relationships between the families of Schizophora remains one of the most challenging problems in the phylogenetics of Diptera. Recent molecular analyses across all dipteran families (FLYTREE project) show good resolution across much of the order, but still fail to resolve deep relationships between families and major lineages of Schizophora. We revisit the FLYTREE dataset for Schizophora, adding sequences for 26 additional acalyptrate taxa chosen to increase sampling within insecurely placed families. The resulting data set was subject to intensive exploratory analyses to investigate the possible effects of alignment, character exclusion, taxon sampling, outgroup selection, choice of model and method, partitioning, and base frequency bias on the resulting topology. We explore several alternative ways to gauge support for nodes with low bootstrap values. Questions addressed include the sister groups of Schizophora, Calyptratae, and Drosophilidae; and the scope of and support for several traditional superfamilies recovered with molecular data, including Ephydroidea, Tephritoidea, and Sciomyzoidea. Evidence for possible alternative relationships between these lineages and remaining families of uncertain placement is evaluated. We conclude with general remarks on possible ways to push the limits of molecular phylogenetic resolution for difficult, rapid radiations

KEY WORDS: phylogeny, Schizophora, rapid radiation, acalyptratae

Molecular phylogeny of the subfamily Empidinae

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The subfamily Empidinae is currently classified into two tribes, Empidini (with two large cosmopolitan genera, *Empis* and *Rhamphomyia*, and a few smaller genera) and Hilarini, (including *Hilara*, also a large cosmopolitan genus, and several south temperate genera). *Empis* and *Rhamphomyia* are widely acknowledged to be mutually non-monophyletic, and their subgeneric classification, based largely on European taxa, is in need of revision. We use molecular data (CAD and COI) and worldwide sampling of empidine taxa to corroborate recent morphological results challenging this traditional classification. These data confirm the monophyly of Hilarini and paraphyly of Empidini, as well as the polyphyly of the three major genera. Gondwanan species of *Empis* form basal branches to both Hilarini and the main clade of temperate *Empis/Rhamphomyia* (= Empidini s.str.). Within Empidini s.str., most diversity is found in three major lineages, one of which includes most Nearctic and Palearctic species of *Rhamphomyia*. We discuss the phylogenetic position of the remaining groups of *Empis* and *Rhamphomyia*, and relationships of the largely unstudied Nearctic fauna. We use our phylogenetic results to explore the evolution of mating-related traits, including female ornamentation, male genitalic elaboration, and behaviors such as swarming and nuptial feeding.

KEY WORDS: *Empis*, *Rhamphomyia*, sexual ornaments, mating systems

Contents

Overview of Afrotropical window flies (Scenopinidae)

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Scenopinidae are a cosmopolitan group of lower brachyceran flies with a maximum body size rarely exceeding 5.0 mm. Twenty-four extant genera of Scenopinidae are presently recognized, containing 436 described species worldwide. Scenopinidae are placed in the superfamily Asiloidea, in a clade comprising families Therevidae, Apsilocephalidae and Evocoidae. Two window fly subfamilies are present in the Afrotropical Region, although 99% of species diversity is represented by Scenopininae (63 spp.). Seven genera are described in Scenopininae (*Caenoneura* Kröber, *Metatrichia* Coquillett, *Prepseudatrichia* Kelsey, *Propebrevitrichia* Kelsey, *Pseudomphrale* Kröber, *Scenopinus* Latreille and *Seguyia* Kelsey) while a single, monotypic genus of Proratinae (*Cyrtosathe* Winterton & Metz) is known. Several new species of scenopinids are known in collections from this region, mostly in *Propebrevitrichia* and the species rich *Scenopinus*.

KEY WORDS: Scenopinidae, window flies

Contents

Cybertaxonomy as a new paradigm for documenting biodiversity: technological advances, opportunities and the culture of taxonomy

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Estimates of undescribed global biodiversity are as varied as they are enormous, but the societal need for documenting biodiversity has never been greater. This is despite the taxonomic impediment (i.e. declines in funding and numbers of taxonomists) limiting our ability to compile a global inventory any time soon. The taxonomic process is inherently slow and careful, but frequently inefficient and tedious with numerous instances of data redundancy. Natural Language Descriptions parsed from Character Matrices is an old idea with significant promise for speeding the process of taxonomic description, but has been poorly implemented in the past resulting in limited uptake by the taxonomic community. Use of character matrices from newer software programs to produce highly standardised taxon descriptions, coupled with the wide availability of high resolution imaging and distributed online databases, means that taxon descriptions can be produced rapidly in machine readable format that is reusable (e.g. monographs, interactive keys, EOL taxon pages). Clearly, a paradigm shift away from traditional handcrafted descriptions towards character matrices is required, and this 'cybertaxonomic' method holds tremendous promise for significantly increasing the output of taxonomists so that we may come close of documenting global biodiversity within our lifetime.

KEY WORDS: Cybertaxonomy, Natural Language Description, character matrix

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Phylogenetic relationships of Acroceridae and Nemestrinidae (Nemestrinoidea)

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Small headed flies (Acroceridae) and tangle wing flies (Nemestrinidae) belong to a loosely defined and possibly paraphyletic clade Nemestrinoidea. Both groups are larval parasitoids of arthropods such as spiders (Acroceridae), beetles and grasshoppers (Nemestrinidae). A phylogeny of these families is presented based on molecular and morphological data. Recent developments in our understanding of the evolution and taxonomy of both extant and extinct groups are discussed.

KEY WORDS: small headed flies, tangle wing flies.

Phylogeny of the therevoid clade (Asiloidea: Therevidae, Scenopinidae, Apsilocephalidae, Evocoidae): a really, really big molecular matrix approach

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Four families of asiloid flies comprise the therevoid clade: Scenopinidae, Apsilocephalidae, Evocoidae and Therevidae. Previous investigations into understanding the phylogenetic relationships of this group have focused on adult morphology of various groupings of stiletto flies, molecular sequence data and even supertree analysis. Despite this recent and extensive activity, our knowledge of the group is still fragmentary. In particular, a robust framework of subfamilial relationships of Therevidae has been lacking. A molecular phylogeny focusing on stiletto flies is presented based on 8 KB of DNA sequence data for over 200 species of the Therevoid clade, analyzed using likelihood and Bayesian methods. Therevidae are confirmed as the sister family to Scenopinidae, and four monophyletic subfamilies are recovered in Therevidae (Phycinae, Therevinae, Agapophytinae and Xestomyzinae).

KEY WORDS: Therevoid clade, molecular phylogenetics

Diptera of Colombia; a preliminary approach

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Colombia, 1,141,748 square kilometres in area, is strategically located in the northwestern corner of the South American Continent. It encompasses a wide variety of bioclimatic zones, from 0 to 5600m in elevation. The country is traversed from south to north by three branches of the Andes mountain chain, creating deep valleys separated by high mountains, which gives rise to a complex mosaic of biogeographic provinces from the Pacific Ocean, with its pluvial forest of the Chocò, to the dry forest of the Caribbean region, to the Páramo Norandino. Its complex faunal diversity, which interdigitates with the biotas of Central America, the Ecuadorian Andes, and Amazonas, has resulted in one of the richest countries in the world in terms of biodiversity. The dipterofauna is no exception and recent efforts to increase sampling have show the high diversity to be discovered. The University of Antioquia houses the main collection of Colombian Diptera, with approximately 50,000 specimens in 86 families. Many of them are new records, showing clearly there is a lot left to be discover, areas such us the Paramo with heights up to 3000m, are a fragile and little studied environments, with high diversity of families like: Anthomyiidae, Calliphoridae, Dolichopodidae, Empididae, Micropezidae, Muscidae, Phoridae, Pipunculidae, Sarcophagidae, Sciaridae, Sphaeroceridae, Syrphidae, Tabanidae, Tachinidae, Tephritidae, Bibionidae, Ceratopogonidae, Chironomidae, Mycetophilidae, Psychodidae, Sciaridae, Tipulidae, Anisopodidae, Keroplatidae and Ditomyiidae. The Norandina region with heights from 2000 to 3000m presents groups such Hybotidae, Dryomyzidae, Nycteribiidae, Pyrgotidae, Scathophagidae, Psylidae. Even in lowland forests, exist rare groups such as Lygistorrhinidae. The important variety of biogeographical regions, show the complexity and diversity of the Colombian biota.

KEY WORDS: Colombia, dipterous diversity

Tachinidae in the era of molecular systematics

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The monophyletic family Tachinidae, one of the largest families of flies, is woefully unprepared for the molecular revolution of the 21st century. Our database already has over 7400 valid species, and genetic analyses of reared specimens from recent studies in Guanacaste suggest that the actual number of tropical species may be 30% higher, in addition to the hundreds, probably thousands, of unnamed species already in collections worldwide.

Classifications vary from 7 families in over 80 tribes comprising well over 1000 genera proposed by Townsend in his Manual of Myiology, to 4 subfamilies (Dexiinae, Exoristinae, Phasiinae, and Tachininae) in 33 tribes, proposed for the Palaearctic Region by Herting in 1984, building on the classification of Mesnil in Die Fliegen der Palaearktischen Region. More recent catalogues have been based on Mesnil's and Herting's classifications. However, many genera are so strange or aberrant that placing them in a tribe or subfamily is still a matter of guesswork, and detailed studies of immature stages and genitalia remain unknown for most genera outside of the Holarctic Region.

All four of the subfamilies, and most of the tribes, have a world-wide distribution, and none appears to be the sister group of another, so that the basic divisions in the family remain unresolved. If capability of retaining eggs to full embryonation has happened more than once in the family, as seems to be the case, perhaps molecular studies may be the only way to determine how often and where these changes took place.

The purpose of this talk is to expose some apparent discrepancies in our existing classification that need further study, both morphological and molecular, using examples from each of the four subfamilies, to show that morphological observations can still contribute to a better understanding of tachinid phylogeny, even as these same taxa are being sequenced.

KEY WORDS: Tachinidae, Dexiinae, Exoristinae,
Phasiinae, Tachininae, classification, phylogeny

Phylogeny of the “orthorrhaphous” Brachycera–progress since 1989

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The publication of the phylogeny volume (Volume 3) of the Manual of Nearctic Diptera in 1989 was intended to summarize our knowledge of Diptera phylogeny down to the family level at the time, as well as present some new morphological character data and analyses. Another intent was to provide a foundation to stimulate further studies in higher level Diptera phylogeny.

In the “orthorrhaphous” Brachycera progress in understanding phylogenetic relationships within the group has advanced on several levels since Woodley (1989). Most studies have continued to postulate that the Brachycera arose from the Psychodomorpha sensu Wood & Borkent in the Upper Triassic, with several studies hypothesizing the Anisopodidae as the actual sister-group of the Brachycera. Some progress has also been made in understanding relationships among the four infraorders left as an unresolved polychotomy by Woodley (1989). Family level taxa, such as Pantophthalmidae and Vermileonidae that were treated as incertae sedis by Woodley have been assigned to infraorders based on convincing evidence. Two new families of “orthorrhaphous” Brachycera have been discovered since 1989 based on newly collected material, the Oreoleptidae (Tabanomorpha) and Evocoidae (Asiloidea, therevoid clade). The infraorder Muscomorpha sensu Woodley (1989) has been corroborated in several studies.

Various aspects of the phylogeny within the Asiloidea have received considerable scrutiny. There is still no consensus as to whether or not the Asiloidea is the sister-group to the Eremoneura, or paraphyletic relative to that group. Also, some infrafamilial groups such as the Proratinae have been reassigned to other families. Progress is being made in understanding the relationships between families of Asiloidea. The Empidoidea has also been the subject of a number of studies, and several family-level taxa within the Empididae sensu lato are now recognized.

KEY WORDS: Diptera, Brachycera, orthorrhapha, phylogeny

Contents

Habitat differentiation of *Chrysomya megacephala* and *Chrysomya pinguis* (Diptera: Calliphoridae)

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In Taiwan, *Chrysomya megacephala* is one of the most important and predominant blow fly species in forensic studies. But according to the literature and to our preliminary survey, *C. megacephala* populations showed localized distributions in some seasons and elevations. It also seems that, at certain times and in certain places, *C. megacephala* is replaced by another species, *C. pinguis*. Hence, to provide more accurate assessment of the post-mortum interval (PMI) it is necessary to understand the relationship and interaction between these two species rather than just focussing on one. *C. megacephala* and *C. pinguis* share very similar morphologies in all life stages. They also have similar life histories and are closely related. These two species usually appear in the same place but at different seasons or in the same season but at different elevations. Because temperature can strongly influence the behavior and physiology of blow flies, we presumed that the two species have adapted to different temperatures, resulting in habitat differentiation. Results of our temperature treatment has suggested, however, that at a high temperature (38°C)larval development of *C. megacephala* was significantly better than that of *C. pinguis*, but when the two species were reared together at 30°C, the larval development of *C. pinguis* was strongly affected by that of *C. megacephala*. We believe that the high temperature created by the maggot mass of *C. megacephala* is probably the key factor that caused the developmental deficiency of *C. pinguis* larvae. The high temperature tolerance and maggot mass formation are apparently an evolutionary strategy of *C. megacephala* allowing them to gain a competitive advantage over *C. pinguis* at high temperatures. This may also explain their habitat differentiation.

KEY WORDS: habitat, temperature effect, forensic entomology, Calliphoridae, Taiwan

The FLYTREE morphological analysis reveals Dipteran evolutionary history

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The Diptera are one of the largest insect Orders, with over 150,000 described species in over 10,000 genera classified in 150 recognised families. FLYTREE is a large international consortium funded by the US National Science Foundation's Assembling the Tree of Life initiative to estimate Dipteran phylogeny. FLYTREE has assembled the largest supermatrices of Diptera, including both molecular and morphological components. 371 morphological characters scored for 42 exemplar fly species spanning the order, and mecopteran outgroups. Trees based on non-additive parsimony analysis of the morphological supermatrix largely confirm Hennig and other author's previous findings, and are consistent with mixed-model Bayesian analysis of concatenated molecular sequences. Well-supported clades (Bremer Support indices > 10) include Diptera, Brachycera, Cyclorrhapha, Schizophora, Calyptratae and Oestroidea. The Nematocera, Orthorrhapha, Aschiza and Acalyptratae are found to be paraphyletic, and support for relationships in these regions of the tree is also poor. The results suggest rapid bursts of fly diversification at the end of the Permian, in the Jurassic, and at the Cretaceous/Tertiary boundary.

KEY WORDS: Diptera, morphology, phylogeny, relationships, evolution

Contents

A systematic review of the Nearctic *Platycheirus* Lepeletier and Serville (Diptera: Syrphidae)

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The Syrphidae is one of the best-known fly families because of its conspicuous diversity, the role of many species as pollinators, and the importance of many syrphines as predators of aphids and other plant pests. Despite this, there are still groups within the Syrphidae that are difficult to identify and are considered taxonomically problematic. One such group is the genus *Platycheirus* Lepeletier and Serville, of which most of the 76 species currently known from the Nearctic Region can be identified only through male secondary sexual characters, leaving females unidentifiable morphologically. We are addressing this issue through the use of morphological and molecular data, using mitochondrial DNA sequences to match females to morphologically identifiable males. After associating both sexes using molecular techniques, females will be reexamined for morphological characters for use in a new photographic key to both sexes of *Platycheirus*. During the course of this review, the monophyly of *Platycheirus* will be tested by examining species groups within the genus and in related genera. Additionally, the validity of several problem species will be reconsidered on the basis of both morphological and molecular characters. We here present preliminary results from our study, which show good correlation between present morphological species concepts and mitochondrial sequence data as well as supporting the monophyly of the genus *Platycheirus*.

KEY WORDS: Syrphidae, *Platycheirus*, Nearctic, systematics, morphology, mitochondrial DNA

Hilarine silk...what it is and its evolution from a fly's perspective

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Silks play a crucial role in the survival and reproduction of many insects. Male hilarine flies (Diptera: Empididae) create elaborate nuptial gifts by wrapping small objects in silk to present to females in mating swarms. The silk is produced from simple class III glandular units grouped in their enlarged prothoracic basitarsi. Tarsal silk glands are not known in any other holometabolous insect.

A partial sequence of the hilarine silk gene has been described. Aspects of the silks composition, together with the proteins predicted architecture, are common to previously described insect silks. Unique aspects of the silk support its genes de novo appearance. In addition, molecular evidence helps to explain how the protein is stored on-masse in the glandular units and how it forms flexible fibres when secreted.

Hilarine silk is likely to represent an independent evolutionary event. Evidence for this is based on the silk gland type, silk protein molecular structure and the phylogenetic relationship of silk producing insects. From the flies' perspective, other categories of insect silk production will be shown in phylogenetic context. The fossil record suggests that male hilarine flies had enlarged basitarsi from ca. 145 million years ago. Some 100 million years earlier, fossilised Embiodea show enlarged prothoracic basitarsi. In conclusion the silk produced by Embiodea, a hemimetabolous insect, will be compared to that of the Hilarini in detail.

KEY WORDS: Hilarini, Empididae, silk, gland, evolution

Possible effects of asynchrony between gall-midge emergence and host-plant phenology on changes in host selection, leading to speciation

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Synchronization between the emergence of herbivorous insects and the phenology of their host-plants is critical especially for short–lived insects such as gall midges. For gall midges, adult emergence is determined by the number of degree-days, or accumulated temperature above a certain threshold, from the onset of their development after hibernation until the emergence season. Conversely, the speed or delay in plant phenology, such as bud burst and blooming, is influenced not only by accumulated temperature in spring but also by cold temperature during winter. Therefore, emergence of gall midges is not always well synchronized with host-plant phenology and under various abiotic and biotic conditions the degree of asynchrony occasionally becomes excessive. Extreme asynchrony forces gall-midge females to search for different plant species or different plant parts for oviposition due to the lack of suitable oviposition sites. Such asynchrony may provide gall midges with opportunities to encounter new plant species or plant parts. Although the probability of successful development in such instances may be low, this is one of the possible triggers for speciation in gall midges. In order to elaborate on this scenario, I present some examples of phenological relationships between gall midges and their host plants, such as Asphondylia aucubae on Aucuba japonica (Aucubaceae), Pseudasphondylia neolitseae on Neolitsea sericea (Lauraceae), Daphnephila machilicola on Machilus thunbergii and M. japonica (Lauraceae) and other gall midges associated with broad-leaved evergreen trees in Japan.

KEY WORDS: asynchrony, emergence, plant phenology, host shift, speciation

The biodiversity of shore flies (Diptera: Ephydridae) in Afrotropical Region

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The shore flies, family Ephydridae, are well represented in the Afrotropical Region with 342 recorded species (20 % of all known shore flies). They belong to 65 genera (out of 110 world genera). Endemism at the species level is high. Distribution of the majority of species (275; 80.4 %) is restricted to the region. There are some affinities with the Palearctic Region (28 species in common; 8.2 %), with both the Palearctic and Oriental regions (3; 0.8 %), with the Oriental Region (4; 1.2 %), with the Australasian Region (3%; 0.8 %), and with the Oriental and Australasian Regions (6; 1.7 %). The remaining species (23; 6.7%) are widely distributed. The endemic genera are members of the subfamily Hydrelliinae, as follows: the tribe Atissini (Isgamera, with two species), the tribe Dryxini (Afrolimna and Corythophora, each with two species) and the tribe Notiphilini (Psilopoidea, with one species). Knowledge of the faunas of the various countries of the Region is uneven; In 7 countries (Benin, Djibouti, Gabon, Guinea-Bissau, Mauritania, Central African Republic and Togo) no shore flies have yet been recorded. Fewer than ten species have been recorded from 25 countries of the continent and its adjacent islands (Ascension Island, Botswana, Burkina Faso, Burundi, Chad, Republic of the Congo, Eritrea, Equatorial Guinea, Guinea, Ivory Coast, Lesotho, Liberia, Malawi, Mali, Niger, Oman, Rodriguez Island, Saint Helena, St. Paul Island, Socotra, Swaziland, Tristan da Cunha, Tromélin, Yemen, and Zambia). Between 10-25 species are known from 11 countries (Aldabra group, Angola, Cameroon, Cape Verde, Ethiopia, Gambia, Ghana, Mozambique, Namibia, Uganda, and Zimbabwe). Seven better known countries, with 26-50 species, are Madagascar, Nigeria, Rwanda, Senegal, Seychelles, Sudan, and Tanzania. Only 4 countries have more than 50 species recorded: Republic of South Africa (58), Sierra Leone (77), Kenya (83), and Democratic Republic of the Congo, with 104 species.

KEY WORDS: Ephydridae, Diptera, biodiversity, Afrotropical Region

Contents

Fly-pollination of umbelliferous plants: how specialized is the system?

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Plants of the family Apiaceae (=Umbelliferae) are usually placed among the species regarded as ‚promiscuous‘ in terms of pollination systems. In fact many of them may be characterized by having a wide range of flower visitors, mostly dipterans. However, recent studies of this plant group suggest that the actual number of anthophilous taxa should not be equated with the number of their efficient pollinators. Studies of pollination biology of three common European taxa (*Heracleum sphondylium* subsp. *sphondylium*, *H. sphondylium* subsp. *sibiricum*, and *Angelica sylvestris*) have shown three attributes, as follows: (1) key pollinators are restricted to a few dipteran groups (*A. sylvestris*are pollinated by muscid and syrphid flies) or even to certain species (*H. sphondylium* is pollinated by the syrphid *Eriozona syrphoides*, and blow flies of the genus *Lucilia*) suggesting at least a level of ecological specialization, (2) all three plant species share a large proportion of the visiting insect taxa, suggesting a similar attraction strategy (3) a large proportion of insect visitors utilize flower resources but do not provide pollination service because of their preference for a particular sexual phase of the flower. Based on these results and new data from the literature we discuss the concept of specialization vs generalization in pollination systems of umbellifers and difficulties in determining their efficient pollinating agents.

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