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ABSTRACTS VOLUME

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Preface

Time flies. Four years have passed by since the preceding Congress was held in Brisbane. This volume contains the abstracts of 264 oral and poster presentations submitted to the Organising Committee of the Sixth International Congress of Dipterology held in Fukuoka, Japan from the 23rd to 28th September, 2006. It may be possible to have a general understanding of recent advance on dipterology from this publication.

Abstracts are arranged in alphabetical order according to the family name of the first author. The name of presenter is underlined when the presentation is oral. The Author Index contains the names of all authors, and the General Index contains the keywords for each abstract.

To avoid possible nomenclatural confusion, it is here stated that any of the new scientific names found in this abstracts volume is disclaimed for nomenclatural purposes. So that the authors concerned are recommended to publish their works in appropriate scientific journals or the like as soon as possible.

Except in a few cases, abstracts are reproduced here as they were submitted to the Congress Organising Committee. I thank Ako Tachi for her help in preparing this volume.

Masaaki Suwa
Editor

September 23rd, 2006

Comparative study on the excito-repellency and irritability phenomena of pyrethroids against *An.stephensi* (Liston) at laboratory and field conditions

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The excito-repellency and irritability phenomena are occurred in the vector populations following the application of definite insecticides. The design of excito-repellency (ER) test box was made of rectangular aluminum frame measuring 30 x 30 x 30 centimeters equipped to exit trap measuring 10 x 10 x 20 centimeters having adjustable opening. A guinea pig was held using locally made aluminum holder. The insecticide treated nets were placed on guinea pig holder and thus allowed the lab-bred mosquitoes (*An.stephnesi*, Beech-Strain), which already released inside ER-box, to feed on animal. In the field condition, based on residual spraying with pyrethoids, the excito-repellency effects may lead to behaviouristic changes of the mosquitoes as diversion either to new hosts or repel mosquito to indoor/outdoor shelters. At these conditions, the mosquitoes leave the sprayed houses to either unsprayed or outdoor shelters before picking up the lethal dose. The result indicated the efficacy of ER- box in relation of ease feeding of mosquitoes on the host as well as directed the excited mosquitoes toward the exit trap. The deterrency effect of treated nets is also studied and the result revealed that the mosquitoes were not able to land on treated net and fed on host. The mosquitoes were seen as either irritated flying or resting at the most distance from treated net. The result also showed that the tendency of the mosquitoes to long resting on the netting of exposure chamber was decreased at high dosage of insecticide. They tried to leave the exposure chamber toward the exit trap.

The mean of the feeding rate was least at higher dosage in comparison of lower one.

Key Words: excito-repellency, irritability, *An.stephensi*, Pyrethroids

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Discoveries of two new psyllophagous gall midges (Diptera: Cecidomyiidae) in Japan, a predacious and an endoparasitic species

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At least 20 genera and 300 species of zoophagous gall midges have been known to occur in the world. In Japan, 8 nominal and 3 unidentified species of predacious gall midges that feed on aphids, scale insects, mites, and other species of Cecidomyiidae have been recorded. During recent field surveys, we newly found 2 species of zoophagous cecidomyiids attacking psyllids in Fukuoka, Japan. One is a species of the genus *Endopsylla*, and another is a species of the genus *Endaphis*. Based on morphological studies, the 2 cecidomyiids are considered to be new to science. *Endopsylla longicaulis* **sp. n.** is a predacious species whose larvae feed on nymphs of *Metapsylla uei* Miyatake (Hemiptera: Psylloidea: Psyllidae) inhabiting their galls on *Melia azedarach* L. (Meliaceae). *Endaphis psyllophag*a **sp. n.** is an endoparasitic species whose larvae feed on adult internal organs of *Calophya nigridorsalis* Kuwayama (Hemiptera: Psylloidea: Calophyidae) on *Rhus succedanea* L. (Anacardiaceae). The findings of these cecidomyiids are remarkable because their feeding habit and host range are different from those observed previously for their respective congeners; species of *Endopsylla* have been known as endoparasitic on adults of Psyllidae or on nymphs of Tingidae (Hemiptera), but not as predacious on nymphs of Psyllidae; species of *Endaphis* have been known as endoparasitic on species of Aphididae, not on those of Psylloidea. The morphological features of 2 new species are described, illustrated, and compared to their respective congeners, and biological notes are briefly given for both species.

Key Words: Cecidomyiidae, Psyllidae, endoparasitic, *Endopsylla longicaulis*, *Endaphis psyllophaga*

Different directions of displacement in two species of leafminer fly in different localities

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Until now, except for two *Liriomyza* species of leafminer fly (Diptera: Agromyzidae), species displacement has not been known to occur in different directions in the same two species under field conditions. The displacement of *L. sativae* by *L. trifolii* in the USA in the 1980s can be attributed to the lower insecticide susceptibility of *L. trifolii*. In Japan, *L. trifolii* was displaced by *L. sativae* after 1999. The different directions of displacement indicate that the reason for the displacement of one *Liriomyza* species by the other appeared to differ between the USA and Japan. Therefore, differences in the insecticide susceptibility, fecundity, effects of natural enemies, and reproductive interference between *L. trifolii* and *L. sativae* are evaluated as possible causes of the species displacement observed in Japan. There was no evidence to indicate that *L. sativae* was highly tolerant than *L. trifolii* to some of the insecticides, but it is possible that the higher fecundity of *L. sativae* is a key factor involved in the displacement. The successful parasitization by a natural enemy *Dacnusa sibirica* (Hymenoptera: Braconidae) on *L. trifolii* without such parasitization on *L. sativae* may have contributed to the displacement of *L. trifolii* by *L. sativae*. Under laboratory conditions, *L. trifolii* and *L. sativae* can mate and produce F1 hybrid females, which do not oviposit if back-crossing occurs. Since courtship and mating discrimination appears to exist between *L. trifolii* and *L. sativae*, interspecific mating between the two species is considered to hardly occur under natural conditions.

Key Words: species displacement, insecticide susceptibility, fecundity, parasitization, *Liriomyza*

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Geographic limits and causal factors for endemisms in the Atlantic Forest, Brazil: biogeography and a HomePage for the Neotropical Diptera (1)

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Biological diversity is heterogeneously distributed in space in such a way that knowledge on biodiversity does not correspond merely to a list of names. Even though attention given to biodiversity has grown in the last decades, quite few is actually known about the geographic patterns of distribution of species and about the causes of these patterns. In the case of the Neotropical fauna, it is still not possible to map the distribution of Brazilian species of most groups. This deficiency has implications for conservation policies and for the understanding of basic evolutionary processes. This ongoing project uses biological material collected with standardized methods along the Atlantic Forest (especially Malaise traps, Moericke and sweeping) to delimit areas of endemism for groups of Diptera and to apply phylogenetic and biogeographic methods of analysis to search for and to examine congruence among these patterns. When biogeographic patterns are congruent with the geological history of South America, it points to groups associated to the geological origin of the continent in the Gondwanaland, in a way that the diversity of these groups would have slowly originated along the last 80,000,000 years. Patterns that disagree from the general biogeographical pattern probably originated in the region due to dispersion. However, groups entering Central and South America coming from the Nearctic Region in Cretaceous or later –e.g., acalyptrate families– and truly Gondwanian clades have undergone the same geological events along the early and late Tertiary, so they exhibit similar patterns. The systematic study of genera belonging to clades at different levels in the phylogeny of the Diptera –from Tipulomorpha to Calyptratae– shall verify the existence of common biogeographical patterns in dipterans. This means finding which areas shall correspond to endemisms, but also which groups of Diptera share the same general patterns. Parallel to this systematic and biogeographic approach, the taxonomic knowledge produced will be gathered and summarized with the construction of a HomePage of Neotropical Diptera. This is an efficient mechanism of making technical information available for a public with different levels of interest on Diptera or on conservation. There will be pages for general subjects on Diptera (as morphology, identification, immature, fossils, biology etc.), pages for each family (with an introduction, identification keys, and illustrations), and pages for each genus (with an introduction, identification keys, descriptions, illustrations, and distribution). The construction of the entire portal will take at least fifteen years, but main chapters and family pages shall be finished within three years. Each page will go online as soon as approved.

Key Words: Diptera, biogeography, Atlantic Forest, endemism, Neotropical Region

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A phylogenetic study of the Bibionomorpha, with emphasis in the Mycetophiliformia (Diptera)

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A phylogenetic analysis of the Mycetophiliformia (=Sciaroidea) was performed to establish relationships between families and to place genera of uncertain position in the system –*Heterotricha*, *Ohakunea*, *Colonomyia*, *Freemanomyia*, *Rhynchoheterotricha*, *Chiletricha*, *Afrotricha*, *Anisotricha*, *Kenyatricha*, *Nepaletricha*, *Sciarosoma*, *Sciaropota*, *Insulatricha*, *Cabamofa*, *Rogambara*, and *Starkomyia*. More than 150 species from 14 families were examined and illustrated. A data matrix was built with 64 terminals and 137 transformation series (202 character steps). A thorough study of thorax morphology brought up robust data. Hennig's system for the Bibionomorpha was adopted, with Mycetophiliformia as a replacement name for Sciaroidea. The Anisopodiformia appeared as sister to the rest of the Bibionomorpha, followed by Pachyneuridae. Bibionidae appears as sister to Mycetophiliformia. Within this clade Cecidomyiidae is sister to the set of the remaining families, followed by the Sciaridae. The Sciaridae appeared in all runs as a clade separated from the Mycetophilidae, Lygistorrhinidae or Rangomaramidae. The Rangomaramidae appeared as the sister group of a clade consisting of (Ditomyiidae + Bolitophilidae + Diadocidiidae + Keroplatidae) and of (Lygistorrhinidae + Mycetophilidae). Rangomaramidae gathered most but not all genera of uncertain placement: a clade is constituted by *Kenyatricha*, *Rhynchoheterotricha*, *Insularotricha*, and *Chiletricha*; two separate clades include respectively *Heterotricha* and *Rangomarama*; *Ohakunea*, *Colonomyia*, *Cabamofa*, and *Rogambara* constitute an additional stem in the family. *Arachnocampa*, usually placed in the Keroplatidae, does not appear within the keroplatids in most runs. *Freemanomyia* apparently fits as a basal clade in the Rangomaramidae.

The position of *Loicia* is still doubtful and may correspond to a clade independent from the Mycetophilidae. *Taxicnemis*, *Sciaropota*, and *Starkomyia* seem connected to the (Lygistorrhinidae + Mycetophilidae) clade. *Afrotricha* may belong to the Sciaridae, a conclusion worth of re-examination. *Anisotricha*, *Nepaletricha* and *Sciarosoma* probably fit within the Rangomaramidae. The similarities gathering Sciaridae and Mycetophilidae showed to be a combination of symplesiomorphies and homoplasies.

Key Words: Diptera, circumantarctic relationships, Gondwanaland, vicariance

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Circumantarctic relationships in Neotropical Diptera: old and new

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Despite advances in biogeography, we are still stuck with the problem of determining whether particular groups with circumantarctic disjunction are truly Gondwanian or more recent. We examined cases of circumantarctic relationships in Diptera and concluded that both, vicariance and dispersion had their own role in producing such patterns. Southern Gondwanaland groups were obviously divided by vicariance due to the break-up of the Gondwanaland itself. A connection between Antarctica and South America lasted until at least the early Cenozoic, so species primarily Laurasian in origin may have reached Gondwanaland by dispersion during the Cretaceous. This means that not all cases of true vicariance in Gondwanian terranes are actually Gondwanian in origin, and explains the cases of groups with typical circumantarctic patterns absent in the Jurassic fossil record. A mild climate was present in Antarctic until at least mid Tertiary, after which global cooling produced ice caps in the poles isolating these faunas. The distribution of groups Diptera of apparent circumantarctic origin in the Neotropical region is examined. Groups present in southern South America and in Australia and/or New Zealand include, e.g., *Zelandotipula* (Tipulidae), *Nervijuncta*, *Autralosymmerus* (Ditomyiidae), *Colonomyia*, *Chiletricha*, *Rhynchoheterotricha*, and *Insulatricha* (Rangomaramidae), *Paraleia* and *Procycloneura* (Mycetophilidae); *Dasyomma* (Athericidae), *Pelecorhynchus* (Pelecorhynchidae) and *Atherimorpha* and *Austroleptis* (Rhagionidae). There are some cyclorhaphans proposed to be circumantarctic (e.g., the Muscidae Reinwardtinae), but there is still no agreement about this. Within the Neotropical region some quite northern areas in South America have species related to clades with circumantarctic distribution. In Colombia, this is related to late Cenozoic uplift of the Andes, generating habitats

suitable for these groups beyond the Equator. Circumantarctic groups in southern Brazil may be due to a geological connection of Brazilian southern areas with Patagonian terranes and/or to the late Cenozoic global cooling resulting in glaciation and also suitable environments in those areas.

Key Words: Diptera, circumantarctic relationships, Gondwanaland, vicariance, dispersion

Polyphagous Agromyzidae as pest species in vegetables in Vietnam

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During the last 40 years South-east Asia has been invaded by several polyphagous Agromyzidae species from America and Europe. They have probably followed international trade with their host plants. Due to difficult taxonomy and lack of local investigations, little has been published about their appearance in this part of the world. To increase our knowledge, a project has investigated their distribution and biology in Vietnam during 2000-2006.

In Vietnam today at least five of these invasive species are important pests in vegetables, potatoes and cotton. The vegetable leafminer, *Liriomyza sativae* Blanchard is by far the most widespread and common species. It is found all over the country. The tomato leafminer, *L. bryoniae* Kaltenbach is found in many vegetable growing areas in most of the country, but not south of Hochiminh city. The pea leafminer, *L. huidobrensis* (Blanchard) is found mainly at higher elevations in the Lam Dong province, but for the time being is spreading also to nearby areas at lower altitude from Hochiminh city to Da Nang. The American serpentine leafminer, *L. trifolii* Burgess is found spread and local in vegetable growing areas in provinces in the middle part of Vietnam from Hochiminh city to Hue. *Chromatomyia horticola* Goureau is found spread in most areas north of Hochiminh city, but in high numbers mainly at higher elevations in the Lam Dong province.

All species appear in vegetable fiends all year round, but they are most numerous during late winter and early spring, in January – April. Distribution within Vietnam, host plant preferences, life cycle and different aspects of their biology will be discussed for each of the five species.

Key Words: *Liriomyza sativae*, *L. huidobrensis*, *L. trifolii*, *L. bryoniae*, *Chromatomyia horticola*

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Monogamy in the Promiscuous Sepsidae? The unique mating system of *Sepsis indica*

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Sepsidae is a family with around 300 species found throughout the world. Sepsid flies are model organisms for studies in sexual selection because they display well documented sexual dimorphism and also have interesting mating behaviour. Here, we describe the courtship and mating behavior of *Sepsis indica*. The males have strongly modified forelegs with large femoral protrusions and spines. These legs are used to hold on to the base of the female wing during mounting. We find that the remaining mating behaviour of *Sepsis indica* is unusual in that almost all virgin females will mate with the first male encountered during mating trials. However, the same females will refuse to mate again when tested one week later with another male. This is unusual for Sepsidae, where most females are very selective during the first mating trial, and will reject male courtship and advances, even when they are virgins. This unusual behaviour of *Sepsis indica* is correlated with a highly reduced repertoire of male courtship behavior as compared to closely related species. The males of the close relatives tend to have 5-10 different elements in their repertoire, while *Sepsis indica* males have only 2-3 minor elements. We are discussing the significance and possible explanations for this unusual behavior.

Key Words: Sepsidae, mating behaviour, sexual selection

Biodiversity in *Drosophila melanogaster* at Evolution Canyon, Israel

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The patterns of biodiversity in *Drosophila melanogaster* were studied at Evolution Canyon, Israel. Sixteen strains collected at the natural population in climatically fluctuating south-facing slop and north-facing slope were analyzed of the mitochondria cytochrome oxidase gene polymorphism based on the RT-PCR method using third instar larvae as the starting material.. The complex pattern of differences could be demonstrated on the molecular biodiversity at the distance of only 100 m. We show significant interslope differences both in protein (isozymes) and genetic (mitochondria DNA) levels. The main differentiating cause seems to be microclimate selection that overcomes the homogenizing effect of migration.

Key Words: *Drosophila melanogaster*, gene diversity, natural population, Israel

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Comparative responses of mosquito vectors of West Nile virus to light traps augmented with chemical attractant and to human hosts

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Scientists in the USA seek to develop Global Information Technology (GIS, GPS, remote sensing)-based systems that can be used to deploy sentinel traps for mosquito vectors and for the implementation and evaluation of mosquito control. Achieving this objective requires the development of methods for unbiased estimation of adult mosquito density. Unbiased estimators will enable the identification and analysis of natural mosquito dispersion parameters and the development of GIT-based models for forecasting mosquito activity and distribution. In North America, the CDC light trap (augmented with attractant CO_2 gas) is used to determine the species composition and abundance of vector populations, as well as the geographic distribution and virus infection rate in these populations. But we do not know the relationship between mosquito capture rates by CDC traps and the numbers of mosquitoes attacking the human population. In the present study, the landing rates (LR) of *Anopheles quadrimaculatus, Culex nigripalpus, Cx. quinquefasciatus*, *Ochlerotatus triseriatus* and *Aedes albopictus* on human hosts were compared with capture rates of the same species by CDC traps (with CO_2). We found significant associations ($P \leq 0.05$) among the day-to-day responses to LR and CDC by *An quadrimaculatus* and *Cx. quinquefasciatus*, and among the hour-to-hour (over 24 hours) responses of all species except *Oc. triseriatus*. CDC traps typically underestimate LR by 40-125%, depending on the mosquito species and time of day, but improved precision (R^2 =0.61-0.70) in these estimates is achieved by the identification/removal of outlier responses and the fit of log-transformed LR data for each species to linear or polynomial models. Temporal variations in the capture rate of mosquitoes by LR and CDC suggest that each method samples separate components of the

mosquito population and/or differentially stimulates competing response patterns in individual female mosquitoes.

Key Words: unbiased estimator, sentinel system, GIS

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Moegistorhynchus Macquart, a remarkable endemic genus of Nemestrinidae and important pollinator of long-tubed flower species along the west coast of South Africa

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About 80% of Afrotropical Nemestrinidae species are restricted to South Africa, where *Prosoeca*, *Moegistorhynchus* and *Stenobasipteron* dominate the fauna. Interest in these genera has increased over the last two decades, because each includes long-proboscid species importance in pollination biology. *Moegistorhynchus* is South Africa's only endemic nemestrinid genus, and is restricted to the west coast. It is immediately recognized by its reticulate wing venation and patterned wings. Most species are large, robust flies, 1.5–2.0 cm in length. Proboscis length varies from *ca* 1–10 cm. Plant species pollinated have an unusually elongate floral tube and offer nectar rewards.

Of the six species in the genus, *Moegistorhynchus longirostris* is by far the most abundant. It has the longest proboscis known in the Diptera (*ca* 3–10 cm) and is widely distributed across much of the genus's range, but at low altitude. *M. perplexus* (proboscis length *ca* 3–5 cm) occurs at higher altitude and has a much more restricted range. *M. brevirostris* and *M. braunsi* have limited ranges in the extreme south, both at low altitude. *M. brevirostris* has the shortest proboscis in the genus (less than 2 cm) and is probably of no significance as a pollinator. Two new species are recorded from southern montane localities; one has a proboscis length of 2 cm and appears to be the unique pollinator of a *Gladiolus* species.

Twenty species of Iridaceae, Geraniaceae and Orchidaceae are pollinated partly or exclusively by *M. longirostris*, which is a keystone species. The incredible variation in proboscis length of this species shows a marked trend of longer forms in the north, ranging to shorter forms in the south, tracking the distribution of flower species with comparable floral tube lengths. *M. longirostris* is of significance in evolutionary biology, given the coevolution of proboscis length and flower tube length.

Key Words: South Africa, Nemestrinidae, *Moegistorhynchus*, pollination

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Sporogony cycle of *Plasmodium vivax* in *Anopheles stephensi mysorensis* and effects of inhibitor carbohydrates on the development of parasite

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The aim of this study was primarily to follow the sporogony cycle of *Plasmodium vivax* in main vector, *Anopheles stephensi mysorensis* and then the effect of inhibitor carbohydrates on development of the parasite. *An. stephensi* were fed with the blood contains gametocyte from donor malaria patients in a restricted insectary. The development of plasmodium was followed by dissecting the infect mosquitoes and taking smear in different interval times. Subsequently, different groups of Anopheles were separately fed with infected blood contain inhibitor carbohydrates as follow; N-acetyle-glucoseamin, N-acetyle- galactoseamin, arabinose, fucose, manose, lactose, galactose and glucose.

Exfellagelation was occurred at 5 minutes after blood meal and then ookinet was observed at 20 hours, while oocysts and sporozoites appeased in day's 8th to 12th. The results indicate that *An. stephensi strain mysorensis* has can extremely transfer *Pl. vivax*. The parasite development was completed in the mosquitoes, which had been fed with N-acetyl-glucoseamine, arabinose, fucose , galactose and glucose, in contrast, lactose, mannose and N-acetyl-galactosamine interrupted the life cycle of the parasite and do not allow sprorosoite to take place into salivary glands.

It seems that several carbohydrate binding protein involved in invasion and development of the parasites in mosquito. However, the results of this study can be used as basic information for developing vaccine against malaria transmission.

Key Words: malaria, sporogony cycle, *Anopheles stephensi,* sporozoite, carbohydra

Molecular and morphological phylogeny of European *Dolichopus* and *Gymnopternus* (Diptera, Dolichopodidae)

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The Dolichopodidae (over 6000 described species in more than 200 genera) are one of the most speciose families of Diptera. Despite its high species richness and the presence of conspicuous morphological characters, few authors have considered the detailed phylogeny of these flies. Molecular data have been used even less frequently. We inferred phylogenetic relationships among 45 species (57 samples) of the subfamily Dolichopodinae. The total data set (1447 characters) was from 32 morphological and 1415 nucleotide characters (810 for COI, 605 for Cyt-b). The monophyly of *Dolichopus* and *Gymnopternus,* as well as the separate systematic position of *Ethiromyia chalybea,* were strongly supported in all analyses, matching and confirming recent findings and hypotheses. Within the genus *Dolichopus*, stable species groups could be assigned to four distinct categories in 8 phylogenetic analyses: (i) clusters significantly supported in all analyses, (ii) clusters supported in trees based on DNA and combined data, but only partly in morphological trees, (iii) clusters supported in trees based on DNA and combined data, but not in morphological trees, and (iv) clusters consistently supported only in morphological trees. The data obtained therefore clarify some previous systematic hypotheses and the phylogeny generated here allows a better understanding of the phylogenetic relevance of some debated morphological characters commonly used in identification keys. This study represent an essential starting point for future projects, particularly for those in which the comparative method is central to experimental design and data analysis.

Key Words: Dolichopodidae, Dolichopodinae, *Ethiromyia*, phylogeny, mtDNA

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Phylogenetic relationships of the nematocerous Diptera inferred from molecular and morphological characters

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Relationships among families of the lower Diptera (suborder 'Nematocera') have been exceptionally difficult to resolve. The status of families assigned to various infraorders is unstable and the inter-relationships between infraorders are even less clear. Multiple hypotheses have been proposed identifying the earliest fly lineages and placing the phylogenetic origin of the higher flies (Brachycera), but convincing support is still limited. Here we provide further evidence on the relationships between families of nematocerous Diptera based on molecular data from two genes (28S ribosomal DNA and CAD) and published morphological data; all traditional nematocerous fly families, except the Perissomatidae, were included. Our analyses provide support for new and existing hypotheses about fly evolution and classification. The earliest lineage appears to be either the family Deuterophlebiidae (mountain midges) or Nymphomyiidae, both morphologically enigmatic among flies. Three major infraorders are supported: the Culicomorpha (containing all traditional families and, perhaps, the Ptychopteridae), a Psychodomorpha defined as (Blephariceridae (Tanyderidae + Psychodidae)) and a Bibionomorpha containing all other families except the Tipulidae s.l. and Trichoceridae. The positions of Ptychopteridae, Axymyiidae, Trichoceridae and Tipulidae s.l. are still uncertain. The Brachycera appear to have affinities to the Bibionomorpha, though high support is lacking. New support for some traditionally uncertain groupings suggests that molecular data will be required to ultimately stabilize a phylogenetic classification for these earliest lineages of extant flies.

Key Words: Nematocera, molecular, morphology, phylogenetics, infraorder

Biogeographic Patterns in southwest Pacific Dolichopodidae: New Caledonia, Fiji, and Australia

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New Caledonia harbours a rich endemic biota and is considered to be a fragment of the ancient Gondwanan supercontinent. Two genera of Dolichopodidae (Medeterinae), *Atlatlia* and a new genus are sister taxa known only from Australia and New Caledonia. In Australia both display a temperate southern distribution often associated with Gondwanan taxa, while in New Caledonia, they occur above 500 m. These two genera have radiated on both landmasses, but are unknown from New Zealand and Melanesia. Two other genera, *Antyx* and *Kowmungia* occur only in rainforests of New South Wales, Queensland, and New Caledonia.

The Australia and New Caledonia pattern suggests a vicariant Gondwanan distribution as these taxa are unlikely to have dispersed between Australia and New Caledonia. Were these genera once widely distributed in eastern Gondwana? The absence of these genera from New Zealand is puzzling. However, during the Tertiary, New Zealand underwent major climactic and tectonically induced extinction events, losing much of its ancestral flora, and probably associated insects as well.

As well, New Caledonia has undergone a remarkable radiation in the subfamily Sciapodinae, with some 75 known species, mostly in the genera *Lapita* and *Parentia.* These two genera are now known to occur in Fiji. As well, Fiji has Sciapodinae of Austro-Papuan affinity, possibly derived from the west via “stepping stone” dispersal. Do the Fijian Sciapodinae represent a composite of both Gondwanan and Papuan biogeographic origins?

Key Words: biogeography, Dolichopodidae, New Caledonia, Fiji, Pacific

Why *Hilara* is not amusing, or the problem of speciose cosmopolitan genera

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Male Hilarini (Family Empididae) often have enlarged fore basitarsus, known to produce silk for wrapping prey or debris to present as nuptial gifts. *Hilara* and related genera are frequently seen cruising back and forth (happy, cheerful little flies) over pools along streams, hence the common name, “dance flies”. The genus is best known in Europe where some 174 species have been described. However, *Hilara* is cosmopolitan and conservatively comprises several thousand species, mostly undescribed/ uncollected. This is complicated by *Hilara* s.l. having a similar facies and suite character expression throughout the world. Further, *Hilara* and the related southern temperate *Hilarempis* are separated by a venation character can be variable among species.

Since many diagnostic characters are variable in expression, supra-specific taxa have to be defined as a mosaic of characters, a "polythetic classification," no character necessarily being diagnostic for all members. Although small, often regional genera/ species groups based on synapomorphies can be defined, one is left with a large paraphyletic residue of species that can only be lumped into large ill-defined genera. Paraphyly is a fact of taxonomic life.

Examples of “open-ended speciose” cosmopolitan taxa from other families are discussed. G.G. Simpson’s “bradytelic” evolution in a stable adaptive zone provides a model. Speciation with a limited suite of morphological characters can result in many species accumulating over time, with homoplasy throughout.

With a conservative estimate of 10 million morphospecies, and some 1.7 million already described (esp. larger, prominent species), then most of the remaining will be such difficult "open ended taxa", mostly uncollected or unsorted from mass trapping residues, and difficult to define at a generic level. Complete taxonomic knowledge on a world level for such groups is unlikely.

Key Words: Empididae, cosmopolitan taxa, speciose taxa, taxonomy, bradytelic evolution

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Australian Hilarini, their biogeography and.....sex lives?

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The Hilarini (Diptera: Empididae) are a cosmopolitan tribe of Empidinae composed of 14 genera. Conservative estimates from European and Australasian institutions suggest there are several thousand species awaiting description. In Australasia and Oceania, 63 species from six genera are formally described. In Australia, 27 species have been described from five genera. Twenty new species from the two largest hilarine genera: *Hilara* Meigen and *Hilarempis* Bezzi, have recently been described from Australia. The trials and tribulations of applying the characters defining these two cosmopolitan genera to Australian specimens are discussed. The biogeography of these species—from the Atherton Tablelands in north Queensland to the state of Tasmania in the south—is outlined. The mating behaviours displayed by members of the tribe are unique. Males have a gland in their fore basitarsus which produces silk, used in elaborate ways to court females. The evolution of, and variation in, the silk-producing basitarsus of males is summarised.

Key Words: Hilarini, Empididae, taxonomy, biogeography, mating behaviour

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The reluctant fly: What makes *Sepsis cynipsea* females willing to copulate?

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A female's willingness to copulate (i.e. her receptivity) can depend on several endogenous, environmental and social factors. The black scavenger or dung fly *Sepsis cynipsea* (Diptera: Sepsidae) is a classic example for strong female reluctance to mate and sexual conflict over mating. Previous laboratory studies found high variability in female receptivity and even virgins unwilling to mate. The aim of this study was to determine the proximate factors influencing female receptivity. Females need to ingest fresh dung to produce eggs. Female receptivity strongly depended on a female's egg laying cycle rather than age: receptivity was highest when females had no ripe eggs. This is probably required for spermatophore transfer, leading to the unusual pre-copulatory guarding and post-oviposition mating of Sepsids. Non-virgins were less receptive than virgins except when they were in need of sperm. Non-virgins were more receptive when they were larger and had previously laid more eggs. Only when not in need of sperm did females copulate with males larger than their previous mate. This suggests sequential female choice, but females typically copulated with the first of up to ten presented males or not at all, provided they were at the appropriate stage of their laying cycle. Female unwillingness to mate in this and probably other species therefore has various, sometimes physiological (intrinsic) reasons. These must be controlled in experiments assessing mate choice, costs and benefits of mating, or sexual conflict. Not taking into account female egg laying state can mask female choice, bias data and suggest wrong associations.

Key Words: female mate choice, mating behavior, reproduction, sexual conflict, sexual selection

Mass sampling, species richness and distribution of scuttle flies (Diptera: Phoridae, *Megaselia*) in a wildfire affected hemiboreal forest

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Species richness and species abundance patterns were estimated for the diverse scuttle fly genus *Megaselia* based on material from a thorough Malaise-sampling project carried out in a hemiboreal forest following a large wildfire. The sampling was carried out in Tyresta National Park and Nature Reserve, south of Stockholm, Sweden. A total of 16 968 males contained 331 species, of which, at least 112 were new for Sweden. Three species (0.9%) constituted 37.6% of all individuals, whereas 102 species (31 %) were singletons and doubletons (species found in one or two individuals). One sample-based rarefaction curve and seven non-parametric species richness estimators were used and showed total species estimates ranging from 378 to 498 (401 to 555 with Chao 1 and Chao 2, 95% CI, lower and upper bound). The sampling was insufficient for a reliable estimate since the species accumulation curves did not reach an asymptote, and furthermore the curves of singletons and doubletons did not flatten out completely. The study demonstrates that species richness estimates and species abundance patterns in species-rich groups require very extensive sampling and may be less reliable for an area in an early succession state. Compared with similar inventories, Tyresta National Park and Nature Reserve has one of the richest temperate scuttle fly communities known to date.

Key Words: species richness estimators, Phoridae, Malaise traps, hemiboreal forest, wildfire

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Migration of light-reactive larval pigment cells in *Chaoborus americanus* (Chaoboridae) during pupation: extra gamete protection for males in the Culicoidea?

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Chaoborus larvae are well known planktonic predators, occurring in aquatic areas worldwide. They follow their plankton prey by migrating vertically within the water column, using tracheal air bladders. These air bladders are covered with light sensitive pigment cells that are able to move around on their surfaces. Studies revealed that these pigment cells have larger surface areas in darker conditions. The pigment cells were also present after pupation, and showed non-random clumping patterns in some pupae. The observed clumping was due to the pigment cells covering the developing testis in male pupae, resulting in two large dark spots at the base of the abdomen. No such cell behaviour was seen in females. These pigment cells and their behaviours may have some systematic value within the Chaoboridae and the Culicoidea.

Key Words: cell movement, Culicoidea, systematics, UV protection, development

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Flower visiting in the genus *Eulonchus* (Acroceridae): pollination or exploitation?

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Species in the Diptera family Acroceridae (spider-parasitic flies) have complex and interesting life histories, and have often proven difficult to study due to their rarity. The adults of many species have been collected on flowers and have morphological characteristics that suggest a dependence on floral nectar, though little study has been made of their role in pollination. The floral visiting behaviour, abundance, and pollen loads of individuals in the genus *Eulonchus* were studied to determine their pollination abilities. This research revealed that *Eulonchus* individuals are good pollinators from a behavioural standpoint, making few revisits to individual flowers, and remaining highly constant to one flowering species in each pollination bout. Individuals are also important in abundance, as they form a large percentage of the pollinator fauna on some plant species. The pollen loads collected from individuals show the same trend, with the majority of pollen belonging to one plant species. However, other pollen species were present, with female *Eulonchus* carrying a greater diversity than males. This difference between the sexes appears to relate to mating behaviour, which takes place within the flower patches. This research shows that acrocerids are important pollinators, both in abundance and behaviour.

Key Words: pollinator behaviour and abundance, pollen loads, mating behaviour, rarity

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Revision of *Australimyza* Harrison (Diptera: Australimyzidae)

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The species of *Australimyza* Harrison are revised. Nine species are recognized and described, including four that are new from New Zealand and Australia. Other taxonomic results, such as a synonymy and lectotype and neotype designations are reported. The larvae of Australimyzidae are described for the first time. Morphological evidence is presented to document our hypothesis of phylogenetic relationships. *Australimyza* is demonstrated to be a well-supported, monophyletic clade. Using four outgroups with *Inbiomyia* as the most immediate to *Australimyza,* the nine species are arranged into an ungrouped species and two species groups. One species group is found on New Zealand and associated subantarctic islands and all other species occur along the maritime coasts of Australia.

Key Words: Australimyzidae, Diptera, Australasian Region, systematics.

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From Fabricius to the Biosystematic Database of World Diptera: An assessment of two hundred years of progress.

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The last comprehensive summary of our knowledge of flies (Diptera) was Fabricius' (1805) Systema Antliatorum. Fabricius documented little over thousand species, which he placed in 77 genera. Today, the Biosystematic Database of World Diptera documents about 150,000 extant species placed in about 150 families and 11,000 genera. Various statistics are presented to assess this growth in knowledge, from the number of workers (over 3,300) and their productivity to error rates (23% synonyms, 1% homonyms). Finally, the prospects for the future are outlined, which are to build an online (internet) taxonomy of flies from our database of names.

Key Words: Diptera, database, statistics

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Mouthpart morphology of larval net-winged midges (Blephariceridae) based on scanning electron microscopy: intergeneric comparisons and their phylogenetic implications.

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Net-winged midges (Diptera: Blephariceridae) are a small group of highly specialized aquatic flies. The larvae are remarkable in their adaptations to torrenticolous habitats, including six ventral suctorial discs, which function as hydraulic suckers and allow secure attachment to current-exposed substrata, and the fused head, thorax, and first abdominal segment (= cephalic division), which keeps the mouthparts close to the substratum while the larva is feeding. Larval mouthparts are specialized for grazing on the thin films of algae, bacteria and other organic matter (= periphyton) on current-exposed rocks. As part of ongoing studies of blephariceridmorphology, taxonomy, and phylogenetics, we used scanning electron microscopy (SEM) to gather structural details on the larval mouthparts of nearly all genera of Blephariceridae. We were especially interested in the "primitive" subfamily Edwardsininae, but made comparisons across major blepharicerid subfamilies, tribes, and generic groups. Although we evaluated features of all mouthparts, our focus was the structure of the larval maxilla, which typically is the largest and most complex mouthpart. These and other mouthparts provided several phylogenetically informative characters.

Key Words: net-winged midges, Blephariceridae, larvae, mouthparts, phylogeny

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Family level phylogeny of the Carnoidea (Schizophora)

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The Carnoidea is one of the most poorly defined superfamilies of Schizophora. Its doubtful monophyly is reviewed and tentatively accepted based on one previously suggested and two newly discovered synapomorphies. The Carnoidea in its redefined sense includes Acartophthalmidae, Canacidae (including Tethinidae), Cryptochetidae, Milichiidae, Chloropidae, Carnidae, Australimyzidae and the recently described Inbiomyiidae. New evidence is provided for the paraphyly of 'Tethinidae' with regard to Canacidae. The relationships of Carnoidea families are analyzed quantitatively for the first time based on a matrix of 58 morphological characters, with Clusiidae and Heleomyzidae as outgroups. The results of the analysis strongly support the previously hypothesized sister group relationship of Milichiidae and Chloropidae. The latter is not the sister group of Cryptochetidae as suggested by J.F. McAlpine (1989). Two other previously hypothesized sister group relationships, (1) Acarthophthalmidae + (Milichiidae + Chloropidae), and (2) Carnidae + Australimyzidae are not supported. Acartophthalmidae is a basal clade of Carnoidea but its sister group remains uncertain. Sister group of the Australimyzidae is the Inbiomyiidae. Separate family status of Australimyzidae (as opposed to subfamily status within Carnidae as suggested by some authors) is therefore necessary.

Key Words: Carnoidea, phylogeny, Acartophthalmidae, Australimyzidae, Canacidae.

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Mitochondrial genome phylogeny of the Schizophora

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The dipteran Tree of Life program is a major collaborative effort to resolve the phylogeny of true flies by combination of morphological and molecular data matrices. At its first stage, tier one species comprising representatives from all major dipteran lineages are being used to construct a backbone phylogeny of Diptera. Our lab has been selected to perform molecular analysis of the Schizophora using a data set consisting of complete mitochondrial genome sequences. The Schizophora are regarded to be a monophyletic group within the Cyclorrapha, representing approximately 44000 known fly species.

Fourteen members of the Schizophora have been selected as tier one taxa. At this point, the complete mitochondrial genome coding regions of the majority of representatives of the Calyptratae covering the families Glossinidae, Tachinidae, Sarcophagidae, Scathophagidae, Anthomyiidae and Muscidae have been sequenced. Preliminary results using concatenated protein sequence alignments have produced robust trees congruent with current hypotheses of calyptrate evolution. Furthermore, preliminary tree reconstruction results including nematoceran and basal brachyceran outgroups (Tabanomorpha) suggests that complete mt genome sequences provide resolution throughout the depth of the Dipteran tree.

Data in progress from sequencing acalyptrate and nematoceran species will be reported as they become available.

Key Words: Schizophora, molecular phylogeny, mitochondrial, systematics

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South American Biogeography: a panbiogeographic and cladistic approach to the Muscidae and Anthomyiidae

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Today, the Muscidae and Anthomyiidae are understood to be sister-groups, both of which occur naturally in all except arctic regions. In the Neotropical region, more than 850 species of Muscidae are found in all enviroments, from above 3000 m in the Andes to sea level, where a few species are found in rocks sprinkled by the sea. To understand South American biogeography, two main questions arise: 1) why do species have specific distributions?; and 2) why do unrelated groups have similar distribution patterns? In attempting to answer these questions, we can ask what are the main processes that caused those patterns. In answer, three main processes are important: dispersal, vicariance and extinction. The distribution patterns for some species of Muscidae in the genera *Apsil* Malloch, *Bithoracochaeta* Stein, *Brachygasterina* Macquart, *Cyrtoneurina* Giglio-Tos, *Cyrtoneuropsis* Malloch, *Micropotamia* Carvalho, *Palpibracus* Rondani, *Polietina* Schnabl & Dziedzicki, *Reynoldsia* Malloch and *Souzalopesmyia* Albuquerque were analysed by panbiogeographical and biogeographical cladistic methods. In contrast, the Anthomyiidae is a less diverse family in South America, with fewer than 100 described species. Only *Coenosopsia* Malloch has been studied using cladistic and biogeographic approaches. The biogeographical pattern of this genus supports the general proposed pattern for the area. This pushes back the origin of the genus in South America. In conclusion: 1) the pattern of the apparent disjunct distributions of some Muscidae and Anthomyiidae species are due to incomplete sampling; 2) more described biogeographic patterns are necessary for consistent comparisons and pattern resolution; 3) regardless, incongruencies may still arise (after better and more sampling) if events of different ages caused those patterns; 4) therefore, we should look to molecular phylogenetic data that may help estimate divergence times through the introduction of explict temporal components in the analyses, thus addressing pseudocongruence.

Key Words: historical biogeography, PAE, panbiogeography, track analysis

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Comparative morphology of "*Sturmia*-spots" in male tachinids – first results (Diptera: Tachinidae)

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Sturmia-spots (also referred to in the literature as "patches of appressed hairs") are hairy areas variable in shape and size, situated in various positions on the abdominal tergites (3–5) of some genera of Exoristinae and in the phasine genus *Besseria*. Though used by taxonomists as diagnostic features, these structures have never received much attention concerning their morphology and biological function.

A careful observation of these structures in many specimens of different species and genera showed that the appressed hairs are glued together by viscous substances (often crystallized), hence the hypothesis of a possible glandular function of these areas. This hypothesis represented the starting point of the present comparative morphological and histological study of these structures in 7 genera and 13 species.

The fine morphological analysis carried out by SEM highlighted a great variety of different types of spots. In most cases they appear as more or less depressed areas of the cuticle, well distinct and rounded; otherwise they are wide and scarcely defined, occupying part or most of the ventral, lateral and dorsal surface of the tergites, or they arise from non-depressed areas. All types are characterized by modified setation, composed by brushes of elongate and thick setae or by thinner, shorter setae, set more tightly together than normal. All setae are deeply corrugated longitudinally like the setae external to the spots. Close to the base of each seta, and slightly anteriorly, a glandular area composed by a variable number of small pores is evident (this area is present only at the base of setae forming the spot); curls of whitish substance have been observed emerging from these pores. The spots show a microsculpture that can be more or less crowded than normal; a peculiar type of microsculpture, filiform, elongate and strongly packed is also present in some species.

The preliminary cytological analysis shows a modified epithelium in correspondence to the spots, characterized by enlarged cells appressed at the base of the hairs, in some cases with evident glandular ducts.

The results obtained so far, though preliminary, seem to confirm the initial hypothesis that such appressed hairs could be part of a more complex exocrine glandular tissue, and are possibly functional to the spreading of substances secreted by the glands.

Future developments include the analysis of the secreted substances and the cytological analysis by TEM of the cells identified, to evaluate homologies and to argue evolutionary implication of such structures.

Key Words: Tachinidae, *Sturmia*-spots, morphology, cytology, gland

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Characteristics and activity analysis of *Bactrocera dorsalis* yolk protein gene 1 (*Bdyp1*) promoter

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In current study, a 2.7-kb upstream fragment of the putative promoter region of the *Bactrocera dorsalis* yolk protein gene1 (*Bdyp1*) was cloned, and the sequence comprises of a series of potential regulatory elements responsible for the regulation of the gene expression, including the binding sites for ecdysone receptor, female specific doublesex, GATA factor and early gene product E75, as well as transcription factors determining the sexual and tissue specific expression of the gene. To analyze the functions of various regions of the promoter, four different lengths of the promoter, i.e. 0.2, 0.7, 1.4 and 2.4 kb, respectively, to drive a reporter gene (*luciferase*) were constructed and transfected into Sf21 cell to assay the promoter activity. Up to now, the results showed that the promoter activity of all four constructs exhibited the greatest activity at treatment with 10^{-11} M of 20-hydroxylecdysone (20E). Nonetheless, there was only minor elevation of the promoter activity in response to the treatment with juvenile hormone III (JH III). Surprisingly, addition of JH either before or after 20E treatment inhibited the 20E-induced activation of the promoter. Currently, in vivo analysis of the properties of the promoter is under investigation using germ line transformation.

Key Words: *Bactrocera dorsalis*, yolk protein, promoter, transcription factors, transgenesis

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ESEM observation of *Liriomyza sativae* Blanchard, *Liriomyza huidobrensis* (Blanchard) and *Chromatomyia horticola* (Goureau) (Diptera:Agromyzidae)

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Since 1975, the economically importance of *Liriomyza spp.* has dramatically risen in the world. The two major species involved are *Liriomyza sativae* Blanchard and *Liriomyza huidobrensis* (Blanchard), which belong to the truly polyphagous insects and are distributed mainly in Nearctic and Neotropical area. However, these two leafminers have been introduced into China in 1993. Afterwards they spread quickly and established in wide areas of China, now have become serious threat to Chinese agriculture. Except that, *Chromatomyia horticola* (Goureau) had been one of important pests in China for a long time.

The ultrastructure of scutum, aedeagus and posterior spiracles on puparium of *L.sativae*, *L.huidobrensis* and *C.horticola* were observed with scanning electronic microscope. It appears that in *L.sativae*, the microtriche on scutum sparse, distiphallus of aedeagus smooth and pod-shaped, posterior spiracles on puparium three horn-shaped; in *L.huidobrensis*, the microtriche on scutum dense, distiphallus of aedeagus wrinkled and trumpet-shaped, posterior spiracles on puparium string-beads-shaped; in *C.horticola*, the microtriche on scutum very thick, distiphallus of aedeagus leaf-shaped and with a medial sharp projection, posterior spiracles on puparium garland-shaped. All these species have distinct difference on ultrastructures whose had been studied. The related taxonomic and morphologic implications are discussed.

Key Words: *Liriomyza sativae* Blanchard, *Liriomyza huidobrensis* (Blanchard), *Chromatomyia horticola* (Goureau), scanning electronic microscope, ultrastructure

Recent findings on the fruit flies of Qianghai-Xizang Plateau (Diptera: Tephritidae)

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The Qianghai-Xizang Plateau is known as the roof of the world. The insect fauna of Qianghai-Xizang Plateau is very complicated and its vertical distribution is magnificent. The Plateau attracts a great number of scientific works over the world by its mystic magnificence.

Although the Chinese fauna of fruit flies has been comprehensively reviewed in 1996, but recent research on more materials and especially from the new specimen collected in Qianghai-Xizang Plateau within recent three years have shown that the diversity of Tephritidae in China is much rich than we have imagined, especially in this special area. Until now, thirty genera have been recognized, with 64 described species; 4 genera and 17 species are recorded to this region for the first time. Except that, at least 7 species have high possibility being new to science. The majority of the taxa (over 70%) are Oriental, and others, Palearctic.

The following research are going on: Firstly, the comprehensive scientific expedition to the Qianghai-Xizang Plateau will be carried on in next two years and more fruit flies will be collected and recognized; Secondly, phylogeographic implications of *Cornutrypeta* Han *et* Wang, *Stemonocera* Rondani and *Ortalotrypeta* Hendel in this region will be carefully discussed; Lastly, the sudden ascent of Qianghai-Xizang Plateau in relation to the fruit fly fauna of this region will be tentatively studied.

Key Words: recent findings, fruit flies, Qianghai-Xizang Plateau, new record, new species

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Rapid discrimination of species of several quarantine important tephritids (Diptera: Tephritidae) by using biochip

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Traditionally, species discrimination of pests found in quarantine inspection has to rely mostly on their morphological characters. However, it is not easy to identify the species of most tephretid larvae or even eggs, which the stages are often occurring in fruits, by morphology. In order to solve above-mentioned difficulty, application of DNA markers to assist in species identification has been adopted in recent years. In this study, we selected 6 fruit and melon flies, including *Bactrocera dorsalis*, *B. Cucubitae*, *B. tau*, *Ceratitis capitata*, *Anastrepha suspensa* and *Rhagoletis pomonella*, which are important tephritid pests on the list of Taiwanese quarantine, to develop a biochip for rapid species discrimination. Three variable genomic regions, *i.e.* cytochrome oxidase I (COI), intergenic spacer 1 (ITS1) and intergenic spacer 2 (ITS2), respectively, were selected to develop specific probes for developing the biochip. We first obtained the DNA fragments from each species with PCR amplification using specific primer sets. After DNA sequencing and alignment, several species-specific probes have been designed by following the most variable regions of species. However, the specificity of each probe is currently under investigation. We expect to develop a chip with rapid, high sensitive and accurate features and to be used to discriminate unknown species of tephritids for quarantine purpose.

Key Words: tephritid fly, discrimination, biochip, cytochrome oxidase I, intergenic spacer 1 & 2

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The achievements of forensic entomology, Japan

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Forensic entomology is a popular component in the practice of forensic autopsy in western countries. To the best of our knowledge, the systematic surveillance and identification of dipteran insects from cadavers which constitute forensic entomology have been conducted in a few institutions in Japan.

The authors performed entomological surveys of forensic autopsies conducted in School of Medicine, Dokkyo Medical University, Japan since 2003 with the cooperation of forensic pathologists, medical entomologists and biologists. From 2003 to the present, 440 cases of forensic autopsy were conducted, 32 of which revealed dipteran eggs, larvae and/or puparia. The Dipteran families detected in these cases were as follows. Family Calliphoridae in 32 cases; Family Sarcophagidae in 9 cases; Family Stratiomyidae in 3 cases; Family Muscidae in 2 cases and Family Dryomyzidae and Family Syrphidae each found in 1 case. The genera and species of dipteran insects found in the autopsy cases are as follows: six *Aldricina grahami*, five *Chrysmya pinguis*, five *Lucilia sericata*, four *Boettcherisca peregrina*, three *Parasarcophaga similis*, three *Hermetia illucens*, two *Calliphora nigribarbis*, two *C. vicina*, two *L. illustris*, one *L. caesar*, one *Triceratopyga calliphoroides*, one *Dryomyza formosa*, one *Hydrotaea ignova*, one *Muscina stabulans*, one *B. septentrionalis*, one *P. dux* and one *Eristalis tenax*.

At present, the authors are trying to analyze if there are relationships between dipteran genera and species and crime or accident scene, season, temperature, environments, postmortem intervals (PMI) and location where victim cadavers were found.

Key Words: forensic entomology, forensic autopsy, Diptera, Tochigi, Japan

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Phylogeny and biogeography of *Philornis* Meinert (Diptera, Muscidae)

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Forty-one species of *Philornis* were analyzed with 64 characters and six outgroups. *Passeromyia* Rodhain & Villeneuve, an Old World genus that shows the same range of association with birds as *Philornis*, was one genus used as outgroup, and appears in this analysis as its sister-group. Six most parsimonious cladograms (243 steps in length; ci=30; ri=69) were produced. According to the analysis the genus *Philornis* is supported by the synapomorphies: acrostichal post-sutural setae not developed; only the pre-scutellar pair of acrostichal post-sutural setae developed and cilia at anepimeron present. The resulting phylogenetic hypothesis (strict consensus) divides the genus into two clades: the most basal one corresponds to the "*aitkeni*- group" of the authors. The second clade is again divided into two others, the first one supported by the homoplasies: cheek hairs brown; cilia at anepimeron black on superior half and yellow on inferior and proepimeral hairs yellow. This group corresponds to "*falsifica*-group" of the authors, and more data on the biology of the species will clarify and/or confirm their relations. *Philornis downsi* Dodge & Aitken is the sister group of all restant *Philornis* species. This third group corresponds to "*angustifrons*-group", defined in this analysis by the synapomorphies: concave shape of posterior end of puparium and by the median width of female frons. These "traditional" groups, the relations among the species and the evolutionary trends are discussed. For biogeographic purposes, panbiogeographic methodology was performed to hypothesize primary biogeographic homology and the cladistics results were employed to test and support the analysis. The coincidence of two or more individual tracks resulted in six generalized tracks which occurred

since Trinidad Island until mid-northern Argentina. Two biogeographic nodes were found: tracks 1 and 2 intersection in Trinidad Island and tracks 3 and 4 intersection in extreme southern Brazil.

Key Words: biology, cladistics, historical biogeography, morphology, panbiogeography.

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Muscidae (Diptera) from Madagascar: identification keys, descriptions of new species, and new records

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The Madagascan Muscidae fauna is known only from scattered publications by a variety of authors, containing mainly descriptions of new species. Previous records of Madagascan muscids amount to 78 species in 27 genera (Pont 1980). The present study of the Muscidae collected by the "Madagascar Arthropod Biodiversity Project", developed by the California Academy of Sciences, San Francisco, California, has provided the stimulus for this paper in which all the genera and species recorded from Madagascar are keyed, 23 new species are described, and 7 species and 3 genera are newly recorded from Madagascar. Almost 80% of the previously known Madagascan muscid fauna has been recognised among the material studied. Replacement names are given for two homonyms: *Dichaetomyia zielkei* new name (for *Dichaetomyia apicalis* Zielke, 1972, preocc.) and *Dichaetomyia frontata* new name (for *Dichaetomyia frontalis* Zielke, 1972, preocc.). One new synonym is established: *Dichaetomyia rangeri* Zielke, 1973 (syn: *Dichaetomyia scutellaris* Zielke, 1974). The species newly recorded from Madagascar are: *Atherigona* (*Acritochaeta*) *orientalis* Schiner, 1868; *Atherigona* (*Atherigona*) *addita* Malloch, 1923; *Brontaea flexa* (Wiedemann, 1830); *Dichaetomyia (Dichaetomyia) albivitta* (Stein, 1906); *Helina lucida* (Stein, 1913); *Lispe niveimaculata* Stein, 1906 and *Lispocephala pectinata* (Stein, 1900). The genera newly recorded from Madagascar are: *Azelia* Robineau-Desvoidy, *Phaonia* Robineau-Desvoidy and *Spilogona* Schnabl. Eggs of the genus *Stylogaster* Macquart (Diptera, Conopidae) were found impaled mainly in the eyes, mesonotum and abdomen of a few specimens (Couri and Pont, in press).

This genus is known to occur in North and South America, Africa south of Sahara, Madagascar, parts of Asia, the Philippines and New Guinea (Smith 1967). Seven species are recorded, for the first time, as new hosts. *Dichaetomyia apicalis* (Zielke); *Dichaetomyia basialaris* (Zielke); *Dichaetomyia tristis* (Zielke); *Deltotus facetus* Seguy; *Deltotus viola* Zielke; *Orthellia setulosa* Zielke and *Phaonia*, n. sp.

Key Words: Madagascan fauna, muscids, taxonomy, *Stylogaster*

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Phylogenetic relationships of the Blephariceridae (Diptera) inferred from morphological and molecular characters

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Relationships among genera and more inclusive clades of net-winged midges (Diptera: Blephariceridae) have been difficult to resolve with confidence. Part of this difficulty presumably reflects common and extreme adaptive constraints on the immature stages, which reside in torrenticolous habitats. 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. In general, monophyly of the tribes Paltostomatini and Blepharicerini, and the relationships between these tribes and apistomyiines have been much more contentious. In order to test hypotheses on relationships between subfamilies, tribes, and genera of Blephariceridae, we examined exemplars of nearly all genera for morphological characters, and two-thirds of known genera for molecular characters. The latter included multiple exemplars of all subfamilies and tribes, and usually at least two species from each exemplar genus. Molecular data were primarily from a new, rapidly evolving, nuclear-encoding gene ("tuftelin-interacting protein"). Our analysis provided support for new and existing hypotheses about relationships among net-winged midges. Data showed strong support for both subfamilies, the tribe Blepharicerini, and a combined Paltostomatini + Apistomyiini. Relationships within these tribes included a range of support values, with paltostomatines and basal blepharicerines being the least resolved.

Key Words: Blephariceridae, phylogenetics, morphology, molecular, net-winged midges

Host race formation by *Eurosta solidaginis* on subspecies of *Solidago altissima*

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Eurosta solidaginis, a gall-inducing fly (Diptera: Tephritidae) shows evidence of having formed host races on two subspecies *Solidago altissima*: *S. altissima altissima* which is found in the forest biome, and *S. altissima gilvocanescens* which is found in the prairie biome. The *E. solidaginis* populations in the prairie and the forest show significant differences in allozyme frequencies indicating partial reproductive isolation between the populations. Gall size and shape of the two *E. solidaginis* populations in the two biomes also differ significantly between prairie and forest populations. Prairie and forest flies had different wing patterns with a cline of wing patterns indicating that there is a hybrid zone. In a common garden experiment both the prairie and forest *E. solidaginis* populations had higher rates of gall induction and survival on the subspecies from their biome. The forest fly population had a strong preference for ovipositing on plants from the forest, while the prairie fly population did not show a preference between host populations. Both populations showed an oviposition preference for tall host plants, and the forest *S. a. altissima* was significantly taller than the prairie *S. a. gilvocanescens* in both the field and in the common garden experiment, and this influenced oviposition preference. We measured gall diameter in the field and in the common garden experiment. We found that gall diameter was significantly influenced by the fly origin and the environment (field versus common garden), but that it was not influenced by the plant origin. These results are the first evidence of host race formation on host plants that are differentiated below the species level.

Key Words: oviposition preference, offspring performance, host race, speciation, gall

Generic limits within the *Microphorella* Becker group (Diptera: Dolichopodidae *s.lat.*; Parathalassiinae)

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Microphorella Becker is a little known genus of small grey parathalassiine flies that has recently been classified in an expanded concept of the family Dolichopodidae. The genus currently includes 16 described species and several undescribed species that generally inhabit marine or fresh-water shoreline habitats in all zoogeographic regions of the world except the Afrotropical Region. Various authors have speculated about whether these species, as well as a few additional *Microphorella*-like shoreline species assigned to separate genera, represent one or several distinct generic lineages. Described and undescribed species of *Microphorella* are analysed phylogenetically and compared with other parathalasiine genera to determine generic limits within the *Microphorella* group.

Key Words: Empidoidea, Dolichopodidae *s.lat.*, Parathalassiinae, *Microphorella*, phylogeny

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The role of female choice on the shape and size of the male phallus in the Sarcophagidae

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Males of the subfamily Sarcophaginae (Diptera: Sarcophagidae) are well known for their complex and distinctive phalli. Species are recognized by the shape of the phallus, new species are described on the basis of the phallus, and most of the evolutionary hypotheses and much of the higher classification of the Sarcophaginae has been based on the morphology of the phallus. A question that has not been adequately investigated nor answered is "why do these males have such extravagant phalli?" This investigation examines the possibility of sexual selection through female choice acting on the shape of the male phallus. Of course, if females do make choices of suitable mating partners based (at least in part) on the shape of the phallus, they need to have sensory structures that would allow such discrimination. The genital openings and vaginal chambers of a variety of female Sarcophaginae were examined for evidence of tactile receptors, with the aid of a scanning electron microscope. These are the only areas that would come in direct contact with the male's exposed phallus during mating. Some ramifications of the presence or absence of sensory structures in these parts of the female reproductive system will be discussed.

Key Words: Sarcophagidae, sexual selection, reproductive morphology

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The *Empis hyalea*-group (Diptera: Empididae: Empidinae) in Asia: phylogenetic systematics, specific richness, distribution and habitats

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The *Empis hyalea*-group is one of the richest species groups within the subfamily Empidinae. It is considerably diversified in the Oriental region, especially in Southeast Asia. Apparently it is the only Empidinae species-group that adapted well to tropical conditions. All other Empidinae occurring in the same habitats are absent, contrary to the northern hemisphere where many different species groups cohabit.

The *Empis (C.) hyalea*-group is a large monophyletic group that can be divided into six well-defined clades. Seventy-two species are now included in this group; however, many new species, especially from the Oriental Region, remain to be described. In addition, several other species already described and for which the taxonomic status is still problematic probably belong to this group. Eventually, after revision of major Asian and Australian collections of Empidinae, the number of species should easily exceed 100 (Daugeron & Grootaert, 2004; 2005; 2006).

Although the present phylogenetic analysis includes only 42 species, the preliminary results show sistergroup relationships between altitude and coastal species (or species groups) in a repeated way. As most species occur in primary or secondary rain forests, it is here hypothesized that the present specific diversity originated in forest fragmentations that occurred during ice ages. Consequently, we propose that the *E. (C.) hyalea*-group is a relevant model for future studies on the impact of Quaternary climate changes on Asian biodiversity. Because we have now a much better knowledge of its taxonomy, phylogeny and ecology, the *E. hyalea* group could also be used as a relevant model to characterize sensible environments by comparing its specific richness in more or less damaged coastal or / and altitude rain forests.

Key Words: Empididae, phylogeny, Oriental, distribution, habitats

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Selection of *Anopheles stephensi* with DDT and Dieldrin and Cross Resistance Spectrum to Pyrethroids and Fipronil, Iran

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In this study the field strain of *Anopheles stephensi*, the main malaria vector in south of Iran colonized in laboratory and selected with DDT and dieldrin in two separate line for 3 generations to a level of 19.5 and 14 fold in DDT and dieldrin resistance respectively synergist test with DMC and pbo on the selected strains indicated that oxidative detoxification and dehydrochlorinase inhibitor might be one of the mechanisms in the dieldrin and DDT selected strains respectively. DDT selections decrease susceptibility to DDT and pyrethroids including lambdocyhalothrin, permethrin deltamethrin and cyfluthrin. Based on our result selection with dieldrin appeared negative and positive cross-resistance to pyrethroid and fipronil respectively. Base line information from these result, besides on metabolic factor, other resistance mechanisms such as mutation in γ aminobutyric acid GABA) and voltage-gated sodium channel might be involved.

Key Words: *Anopheles stephensi*, selection, cross-resistance, Iran.

Recent developments in the systematics of African Ceratitidina and Dacina (Diptera, Tephritidae, Dacini).

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African Dacina and Ceratitidina comprise 372 described species, of which several are considered serious pest organisms, attacking a wide variety of commercial fruits and crops. Since the state of the art meeting in Xalapa, Mexico in 1998 our knowledge of this group has increased dramatically. We hereby present an overview of the recent accomplishments in the taxonomic studies of the African representatives of these groups.

The almost exclusively African Ceratitidine genera *Ceratitis* MacLeay, *Capparimyia* Bezzi, *Carpophthoromyia* Austen and *Trirhithrum* Bezzi have been taxonomically revised during the last decade. In the course of these studies 44 species new to science were described. Altogether the revised genera comprise 159 species or 88% of all known African species belonging to Ceratitidina. Molecular (for some representatives of *Ceratitis* and *Trirhithrum*) and morphological (for all representatives of *Ceratitis* and *Capparimyia*) phylogenies were proposed. The phylogenetic relationships in *Ceratitis*, were studied in relation to the subgeneric classification and evolutionary tendencies on host plant specificity.

The African (and Middle Eastern) representatives of the Dacine genera *Bactrocera* Macquart and *Dacus* Fabricius were taxonomically revised. Fifteen *Bactrocera* and 177 *Dacus* species were recognized of which 26 are new to science. For *Dacus*, a preliminary phylogeny based on a selection of 30 exemplars from among the 66 recognized species groups was performed, and discussed in relation to formally established subgenera, and to host specificity.

It is envisaged that when all taxa are revised at a generic level, this will form the basis of a proper suprageneric phylogeny reconstruction.

Key Words: taxonomy, phylogeny, *Ceratitis*, *Dacus*, *Bactrocera*

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A new species of *Goniophyto* with a revised key to species from China (Diptera: Sarcophagidae)

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Six species of *Goniophyto* Townsend were described in the world, among them, two from China. A new species has been found during the course of fly investigation in Shanghai, China. The present paper deals with a description of the new species both sexes and a key to the Chinese species of *Goniophyto* in detail.

Key Words: Diptera, Sarcophagidae, *Goniophyto*, new species, China

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Morphological studies on the preimaginal stages of *Atherigona biseta* Karl (Diptera: Muscidae)

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The larvae of Millet shootfly as a pest will reduce the production of millet, which is one of the primary cultivated plants in northern area of China. No morphology of the preimaginal stages of *Antherigona biseta* Karl was reported in detail before. The definite adult from feed reared within a cage with millet in laboratory. And their offspring will be obtained. Then taken and preserved as specimens was studied. The morphology of the egg, 1st-3rd larval instars and puparium of *Antherigona biseta* Karl will be given in the present paper.

Key Words: *Antherigona biseta*, morphology, preimaginal stages

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New insight on the phylogenetic relationships within Mydidae and its relationship to Apioceridae (Diptera: Asiloidea)

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Presently, Mydidae is a rather species-poor taxon incorporating only 65 genera and approximately 360 described species from arid areas world-wide. However, it is an outstanding taxon within Asiloidea needing more attention in future studies, which will certainly reveal new species with targeted collecting. Many species are very large and the largest known true fly, *Gauromydas heros* (Perty, 1833) from Argentina, belongs to this taxon. A very short annual activity period and the remoteness of their habitats make them rare in collections and this is especially true for ethanol-preserved specimens suitable for molecular studies. Only a few publications address the world-wide fauna and recently Yeates & Irwin postulated the only higher-level phylogenetic hypothesis for Mydidae. The Apioceridae are regarded as the adelphotaxon of Mydidae and a close relationship has been substantiated by the removal of several genera from Apioceridae to Mydidae, apparently changing not only the delimitation of Apioceridae, but also of Mydidae. Now that the Apioceridae, with the only included genus *Apiocera* Westwood, 1835, is rendered monophyletic, the validity and delimitation of the ‘plesiomorphic’ and ‘apomorphic’ Mydidae *sensu* Yeates & Irwin remains to be addressed. This presentation aims to provide new insight on the higher-level phylogeny of Mydidae and its relationship to Apioceridae by incorporating nucleotide-sequence data from three nuclear genes (28S rDNA, *EF-1alpha*, & *CAD*) and evaluating some of the autapomorphic morphological characters previously hypothesised to support the monophyly of Mydidae. Included in this analysis are representatives of two of the subgenera of *Apiocera*, *Apiocera* from Australia and *Pyrocera* from the USA, and eight of the eleven subfamily taxa of Mydidae, including the ‘plesiomorphic’ Megascelinae

and Rhaphiomidinae; making it the most comprehensive molecular study to date. Only the two monogeneric taxa, Anomalomydinae from Australia and Cacatuopyginae from the Oriental Region, and the species-poor Rhopaliinae are missing.

Key Words: Asiloidea, Mydidae, Apioceridae, phylogeny

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Phylogeny of Asilidae with special reference to the position of Leptogastrinae based on morphology of imagines (Diptera: Asiloidea)

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Despite ongoing interest in species-level revisionary studies, phylogenetic relationships within Asilidae are poorly understood and have never been addressed in a comprehensive morphological analysis. The present analysis aims to provide the first detailed higher-level phylogenetic hypothesis with particular reference to the position of Leptogastrinae within Asilidae. The outstanding morphological characteristics of Leptogastrinae made Martin postulate in 1968 that it should be ranked as a distinct family sister to Asilidae. This adelphotaxa relationship was supported by a recently published molecular phylogenetic study involving 26 Asilidae species of which 2 were representatives of Leptogastrinae. In the present study, morphological features of the imagines are used to resolve relationships among 158 species sampled from 139 genera, 39 of the 42 recognised tribal taxa, and all 11 currently recognised subfamily taxa. Asilidae is supported as monophyletic based on a number of autapomorphies with respect to the included outgroup taxa (1 Nemestrinidae and 14 Asiloidea exemplars). A taxon comprising Apioceridae and Mydidae is the sister-group to the Asilidae. The analysis supports monophyly of six Asilidae subfamily taxa and non-monophyly of five. Leptogastrinae is monophyletic and nested deep within Asilidae, contradicting its previous placement as adelphotaxon to all other Asilidae. *Acronyches maya*, a morphologically distinct Stenopogoninae from Mexico, is supported as the sister-taxon of Leptogastrinae. Dasypogoninae and Stenopogoninae, both morphologically heterogeneous taxa, are shown to be non-monophyletic. The monophyly of Apocleinae and Laphystiinae with respect to Asilinae and Laphriinae, respectively, assumed by previous authors, could not be demonstrated. Many tribal taxa were recovered as monophyletic. Based on the world-wide sample employed here, the concepts of some geographically restricted tribal taxa have to be re-evaluated. Comments on a tentative higher-level classification of Asilidae are made based on the morphological synapomorphies resulting from this hypothesis. The findings are compared to a preliminary molecular and total-evidence analysis.

Key Words: Asiloidea, Asilidae, phylogeny

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Goldenrod gall midges revisited: cecidomyiid biodiversity on *Solidago* and *Euthamia* (Asteraceae) in North America

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Goldenrods are hosts to 24 recorded species of gall-inducing cecidomyiids in North America, making these plants one the most species-rich host taxa for gall midges, second only to *Artemisia* among the Asteraceae. While much ecological research has been done on some of the goldenrod-infesting midges, most species are only superficially known, several seem to be synonymous, and some have not been found since their description almost 100 years ago. The major cecidomyiid genera associated with goldenrods are *Rhopalomyia*, *Asteromyia*, and *Dasineura*, which account for 16, 4, and 4 described species, respectively. The genera *Asphondylia*, *Lasioptera*, and *Schizomyia* are each represented by 1-2 described species. Galls induced by these species are found on most plant organs, from rhizomes to stems, leaves, buds, and flowers, and exhibit great diversity in size, shape and structure. However, the life history of most species is virtually unknown.

Along with studies focused on behavioral ecology and systematics of certain species in this group, we conducted a field survey of goldenrod gall midges in an attempt to rear little-known species and learn about their basic biology. This survey has yielded numerous new host and gall records, which might prove to represent undescribed species, especially in the genus *Asphondylia*. Life-history data gathered elucidate complex life cycles in *Rhopalomia* and *Dasineura* spp., including induction of different types of galls at different times of the year, and the occurrence of natural enemies. While the large number and biological diversity of goldenrod gall midges make them ideal models for evolutionary ecology and systematic studies, lack of knowledge of their basic biology and taxonomy has hindered such research. The information we are gathering will not only lead to a better understanding of basic life-history strategies of the gall midges, but also facilitate their use in future systematic and evolutionary research.

Key Words: biodiversity, goldenrod, galls

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Behavior, ecology, and genetics of *Dasineura folliculi* (Diptera: Cecidomyiidae) - another case of host-race formation in goldenrod gall midges?

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Host-race formation is considered to be the first step toward sympatric speciation in phytophagous insect species, a concept that keeps gaining support from behavioral and genetic studies in different insect taxa. Gall-inducing insects in particular serve as ideal models for such studies due to their close and highly specific interaction with their hosts. In recent years, several insects associated with goldenrods (*Solidago altissima* and *S. gigantea*) in North America have offered evidence for host-race formation based on ecological and genetic data. In two of these cases, involving parasitic wasps and predatory beetles, it has been found that the natural enemies differentiate on the two plants following the gall inducers, in a process known as sequential radiation.

We are currently studying host-race formation and sequential radiation in the gall midge *Dasineura folliculi*, which induces loose bud galls on *S. gigantea* and *S. rugosa*, and in an inquilinous gall midge that is associated with the galls. As host preference in herbivorous insects is frequently linked to mate choice, the requirement for simultaneous mutations leading to host shifts may be alleviated. Preliminary mate-choice experiments indicated significant preference for mates from the same host-associated population among the gall inducers. However, host-preference experiments were inconclusive and will be repeated in an improved setting this summer.

One of the factors that may facilitate shifts to new hosts is the acquisition of enemy-reduced space, in which the rates of enemy attack are lower on the novel host. Documenting inquiline infestation in galls on *S. gigantea* and *S. rugosa* showed inquilines are significantly more common in the latter, suggesting *S. gigantea* might be the more recent host. Molecular analyses of the COI mitochondrial gene of the gall inducer and the inquiline, currently

underway, will further enable us to conclude whether host-race formation and sequential radiation occur in this system.

Key Words: gall midges, host races, mate choice, sequential radiation

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Biting and resting behaviors of the main malaria vector, *Anopheles stephensi* liston in an endemic area of southern Iran

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Malaria is one of the most common parasitic infections that had infected and killed many people from long time ago. Malaria is still endemic in southern parts of Iran particularly in Sistan and Baluchistan, Hormozgan and south of Kerman provinces . *Anopheles stephensi* is the main malaria vector in those areas where anti-malaria program highly concern. This study was carried out in the mountainous area of Hormozgan province with respect to biting and resting behavior. In order to determine biting activity of this species, human and animal landing collection method was used. The results showed that, this species is active during the night from sunset to sunrise and the maximum biting activities was observed between 22:00 and 02:00 hours. The number of collected specimens on animal was 12 times more than human. With the purpose of study on resting behavior, different methods of mosquito collecting from outdoors and indoors shelters were performed. Totally, 2878 *Anopheles stephensi* were caught while 67% (n = 1928) of them collected by pyrethrum spray collection methods from indoor places which indicated that, this species is highly endophil. Therefore, the residual insecticides would be more effective to control of this species.

Key Words: malaria, *Anopheles,* resting, biting, southern Iran

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On the infestation of warble fly - larvae in the Antlered Ruminants in "Szigetköz Region" (Hungary)

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Prior to our analyses we did not find any data on the warble fly infestation in wild *Cervidae* in „Szigetköz Region"in the North-West of Hungary. Between 25th June 2005 and 27th February 2006 we examined 51 red deer and 32 roe deer of which all were shot on hunting. The aims of our observations were to declare the incidences and rates of different larvae of *Hypoderma*-species. The above mentioned larvae were found to occur in 74.5% of red deer and 84.3% of roe deer. As a result of identification (by Minař, 2000) of 2601 larvae, the incidence of 2 species was established. The 1811 larvae of *Hypoderma diana* (Brauer, 1858) were found to occur in 84.3% of roe deer and 46.08% of red deer, while 790 larvae of *Hypoderma actaeon* (Brauer, 1858) showed 53.92% incidence in red deer. Data related to the QP 2.0 quantitative parasitological analysis (by Rózsa et al., 2000) was discussed.

Key Words: *Hypoderma diana, H. actaeon,* infestation, *Cervidae,* North-West Hungary

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Studies on the leafminers : *Liriomyza sativae* (Blanchard) and *Liriomyza congesta* (Becker) (Diptera: Agromyzidae) and their parasitoids in Egyptian clover in Egypt.

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Liriomyza sativae (Blanchard) is a new recorded pest species attacking Egyptian clover, *Trifolium alexandrinum* L., with *Liriomyza congesta* (Becker), *Agromyza nana* Meigen and *Chromatomyia* (= *Phytomyza*) *horticola* Goureau in Egypt. Incidence and intensity of infestation as well as parasitism were studied on untreated clover plants at Al-Aiat (40 km south Cairo) during 2002- 2003 and 2003- 2004 seasons. Infestation rate and number of mined leaflets per leaf not varied with general means of about 10% and 43%. The highest infestation rate about 22% was recorded by late January and February in 2004 and 2003, respectively. Larval or pupal parasitism not varied in each season, but reached higher rates of 38.1 and 37.2% (2002- 2003) opposed to 29.2 and 29.9% (2003- 2004). Its highest rates coincided with lower infestation by early March, in both seasons. Synchronization was found between the time of host emergence and larval parasitoids, which were the abundant species *Diglyphus isaea* (Walker), *Hemiptarsenus zilahisebossi* (Erdös), " *Chrysonotomia* (*Achrysocharella*) sp." and *Pnigalio* sp. (Eulophidae) in active seasons. Majority of flies and the dominant larval- pupal parasitoid species *Opius* sp. (Braconidae) as well as *Chrysocharis* sp. (Eulophidae) were emerged from active pupae. Asynchrony was observed in their timing of emergencies in active or diapause seasons, but not in the second diapause one. Parasitic activity by larval and larval- pupal parasitoids resulted in an obvious decrease about 34% of the leafminers population. Clover can be used as an banker crop to conserve and promote the natural enemies against the leaminers.

Key Words: *L. sativae, L. congesta,* Egyptian clover, infestation, parasitism.

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The sorghum shoot fly, *Atherigona soccata* Rondani (Diptera: Muscidae), attacking some gramineous forage crops in Egypt.

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The sorghum shoot fly, *Atherigona soccata* Rondani, attacks sorhgum ratoon (*Sorghum bicolor* (L.) Moench) at Sids and Al-Aiat with *Atherigona humeralis* (Wiedemann) on sudan grass (*Sorghum vulgare var. sudanense* Hitch.) and *Atherigona* sp. on barnyard grass (*Echinochloa crus-galli* (L.) P. Beauv) at Al-Aiat in Middle Egypt. The shoot flies were generally active during the year and passing from crop to crop. It infested ratoon of sorghum plants left in the field after harvest reach about 12% and 14% at Sids and Al-Aiat in 1998-1999 and 2002. Infestation was lower (about 5%) on barnyard and sudan grasses at Al-Aiat in 2202-2003 and 2003. Larvae peaked by early January on (barnyard grass) and at early and late July as well as the third week of August on (sudan grass) at Al-Aiat. Two peaks were attained by the third week of November and December on (sorghum ratoon *Atherigona soccata*) at Sids. Flies emerged from infested plants of the forage crops during the most months in the year. Four peaks were observed on late January, July and August as well as mid December. Larval parasitism was higher (about 61% and 55%) on barnyard and sorghum ratoon at Al-Aiat, but declined to (about 1% and 9%) on sorghum ratoon and sudan grass at Sids and Al-Aiat. Three hymenopterous larval parasitoids i. e. *Neotrichoporoides* sp. near *nyemitawus* Rohwer, *Pediobius*

sp. and *Pnigalio* sp. (Eulophidae), two pupal parasitoids i. e. *Callitula* sp. (Ptromalidae) and *Dacnusa* sp. (Braconidae) and one undetermined hyperparasitoid belongs to Cynipidae had emerged. These species are newly recorded on *A. soccata* in Egypt. The first and the second species were abundant on larvae infested (sorghum ratoon or barnyard grass) at Al-Aiat and on (sorghum ratoon or sudan grass) at Sids and Al-Aiat. Plowing sorghum fields and collecting stubbles could be useful as a cultural control method for decreasing the population size of the sorghum shoot fly.

Key Words: *A. soccata, S. bicolor, S. vulgare var. sudanense, E. crus-galli,* infestation

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Developmental stability and hybridization: a test case in two *Ceratitis* species (Tephritidae, Diptera)

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Developmental stability (DS) is defined as the ability of an organism to buffer its development against genetic or environmental perturbations, and is most commonly estimated by the level of fluctuating asymmetry (FA), i.e. small random deviations from perfect symmetry in bilateral traits. DS is hypothesized to be affected by genome-wide properties such as the level of heterozygosity and genetic co-adaptation. For instance, merging of different genomes as a result of hybridization may destabilise developmental processes due to the disruption of co-adapted gene complexes. We tested this hypothesis by comparing patterns of FA in three meristic and four metric traits on the wings and legs of two Tephritid species (*Ceratitis (Pterandrus) rosa* Karsch and *Ceratitis (Pterandrus) fasciventris* Bezzi) and their lab-reared hybrids (males x females of either species). Within each cross type, unbiased FA estimates of male and female offspring were obtained through mixed regression analysis. Hybrids showed higher levels of FA than parentals, especially so in meristic traits. Among hybrids, males showed higher levels of stability than females, possibly due to stronger buffering of traits that are functionally important during male display. These results hence provide evidence for the use of FA as an estimator of disruption of developmental stability due to genetic stress.

Key Words: fluctuating asymmetry, *Ceratitis*, hybridization, developmental stability

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Fauna Sinica-Insecta: Diptera: Muscidae, I

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The Fauna Sinica, Diptera: Muscidae is divided into 3 volumes compiled by 3 chief editors respectively. Present vol. 1 Chief-edited by FAN Zi-de includes the general account for the family as a whole, in which, a modification of the Hennig-Pont-Skidmore System is proposed for classification under the family, and the systematic account with 7 subfamilies, 30 genera, 363 species, and 4 subspecies, in which 32 new species are reported:

1. Eginiinae	2 gen.,	26 spp. (including 6 n. spp.)
2. Achanthipterinae	1 gen.,	1 sp.
3. Azeliinae	9 gen., 2 subspp.	170 spp., (including 12 n. spp.)
4. Muscinae	10 gen., 2 subspp.	111 spp., (including 12 n. spp.)
5. Stomoxyinae	3 gen.,	12 spp.
6. Reinwardtiinae	3 gen.,	8 spp. (including 1 n. sp.)
7. Atherigoninae	2 gen.,	35 spp. (including 1 n. sp.)

The new species appear in following genera: *Xenotachina* (6 spp.), *Ophyra* (1 sp.), *Hydrotaea* (6 spp.), *Xestomyia* (1 sp.), *Drymeia* (1 sp.), *Megophyra* (1 sp.), *Thricops* (2 spp.), *Polietes* (1 sp.), *Neomyia* (3 spp.), *Rypellia* (3 spp.), *Eudasyphora* (3 spp.), *Dasyphora* (2 spp.), *Muscina* (1 sp.), *Atherigona* (sp.)

Key Words: Muscidae, fauna, China

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Biosystematics of New World Andrenosomatini Robber Flies (Diptera: Asilidae: Laphriinae).

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A review of the classification and biology of the American genera of Andrenosomatini is presented. Nine New World genera (comprising about 65 described and 35 undescribed species) are presently recognized: *Andrenosoma*, *Cerotainiops*, *Dasyllis*, *Neophoneus*, *Pilica*, *Pogonosoma*, plus three undescribed genera related to *Dasyllis*. Taxonomic characteristics of the tribe and these nine genera are shown, their phylogenetic relationships are briefly discussed, and biological and natural history data for both adult and immature stages are given.

Key Words: Asilidae, Laphriinae, Andrenosomatini, systematics, biology.

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Taxonomic study of stalk-eyed flies on the example of the *Diasemopsis aethiopica* species group (Diptera, Diopsidae)

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Members of the family Diopsidae are remarkable insects carrying their eyes and antennae at the end of lateral projections of the head in all genera except *Centrioncus*. The number of species described so far is ca. 150 world-wide. Despite the fact that numerous earlier authors have been working on the group there are currently but a few taxonomic specialists publishing on this group. On the other hand, several research groups are working on the behavioural aspects and genetics of Diopsidae and in many cases the species identity of the live populations used for experiments, is in doubt. This results in information accumulation without reliable species reference. Therefore, a more accurate taxonomic knowledge at species level is required. We have studied types of *Diasemopsis aethiopica* and its closest relatives as well as identified material deposited in Tervuren (RMCA) and London (BMNH). Five morphologically different entities (probably species) were incorporated in the RMCA collection under *D. aethiopica*, some of them clearly distinguishable on the basis of external characters. Earlier authors did not use genital characters, their descriptions are superficial, and their drawings are restricted to general parts (mostly "habitus") but do not show many taxonomically important details. Based on our studies with *D. aethiopica* and related species there are several synonyms. These types have to be studied in order to establish stable species identities. Similar research on other genera would be desirable in the future which can be supported by behavioural, allometric and genetic data from the live populations. The stocks in laboratories also provide long series of specimens which may solve problems when using scattered material deposited in dry collections.

Key Words: taxonomy, Diopsidae, synonyms, genitalia, variation

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Tephritoid systematics and biology at the beginning of the third millennium

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The extremely diverse superfamily Tephritoidea currently contains the following families: Ctenostylidae, Lonchaeidae, Pallopteridae, Piophilidae, Platystomatidae, Pyrgotidae, Richardiidae, Tephritidae and Ulidiidae. Recent progress in the systematics and biology of the group is reported in response to various previously stated 'needs' and the global ‘biodiversity crisis’. The uniqueness of the superfamily derives from its impact on mankind, size, distinctive biological traits and aesthetic appeal. The differential attributes of the component families are elaborated. In particular, an overview on the higher classification, important revisions, monographs, catalogs, keys, phylogenies, and host lists, as well as other information, such as on immature stages, biology and ecology, are given. Dissemination of taxonomic and biological expertise, especially via the internet and by the production of computerized interactive keys, is highlighted. The status of two very different families is compared. For the main family, the Tephritidae, a detailed higher classification now exists that is largely based on a fairly rigorous cladistic analysis. There is also a glossary of tephritid terminology, which should be used and expanded for the rest of the Tephritoidea, and indeed for the entire Diptera. At the other end of the range is the Piophilidae, a small family of about 70 known species, the biology of several of which has been studied in considerable detail. A cladistic analysis, albeit intuitive, was recently published within the framework of a quite comprehensive revision of the family.

Recommendations for the future include: Scientific cooperation among scientists, including periodical meetings; training of junior staff and educating the new generation of tephritoid taxonomists; and creating special funds for the study of tephritoid taxonomy. A special effort should be made to discover the still missing taxa and to improve the quality of preservation procedures. For taxonomic research both traditional and molecular techniques should be employed.

Key Words: Tephritoid, biosystematics, past, present, future

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Experimental and natural infections of black flies (Diptera: Simuliidae) with larvae of *Onchocerca dewittei japonica*, the causative agent of zoonotic onchocerciasis in Japan

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To determine the vector(s) of *Onchocerca dewittei japonica* Uni, Bain and Takaoka, a common filaria parasite of wild boars and the causative agent of zoonotic onchocerciasis in Japan, we investigated the experimental and natural infections of female black flies with larvae of this parasite. The microfilariae of *O. dewittei japonica* were injected intrathoracically into 86 newly-emerged females of seven *Simulium* species collected in Oita, Japan. After 10 days post-infection, the third-stage larvae were found in 4 of 21 *S. aokii* (Takahasi) dissected, 12 of 14 *S. arakawae* Matsumura, 6 of 11 *S. bidentatum* (Shiraki), 1 of 1 *S. japonicum* Matsumura, 1 of 1 *S. quinquestriatum* (Shiraki) and 3 of 4 *S. rufibasis* Brunetti. No larva was found in 1 *S. uchidai* (Takahasi) dissected. The infective third-stage larvae were 772–1,059 µm long by 17–22 µm wide. It has been proved for the first time that these six black-fly species are able to support the larval development of *O. dewittei japonica*. Moreover, female adult black flies attracted to a man and/or an automobile were collected in the field and maintained in tubes with sugar solution for 10 or 11 days until dissections. One of 100 *S. bidentatum* and 1 of 11 *S. quinquestriatum* examined had one third-stage filaria larva. The third-stage larvae found from field-collected *S. bidentatum* was 964 µm long by 21 µm wide, and that from *S. quinquestriatum* was 856 µm long by 25 µm wide. Morphometric analysis shows that the former filarial larva is likely to be *O. dewittei japonica*. These findings may suggest a possibility that black flies play a role in the transmission of zoonotic onchocerciasis due to *O. dewittei japonica* in Japan.

Key Words: *Onchocerca*, infection, *Simulium*, vector, zoonosis

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Examination of Diabetic Necrotic Foot Treated with Maggot Debridement Therapy And Split Thickness-Skin Graft

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We announced that we examinated Diabetic Necrotic Foot Treated with Maggots. We got Good Result. We recognized that Maggots is effective to Wound Repair from any thousands years ago. Maggots grew up flies one week. We changed maggots two times per a week. We judged operation at each wound dressing change. This time patient had many pus at rawsurface (NecroticUlcerWound), we performed Split Thickness-Skin Graft from inguinal area skin. Conclusionaly patient preserved lower leg. We used Sterilized Maggots. Maggots ate only necrotic tissue, preparated wound bed and promoted granulation tissue. We got good result adding to Split Thickness-Skin Graft to reduction rawsurface. We reported a few Maggot Debridement Therapy in Japan.

Key Words: maggot debridement therapy (MDT), split thickness-skin graft, diabetic necrotic foot

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One less acalyptrate family? The status of Eurychoromyiidae

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The Neotropical genus *Eurychoromyia* Hendel was described for the single species *E. mallea* Hendel, based on four specimens collected over 100 years ago by Carl Schnuse in the lower elevation Andean foothills north of La Paz, Bolivia. When described, the species was considered an isolated group, classified in its own family-group coordinate in rank with Hendel's subfamilies Lauxaniinae (=Lauxanioidea) and Sciomyzinae (=Sciomyzoidea). Hennig was first to align the family with Lauxanioidea (in the current sense), a placement followed by the few subsequent authors dealing with this issue, but being specifically aligned, in turn, with each of the other lauxanioid families. Hennig and Griffiths based an affinity with Chamaemyiidae on presence of four spermathecae (2+2), while all lauxaniids known at the time had three (2+1). J.F. McAlpine at first suggested placement near Lauxaniidae (or Ropalomeridae, an idea quickly dismissed), but 20 years later suggested Celyphidae. Characteristics used to support Celyphidae + Eurychoromyiidae either represent clear trends towards reduction that have evolved in parallel in several lauxanioid lineages (e.g., reduction of macrosetae), general conditions also found in many lauxaniids (e.g., widened fronto-orbital plates, elongated scape), and misinterpretations of character states (e.g., convex bulging face, reduced costal setulae). Even the autapomorphies McAlpine listed for Eurychoromyiidae relative to the lauxanioid ground plan are conditions found in some lauxaniids (e.g., reduction of gonopods and parameres, four spermathecae). Griffiths suggested (from an illustration of Henning) that another autapomorphy was the fusion of the 7th tergite and sternite into a ring – a condition now known in various lauxaniid genera. The current study provides evidence for reducing Eurychoromyiidae to a subfamily within Lauxaniidae, demonstrating the close relationship of *Eurychoromyia* with three unequivocal Neotropical lauxaniid genera

(*Tauridion* Papp & Silva, and two undescribed), based on numerous synapomorphies from the head, legs, wing, female terminalia, and male genitalia.

Key Words: Acalyptratae, Lauxanioidea, Lauxaniidae, Eurychoromyiidae, *Eurychoromyia*

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Raman-atomic force microscopy revealing nanometer-scale morphology and spectro-chemistry of the ommatidial surfaces of Dipteran compound eyes

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The ommatidial lens surfaces of the compound eyes in several species of Diptera and the related order Mecoptera were analyzed using a recently developed Raman-atomic force microscope, which is capable of acquiring sub-micron scale topographic and spectro-chemical information from surfaces. We demonstrate in this work that the atomic force microscope is a potentially useful instrument for observing nanometer-scale surface morphology, and that the newly developed Raman-atomic force microscope extends this application by revealing spectro-chemical information that can be inferred at sub-nanometer resolution. This is the first demonstration of apertureless near field Raman spectroscopy on an intact biological surface. A full analysis (surface morphology and spectro-chemistry) was done for *Chrysopilus testaceipes* Bigot (Rhagionidae), revealing a surface with cerebral cortex-like ridges with periodic variation in height, with corresponding differences in surface chemistry both on and off ridges. For example, ridge tops displayed more protein character and hydrophobicity, while troughs displayed more carbonyl functionality associated with the esters of fatty acids. Several other taxa were examined for their sub-micron surface morphology, most of which displayed a similar pattern (i.e., *Sylvicola fenestralis* (Scopoli) (Anisopodidae), *Symphoromyia* sp. (Rhagionidae), *Platycheirus obscurus* (Say) (Syrphidae), *Musca domestica* Linnaeus (Muscidae), *Phormia regina* (Meigen) (Calliphoridae)). Other taxa displayed various other characteristics, such as a nodule-like morphology (i.e., *Tipula (Triplicitipula)* sp. (Tipulidae)), pseudo-nodular (coalescing nodules) morphology (i.e., *Tabanus punctifer* Osten Sacken (Tabanidae)), a pitted and grooved morphology (i.e., *Dilophus orbatus* (Say) (Bibionidae)), or an entirely smooth surface (i.e., *Bittacus chlorostigma* MacLachlan (Mecoptera: Bittacidae)). Variation in sub-micron surface structure and spectro-chemistry provides an unexplored source of potentially interesting information, suggesting that Raman-atomic force microscopy could provide a new tool useful to systematic, evolutionary, and other lines of inquiry.

Key Words: Raman spectroscopy, atomic force microscopy, surface chemistry, ommatidia, *Chrysopilus*

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Fine morphology of Sciomyzidae (Diptera) female head sensory system

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The morphology of the sensory system of Sciomyzidae from genera *Pherbellia*, *Pteromicra*, *Coremacera*, *Elgiva*, *Sepedon*, *Limnia*, *Tetanocera* and *Trypetoptera* was investigated using scanning electron microscope. Distance chemoreceptors are presented by several types of olfactory sensilla, located mainly on the antennae (especially on the flagellum and arista). Olfactory cavities with basiconic sensilla were found at the flagellum. The short scapus bears several trichoid sensilla, while a group of trichoid olfactory sensilla is located on the pedicel. Basiconic sensilla are usually surrounded with microtrichia and are distinguished by their shape and thickness. Cylindrical and conic hair with narrow or round top are widespread. In *Pteromicra*, they are hook-shaped. The flagellum has cuticle invaginations, represented by double-walled coeloconic sensilla (their cuticle is perforated with multiple pores). Besides basiconic and coeloconic sensilla, there are thichoid and club-shaped sensilla. Trichoid sensilla are thick-walled receptors with an olfactory sensila structure, while club-shaped sensilla are typical thin-walled olfactrory ones. Basiconoc sensilla can be smooth and grooved. The arista is covered with short and sparse hair (*Pherbellia*), but in some species this hair forms compact clusters. The arista can also be covered with chetae (*Sepedon*), or with long and dense hair (Coremacera). In *Tetanocera* and *Pteromicra* arista, hair is located irregularly (dense at the base and sparse at the apex of arista). Contact chemical receptors (gustatory sensilla) are located at the labellum in rows (*Trypetoptera punctulata*, *Sepedon sphegea*) or irregularly (*Tetanocera robusta*). Trichoid, basiconic and coeloconic sensilla are located on the labellum of all studied species. Basiconic sensilla are by far the most numerous and usually form receptor fields. In some species basiconic sensory chetae are found between the ommatidia (mechanoreceptors). Mechanoreceptors form a field for receiving

information from air streams. There are separate mechanoreceptory chetae at the occiput. Paired gravitational receptors are located at the lateral sides of the occiput aperture. The location of sensilla on the flagellum might correlate with the method of reproduction of discrete species and with the method of egg laying.

Key Words: sensilla, Sciomyzidae, antennae

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Fine morphology of Conopidae (Diptera) female head

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The sensory system of the female head of conopid flies of 7 species (*Myopa testacea* L., *Zodion andersoni* Kr., *Thecophora sundewalli* Ztt., *Conops ceriaeformis* Mg., *Melanosoma bicolor* Mg., *Sicus nigritarsis* L., *Physocephala truncata* Lw.) was investigated using scanning electron microscopy. Most sensilla are located on the antennae. The scapus of these species is short and covered with a row of trichoid and basiconic sensilla. Trichoid sensilla were found mainly on the dorsal (and partially on the lateral) surfaces of the pedicel. Grooved (*Thecophora*) and smooth basiconic sensilla were found on the pedicel. These sensilla provide thermal and chemical reception. Conic and caved coeloconic sensilla as well as areas with pores (*Conops*, *Physocephala*) cover the flagellum. Distant chemical receptors are represented by several types of olfactory sensilla at the flagellum and flagellomers. Basiconic sensilla may be contact receptors or olfactory ones, and they vary in their size, shape and thickness. Thin chetoid sensilla with smooth or grooved surfaces were found on the head. Trichoid sensilla are common at the pedicel surface. Separated mechanoreceptors were discovered between ommatidia of the compound eyes. Some Conopidae (*Myopa*, *Zodion*, *Physocephala*, *Conops*) have 5-7 mechanoreceptors at the occipital area. Other representatives of the family (*Sicus*, *Melanosoma*) have 7 long trichoid sensilla and 13-15 short stick-walled senscilla in this zone. Variety and function of different sensilla are discussed.

Key Words: Conopidae, sensillae, antennae

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Phylogenetic implications of the male genitalia in Sarcophaginae (Diptera: Sarcophagidae)

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Male sarcophagine genitalia are highly distinctive at the species level and provide excellent species identification characters as well as phylogenetically informative characters for higher classification. However, to date, male genitalic characters have rarely been used for genus-level phylogenetic analyses. Considering the complexity and the high degree of sclerotization of the sarcophagine phallus, a comprehensive Scanning Electron Microscopy (SEM) study of the male acrophallus was undertaken to clarify its morphology and to homologize its parts. In addition, to test the phylogenetic implications of the male genitalia, 52 male genital characters were defined and included in a matrix with 47 other morphological characters. Based on a parsimony analysis, this work provides a preliminary hypothesis of sarcophagine phylogeny of 72 examplar species, representing 19 genera. On the basis of those results, the monophyly of *Ravinia* Robineau-Desvoidy, *Oxysarcodexia* Townsend, *Titanogrypa* Townsend, *Helicobia* Coquillett, *Lepidodexia* Brauer & Bergenstamm and *Sarcophaga* s.l. Meigen is supported but *Blaesoxipha* Loew appears paraphyletic. The genus *Helicobia* is nested within *Sarcophaga.* Given that modern phylogenetic techniques were rarely applied to test the numerous generic classifications of the Sarcophaginae, this analysis provides one of the first relevant phylogenetic data clarifying sarcophagine generic classification. The male genitalia morphology dataset is also highlighted as an important source of informative phylogenetic characters.

Key Words: Sarcophaginae, male genitalia, morphology, phylogeny, scanning electron microscopy

Diptera in the cartographical database of agricultural plant pests of Russia and adjacent countries

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The first version of the interactive Agricultural Atlas of the former USSR territories is now completed and can be reviewed at http://www.agroatlas.spb.ru/. The Atlas presents maps reflecting the distribution and incidence of major and minor crop pests (150), crop diseases (150), and weeds (150 species), in addition to distribution maps of crops and wild crop relatives, as well as agroecological maps of major climatic parameters that influence agricultural production. Only 13 dipteran species have been selected to be included in the Atlas, i.e., pests of small grains (*Mayetiola destructor* Say, *Phorbia fumigata* Mg., *Opomyza florum* F., *Oscinella frit* L. & *O. pusilla* Meig., *Chlorops pumilionis* Bjerk., *Contarinia tritici* Kirby, *Stenodiplosis panici* Rohd.), vegetables (*Delia radicum* L., *Delia floralis* Fall., *Delia antiqua* Meig., *Chamaepsila rosae* L.) and stone-fruits (*Rhagoletis cerasi* L.). Each object is represented by a number of standard files. The Map file is composed of 2-5 layers reflecting the geographical spread and levels of harming activity. *O. frit* & *O. pusilla* joint map only reflects zones of high, moderate and low damage. Two geographical zones of damage are allocated for 4 species, low and moderate, or low and high. In other cases, available materials have allowed to allocate low damage zone only inside the area. The Description file includes Taxonomic Position, Morphology and Biology, Distribution, Ecology, and Economic Significance. There is also an image, usually original photograph illustrating the pest. The Metadata file includes Scale, Accuracy, Projection, Content, Accuracy of Qualifier, Method of Map Construction, and References. The second version of the Agricultural Atlas is planned to be created soon. More than 100 insects and other animal species will be added, but only 7 more dipteran pests (of grains, legumes, sugar beet and pear) will be included. Preliminary analysis shows that they all have low harming activity in Russia.

Supported by ISTC grant no.2625p.

Key Words: Russia, cartographical database, crop pests

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Notes on taxonomy of Dolichopodinae (Diptera: Dolichopodidae)

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Dolichopodinae is the largest subfamily with approximately 1765 species in 20 genera (25% and 8% of total number for the family), including species-abundant genera *Dolichopus* and *Hercostomus*, but probably the same number of species is to be described. After a long pause four reviews have recently appeared, dealing with Dolichopodinae as a whole subfamily. The works of Grichanov, 2004, and Rodionova, 2004 (who follows Negrobov, 1986), contain verbal description and reasoning for their classifications. The works of Brooks, 2005 and Zhang & Yang, 2005 are based on cladistic analysis. The main methodical difference between the last two works is that Zhang & Yang have included into analysis characters of only generic and subgeneric rank, while Brooks has used both generic and specific characters. This is probably the cause of different results produced by their computer software. The work of Brooks is remarkable in that the author has redescribed and figured type species of almost all known dolichopodine genera. The recent papers have revealed a number of very close genera that have been united, and have found important characters that allow to split some holding taxa. Thus, the *Paraclius arcuatus* and *Pelastoneurus vagans* lineages seem to be restricted to North America, being absent in the Old World tropics where at least 6 new genera are proposed to create instead. Similarly, several new genera should be erected in tropics for *Hercostomus* species in addition to already created ones. Then it will be possible to assign finally generic rather than subgeneric status to Holarctic *Gymnopternus* differing now in only one morphological character from other species of *Hercostomus*. The largest (with more than 600 species), mainly Holarctic genus *Dolichopus* seems to be monophyletic, and it will never be splitted despite holding many doubtful names and possible synonyms.

Key Words: taxonomy, Dolichopodinae, Dolichopodidae

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Dolichopodidae in mangroves of Southeast Asia: diversity, community structure, zonation and phenology: a case study in Singapore

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In contrast to marine and brackish water habitats in temperate regions, mangroves in Southeast Asia have a very diversified dolichopodid fauna. A one-year study of mangroves in Singapore revealed the presence of 92 species, excluding the typical sandy and rocky beach species. A distinct zonation of the species was observed with species typical for areas directly exposed to the sea and direct sunlight, species living in areas covered by mangrove forest and gentle tidal currents and, a third group that is confined to the backside of the mangrove forest, around pools with low salinity or upwelling fresh water in areas that are flooded only during spring tides. Anthropogenic sites and fresh water affluents host tramp species. Some *Thinophilus* and *Nanothinophilus* are identified as colonizers i.e. occupying freshly exposed mud flats (after logging and digging) that start to be re-colonized by mangrove tree saplings. The tree trunk inhabiting *Medetera* and *Neurigona* also have typical mangrove species that are not found in nearby rain forest.

All dolichopodid subfamilies have representatives in mangroves as shown in the Singapore case study. Genera such as *Ngiraphium*, *Nanothinophilus* and *Phacaspis* only occur in mangroves. Although mangroves are characterized by a rather constant humidity, 2 distinct periods of activity are observed.

The high diversity of mangrove dolichopodids is explained by the fact that the habitat seems to be old (genetic distance between species is very large). Secondly, some species have a disjunctive distribution pattern, occurring in both mangroves and mountainous areas, suggesting that the humid mangroves acted as refugia during the arid spells caused by the glaciations. Diversity of dolichopodids in mangroves in Thailand, Malaysia and Indonesia will be discussed.

Key Words: Dolichopodidae, mangrove, Southeast Asia

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Human blood propensity of *Anopheles stephensi* the main malaria vector of Malaria in coastal and mountainous areas of Bandar Abbas , southern Iran

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This study was conducted to investigate hematophagic tendencies of the malaria vector base on a seasonal basis as well as by geographical region in a two malaria endemic areas situate in north of Persian Gulf, Bandar Abbas, Southern Iran. This study was carried out for 12 months from Apr. 2003 up to the end of May 2004. Female anophelines were collected from indoor and outdoor shelters in hilly and plain regions of Baddar Abbas district and their blood meal was tested using ELISA test methods. In mountainous area, *An. stephensi* was active during whole year except winter and reached a peak in December. In contrast in flat regions *An. stephensi* showed strongly endophilic behavior with two seasonal activity peaks. The anthropophilic index *An. stephensi* was estimated at 48% in hilly area where residents sleep outside during transmission season while the anthropophily index was 28% in plan area. In the study area, the most malaria cases occurred in the hilly area and it seems that *An. stephensi* was responsible for transmission of malaria in hilly and coastal. However, malaria transmission in this study area is much influenced by resident's rest habits. Thus, adapting people to use personal protection such as a bed net instead of residual spraying may be considered as an effective measure in malaria control in both regions.

Key Words: anthropophily, *Anopheles*, seasonal activity, geographical region, malaria

Molecular phylogeny and classification of the family Tephritidae: current status and future perspective

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The phylogeny of the family Tephritidae was reconstructed from mitochondrial 12S and 16S ribosomal RNA gene sequences using over 60 species representing many currently recognized higher taxa within the family. Patterns of nucleotide composition and substitution were assessed based on sequence comparison. The minimum evolution and Bayesian trees suggested many interesting new phylogenetic relationships including the followings: (1) sister group relationships between the subfamily Tephritinae and the tribe Blepharoneurini; (2) possible close relationship between the Palearctic *Cephalophysa* and Neotropical Blepharoneurini; (3) monophyly of Acanthonevrini plus Phytalmiini; (4) membership of New World genus *Alujamyia* to the Old World tribe Acanthonevrini; and (5) membership of the little known genus *Esacidia* to the tribe Carpomyini. Our results, therefore, convincingly suggest that an extensive rearrangement of the higher classification of the Tephritidae is necessary. Since our sampling of taxa heavily relied on the current accepted classification, some lineages identified by the present study were severely under-sampled and other possible major lineages of the Tephritinae were probably not even represented in our dataset. We believe that our results provide baseline information for a more rigorous sampling of additional taxa representing all possible major lineages of the family, which is essential for a comprehensive revision of the tribal and subfamily classification.

Key Words: Diptera, Tephritidae, classification, molecular phylogeny, DNA

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Molecular phylogeny of the superfamily Tephritoidea reanalyzed with addition of rare taxa including Ctenostylidae, *Eurygnathomyia* and *Tachinisca*

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The phylogeny of the superfamily Tephritoidea (Diptera: Muscomorpha) was reanalyzed from three mitochondrial gene fragments (12S, 16S, and COII) using previously published dataset plus some additional species representing various taxa critical but not used in the past mostly because of their rarity. These additional taxa include Tanypezidae, Ctenostylidae, *Tachinisca*, *Ortalotrypeta*, and *Eurygnathomyia*. Phylogenetic signal present in different gene fragments as well as combinations of gene fragments was examined using the minimum evolution method as well as Bayesian inference. We have tried to answer the following questions based on this expanded dataset. (1) Is the Tephritoidea monophyletic? (2) Are the families Tanypezidae and Conopidae closely related to the Tephritoidea? (3) What is the phylogenetic position of the family Ctenostylidae? (4) Does *Tachinisca* belong to Tephritidae or Pyrgotidae? (5) What's the phylogenetic position of the genus *Eurygnathomyia*? Does it deserve its own family status? (6) Are the important conclusions from the previous study still hold when substantial number of species added?

Key Words: Diptera, Tephritoidea, 16S rRNA, 12S rRNA, COII

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Evolution of *cis*-regulatory Sequences in acalyptrate Cyclorrhapha: sequencing and analysis of 300 developmental loci in *Sepsidae*, *Tephritidae* and *Diopsidae*.

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Although it is widely believed that changes in developmental gene expression play a role in the evolution of organismal form and function, the molecular basis is poorly understood. Developmental gene expression is precisely regulated by networks of regulatory proteins that interact with *cis*-DNA sequences associated with every gene. We are studying how these *cis*-regulatory sequences change over different evolutionary time scales, how these changes affect regulatory output, and how regulatory changes contribute to morphological and developmental diversification. Evolutionary analyses in *Drosophila* suggest that developmental enhancers are highly plastic, and that functional constraints on enhancer sequences manifest in the composition and architecture of transcription factor binding sites rather than in the linear sequence of the region. However, there is insufficient sequence and functional divergence among the sequenced *Drosophila* species to fully characterize the dynamics of enhancer evolution, while extensive functional divergence between drosophilids and mosquitoes (the closest outgroup with sequenced genomes) makes comparisons of these taxa difficult to interpret. To overcome these limitations, we have sequenced (in collaboration with the Joint Genome Institute) fosmids containing 18 developmentally important loci in 16

species of tephritids (5 species), sepsids (5) and diopsids (6). The families were chosen to provide more optimal evolutionary comparisons with drosophilids, and individual species were chosen to facilitate the identification of functional sequences by intrafamily comparison. We are identifying potential regulatory regions in these targeted loci based on the content and evolutionary properties of their DNA sequence and testing their function in transgenic *D. melanogaster* embryos. In parallel we are characterizing the endogenous gene expression patterns in select species by RNA *in situ* hybridization and antibody staining. By studying enhancer evolution in increasingly divergent species we are developing a better understanding of the natural variation in functional enhancers and how changes in these enhancers lead to the morphological and developmental diversity in Diptera.

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Amplification of DNA from preserved specimens shows blowflies were preadapted for the rapid evolution of insecticide resistance

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Mutations of esterase E3 confer two forms of organophosphate resistance on contemporary
Australasian *Lucilia cuprina*. One form, called diazinon resistance, is slightly more effective against commonly used insecticides and is now more prevalent than the other form, called malathion resistance. We report here that the single amino acid replacement associated with diazinon resistance and two replacements associated with malathion resistance also occur in E3 in the sibling species *Lucilia sericata*, suggesting convergent evolution around a finite set of resistance options. We also find parallels between the species in the geographic distributions of the polymorphisms: in both cases the diazinon resistance change is absent or rare outside Australasia where insecticide pressure is lower, whereas the changes associated with malathion resistance are widespread. Furthermore PCR analysis of pinned specimens of Australasian *L. cuprina* collected before the release of organophosphate insecticides reveals no cases of the diazinon resistance change but several cases of those associated with malathion resistance. Thus the early outbreak of resistance in this species can be explained by the pre-existence of mutant alleles encoding malathion resistance. The pinned specimen analysis also shows much higher genetic diversity at the locus prior to organophosphate use, suggesting that the subsequent sweep of diazinon resistance in Australasia has compromised the scope for the locus to respond further to the ongoing challenge of the insecticides.

Key Words: *Lucilia*, resistance, evolution, mutation

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Influence of multi-species host distribution on abundance and blood-feeding of JE-vectors in a northern Vietnam village.

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Japanese encephalitis (JE) vectors, *Culex vishnui* group and *C. gelidus* have reported to be zoophilic and feed on human opportunistically. Zooprophylaxis is an idea that the diversion of vectors from humans to animals may reduce transmission. More field data has been required to prove its efficiency. We investigated the influence of multiple species animal host availability on the abundance and blood feeding of JE vectors. The field survey was carried out at a paddy farming village, JE endemic area, in the suburb of Hanoi, on June 2003. Adult mosquitoes were collected from neighboring 50 house compounds using insecticide indoor spray catch as well as light trap catch at animal shed during two weeks. Engorged mosquitoes were sorted their host into human, bovine, swine, chicken, and another, using sandwich-ELISA. The host abundances were recorded by direct interview at 79 houses including the mosquito collected 50 houses. Redundancy analysis was applied to study the relationships between host availability and mosquito abundance and their blood feeding. Our results indicated that the existence of bovine close to human increase the human risk of getting JE vector bites.

Key Words: Japanese encephalitis, *Culex tritaeniorhynchus*, *Culex vishunui*, blood feeding, zooprophylaxis.

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The basal radiation of stiletto flies: Evidence throughout time and space

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Chronology of the early radiations of stiletto flies (Therevidae) remains poorly understood. Of the five subfamily level groups of Therevidae the Xestomyzinae and Phycinae had been previously proposed to represent the basal groups, but the data supporting a monophyletic Xestomyzinae and Phycinae as proposed previously in the published literature are ambiguous. The distribution of extant Xestomyzinae in southern Africa, South America and in the southern North America agrees with a typical Gondwana pattern. The discovery of Xestomyzinae in Madagascar raises the question of whether vicariance or dispersal lead to the occurrence on this island. To resolve these questions and to test the monophyly of Xestomyzinae and Phycinae, data from two genes (EF1alpha and 28S), morphology of adults and immatures were analyzed in addition to evidence from the fossil record. The results support a new classification of the basal clades of Therevidae and rejects vicariance as the most likely explanation for the distribution.

Key Words: Biogeography, stiletto flies, Therevidae, fossil record.

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Taxonomy and distribution of *Poecilosomella borboroides* species group (Diptera, Sphaeroceridae)

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Poecilosomella borboroides was described (as *Ephydra borboroides*) based on female specimens from Celebes (Sulawesi), Indonesia (type locality: Makassar = Ujungpandang) in 1860. Thereafter, closely related species, *P. ornata* (as *Limosina ornata*) and *P. picturata* (as *Limosina picturatus*) were described from Indonesia in 1908 and Philippines in 1913 respectively, but some authors treated these species as synonyms of *P. borboroides* for a long time. Papp (2002) reviewed the Oriental species of the genus *Poecilosomella*, and treated *P. ornata* and *P. picturata* as distinct species. Furthermore, he described 2 more related species, *P. borborus* from Philippines and *P. formosana* from Taiwan. This species group is rather complicated, and it is necessary to revise the former records to make clear the distribution of each species. I studied the specimens of this group from the Oriental and Australasian Regions. I recognized these 5 species and one new species. *Poecilosomella borborus* is recorded from the Australasian Region for the first time in this species group. Male of *Poecilosomella borboroides* was discovered for the first time from Sulawesi Is. which is the type locality of this species, and redescribed. *Poecilosomella borboroides* of Papp (2002) was conspecific to *P. borborus*. The specimen records I examined are as follows:
Poecilosomella borboroides: Indonesia (Sulawesi).
Poecilosomella borborus: Bangladesh(new record), Indonesia (Java and Bali)(new record), Malaysia (Malaya and Borneo) (new record), Papua New Guinea (new record), Philippines, Singapore (new record), Taiwan (new record) and Thailand (new record).
Poecilosomella formosana: Bangladesh (new record), Indonesia (Java)(new record), Japan (Ryukyu Isls)(new record), Laos (new record), Malaysia (Malaya and Borneo)(new record), Nepal (new record),

Philippines (new record), Taiwan, Thailand (new record) and Vietnam (new record).
Poecilosomella ornata: Laos (new record), Singapore (new record), Sri Lanka and Taiwan.
Poecilosomella picturata: Malaysia (Malaya and Borneo) (new record).
Poecilosomella sp. nov.: Indonesia (Seram).

Key Words: *Poecilosomella borboroides* group, Sphaeroceridae, new records, redescription, a new species

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Larvicidal activity of Japanese *Bacillus thuringiensis* isolates against the biting midge, *Culicoides oxystoma* (Diptera: Ceratopogonidae)

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In Japan, the biting midge *Culicoides oxystoma* is a major vector of bovine arboviruses including Akabane virus, Aino virus, and Ibaraki virus. This study was an attempt to screen environmentally safe microbial agents effective for control of the biting midge. A total of 3,314 Japanese isolates of *Bacillus thuringiensis*, belonging to at least 60 H serogroups, were examined for larvicidal activity against *C. oxystoma*. Of these, seven isolates exhibited >80% mortality in 72 h, while the majority (99.7%) showed no larvicidal activity. One of the seven toxic isolates belonged to H5ac (serover *canadensis*) and the others H5ab/21 (serovar *galleriae/colmeri*). Isolates of H14 (serovar *israelensis*), as well as the mosquitocidal reference strain of H14, gave no mortality against *C. oxystoma*. Parasporal inclusions of the toxic isolates had a common morphological feature, spherical in shape, when observed under a phase-contrast microscope and SEM. TEM revealed that these inclusions were surrounded by electron-dense envelopes. When examined with SDS-PAGE, a common protein profile was observed among the inclusions of the H5ab/21 isolates. Protein profiles of the seven toxic isolates were markedly different from that of the mosquitocidal reference strain of serovar *israelensis*.

Key Words: *Bacillus thuringiensis*, biting midge, *Culicoides oxystoma*, bovine arbovirus

Cladistic approach to Cecidomyiidae (Diptera) phylogeny, with a revised subfamily classification

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A cladistic analysis of Cecidomyiidae was performed, with representative genera from all usually recognized tribes or subfamilies as the ingroup, and with *Rangomarama* (Rangomaramidae or Sciaridae: Rangomaraminae) as the outgroup. The resulting cladogram has the following successive main clades (the rest of the ingroup always being the sister group of the former clade), suggesting a subfamily rank for the following taxa: Catotrichinae, Lestremiinae, Catochinae, Heteropezinae, Strobliellinae, Micromyinae, and Cecidomyiinae + Porricondylinae. The placement of Heteropezinae varies from that above to the sister group of Cecidomyiinae + Porricondylinae. There is a monophyletic Porricondylinae including Porricondylini, Asynaptini, Diallactini and Winnerzini, but the status of Leptosynini, which usually is placed in Porricondylinae, remains uncertain. Thaumacecidomyiinae is a synonym of Diallactini.

Key Words: Cecidomyiidae, phylogeny, subfamilies

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Distribution pattern of crane flies (Diptera: Tipulidae) in the upper and middle reaches of the Shinano River in Central Japan

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This is the first report on crane flies communities captured in summer, 2002 by light traps at the upper and middle reaches of the Shinano, Japan's longest river. A total of 1,096 adults (male 871, female 225) were collected. We identified a total of 13 genera and 23 species belonging to two subfamilies, i.e., 17 species of Limoniinae (98.3%) and 6 species each of Tipulinae (1.70 %). The most abundant genera was *Tipula* (4 species), followed by *Antocha* and *Dicronomyia* (3 species). The dominant species was *Antocha* (*Antocha*) *bifida* (83.3%), followed by *Symplecta* (*Psiloconopa*) *laudatrix* (9.9%). These two species accounted for 93.2% of the overall individual numbers. Focusing on the abundance of crane flies species along the river flow from Stations 1 toward Station 4, changes in the fauna of crane flies and the number of individuals collected were found to increase, whereas the number of species and the index of diversity decreased. In the relative frequency of the functional feeding group, the percentage of shredders decreased, while that of collectors increased.

Key Words: crane fly, distribution pattern, *Antocha (Antocha) bifida*, Shinano River, species diversity index (H'), upper and middle reach

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Egg placement of the tachinid fly *Sturmia bella* on leaves of the evergreen milkvine *Marsdenia tomentosa* and the feeding habit of its host butterfly *Parantica sita*

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We investigated the egg placement of the microtype tachinid fly *Sturmia bella* on leaves of the evergreen milkvine *Marsdenia tomentosa*, one of the foodplants of the host butterfly *Parantica sita,* in the southern Kinki district of Japan. Most *S. bella* eggs were found on the undersurface of young *M. tomentosa* leaves around leaf tips or along leaf margins. Choice of oviposition sites was independent of leaf size and existence of leaf damage made by the host larvae. *P. sita* changed its feeding patterns with larval development and left three types of characteristic feeding marks on *M. tomentosa* leaves. Since fourth and fifth instar larval *P. sita* ate the marginal areas, apical areas and sometimes even entire leaves, most *S. bella* eggs are considered to be ingested during these stages. Both female adults and larvae of *P. sita* showed no age preference for the *M. tomentosa* leaves. The relationship between the feeding habit of *P. sita* and the egg placement of *S. bella* on *M. tomentosa* is discussed.

Key Words: *Sturmia bella, Parantica sita, Marsdenia tomentosa*, host-parasite relationship

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Role of insects in practical forensic medicine

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Entomological information can sometimes help to determine the minimum time that has elapsed since death when medical parameters are no longer relevant. Flies are the first insects to colonize decomposing cadavers. Therefore, collecting adult insects and larvae can identify fly species and instar stage, respectively, and thus provide useful entomological evidence. We present some actual cases in which forensic entomology has contributed to estimating postmortem duration.

1) Burned cadaver

Postmortem interval cannot be determined from the superficial appearance or from decompositional changes in the organs of severely burned cadavers. We collected third instar larvae of the flesh fly, *Parasarcophaga similis,* from a severely charred cadaver discovered in a coppice. Entomological evidence confirmed that the postmortem interval was about 4 days.

2) Cadaver near water

Although flies and other terrestrial insects cannot access submersed cadavers, they can be attracted to them when they float to the surface. Third instar larvae of the flesh flies, *Parasarcophaga similis* and *Boettcherisca peregrina,* and dermapteran larva, *Euborellia* sp. were collected from a severely decomposed cadaver discovered beside a river. The entomological evidence indicated that the body had been out of the water for about 7 days.

3) Cadaver inside a car

Automobiles are frequent disposal sites of cadavers. Third instar larvae of the flesh fly, *Boettcherisca peregrina* were collected from a body found in the closed trunk of a car. Since the flies were trapped in the trunk, the entomologic evidence confirmed that the woman had died 14 days before discovery.

Key Words: forensic entomology, postmortem interval, cadaver, fly larvae

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Life history parameters of the parasitoid fly *Zenillia dolosa* (Diptera: Tachinidae)

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Life history parameters of the tachinid fly, *Zenillia dolosa*, that lays microtype eggs on host plants of some lepidopteran larvae was studied in the laboratory at 25˚C, 60-70% RH and 16L: 8D photoperiod on the host *Mythimna separata*. Newly emerged and mated females started laying eggs on host food plants approximately 6 days after emergence. The duration of mating averaged 90 min. Females of *Z. dolosa* showed a daily oviposition rate of 70 eggs and oviposited 900-2600 eggs in total during their mean longevity of 25 days, which was not significantly different from longevities of unmated females and males. We also discuss about effects of the number of eggs eaten by a host on developing time, body size of the parasitoid and percentage parasitism.

Key Words: parasitoid, *Zenillia dolosa*, biology, clutch size, Tachinidae

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The use of air curtains to prevent entry of flies and mosquitoes on commercial aircraft

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Dispersal of insects, particularly species that transmit zoonotic diseases, by commercial aircraft is a concern of many nations world wide. Another concern, particularly by flight crews and passengers, are the current pesticide-based methods mandated for treatment of aircraft prior to landing in countries anxious to prevent entry of vector species. The USDA, supported partially by a grant from the Federal Department of Transportation, investigated the potential use of air curtains as an alternative method for management of insects that might enter and disperse via commercial air craft. The method involves preventing insect entry during servicing and boarding of aircraft and prevention of insect exit from aircraft after landing. Tests were performed in rooms especially designed to simulate boarding bridges attached to an aircraft cabins. Air curtains, used commercially to prevent insect entry over doorways, were mounted vertically on either side of the door between the simulated boarding bridge and aircraft so that air blew into the boarding bridge and air streams from each unit intersected at a 90° angle just inside the center of the doorway of the boarding bridge. To perform a test, 50 mosquitoes of 3 different species (150 total) and 50 house flies, *Musca domestica*, were released in the simulated boarding bridge when air curtains were in operation. Next, staff members made 25 passes through the boarding bridge, through the air stream of the air curtains and into the aircraft to simulate passenger boarding. After the 25th 'passenger' entered the aircraft, the door separating the two rooms was closed and any insects that passed into the aircraft were counted and identified. The system excluded 95-99% of the mosquitoes and 95-100% of the house flies.

Key Words: *Musca domestica*, *Aedes aegypti*, *Anopheles quadrimaculatus*, *Ochlerotatus taeniorhynchus*, air curtains

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Ecological Modelling Using Stiletto Flies (Diptera: Therevidae)

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The ability to examine primary data for underlying patterns is crucial for documenting and investigating asiloid biodiversity, and many asiloid species have been designated rare or threatened. Ecological characterizations for species of Asiloidea, however, are notably limited to qualitative local and regional assessments. A shift to quantitative approaches in developing these assessments is becoming increasingly important as taxonomic and phylogenetic resolution improves and the need for robust characterizations becomes more critical. Extending acquisition protocols for physical collections of Asiloidea to complementary repositories of specimen-level data provides resources relevant to these assessments, exemplified by collaborative research on stiletto flies. Expansive geospatial datasets that are available for download from Mandala, the biosystematic database developed for Therevidae, are being used to develop the first ecological models for therevid species in a context suitable for robust comparative studies. Results from these comparative studies have provided tests for ecological hypotheses, which include hypotheses based on patterns described for well-studied organisms. These models extend the study of stiletto fly biodiversity to geographic scales encompassing entire species distributions, providing an important perspective in evaluating results from local ecological studies. Ecological modelling using specimen-level data is a promising approach towards

improving our understanding of stiletto fly ecology and providing baseline assessments for uncharacterized taxa. Considering the wide ecological range, extensive geographic distribution, moderate to high level of taxonomic resolution, and documented habitat fidelity among species, Asiloidea is considered a prime dipteran group for further ecological modelling.

Key Words: ecological modelling, Therevidae

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The role of tachinid fly complex in the population dynamics of the mulberry tiger moth (*Lemyra imparilis* (Butler)) in western Japan

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The mulberry tiger moth, *Lemyra* (=*Thanatarctia*, *Spilarctia* or *Spilosoma*) *imparilis* (Butler), is a univoltine arctiid moth, of which is distributed throughout Japan. Population density of the moth increases and decreases in southwestern Japan. The larvae in spring are often a serious insect pest of various crops such as citrus, pears and vegetables, when the density is high. To evaluate the effect of parasitoids and pathogens on *L. imparilis* larvae, sprig larvae of *L. imparilis* were collected every year from three sites in the Kinki region, western Japan during the periods of 1990-1994 and 2003-2005. Mortality of spring larvae caused by parasitoids and pathogens decreased with increasing density and increased at decreasing phase. Mortality by parasitic wasps (two species) decreased with increasing density and increased with decreasing density. Mortality by pathogens (one virus, one fungi and one bacteria) was low value except at the peak density. In contrast, mortality by tachinid flies was constant (15-20%) with the host density. Five species of tachinid flies, *Carcelia rasa*, *Carcelia* sp., *Thelaira nigripes*, *Pales angustifrons* and *Compsilura concinnata* were found. *Carcelia* was the most abundant species (50% of all flies emerged), followed by *T. nigripes* (35%), *P. angustifrons* (8%) and *C. concinnata* (7%). From spring larvae of *L. imparilis*, firstly *C. concinnata* emerged from the 7th instar larvae, followed by *Carcelia* (from the 8th instar larvae), *T. nigripes* (from the 8th and 9th instar larvae) and *P. angustifrons* (from the pre-pupae). It is suggested that tachinid fly complex is a major and constant mortality factor in spring larvae of *L. imparilis* in the Kinki region, Japan.

Key Words: *Carcelia rasa*, *Thelaira nigripes*, *Pales angustifrons*, *Compsilura concinnata*, parasitoids

Dengue fever and insecticides resistance in *Aedes aegypti* in Taiwan

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Taiwan has been island-wide epidemics of dengue fever, 80% of population was infected during 1942-1945. There was no case reported until 1980 resulted from the anti-malaria campaign by the massive DDT & γ -HCH sprays. In 1982 there was an outbreak of dengue fever in Liuchiu village 80% of inhabitants were infected. There was no case reported (may not be recognized in clinics) in 1982-1985. The dengue fever stated epidemics since 1986. The strengthen control programs were put on by Health Department and Environmental Protection Administration. Dengue fever was control under acceptable situations since then. The insecticides have been routinely applied for *Aedes aegypti* control by pest control operators when dengue fever cases occurred in the Tainan and Kaohsiung areas of Taiwan. But it was failed to control in 2002 the insecticide resistance and control strategy were re-examined. The poor efficiency of the insecticides application and under estimated the mosquito population density result the control failure in 2002. The resistance ratios of adult mosquito of the Chianjen, Lingya (2002), and Lingya (1900R) strains for permethrin compared to susceptible strains were above 312.5X, while those of the 4th instar larvae were 20.8, 30.5 and 102.1, respectively. Results of synergism study on larvae resistance to permethrin showed correlations to the activities of microsomal monooxygenases and esterases. The effect alternative insecticides should be prepared for the mosquito emergence control.

Key Words: dengue fever, *Aedes aegypti,* insecticide resistance, esterases, microsomal monooxygenases

Chlorophyll biosynthetic and degradative pathway in the leaf-derived galls

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The aim of this research was to test a hypothesis that the galls derived from infected leaf alter the biosynthetic and degradative pathway of chlorophyll (Chl). The contents of chlorophyll (Chl), biosynthetic intermediates such as protoporphyrin IX (PPIX), magnesium protoporphyrin IX (MGPP) and protochlorophyllide (Pchlide), breakdown intermediates including chlorophyllide (Chlide), pheophytin (Phe), pheophorbide (Pho), carotenoid (Car), anthocyanin, flavonoid and tannin in the four different galls and their host leaves were determined. Three of the galls were formed by cecidomyiids, which are two *Dephnephila* spp. from *Machilus thunbergii* (Lauraceae) and *Pitydiplosis* sp. from *Pueraria montana* (Leguminosae), and one was formed by psyllid, *Sympauropsylla triozoptera*, from *Ficus amplelas* (Moraceae). For UV-related pigments, anthocyanin and tannin are extremely higher in galls than in infected leaves, but flavonoid is reversed. For photosynthetic pigments, both Chl and Car are much lower in galls than in host leaves, and the galls obviously have decreased Chl a/b ratio but increased Car/Chl ratio. The total content of PPIX, MGPP and Pchlide in galls is about 10% of that in host leaves, and their mole percentages are 64.4%, 30.3% and 5.4%, respectively, changing from 47.6%, 33,8% and 18.7%, respectively, in host leaves. The data indicated that non-lethal leakage happens in the Chl biosynthsis of galls and that Mg-chelatase is one of the partial blockage site. The contents of Phe, Pho, phytylated and dephytylated compounds in galls are only 7.4%, 26.6%, 7.0% and 0.4%, respectively, of host leaves. The above data apparently suggested that Chl→Chlide→Pho is the major rout and Chl→Phe→Pho is

the minor route of Chl degradation in galls, in contrast to that of their host leaves.

Key Words: biosynthetic and degradative pathway, chlorophyll, major route, minor route

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Photosynthetic reflectance properties of three cecidomyiid galls of *Machilus thunbergii* and *Litsea acuminata* leaves

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The aim of this study was to test two hypotheses that leaf-derived cecidomyiid galls of *Machilus thunbergii* and *Litsea acuminata* leaves have different surface reflectance characteristics from their host leaves, and that the spectral properties of galls are directly related to photosynthetic processes and pigment composition, as well as their host leaves. By using the reflectance spectrum from 200-900nm, the reflectance between 280-320nm ($R_{280\text{-}320}$), photosynthetic reflectance index (PRI), red/green ratio (R/G), adjusted normalized difference vegetation index (aNDVI) and cold hard band (CHB), were calculated to investigate the cecidomyiid gall pigment such as chlorophyll, carotenoid and anthocyanin and photosynthetic properties indicated by Fv/Fm. The $R_{280\text{-}320}$ suggested that all galls may reflect more UV radiation than the host leaf to avoid UV damage. The PRI and R/G data indicated that xanthophyll cycle pigments and anthocyanin content are higher in galls than in host leaf. In contrast, the aNDVI and CHB values suggested that chlorophyll content and pigment-protein complexes are much lower in galls than in host leaf. The Fv/Fm ratio also indicated photosystem II is much less efficient in galls than in host leaf. Either PRI or CHB is positively correlated to Fv/Fm. The above reflectance analysis of three cecidomyiid galls strongly suggested that the photosynthetic efficiency of galls is much less than that of host leaves which is consistent with the results of our earlier analyses showing a deficiency in structures of chlorophyll and pigment protein complexes. As a result, the spectral reflectance revealed the possibility to be utilized as a tool for studying the ecophysiology of galls.

Key Words: aNDVI, cecidomyiid gall, CHB, Fv/Fm, photosystem efficiency, photosynthetic reflectance properties, PRI, R/G

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Muscid flies associated with grazing cattle and water buffallos in Taiwan

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In spite of the animal husbandry is well developed in Taiwan, the knowledge on the flies injurious to the grazing cattle and water buffalos is still incomplete. Hence an investigation on muscid flies associated with grazing cattle and water buffalos have been carried out at the 9 localities in Taiwan by the use of NZI traps and hand netting methods from 2002.

From the results of this investigation, 10 non-biting species belonging to 2 genera, and 6 biting species belonging to 3 genera were recorded. In addition, 5 dung breeding species of 2 genera, and 2 genera and 2 species their bionomics are unknown, are also recorded.

The predominant non-biting species are *Musca conducens*, *M. domestica* and *M. seniorwhitei*. Those of biting species are *Stomoxys calcitrans* and *Haematobia irritans exigua*.

The species composition varied according to the surveyed locations. The most multiple population was obtained at the pasture of Hengchun, the southern part of Taiwan, where 7 genera and 18 species were captured.

Key Words: Taiwan, Muscidae, cattle, water buffalo

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Light effect on the photosynthetic reflectance properties of an oval-pointed cecidomyiid gall of *Machilus thunbergii* leaves

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An oval-pointed cecidomyiid gall (*Dephnephila* sp.) residing on the lower epidermis of *Machilus thunbergii* leaf has red side exposing to light and green side unexposing to light, i.e. while the latter attaches to the host leaf, the former not. Therefore, the aim of this study was to test the hypotheses that the surface reflectance characteristics of red and green side are different in the same gall, and that the spectral properties of both sides of the same gall are directly related to photosynthetic processes and pigment composition. The galls were divided into four stages on the basis of size to stand for its various development stages. By using the reflectance spectrum ranging from 400-900nm, seven indices such as photosynthetic reflectance index (PRI), red/green ratio (R/G), normalized difference vegetation index (NDVI), adjusted NDVI (aNDVI), cold hard band (CHB), the structure independent pigment index (SIPI) and normalized pigment chlorophyll ratio index (NPCI), were applied to investigate the surface reflectance characteristics of galls. While the PRI, NDVI, aNDVI and CHB of inner green side gradually increased during the gall development, the R/G, SIPI and NPCI were reversed. Meanwhile, the PRI, R/G, NDVI, aNDVI and CHB of outer red side gradually decreased, the SIPI and NPCI were inverted. It is concluded that exposure to light affect the surface reflectance properties and their corresponding photosynthetic, and nonphotosynthetic pigments of galls.

Key Words: aNDVI, cecidomyiid gall, CHB, NDVI, NPCI, oval-pointed, photosynthetic reflectance properties, PRI, R/G, SIPI

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A Close Correlation among Histone Acetylation, *hsp70* Gene Expression and Longevity in *Drosophila melanogaster*

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The heat shock proteins (Hsps) play a positive role in lifespan determination, and histone acetylation has been shown to be involved in transcription of *hsp* genes in *Drosophila*. To further determine if *hsp70* expression is correlated with lifespan, and if histone acetylation participates in this process, RNA levels for *hsp70* were analyzed throughout the lifespan in the long-lived and short-lived iso-female lines. The results showed that *hsp70* RNA levels were higher in long-lived line than in short-lived line and that the longlived flies responded more rapidly to heat but were more tolerant to high temperature. Moreover, we investigated the influences of histone acetylation modification on longevity and on *hsp* gene expression by using histone deacetylase (HDAC) inhibitors. The results demonstrated that both inhibitors were able to extend the lifespan and promote *hsp70* expression. However,The mechanisms of their actions may vary with the genetic background. In addition, we showed that HDAC inhibitors caused the hyperacetylation of core histone H3 at the promoter and the transcribing regions of *hsp70* gene.

Key Words: *hsp70*, lifespan, histone acetylation, histone, deacetylase inhibitor, *Drosophila melanogaster*

Larval behaviour of the tachinid fly, *Compsilura concinnata*, within the host midgut

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How and where they live within the body of their host is very important for endoparasitic insects. Immature parasitoids must defend themselves from host immune systems, obtain nutrition, and respire. The larva of *Compsilura concinnata* (Meigen) (Diptera: Tachinidae) stays in the midgut of the host during the larval stage and achieves respiration by utilizing the tracheae of the host. In this study, heretofore never attempted, we directly observed the behaviour of *C. concinnata* larva from the penetration into the midgut through to the achievement of respiration. The last instar larva of a noctuid, *Mythimna separata* Walker (Lepidoptera: Noctuidae), was dissected alive and exposed the midgut. *C. concinnata* larva was then applied to the exposed midgut of *M. separata*. The larva of this tachinid made an opening on the wall of the midgut using the anterior portion of head skeleton and then entered into the cavity between the peritrophic membrane and the midgut wall of the host. The crawling larva searched for the host trachea and then pulled it by using its anterior portion of head skeleton. On the pulled point, the fly larva turned its body around and attached the posterior abdominal spiracle to the drawn trachea. The midgut lumen appeared to be an ideal place for *C. concinnata* larva to escape from the host immune response and to evade aggressive competitors.

Key Words: Tachinidae, larval behaviour, *Compsilura concinnata*, midgut, parasitoid

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Species microdistribution of larval Chironomidae (Diptera) on riverbed cobbles at riffles: a quantification using artificial substrates

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Species composition and density of chironomid larvae attached to standardized artificial substrates placed on riffles were investigated in Japanese temperate low-order streams. The surfaces of the substrates, quartets of holed cubic blocks of concrete (L19×W19×H19cm), were classified into three types, i.e. ‘exposure’, ‘hollow’ and ‘interstices’, so that they might reflect different conditions in relation to the water flow. The substrates were set in August 2003 then chironomid collection was replicated twice, in October and December 2003, in each stream. At streams with riparian canopy coverage where leaf litter was provided to benthic macroinvertebrates as a food, larval density of Chironomidae on ‘interstices’ reached 234.0 indiv.m^{-2} in average, about eight and ten times as high as those on ‘hollow’ and ‘exposure’, respectively. As to species richness, 12.3 species were attached on ‘interstices’ in average, about four and five times as many as those on ‘hollow’ and ‘exposure’, respectively. Partial ReDundancy Analysis (RDA) where the environmental variables other than the surface type, e.g. water temperature, depth, surface current velocity and specific conductance of streams, were used as covariables revealed that distribution of 9 species, i.e. *Corynoneura celtica*, *Neobrillia longistyla*, *Polypedilum akisplendens*, *Polypedilum tamanigrum*, *Cladotanytarsus vanderwulpi* and four *Rheotanytarsus* species, were significantly associated with ‘interstices’, while no species showed significant association both with ‘hollow’ and ‘exposure’. On the other hand, at streams without riparian canopy, no significant difference was found both in species richness and density among the three surface types. In addition, both species richness and density at streams without riparian canopy were much lower than those at streams with riparian canopy. These results indicate that interstices in riverbed are the major microhabitat of larval Chironomidae at riffles. Leaf litter caught in interstices would allow most species to colonize at relatively higher density than on exposed surfaces.

Key Words: Chironomidae, riffles, microhabitat, artificial substrate, interstices

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Making of artificial diets for an aphidophagous hoverfly, *Eupeodes frequens* (Diptera: Syrphidae)

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The larvae of an aphidophagous hoverfly, *Eupeodes frequens* are effective predators and potential biological control agents of aphids. However, rearing the aphidophagous hoverfly is much labor- and time-consuming because of cultivation of 3 organisms is necessary; host plants, prey aphids, and the flies. The development of artificial diets would be indispensable for a labor-saving technique but there have been few reports of successful artificial diets for them. We invented an agar-gelled diet containing lyophilized and pulverized drone honeybee brood (drone powder, DP) which offered the minimum nutrition necessary for *E. frequens* larval development, but the larval period and adult body size on the diet was significantly inferior to the insects on aphid. In this report we examined the effect of three fatty acids (myristic, linoleic, and oleic acids) on the larval development and adult body size in order to obtain normal size adults. The addition of each one of fatty acids to DP improved the adult emergence ratio and significantly shortened developmental period of the third instar larvae. The combination of linoleic acid and oleic acid was the most effective for adult body size. We challenged to make better artificial diet for the syrphid. Physical property and amount of fatty acids and sugar added was changed during early stage to the 3rd instar larval period. More than 80% of larvae reach to the adults and their body size was equal to ones feeding on aphids. Thus, we succeeded to rear *E. frequens* larvae on the artificial diets and this would be a step to develop mass rearing of syrphids.

Key Words: *Eupeodes frequens*, Syrphidae, artificial diet, biological control agent

Genetic survey of *Haematobia irritans irritans* and *H. irritans exigua*, and phylogeny of Japanese Stomoxyini flies (Diptera, Muscidae)

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The horn fly, *Haematobia irritans* (Linnaeus) which is an obligate blood-sucking fly of cattle is divided into 2 subspecies: *H. irritans irritans* (Linnaeus) in the northern hemisphere and *H. irritans exigua* de Meijere (buffalo fly) in tropical and subtropical areas. In these 2 subspecies, genetic difference in relation to distribution were investigated by analysis of mitochondrial DNA (mtDNA) of the populations obtained from 4 localities (Japan:Obihiro and Morioka; Taiwan, Vietnam). Furthermore, phylogenetic relationship of the Japanese 4 Stomoxyini species, *Stomoxys calcitrans* (Linnaeus*)*, *S. indicus* Picard*, S. uruma* Shinonaga et Kano and *Haematobosca sanguinolenta* (Austen) was also examined by analysis of mtDNA. For the phylogenetic analysis, 3 species of the genus *Musca*, *M. domestica* Linnaeus, *M. crassirostoris* Stein , *M. bezzii* Patton et Cragg were used as an outgroup.

In *Haematobia irritans*, the populations obtained from Obihiro and Morioka and the populations from Taiwan and Vietnam were almost identical at genetic level, respectively. However, there was genetic difference between populations of Obihiro-Morioka (*irritans irritans*) and the populations of Taiwan-Vietnam (*irritans exigua*). This result agreed with classification and distributional phenomena based on morphology. However, genetic distance between *irritans irritans* (Obihiro-Morioka) and *irritans exigua* (Taiwan-Vietnam) was shorter than those of between independent species in other Stomoxyini flies. There were some genetic variations in the population of *H. irritans exigua* from Vietnam compared with those from Obihiro and Morioka.

In the species level of other Stomoxyini flies, *Haematobosca sanguinolenta* closed to *Haematobia* cluster than *Stomoxys*. Within *Stomoxys* cluster, *S. calcitrans* and *S. uruma* were rather closely related each other: *S. indicus* was distantly related with these 2 species.

Key Words: mitochondorial DNA, *Haematobia irritans*, Stomoxyini, phylogeny, Japan

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Host Habitat and Host Location Behavior in the tachinid Fly, *Exorista japonica*

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We demonstrated by a wind tunnel bioassay that the tachinid fly, *Exorista japonica*, is attracted to corn plants damaged by the noctuid larva, *Mythimna separata*. Mated female flies oriented to damaged corn plants, but did not respond to undamaged corn plants. This orientation occurred to the damaged plant itself, but not the host larva or larval frass. In order to test the effect of plant color, blue, green, yellow and red paper models were placed in front of damaged corn plants hidden with a mesh screen. The landing rate of flies was highest on green and lowest on red paper models. In addition, flies did not respond to the green model without a damaged plant or in the presence of a healthy plant. The behavior of flies to chemicals in the host frass were tested by placing a filter-paper patch treated with the frass in a plastic cage. Flies stayed longer in a patch treated with host frass or host frass extracts than in untreated patches and this response was dose-dependent. Responses were strongest to the methanol extract among several solvents. These experiments indicate that *E. japonica* females find the host habitat not only by long-range olfactory cues (damaged plant odor) but also visual cues (plant color), and once in a host habitat they tended to stay longer in a patch with close-range olfactory cues (host frass). Finally, flies use visual cues to attack the host larvae.

Key Words: *Exorista japonica,* Tachinidae, host location, host habitat location, wind tunnel

Effect of Neem Seed Kernal Extract and Neem based biopesticide, Nimbecidine for the control of Aedes aegypti

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Neem Seed Kernel Extract (NSKE) and Nimbecidine has been tested against larval and pupal of *Aedes aegypti* . NSKE and Nimbicidine has greatly affected during life stages of Mosquito. Higher mortality of *A. aegypti* was evident at higher concentrations NSKE and Nimbicidine. Lethal concentration has been worked for each stages of *A.aegypti*. Increased mortality was noted by the treatment of Nimbicidine than the NSKE and this may be due to the specific formulation and concentration of active compounds in Nimbecidine. After the treatment of NSKE and Nimbicidine on the larval and pupal showed significant mortality, and it may be due to the ovicidal action of neem on Mosquito eggs. Reduction in the developmental duration and treated Mosquito also showed deformities suggested that the Neem action on hormonal interference in molting process of Mosquito. This paper discusses on the use of Neem based Biopesticide for the control of Public he! alth insect pest.

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Acoustic signals in taxonomy of Agromyzidae and Chloropidae

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Past bioacoustic studies on the mating behavior of Acalyptrate flies were only restricted to a few genera of Tephritidae, Drosophilidae, and Chloropidae. Males of preceding two families produce intermittent sounds by controlling free wing fanning. Males of chloropid genera, *Lipara, Calamoncosis*, *Kurumemyia*, *Pseudeurina* of Oscinellinae, and *Chryptonevra* and *Terusa* of Chloropinae, produce substrate-borne vibratory sounds, which have said to be exclusively known in Diptera. Recently, I first recognized male acoustic signals in several genera of Agromyzidae, *Agromyza*, *Cerodontha*, *Chromatomyia*, *Liriomyza, Melanagromyza*, and *Nemorimyza*. Their mating sounds are also substrate-borne vibration except for those of *Chromatomyia horticola* by wing fanning. In this paper, I additionally recorded mating sounds in chloropid genera: *Togechiphus* and *Elachiptereicus*. For Agromyzidae, I proposed enough data for separating *Liriomyza*-species, *chinensis, bryoniae, sativae,* and *trifolii* based on acoustic properties. These sounds are species-specific courtship signals for female receptiveness. It seems probable that most of plant-dwelling Acalyptrates make substrate-borne vibrations for courtship signals or sexual interaction. The mid-coxal protuberance associated with contact between coxa and trochanter appears to be a mechanoreceptor to detect substrate-borne vibration.

Key Words: mating behavior, acoustic signals, substrate-borne vibration, Diptera, Acalyptratae

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Insecticide resistance of major West Nile virus-transmitting mosquitoes in Japan

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Culex pipiens group and *Aedes albopictus* are potentially important vectors of West Nile fever in residential areas in Japan. We investigated the larval insecticide susceptibility of these mosquitoes against the invasion of the disease, using mosquitoes colonized in 2003 and 2004. The efficacy of 5 insecticides grouped into organophosphate (temephos and fenitrothion), pyrethroid (etofenprox), and IGR (diflubenzuron and pyriproxyfen) were tested. None of the resistance was detected in the 11 colonies of *Ae. a.* tested, while resistant larvae were more or less segregating for all the applied insecticides but fenitrothion in some of the 54 colonies of *Cx. p.* group tested. Among the tested compounds, etofenprox revealed the most prominent resistance in *Cx. p.* group populations in Japan. The numbers of colonies that showed more than 5% survival at 100X *LC*99 (5.7 ppm) of etofenprox for a reference susceptible strain of *Cx. p. pallens* were 19 in *Cx. p.* pallens (*N*=37) and 7 in *Cx. p. molestus* (*N*=17). Etofenprox-resistant strains of *Cx. p. pallens* and *molestus* were established from some of the laboratory colonies by larval selection. The selected strains also showed cross resistance of larvae to permethrin and phenothrin. The mechanisms of pyrethroid resistance involved increased detoxifying activities of cytochrome P450s and decreased sensitivity of the nerval target, sodium channel. Amino acid substitution mutations in sodium channel gene were unique between *Cx. p. molestus* (as Leu999Phe, the position being equivalent to 1014 in *Musca domestica* orthologue) and *Cx. p. pallens* (as Leu999Ser).

Key Words: insecticide resistance, mosquito, *Culex*, *Aedes*, sodium channel, cytochrome P450

Morphological and genetical relationships among the Japanese chironomid species of the genus *Polypedilum.*

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The phylogenetic trees of the Japanese species of the chironomid genus *Polypedilum* were constructed on the basis of 29 morphological characters of male adults and of the sequence of *CO* I region of mtDNA and compared. All the members of the subgenus *Tripodura* and a group of the subgenus *Polypedilum* each constructed a single cluster by themselves whereas those of other subgenera, *Pentapedilum*, *Uresipedilum* and other groups of *Polypedilum*, constructed such clusters that comprize multiple subgenera in the morphological tree. There were many exchanges in member of cluster between morphological and genetical trees. For example, *P.(U.) cultellatum* constructed a cluster with *P.(U.) hiroshimaense* in the morphological tree whereas it constructed a cluster with *P. (T.) decematoguttatum* in the genetic tree. On the contrary, a few pair, e.g., *P.(P.) pedestre* and *P.(P.) tamaharaki*, constructed a cluster in the genetic as well as morphological trees. These results suggest that many characters of the adult male of this genus be a product of convergence.

Key Words: adult male, chironomid, mitochondria DNA, morphology, *Polypedilum*

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FLYTREE MOLECULES: The first tier phylogeny of Diptera using multiple nuclear genes

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We report preliminary results from phylogenetic analysis of nuclear genes for the first tier taxa of the NSF Assembling the Tree of Life FLYTREE project. Relationships among the major lineages of Diptera remain either poorly resolved or hotly debated. Major questions surround the composition, monophyly, and relationships among dipteran infraorders and superfamilies. For example, exact sister groups for several major dipteran lineages, e.g., Brachycera, Calyptratae, are still undetermined. Existing molecular phylogenies of Diptera are based on relatively few molecular markers. Despite some progress resolving relationships within major superfamilies and families, most molecular datasets are still too limited in taxa, genes, or both, to answer conclusively many questions of higher-level relationships. As a major goal of the FLYTREE project, we are gathering sequence data from nuclear protein encoding genes. To provide a preliminary assessment of progress to date, we combined nucleotide sequences from fragments of 12 nuclear genes along with full-length 18S and 28S ribosomal DNA sequences, from 42 dipteran species plus three outgroups. Parsimony and Bayesian likelihood analyses of these data yields trees that are largely concordant with morphology-based relationships and with a recent supertree analysis. High parsimony bootstrap values (>70%) support the monophyly of the following dipteran clades: Brachycera, Eremoneura (Empidoidea + Cyclorrhapha), Cyclorrhapha, Schizophora, and Calyptratae. We find paraphyly for lower Diptera (="Nematocera"), lower Brachycera (="Orthorrhapha"), basal Cyclorrhapha (="Aschiza"), and Acalyptratae. Our nuclear gene data for the FLYTREE first tier demonstrates the great potential of nuclear gene sequences to add significant resolution to the dipteran Tree of Life.

Key Words: phylogeny, molecular systematics, FLYTREE, gene

The first record of adult cranefly (Diptera: Tipulidae) in Nishina Three Lakes

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Lake Aoki, Lake Nakatsuna and Lake Kizaki, form a chain of lakes, called the Nishina Three Lakes. The trophic status of each lake has been differed. Nishina Three Lakes is one of the most intensively investigated lakes in Japan. The aquatic insects fauna and its behavior has been studied in these lakes; macroinvertebrates (Miyadi, 1931; Kitagawa, 1973; Chino, 1975; Hirabayashi and Hayashi, 1994; Yoshida and Uenishi, 2001), Trichoptera (Kawamura, 1918; Iwata, 1927a, 1927b, Yoshida and Uenishi, 2001), Odonata (Kurasta, 1965, 1971), Diptera especially chironomidae (Asakawa, 1977; Yasuno et al., 1983; Hirabayashi and Hayashi, 1996; Hirabayashi et al., 1996). However, studies of adult craneflies have never been because of the difficulty of species identification. The objective of this study is to clarify species composition and abundance of adult craneflies in Nishina Three Lakes. The abundance of adult craneflies were monitored using light traps in May, August and October in 2005 and February in 2006. We collected 26 species of adult craneflies in Lake Aoki, 16 species in Lake Nakatsuna and 17 species in Lake Kizaki. A total of 39 species were collected in Nishina Three Lakes. Only 2 species (*Antocha bifida* and *Dicranota* sp.) were captured from all lakes. *Antocha bifida* was dominant species in Lake Nakatsuna and Kizaki, and *Gonomyia incompleta* was dominant species in Lake Aoki. The species number of craneflies increased from May to August, decreased from August to February in all lakes. The individual number showed different seasonl trend each lake.

Key Words: adult cranefly, light trap, species composition, seasonal trend, different trophic status

Nordic fungus gnats (Diptera: Sciaroidea) and the Swedish Taxonomy Initiative: Preliminary results and prospects for a complete inventory

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The Swedish Taxonomy Initiative (STI) has set its goal for making Sweden the first country to complete an inventory of all the multicellular species living within its borders. As a part of this giant endeavor taxonomic research of Nordic fungus gnats (Diptera, Sciaroidea) has been initiated at the STI. The Nordic countries, and especially their boreal forests, have a high species diversity of fungus gnats, and the Nordic fauna constitute a major part of the known European and even of the entire Palaearctic fauna of this diverse assemblage of nematocerous flies. Exclusive of Cecidomyiidae (sometimes included in Sciaroidea), Sciaridae and the unplaced *Heterotrichia*-group genera, that are being treated separately, some 925 species belonging to the following five families are so far known from the Nordic countries: Bolitophilidae (27), Diadocidiidae (6), Ditomyiidae (3), Keroplatidae (59), and Mycetophilidae (approx. 830). The first modern checklist for Sweden will be presented soon, and the goal is to illustrate and describe all Nordic species in four planned volumes of the national encyclopaedia "Nationalnyckeln". The mycetophilid tribe Exechiini is first out to be reviewed with regional revisions of some 260 species in 17 genera.

Key Words: Sciaroidea, fungus gnats, Nordic, diversity, taxonomy

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Orysmia gen. n. from Hokkaido, Japan and Sakhalin, Russia, with a revised phylogeny of the *Allodiopsis* s. l. genus group (Diptera: Mycetophilidae)

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The genus *Myrosia* Tuomikoski is known with two species: *M. maculosa* (Meigen, 1818) and *M. orientalis* (Zaitzev, 1993). A phylogenetic analysis of the genera in the *Allodiopsis* s.l. genus group reveals *Myrosia* as paraphyletic and suggests that *M. orientalis* should be regarded as representing a separate, monobasic genus. Hence, *Orysmia* **gen. n.** is established for *O. orientalis* (Zaitzev, 1993) **comb. n.**, known from Sakhalin Island, Russia and new material from Hokkaido, Japan. The new genus is described, and *O. orientalis* (males) and *M. maculosa* (both sexes) are re-described accompanied by detailed illustrations of their terminalia. *O. orientalis* has rather different terminalia compared with *M. maculosa* and is characterized by several autapomorphies.

Key Words: Mycetophilidae, Exechiini, new genus, taxonomy, phylogeny

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Japanese *Lipiniella* species assigned to *L. moderata* Kalugina, 1970 (Diptera, Chironomidae, Chironominae, Chironomini)

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For several years Japanese researchers have noticed that a *Lipiniella* species occurs in Japan (e.g. Kitagawa 1997a, 1997b, 2000, 2004; Kobayashi & Yamamoto 2001; Yamamoto 2005). Midges belonging to this genus are actually rather common in the big rivers, lakes and marshes. To establish the true identity of the Japanese *Lipiniella* species was urgent. The genus *Lipiniella* comprises 4 described species: *L. araenicola* Sihlova, 1961; *L. moderata* Kalugina, 1970; *L. prima* Shilova, Kerkis and Kiknadze, 1992; and *L. secunda* Shilova and Prowiz, 1997. *L. prima* is described based on larval morphology and karyotype only. We examine the morphology of the Japanese specimens to establish if they truly belong in the genus *Lipiniella*, and if so, if they are conspecific with any of the previously described species. As a result we consider the Japanese material to include only one species, namely *L. moderata*. We also compared *Glyptotendipes goryoense* (= *Demeijerea goryoensis*) and *Chironomus fujiprimus*, and found them both to be junior synonyms of *L. moderata*. Japanese specimens of *Lipiniella* Shilova, 1961 are assigned to *L. moderata* Kalugina, 1970, and *Glyptotendipes goryoensis* Ree & Kim, 1981 and *Chironomus fujiprimus* Sasa, 1985 are found to be junior synonyms of *L. moderata*.

Key Words: Chironomidae, *Lipiniella moderata*, Japan

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Bactrocera dorsalis Hendel (Diptera: Tephritidae) successfully eradicated in Okinawa Island, southwestern Japan in 2002

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The oriental fruit fly, *Bactrocera dorsalis* Hendel, was eradicated from Okinawa Prefecture in 1986. After that, however, fruit fly outbreaks (detection of the fly larvae on infested fruits) occurred five times in that area in the past 19 years (1986 through 2005). In May 2002, a major outbreak of the oriental fruit fly occurred in the southern part of Okinawa Island. The male annihilation technique (MAT) and protein bait spray were applied to control the fruit fly within a 5 km radius from the detected trap. For MAT, wood fiberboard squares containing male attractant and insecticide were distributed in the control area. Protein bait spray that contains insecticide was applied on the areas where the fruit fly was found. Host fruits were also removed in the infested areas. From May 2002 through January 2003, a total of 91,345 fruits were collected from a total of 3,639 points. Subsequently, we found numerous infested fruits at 68 different points, and a total of 4,130 adult flies emerged from those fruits. During this period, a total of 375 flies were captured in monitor traps. As a result of the control, both the number of infested fruits and the number of adult flies emerging from the fruits decreased. No infested fruits were found from September 2002 until January 2003, and no flies were captured in monitor traps from October 2002 until January 2003. The flies ceased to recur within approximately five months. Therefore, we considered that the oriental fruit fly was again successfully eradicated from the southern part of Okinawa Island.

Key Words: methyl eugenol, male annihilation technique, fruit-fly exclusion program, exotic insect pest, invasion

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Drosophilid Fauna in Kume-jima, a Subtropical Island of Japan

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The Ryukyu archipelago is continental islands located in subtropical region of Asia, and its fauna and flora appear to consist of complex combinations of tropical, subtropical and temperate elements. We are studying the drosophilid fauna of the archipelago in regard to the climates, size of islands and distance from the continent and other islands. In this archipelago, intensive surveys (Hirai et al. 2000) have been performed on drosophilid fauna in Iriomote-jima, the southwestern island of the archipelago, where about 65% of drosophilids were tropical and subtropical species and about 30% temperate. However, only a fragmental survey was conducted in other islands.

We study the drosophilid fauna in Kume-jima, an island located in the central part of the archipelago. Collections were made by traps baited with bananas and mushrooms by net sweeping on undergrowth plants and from naturally-occurring fungi and tree trunks from April 2002 to February 2003. As a result, a total of 37 species representing 16 genera were collected. We compare the present results with the results of surveys in Iriomote-jima and the main islands of Japan, and discuss the characteristics of drosophilid fauna in this island.

Key Words: Drosophilidae, fauna, Kume-jima, subtropics

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The influence of particle size of sandy substrates on the survival rates of two chironomid species inhabiting in the middle reaches of the Kiso River, Japan

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The psammophilous species is often influenced by the particle size of sandy substrate. The influence of particle size of sandy and artificial substrates on the survival rates and developments of larvae of *Hydrobaenus kondoi* and *Stictochironomus akizuii* was investigated.

The survival and development of the two species were observed by rearing test using several sandy substrates of different particle sizes (>500, 250-500, 150-250, 75-150, <75µm). The just hatched larvae of both species were used in the experiments.

Very low survival rates of *H. kondoi* were observed with particle size of 150-250 and 75-150µm. None of the larvae of *S. akizukii* was survival in particle size <250µm.

H. kondoi larvae exhibited lower survival rate and delayed development in the particle size of <75µm in comparison with >500, 250-500µm and control (muddy substrate). In glass bead substrate (<150µm), lower survival rates of *S. akizukii* larvae and delayed development to *H. kondoi* larvae were observed.

However, 5 day old *H. kondoi* larvae exhibited normal rates of development at the same conditions of sandy substrates. This suggests that the chironomid larvae were immediately influenced after hatching on the substrate.

Key Words: Chironomidae, particle size, substrate, *Hydrobaenus kondoi*, *Stictochironomus akizukii*

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Larvicidal Activities of traditional medicinal plant, *Portulaca oleracea* against *Aedes albopictus* (Culicidae) and *Paratanytarsus grimmii* (Chironomidae)

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We are searching for the target-specific insecticidal constituents of traditional medicinal plants for the purpose of the prevention of physiological resistance and of the environmental contamination prevention by use of synthetic pesticides. We found some traditional medicinal plants showing the selective larvicidal activities against *Aedes albopictus* (Diptera: Culicidae) and *Paratanytarsus grimmii* (Diptera: Chironomidae).[1)]

The larvicidal activities of the extract of *Portulaca oleracea* (Portulacaceae) against *Ae. albopictus* and *P. grimmii* were examined. Methanol extract showed highly mortalities at a concentration of 1000 μg/ml against the larvae of *Ae. albopictus* within 24hrs. But it did not entirely show lethal effects against the larvae of *P. grimmii* at same concentration. Methanol extract partitioned with four organic solvents (hexane, chloroform, ethyl acetate and *n*-butanol) and water. Chloroform, ethyl acetate and *n*-butanol-soluble fractions showed lower mortalities against *Ae. albopictus* and *P. grimmii*. However, hexane-soluble fraction showed high selective toxicity against the larvae of both species at 1000 μg/ml. Hexane-soluble fraction was provided seven fractions (Fr.1-7) by chromatography. Fractions 2 and 5 showed significant mortalities (61.9% and 100%) against the larvae of *Ae. albopictus* within 48hrs at 500 μg/ml. A fraction 5 also exhibited 56.5% mortality at 50μg/ml against *Ae. albopictus,* but this fraction showed no mortality at 500 μg/ml against *P. grimmii*. This suggests that fraction 5 contains the constituents which showed selective toxicity. We are investigating the selective toxicity constituent now.

1) T. Konishi *et al.*, International Conference on Biodiversity of Insects: Challenging Issues in Management and Conservation (BIMC, 2006), Coimbatore, India.

Key Words: *Aedes albopictus, Paratanytarsus grimmii, Portulaca oleracea*, larvicidal activity

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Phylogeny of Sarcophagid flies based on the comparative morphology of female postabdomens

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It has been not easy to identify the females of Sarcophagid flies, although the male genitalia are very useful for identification. However, the male genitalia do not seem to be good for phylogenetic analysis because they are very complex in structure and modified among species. The phylogeny of the Japanese Sarcophagidae including some Oriental species was analyzed based on 41 morphological characters by using the UPGMA program. The study material consisted of females collected in copulo with males that could be identified or specimens identified by a taxonomic authority. These 41 morphological characters were mainly selected based on ground plans of the calyptrate muscoid female postabdomen. tergites 5-9, sternites 5-9, SPAP, SUAP and spermathecae were classified based on their shapes, vestitures, and apparent homologies. Their character states were scored as 0: primitive state, 1: intermediate, 2: advanced, 3: more advanced.

Among the Asian sarcophagid flies, three big clusters were produced. The first one is the Subfamilies Miltogramminae+Paramacronychinae, and the second group was the tribes Raviniini+Protodexiini+Goniophytoini. The 3rd cluster was the biggest and most complex, and consists of Tribe Sarcophagini. The dendrogram of Sarcophagini had 6 main branches and comprised more than ten small clusters. The first and second groups seem to be more morphologically primitive than Sarcophagini and distinctly separated from each other and from the third group.

The further detail examination and analysis based on the world wide materials may contribute to discuss the generic taxonomy of tribe Sarcophagini.

Key Words: phylogeny, Sarcophagidae, comparative morphology, female postabdomen

Is the Japanese blow fly, *Calliphora nigribarbis*, a mechanical carrier of highly pathogenic avian influenza virus ?

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In the winter (December 2003 to March 2004), four cases of highly phathogenic avian influenza (HPAI) were reported from poultry houses and farms in Yamaguchi, Oita and Kyoto Prefectures, western part of Japan. We entomologists surveyed the first infected poultry farm in Tamba-Town, Kyoto, and collecting fly samples on fish baits at six stations A-F which located 600-2,300m far from the facility. A number of *Calliphora nigribarbis,* (*Cn*) and *Aldrichina grahami* were observed and collected on baits, especially at station A. The H5 influenza A virus genes were detected by RT-PCR from 10-30% samples of both species and the viruses were isolated from 20% (2 positives among 10 examined) of *Cn* blow flies. The virus isolated was characterized as H5N1 subtype influenza A virus. Laboratory experiments showed *Cn* flies ingested carried viruses having an infectious titer in their alimentary canales and crops for 24 h under 20℃, 70-75% RH.

Seasonal migration and characteristic landing of *Cn* were annually observed in the end of October in Fukuoka, northern Kyushu. A thousand of male and female flies were flying from sea of Genkai-Nada through Fukuoka to the direction of south.

Their behavior including short distance migration might be associated with some of outbreaks in Japan during 2003 to 2004, especially the case of the 2nd poultry farm in Tamba which located ca. 2 km far from the first. A mark-release and recapture field experiment showed that female flies can migrate at least 2-3 km within the same day.

In addition to other possibilities such as by wild birds, the blow fly also should be considered a mechanical carrier of HPAI virus.

Key Words: highly pathogenic avian influenza, migration, blow fly, *Calliphora nigribarbis, Aldrichina grahami*

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European species of the genus *Cordyla* Meigen (Diptera: Mycetophilidae). A morphological study

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The genus *Cordyla* Meigen, 1803 is a well marked monophyletic group of fungus gnats (Mycetophilidae), consisting of small, about 5 mm in size, species whose larvae mainly feed on mushrooms. *Cordyla* is characterized by a number of apomorphies: swollen antepenultimate segment of palpi, vein m2 does not reach wing margin etc. The number of flagellar segments as an important character for identification was outlined by C. Landrock in 1926 already, and this, in combination with morphological characters of male terminalia, is also substantial today. Species groups were discussed briefly in Kurina (2001), but the approach is critically reviewed and new data have been added.

The structure of male terminalia is considered to be the most important set of morphological characters followed by number of flagellar segments and the colour of the swollen segment of palpi. The characters in male terminalia allow to distinguish three groups: *fusca*, *semiflava* and *crassicornis* species groups. There are 21 *Cordyla* species known in Europe: viz. 11 species from the *fusca* group, 8 species from the *semiflava* group and 2 species from the *crassicornis* group. Judging by the structure of medial and ventral parts of gonostylus, the *fusca* group is most variable, while the species are most similar in the *semiflava* group. At identification of species of the *semiflava* group, the outlining of hypoproct, which can be bifid, club-like or rudimental, should also be observed.

Key Words: Mycetophilidae, *Cordyla*, systematics, Europe

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Biogeographic analysis of Crocidiinae (Diptera, Bombyliidae): when congruence exists among morphological, molecular, fossil and paleogeographical data indicating a Gondwanan origin of the beeflies.

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A cladistic biogeographic analysis of the Crocidiinae (Diptera, Bombyliidae) is presented, in order to discuss a biogeographic hypothesis for the subfamily and the entire Bombyliidae family. It is based on previously published phylogenetic results ((*Inyio* + *Desmatomyia*) + (*Apatomyza* + (*Crocidium* + (*Mallophthiria* + *Megaphthiria*)))), which were modified to include the two problematic genera *Semiramis* and *Timiomyia* polytomic to *Crocidium*, with which they are probably synonyms. The Crocidiinae is mostly distributed over arid areas of the early components of Gondwanaland: Chile (*Mallophthiria* + *Megaphthiria*) and Southern Africa (*Apatomyza* + *Crocidium*), but also in the Southwestern Palaearctic (*Crocidium* + *Semiramis* + *Timiomyia*) and Southwestern Nearctic (*Desmatomyia* + *Inyo*). For the biogeographical analysis we performed the Brooks Parsimony Analysis (BPA) aiming to reconstruct the historical relationships among the areas of endemism inhabited by Crocidiinae taxa. Five areas were used: Chile, SW Nearctic, Southern Africa, Northern Africa and SW Asia, and an all zero outgroup area to root the trees. The absence/presence of Crocidiinae taxa into these areas was reconciled to its resolved phylogenetic hypothesis previously published. The program NONA version 2.0 was used for cladogram searching, and WINCLADA for the tree viewing and editing. The vicariance events affecting Crocidiinae biogeography, obtained by performing BPA at genus level, seems to be the sequential separation of the Holarctic from Gondwanaland and then the splitting of the latter into its smaller components. The biogeographic results were corroborated by the known fossil records and molecular-based dating. The association of Crocidiinae diversification with the Gondwanaland splitting supports the

origin of the subfamily during the Middle Jurassic, the same period in which other bombyliid lineages arose and radiated. We found evidence from molecular phylogeny and from the fossil record supporting a Middle Jurassic origin of the Bombylioidea.

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Key Words: biogeography, Bombyliidae, Crocidiinae, Diptera, Gondwanaland.

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FLYTREE MORPHOLOGY: Preliminary analysis of the first tier dataset

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We report the results of the preliminary analysis of the morphological dataset for the first tier taxa for FLYTREE, a large international collaboration producing new, comprehensive data sets for Diptera phylogenetics funded by the US National Science Foundation's Assembling the Tree of Life (ATOL) initiative. This international team of scientists is bringing together existing and new morphological evidence on fly relationships across the entire order, producing data sets unprecedented in their size and the breadth of their coverage of taxa. New and traditional morphological character interpretations across the entire order have been assembled and developed. Here, we summarize our current progress in one of the principal tasks of the project; the construction and preliminary analysis of large morphological data matrices for a backbone phylogeny, based on a matrix of 42 ingroup taxa and over 350 characters. This comprehensive new phylogeny will provide a valuable framework for testing evolutionary hypotheses and will be critical to comparative studies of dipteran development, behaviour, genomics, and neurobiology.

Key Word: Assembling the Tree of Life

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A Supertree for the stiletto flies (Diptera: Therevidae) using constraint trees and the parsimony ratchet to overcome low taxon overlap

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We explore the use of the three most common approaches to calculating globally inclusive phylogenies from smaller, more exclusive analyses; supertree methods, ‘supermatrix’ methods, and total evidence. Supermatrix and total evidence approaches are often unsuitable for use in species-rich clades such as insects because these methods require significant overlap in both terminal taxa and data classes. Supertree methods require no overlap in data class between source analyses, performing well even with incomplete taxon overlap; hence they are suitable for use in species-rich clades. We describe a method for handling low taxon overlap in supertree analyses. A therevid supertree was produced using matrix representation with parsimony (MRP) analysis in combination with the parsimony ratchet and constraint tree techniques, from 24 phylogenetic studies containing a total of 362 terminal taxa despite only 34% of the terminal taxa found in more than one source tree. The resulting supertree is a complete phylogenetic hypothesis for Therevidae that incorporates extensive sampling of major lineages, and summarises all past phylogenetic work on the family. The resultant inclusive metaphylogeny robustly retrieves the subfamilies Agapophytinae, Phycinae, Therevinae, and Xestomyzinae, and the tribes Cyclotelini and Therevini. MRP supertree methods can be used to produce inclusive metaphylogenies in situations where source trees have poor data overlap and low taxon overlap, and are therefore valuable in species-rich groups such as insects. These methods may be necessary for constructing the 'Tree of Life', representing phylogenetic relationships between the millions of known species.

Key Word: matrix representation with parsimony

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Australasian stiletto flies (Diptera: Therevidae): Divergence time estimates indicate Gondwanan separation, evolutionary radiations with aridification, and recent dispersal

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Why are there so many stiletto flies (Therevidae) in Australia? Intensive field and systematic research over the last decade has revealed a fauna we estimate at 700 species, arranged in three independent lineages; the Agapophytinae, the *Taenogera* group of genera, and the *Anabarhynchus* group of genera. While the Agapophytinae is endemic to Australasia, the other two lineages also have a few species in Chile or Argentina. We discuss the latest divergence time estimates for the Australian Therevidae and the implications for studies of evolutionary radiations of Australian fauna. Preliminary research showed that Australian therevid divergence times correlated with known gondwanan biogeographical events. Recent paleontological research has provided accurate phylogenetic assignments and ages for key fossils required to calibrate the molecular clock. Analysis of a dataset comprising intense taxon samples from the three radiations shows that while these lineages arose in the late Cretaceous or early Tertiary, the intense species-level evolutionary diversification did not begin until the mid Tertiary. At least six Australian genera have radiated in conjunction with the aridification of Australia. The New Caledonian fauna appears to have been a result of recent dispersal from Australia, rather than Gondwana vicariance.

Key Words: biogeography, stiletto flies

Surviving the test of time: Testing species boundaries and the subfamily concepts in Dolichopodidae using South-east Asian species

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The Dolichopodidae with its 7000 described species is particularly speciose in the Oriental and Australasian Regions, but little is known about many of the diverse genera. Here, we report the results of a molecular study on the terrestrial genus *Teuchophorus* and the mainly marine genus *Thinophilus*. We find that interspecific distances for mitochondrial genes are small in the former and remarkably large in the latter, thus requiring conserved genes to resolve relationships. These results imply that *Thinophilus* may be a very old genus. We also document that the intraspecific variability can be very high for *Teuchophorus* and that identifying species based on *COI* sequences as proposed by the DNA barcoding consortium is not feasible. We attempt to place *Thinophilus, Teuchophorus*, and several *incertae sedis* genera from South-east Asia into the subfamily classification of Dolichopodidae by using information from several genes (e.g., *12S, 16S, 18S, 28S*). Our results agreed with morphological data on the placement of *Teuchophorus* and *Thinophilus* in the sub-families Sympycninae and Hydrophorinae respectively. However, several other genera are difficult to place based on morphological and molecular data.

Key Words: Dolichopodidae, South-east Asia, genetic distances

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Conflict between larval and adult data: Which has more homoplasy and which provides more information for phylogenetics?

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Convergent evolution can be studied by comparing the results of separate cladistic analyses based on larval and adult characters for endopterygote taxa such as Diptera. The adult and larval stages of the same species usually occupy radically different niches and hence many external morphological features evolve autonomously. This interest in convergent evolution and new DNA-based techniques that allow for an easier identification of immature stages make it important to revisit the question whether adult or larval characters are more homoplasious and/or provide more characters for phylogenetic research. Here, we use Partitioned Bremer Support (PBS) from 20 datasets with an average of 33 larval and 74 adult characters to answer two related questions. (A) Are larval or adult character more homoplasious? (B) Which partition provides more phylogenetic signal? Overall, we find that adult characters are less homoplasious as measured by RI and CI and provide more information than larval characters, with the average adult character providing 74% more support than the average larval character. Surprisingly, we also find that levels of homoplasy are only weakly correlated with phylogenetic signal as measured by total PBS.

Key Words: Endopterygota, Partitioned Bremer Support (PBS), morphology, homoplasy

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Liriomyza leaf miners of economic significance to Australia (Diptera: Agromyzidae)

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The family Agromyzidae is represented in Australia with only about 150 identified species. The genus *Liriomyza*, which has over 376 species worldwide and has many species of economic importance, is sparsely represented in Australia with only 18 species. Only *Liriomyza brassicae* and *L. betae* (syn. *L. chenopodii*) have some economic significance in Australia.

However, seven species of *Liriomyza* that have significant pest status in many countries around the world but are not yet present in Australia, are *L. huidobrensis, L. sativae, L. trifolii, L. chinensis, L. bryoniae, L. strigata* and *L. cicerina* . Some of these, particularly *L. huidobrensis, L. sativae* and *L. trifolii*, are highly polyphagous and invasive. While they are not yet reported in Australia, *L. huidobrensis* and *L. sativae* have recently invaded Indonesia and *L. trifolii* is currently present in Tonga, New Caledonia, the Cook Islands and French Polynesia, giving these species significant quarantine importance for Australia.

We have studied the Australian major economic as well as exotic quarantine species mentioned above with a view to develop Lucid identification keys and diagnostic protocol capability for certain exotic species (e.g. *L. cicerina*, *L. huidobrensis*, *L. sativae* and *L. trifolii*) as part of Australia's preparedness for exotic biosecurity threats. Additionally, we are using molecular diagnostics developed for a few exotic species using a rapid PCR-RFLP method based on COI and CO II genes.

Key Words: Agromyzidae, *Liriomyza,* Australia

An assessment of the utility of DNA barcoding for differentiating species in chironomids

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Chironomids have been investigated extensively in paleogeographic and biomonitoring studies. However such studies are hampered by the difficulty of accurately separating species, particularly in the larval stage. Consequently it has been common to use only family level identification, but recent studies are showing this results in loss of much important information and that species level identification is preferable. DNA barcoding, using the mitochondrial COI gene, has been advocated as a solution to these problems. However, in chironomids there are potential problems from complexes of sibling and cryptic species, as well as from mitochondrial introgression between closely related species. Since the group includes both species with extremely broad and with very limited distributions, the amount of intraspecific sequence divergence could be quite variable. We are investigating the genus *Chironomus* and related taxa that will enable a comparison of the levels of intra- and inter-specific sequence divergence, with the aim of establishing whether COI sequence offers a real solution for rapid and accurate identification of species in this group.

Key Words: Chironomidae, species complex, COI, intraspecific variability

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Asphondylia sp. (Diptera: Cecidomyiidae) Infesting Chili Pods in Bogor, West Java, Indonesia

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A gall midge that is known to infest pods of chili, *Capsicum annuum* L., in Padang, West Sumatra, Indonesia was tentatively identified as *Asphondylia capsici* Barnes (Diptera: Cecidomyiidae). *A. capsici* is now considered to be identical with *Asphondylia gennadii* (Marchal), but we need further investigations to confirm if the Indonesian gall midge is identical with *A. gennadii* or not. Recently we found this gall midge in Bogor, West Java. The females lay their eggs in flower buds or very young pods of chili and larvae transform chili pods into galls. When young pods were attacked, they cannot grow normally and remain smaller than normal pods. When older pods were attacked, they are twisted or irregularly distorted. At the same time, the color of infested chili pods remains green, sometimes with reddish tinge. In order to establish control measures against the gall midge, we conducted field surveys in Cisarua and Darmaga, Bogor from February to June 2005 to obtain basic information on the gall midge. The percentage of chili pods damaged by the gall midge at Cisarua and Darmaga was 0.91–3.97% and 0.69–7.49%, respectively, and the percentage of chili plants that bore galled pods was 11 – 41% at both fields. We also found the following parasitoid species that attacked the larvae of the gall midge: one species of *Eurytoma* (Hymenoptera: Eurytomidae) and two species of *Sigmophora* (Hymenoptera: Eulophidae). *Eurytoma* sp. was found more frequently than *Sigmophora* spp. It is remarkable that we could not rear any braconid parasitoids from the chili pod galls, although they have been frequently found in galls induced by *Asphondylia* gall midges in the Temperate Zones.

Key Words: *Asphondylia* sp., chili pod, gall midge, pest, parasitoid

Biogeography and phylogeny of marine dolichopodid flies in the Hawaiian Islands (Diptera, Dolichopodidae)

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Among dolichopodid flies, which have their greatest diversity near fresh water, one group lives exclusively on rocky (or coral) seashores. Because these marine-shore dolichopodids are confined to a linear habitat, the distributional ranges of species of this group can easily be represented as lines, instead of areas as is done for inland dwellers. This property is one of the exceptional merits of this group for studying biogeography. We investigated six of the main Hawaiian Islands (Hawai'i, Maui, Lanai, Molokai, Oahu, Kauai) to characterize the fauna and clarify the origin of the Hawaiian species. We found the only previously recorded Hawaiian dolichopodid species, *Conchopus acrosticalis* Parent, 1938 (which has also been assigned to *Thambemyia* Oldroyd, 1956), and five undescribed species also belonging to the genus *Conchopus* Takagi. Only species of this genus appear to be distributed in the Hawaiian Islands. Other genera distributed in surrounding Pacific areas, such as *Cymatopus* Kertész (pan-tropical), *Paraphylosylus* Becker (west coast of North America), and *Acymatopus* Takagi (East Asia) were not found there. We attempted to clarify the phylogenic position and origin of the Hawaiian species of *Conchopus* by contructing a molecular phylogenetic tree based on mtDNA ND5 gene sequence data. Immigration of this group into the Hawaiian Islands probably took place on two occasions. The Hawaiian species prove to be the sister-group of the *rectus*-group of the genus *Conchopus*, with no immediate relation to species of *Thambemyia*.

Key Words: Dolichopodidae, *Conchopus*, Hawaiian Islands, ND5 gene, biogeography

Discovery of the South American Rice Miner in Southeastern United States (Diptera: Ephydridae)

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The South American Rice Miner (*Hydrellia wirthi* Korytkowski), a recently discovered, invasive pest in rice, is reported from southeastern United States (Louisiana and Texas). A detailed description and diagnosis with illustrations and photographs are provided to facilitate identification of this pest, along with descriptions of its damage as a miner in rice whorls, stems, and leaves. The localities where this invasive species has been found in surveys in Louisiana and Texas are provided.

Key Words: *Hydrellia wirthi* Korytkowski, shore flies, invasive species

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Evaluation of control measures for Oriental fruit fly, *Bactrocera dorsalis* Hendel, during an outbreak in the southern part of Okinawa Island, Japan

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An outbreak of oriental fruit fly, *Bactrocera dorsalis* Hendel, occurred in the southern part of Okinawa Island, Japan, in 2002. The male-annihilation technique (MAT) and protein bait spray were applied to control the oriental fruit fly. For MAT, fiberboard squares soaked with lure-toxicant, a mixture of an attractant (methyl-eugenol) and an insecticide (BRP), were distributed in infested areas. Protein bait spray that contains insecticide was also applied on the areas where the oriental fruit fly was detected. Since the male-attractant trap contained the same attractant (methyl-eugenol) as fiberboard squares, the ability of the traps to catch the flies should have declined in these areas. Therefore, to evaluate the control measures, adult flies were captured using an insect net, then the sex ratio of captured flies, mating rate, and sex maturity of captured females were investigated. Furthermore, yellow sticky-trap surveys and fruit-collecting surveys were conducted to investigate the duration of fly infestation at each detected point. The proportion of males decreased in the early phase of control, and the mating rate of females decreased rapidly in the controlled areas. These results indicate that MAT effectively controlled the oriental fruit fly. Even though MAT works for only males, the number of matured females was decreased with the passing time of control. It is considered that matured female flies were controlled with protein bait spray. Yellow sticky-trap surveys and fruit-collecting surveys revealed that the average duration of fly infestation at each detected point was only about nine days. This suggested that the control measures prevented additional ovipositions by the remaining matured females or next generation flies, and that the combination of MAT and protein bait spray was an appropriate and effective control measure against the oriental fruit fly.

Key Words: Oriental fruit fly, male-annihilation technique, protein bait spray, yellow sticky-trap survey, evaluation

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Sciomyzids and slugs: potential for biological control in southern California

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It has been estimated that approximately 15% or US$75 billion of global food production is lost annually to pest organisms before it reaches the consumer (Oerke *et al.,* 1994). Of these, pestiferous slugs are among the most important and are the primary pests in many regions of the world (Reidenbach *et al.*, 1989). In California, agri-production has been estimated at US$30 billion (single most important contributory U.S state) and in surveys of horticultural and agricultural systems in southern California only slugs which are native to Europe have been found. These include *Deroceras reticulatum* (Müller)*, Deroceras panormitanum* (Lessona and Pollonera)*, Lehmannia valentiana* (d'Audebard de Férrusac)*, Limacus flavus* (L.), *Milax gagates* (Draparnaud) and *Arion hortensis* d'Audebard de Férrusac. Details on relative abundance and pest status of these species are presented. Current slug control measures are either overtly toxic to non-target organisms (molluscicides), impractical for large areas (copper fences) or only successful against certain slug species (nematode use). There is, hence, a real need for an alternative control strategy. One such option is biocontrol using flies in the Family Sciomyzidae. Eight sciomyzid species are known parasitoids and/or predators of slugs. *Tetanocera plebeia* Loew*, Tetanocera clara* Loew and *Tetanocera valida* Loew have a Nearctic distribution while *Tetanocera elata* (Fabricius)*, Euthycera cribrata* (Rondani)*, Euthycera stichospila* (Czerny)*, Euthycera chaerophylli* (Fabricius) and *Limnia unguicornis* (Scopoli) are native to Europe. Information on prey acceptability, prey preference, prey location mechanisms and rearing success for selected sciomyzids are presented and the biocontrol potential of each species

assessed. This information will ultimately be used for the selection of a species for preliminary release trials in greenhouses in southern California.

Key Words: Gastropoda, slugs, pests, Sciomyzidae, biological control, California

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Significance of gall polymorphism in the speciation of galling cecidomyiids (Diptera: Cecidomyiidae)

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Generally, gall shape is species-specific to gall midges (Diptera: Cecidomyiidae), but some species exhibit gall polymorphism. *Masakimyia pustulae* induces thin and thick type galls on the leaves of *Euonymus japonica* and *E. fortunei* (Celastraceae). Leaf galls induced by Pseudasphondylia neolitseae on Neolitsea sericea (Lauraceae) are apically rounded subconical on adaxial surface and hemispherical on abaxial surface, and are divided into two types: the adaxial side protrudes prominently in one type and the abaxial side does so in another. *Hartigiola faggalli* induces bivalve-shaped galls on adaxial- or abaxial surface of *Fagus crenata* (Fagaceae) leaves. In any case, individuals inhabiting different types of gall cannot be distinguished morphologically from each other. To discuss the significance of gall polymorphism in the speciation of galling cecidomyiids, we analyzed a region of the COI gene of mtDNA for these gall midges to detect differences at the molecular level between individuals inhabiting different types of gall. The sequencing data indicated that the gall dimorphism was represented by the individuals with different haplotypes in *M. pustulae* and *H. faggalli*. Differences between the haplotypes were 2 bp (0.5 % of 439bp) in *M. pustulae* and 7 bp (1.6 %) in *H. faggalli.* There were 2 (1.4%) differences in the 146 deduced amino acid residues in *M. pustulae* and 1 (0.7%) in *H. faggalli*. In *P. neolitseae*, different haplotypes did not represent individuals from different gall types. In all three cases, genetic distance between the haplotypes varies with species but it was not great enough to regard them as distinct species. Thus, gall differentiation starts at the molecular level prior to the morphological differentiation of gall midges and may lead to speciation because mortality factors would operate differently on the individuals inhabiting different types of gall.

Key Words: COI sequence variation, gall dimorphism, speciation, genetic distance, Cecidomyiidae

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Excellent combination therapy of maggot debridement therapy (MDT) and bioaritificial dermis with therapeutic angiogenesis and/or autograft skin transplamtation

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We investigated efficacy and safety of autologous bone marrow-mononuclear cells plus platelets including endothelial progenitor cells (EPCs) implantation for recovering refractory chronic peripheral arterial disease (PAD). But also simultaneously the refractory PDA patients are needed the control of multiple drugs resistance bacterial infections (MRSA, MDRP etc.). We performed 17 cases of MDT for severe refractory limb ulcers and gangrenes. 15 cases of total 17 cases (88.2%) were diagnosed limb amputation or were going to be performed limb amputation in the near future by former hospitals and departments. In the clinical results, 12 cases of total 15 cases (80.0%) were successfully salvaged the limbs of these patients. And also we succeeded the bioaritificial dermis with therapeutic angiogenesis and/or autograft skin transplamtation
in 7 cases of total 8 cases (87.5%) that all 8 cases of autologus skin graft were rejected in former hospitals and departments.

Our new combination therapy of maggot (*Lucilia sericata)* debridement therapy (MDT) and bioaritificial dermis with therapeutic angiogenesis and/or autograft skin transplamtation are very effective for severe refractory PAD ulcers or gangrenes. This therapy may be possibility as newly limb salvage method.

Key Words : maggot debridement therapy (MDT), bioartificial dermis, *Lucilia sericata,* therapeutic angiogenesis, refractory ulcers and gangrenes

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Anopheline vectors and malaria transmission in irrigated areas of Southeastern Iran

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In a study carried out in the Zar -Abad Division (Baluchistan, Iran) from March through February 2005, the objective of this study was to assess the malaria disease risks in a new-established agro-ecosystem. Clinical malaria was monitored in 10 rural villages by passive and active case detection s. Adult mosquitoes were collected by pyrethroid spays spray catch of living quarters and stables , cattle bait and pit shelter catches. Overall, *An. culicifacies* Giles s.l predominated (49.8%) ,followed by *An stephensi* Liston s.l. (36.9%), *An pulcherrimus* Theobald (7.3 %), *An dthali* Patton (5.7%) and *An.fluviatilis* James (0.3%). Most mosquitoes (88.8%) were collected from indoor resting-sites whereas collections from potential resting-sites outdoors accounted for 11.2% of total anopheline densities. *Anopheles stephensi* Liston s.l. and *An. culicifacies* Giles s.l populations peaked in April-May and August-September, respectively. This study indicates that, in South Baluchistan, Banana irrigation-related sites support the breeding of anopheline mosquitoes, including the vectors of malaria.

Key Words: malaria, vectors, species, Baluchistan, Iran

Some ecological aspects of *Anopheles culicifacies* s.l. in Baluchistan, Iran

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Studies were conducted on the ecology of *Anopheles culicifacies* **s.l.** over a period of 20 months in the villages of Bent area, Sistan and Baluchistan Province, southeastern Iran This Province is located in the bordering the Oman sea and malaria is still considered a major health problem. Monthly malaria incidence generally followed fluctuations of *An.culicifacies* **s.l.** density, usually with a peak in September-October. Adult mosquitoes were collected during 2005-2006 by four methods of sampling: knock-down pyrethrum space-spray indoors, human and animal bait (18.00-05.00 hours), and pit shelters collections. , The species was active throughout the year with 2 peaks of activity, April-May and August-September. knock-down pyrethrum space-spray indoors captured the highest number of *An. Culicifacies* s.l. females (75%) as compared to human and cattle bait collections (9.3%), pit shelter catches (15.7%), Larval habitats of malaria vectors varied from clean to brackish water, as well as sewage water, under palm trees, marshland, pools, pounds, drainage, irrigation canals, wells, and water containers .

Key Words: malaria, *Anopheles culicifacies* s.l., Baluchistan, Iran

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Physiological studies of four forensically important flies found in different seasons in Japan

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Flies that develop in different seasons have different physiological characters and life styles. We studied a physiology of flesh flies, *Boettcherisca peregrina* and *Parasarcophaga similis*, that breed late spring to early autumn and of blow fly, *Aldrichina grahami* and *Calliphora nigribarbis,* that breed late autumn to early spring in Japan. Larvae of these flies feed on dead animals and dead bodies, so that they are forensically important. Flesh fly larviposit first inster larvae, while blow flies oviposit. Larvae of the flesh fly enter pupal diapause under a short day condition at 20°C but do not enter diapause under a long day condition. Larvae destined non-diapause develop adults in 4 weeks at about 20°C. Flesh fly females can larviposit in 10 days at 25°C, and it takes 5 days from first inster larvae to mature larvae. Mature larvae are inhibited to become pupae by contact with a little water (water immersion treatment). The treated mature larvae survived 20 days at 25°C and 30 days at 20°C, respectively. Percentages of triacylglycerol (TG) and arachidonic acid of lipid extracted from the survived larvae especially decreased by water treatment. Adult blow flies, *A. grahami* and *C. nigribarbis* aestivate in highlands or northern areas in summer, and appear in lowlands during autumn to winter, which is a short day condition, and lay eggs. In the experimental condition at 20°C under a short day condition, *A. grahami* can lay eggs 6 or 7 day after eclosion but *C. nigribarbis* takes about 21 days. High peaks of ecdysteroid hormone for egg development of *A. grahami* and *C. nigribarbis* were found only in females grown under a short day condition. After adult emergence, percentage of palmitoleic acid increased gradually and the acid finally became more than 40%.

Key Words: *Boettcherisca peregrina, Parasarcophaga similis, Aldrichina grahami, Calliphora nigribarbis,* ecdysteroid hormone

A preliminary phylogeny of the horse flies (Diptera: Tabanidae).

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Horse-flies (Diptera: Tabanidae) are both vectors of disease and important pollinators. The monophyly of Tabanidae is supported with molecular and morphological evidence. However, current phylogenetic hypotheses within Tabanidae are based on intuitive classification. Many species of Pangoniinae have proboscides at least as long as their heads, but the longest are all in the old world genus *Philoliche* (Wiedemann). These "long-tongues" are used to probe for nectar in deep-throated flowers; for some flower species, these flies are the only known pollinators. Here I present a phylogenetic hypothesis for the Tabanidae, with an emphasis on *Philoliche*, based on molecular data from one nuclear (CAD) and one mitochondrial (COI) gene. Using an exemplar approach, I sampled species from 8 of 9 tribes in all 3 subfamilies in Tabanidae. I have also sampled all 9 subgenera of *Philoliche*, and multiple geographic representatives of the subgenus *P.* (*Philoliche*) in southern Africa. My analysis on the whole supports Mackerras and Oldroyd's classifications but does not support the maintenance of three monophyletic subfamilies.

Key Words: Tabanidae, *Philoliche*, phylogeny

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Bloodsucking pollinators converge: evidence for local adaptation from the first molecular phylogeny of horse flies (Diptera: Tabanidae).

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Horse-flies (Diptera: Tabanidae) are both vectors of disease and important pollinators. Pangoniinae, especially *Philoliche* (Wiedemann), often have extremely long-proboscides specialized for nectar-feeding. The *P. aethiopica* (Thunberg) species complex in South Africa is known for its taxonomic confusion with extreme variation in proboscis lengths which may be due to adaptation to floral resources. It historically includes two species, *P. aethiopica* and *P. rondani* (Bertoloni). Based on this, I address the following questions: 1) What are the phylogenetic relationships within the *Philoliche aethiopica* species complex? 2) Is long-proboscis (LT) morphology derived in *Philoliche*? 3) Has LT morphology evolved multiple times? 4) Is there a trend in proboscis length evolution? I produced a phylogeny from the nuclear gene CAD and the mitochondrial gene COI by sampling species from 8 of 9 tribes in all three subfamilies in Tabanidae to produce a fossil calibrated chronogram in the program r8s. The molecular data combined with a new morphological character and biogeography support 6 lineages in the *P. aethiopica* species complex. *P. aethiopica* and *P. rondani* are mutually exclusive, but both have long and short proboscid lineages. The LT taxa both occur in the Albany Center of endemism. Reconstruction of ancestral character states using weighted squared change parsimony shows that LT morphology is derived in *Philoliche* and supports convergence for long proboscides in the Albany Center between *P. aethiopica* and *P. rondani*. Proboscis length was also analyzed as a discrete character using Maximum Likelihood. A model of increasing proboscis length evolution over evolutionary time under a two rate model is significantly more likely than a one without a trend in proboscis length (one rate model) based on a log likelihood ration test.

These results show evidence for parallel evolution in proboscis length and are consistent with the hypothesis of local adaptation to floral resources.

Key Words: Tabanidae, *Philoliche*, convergent evolution, pollination

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Behavioral Diversity of Oestroidea Maggots on Rotten Flesh

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The behavior of Oestroid fly larvae was compared. Larvae of Cyclorrhapha are usually considered to have a simple life, only eating digested flesh externally and crawling randomly on food. But some remarkable behavioral differences between species have been observed. Oestroidea larvae are generally grouped into aggregative species and solitary species. Most Salcophagid maggots are solitary, and many Calliphorid maggots are aggregative. In some species of aggregative maggots, masses of maggots are formed separately from food, although almost all species form masses near or inside foods. In such species, for example *Lucilia illustris*, larvae goes back and forth between the feeding site and maggot mass site. Aggregative maggots of some Calliphorid fly species can not easily grow into adults in small populations or solitarily, and this feature is remarkable considering that these species form masses separately from feeding sites. In addition, some solitary maggots show aggressive behavior. These behavioral features appear to be correlative with morphological characters and phylogeny. It is believed that these behaviors are necessary to form an insect community on carrion.

Key Words: Calliphoridae, Sarcophagidae, carrion, maggot mass, behavior

Larvicidal and pupicidal effect of *Datura metal* L. var. on filarial vector, *Culex quinquefasciatus* Say

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A study has been made to evaluate the larvicidal and pupicidal effect of *Datura metal* (leaves, flower and seeds) against *Culex quinquefasciatus*. Plant extracts at different concentrations had considerable toxic effect on 4th instars and pupa of mosquito and it was dose dependant. Lethal (Lc50 and Lc90) doses were worked out on the effect of plant extract against mosquito larva and pupa. Evidence of larval and pupal mortality of filarial vector after the treatment of plant extracts may be due to the action of toxic alkaloids (hyoscyamine and Atropine etc.,). Growth regulatory activity was noted at lower dose of plant extract treatment. Larval and pupal durations were considerably extended after the treatment. The longevity and fecundity were also greatly affected by the treatment and suggested that plant extract greatly interfered the egg laying capacity of mosquito. Applications of plant extract in the breeding sites of filarial vector showed that the higher percentage of larval reduction after 24 h, 48 h and 72 h., predicts that the *Datura metal* extract can be used for environmentally safe vector control programme at the sewage water system.

Key Words: *Culex quinquefasciatus, Datura metal*, larva/pupal toxicity, growth, control

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Mating behaviour of the parasitoid fly: Female choice for large males?

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Although there have been many works on oviposition behaviour and strategies of female parasitoids, studies on behaviour of male parasitoids are very few. In most species of parasitoid wasps, females are usually larger than males, and the advantages of being larger are believed to be relatively less for males than females. Therefore, many studies on behaviour and body size of parasitoids have focused only on those of females. Parasitoid flies are not exceptional in this trend, but in *Exorista japonica* (Diptera: Tachinidae), a gregarious endoparasitoid of lepidopteran larvae, males are on average larger than females. In this species males try to overtake and grasp females without any specific pre-mating behaviour. They usually grapple females on the ground, and females struggle vigorously to get rid of males. When a male seizes a female, males can successfully copulate with females.

We conducted an experiment on how male body size affected its mating success. We divided males and females into three different body size groups and observed combinations of mating pairs. While large males could mate with all sizes of females, smaller males had difficulties in mating with females larger than themselves. Large males could thus control female resistance against male mating attempts and males enjoy the advantage for being large. As *E. japonica* takes 5-6 hr for mating which is longer than reported mating durations of other species of tachinid flies, this long duration could be a mating guard behaviour, even females of this species are believed to mate only once in their life time. We also examined a possibility of multi-mating of females and discuss whether females intend to choose a large male for mating to increase their fitness.

Key Words: parasitoids, Tachinidae, mating behaviour, sexual selection

Systematic Study of the Genus *Cladura* Osten Sacken (Tipulidae) : Definitions and Diagnoses of its Species Groups

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The genus *Cladura* Osten Sacken is a group of medium sized tipulid craneflies, classified in the tribe Eriopterini of the subfamily Limoniinae, characterized by presence of cell m1 in wing venation. This genus is supposed to be one of the closest relatives of the flightless cranefly genus *Chionea* Dalman. It is distributed in North America, Far East Russia, and East Asia. Thirty-three species are described so far (five species in North America, 26 in Japan and Russia, one in China, and one in Taiwan). Adult flies appear chiefly in late autumn.

Recent study has revealed that the Japanese fauna of *Cladura* consists of more than 50 species, including at least 25 undescribed species. They can be divided into five well distinguishable species groups, mentioned below.

(1) *C. decemnotata* species group: Gonostylus with two apices.

(2) *C. nipponensis* species group: Gonocoxite long and slender. Gonostylus simple, tapered apically, and hook shaped.

(3) *C. autumna* species group: Ninth tergite with small tubercles at middle of posterior margin. Gonostylus with blunt tip.

(4) *C. megacauda* species group: The largest group. Gonocoxite with apical prolongation and mesial projections. Gonostylus variable in shape.

(5) *C. machidella* species group: Wing with supernumerary crossvein in cells r3 and r4. Gonostylus broad hook shaped.

C. japonica, the first described Japanese species, could not be assigned to any species groups, as it was described quite insufficiently with only female specimens.

In this presentation, I will demonstrate the magnificent diversity of the genus in Japan and the diagnoses of each species group, and discuss the phylogeny of these groups.

Key Words: *Cladura*, Limoniinae, Tipulidae, species groups

Sinistral coiling observed in the aedeagus of Phoridae (Insecta: Diptera)

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The epandrium and hypandrium in the male genitalia of the Phoridae are known to show left-right asymmetry. The aedeagus of the male genitalia in the Phoridae also shows asymmetric feature, but components of the aedeagus have been uncertain. The genera of the subfamily Phorinae sensu Schmitz were investigated, and their aedeagi to form asymmetric structure were examined. The aedeagus of Phoridae examined consists of only two major sclerites, inner core plate and outer jacket plate. Inner core plate is nearly tube-shaped and its proximal portion is modified to a ring which is called the basal ring by phorid researchers. Outer jacket plate is derived from right lateral portion to dorsal portion (when proximal-distal axis of the aedeagus is parallel to long body axis) and extends to the left side through ventral portion of the core plate. The jacket plate always surrounds the core plate counterclockwise (in anterior (proximal) view), and also as sinistral coiling. The basal ring is often twisted a little clockwise (in anterior (proximal) view). This feature of the aedeagus is common to genera examined. The genus *Stichillus* has simple tube-like aedeagus, and it is different from the general type consisting of the core and the jacket. Outer jacket plate in *Stichillus*, however, should be reduced to a small arm on inner core plate. Simple tube-like aedeagus in *Stichillus* is regarded as bare core plate without the jacket plate. Morphology of phorid aedeagus consisting of inner core plate and outer jacket plate is spiral, and similar to shell coiling to some extent, but coiling direction is always sinistral.

Key Words: aedeagus, basal ring, male genitalia, Phoridae, sinistral coiling

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Zoogeographical aspects of the North European fauna of Chloropidae (Diptera, Cyclorrhapha)

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The territory in question covers Scandinavian countries (Norway, Sweden, Finland), Denmark and Northwest Russia (the Kola Peninsula, Karelia, the Karelian Isthmus). The investigation of the fauna of this territory is of scientific and practical interest in different aspects: type localities and northern limits of ranges of many species are situated there, phytophagous Chloropidae play an important role in grass ecosystems, some of them being pests of cereals and cultivated fodder grasses. Chloropidae are perspective group for bioindication and ecological monitoring.

Some species Chloropidae are distributed to the North up to the coast of the Arctic Ocean, but 10 genera from recorded in the European fauna do not occur in Fennoscandia and Denmark. 204 species are found up to now in Fennoscandia and Denmark. They represent 6 groups as regards of the northern limits of their ranges. 1. Species recorded on the whole investigated territory, including Lapland and the Kola Peninsula - 44 species (21.5 %). These species are Holarctic and widely distributed transpalaearctic. 2. Species extending northwards to approximately 66^o N L (nearly to Arctic circle) - 46 species (22.5 %). Eurasian, European and Euro-Caucasian geoelements added there 3. Species extending northwards to the central part of Fennoscandia, to approximately 64-62^o N L - 32 species (15.5 %). 4. Species extending up to 60^o N L (nemoral zona) - 43 species (21.0 %). European and Euro-Caucasian species are here predominant. 5. The southernmost group includes species, recorded only in Denmark and southern Sweden - 31 species (15.1 %). The majority species are European. 6 Islands of Baltic Sea are localities for some species, which are not known on mainland – 8 (3.9 %). Species distributed far to the North are mainly Holarctic and widespread transpalaearctic, and

species recorded only in the southern part of Fennoscandia are predominantly European or Euro-Mediterranean.

Main recolonisation route after retreating ice went from southern Europe, and species groups discussed above reflect the rate of colonisation by different species and their cold tolerance. Western colonisation route along sea cost is possible to presume for coastal species *Eutropha fulvifrons* and *Eurina lurida* with Euro-Mediterranean distribution and eastern rout for some species of eastern origin. Two species *Chloropsina distinguenda* and *C. rohaceki* probably may be considered as relicts of warmer Atlantic time. A few new species of Oscinellinae, especially from the genus *Conioscinella*, are described from northern Sweden (Abisko, Norrbotten).

Key Words: Chloropidae, Fennoscandia, Denmark, North-West Russia, biogeography

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A comparison of the dolichopodid faunae of the Russian Far East and Japan

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The study of the dolichopodid fauna of the Russian Far East began with descriptions of new species of *Dolichopus* from Primorsky Krai by Stackelberg (1928). Since that time, 44 papers have been published by Stackelberg, Smirnov, Udovenco, Negrobov and their co-workers. As a result, 206 species plus 1 subspecies have been recorded, which belong to the following genera: *Argyra* (4 species), *Asyndetus* (2), *Campsicnemus* (9), *Chrysotimus* (2), *Chrysotus* (11), *Diaphorus* (4), *Dolichophorus* (1), *Dolichopus* (75 species, 1 subspecies), *Hercostomus* (19), *Hydrophorus* (4), *Medetera* (36), *Mesorhaga* (1), *Nematoproctus* (1), *Neurigona* (5), *Paraclius* (1), *Pseudoxanthochlorus* (1), *Suschania* (1), *Rhaphium* (14), *Scellus* (2), *Sciapus* (4), *Syntormon* (2), *Systenus* (1), *Teuchophorus* (1), *Thinophilus* (2), *Thrypticus* (2), and *Xanthochlorus* (1). Although the faunae of Sakhalin, the Kuriles and Kamchatka are imperfectly known, the numbers of recorded species amount to 47 (+ 1 subspecies), 29 and 48 respectively.

In contrast, the Japanese fauna of dolichopodid flies is imperfectly known. Since Matsumura (1905), who described *Dolichopus nitidus* Fallén, there have been published 29 papers by Matsumura, Becker, Parent, Takagi, Smirnov, Negrobov and co-workers, Meuffels, Kasagi, Hirashima (ed.), Saigusa, Satô, Ohishi, Saitama Kontyu Danwakai (ed.), Masunaga and Yang. There are 80 species recorded to date, which belong to the genera *Acymatopus* (5 species), *Argyra* (2), *Australachalcus* (1), *Chrysosoma* (1), *Conchopus* (17), *Condylostylus* (3), *Diostracus* (12), *Dolichopus* (5), *Hercostomus* (3), *Hydrophorus* (1), *Liancalus* (1), *Medetera* (16), *Mesorhaga* (3), *Neurigona* (4), *Rhaphium* (2), *Syntormon* (1), *Tachytrechus* (1), *Teuchophorus* (1) and *Thambemyia* (1).

Key Words: Dolichopodidae, fauna, Russian Far East, Japan

The utility of the COI barcode for identification of forensically important Australian *Chrysomya* (Calliphoridae)

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A DNA barcoding approach shows potential to be advantageous for the identification of taxa for which the use of morphology, or the association of different life stages, is problematic. For these reasons, we tested the efficacy of cytochrome oxidase I (COI) DNA barcodes for the identification of forensically important blowflies of the genus *Chrysomya* (Diptera: Calliphoridae), collected from the east coast of Australia. The identification of several *Chrysomya* species is hampered by their similar morphologies, even as adults. A 658 bp fragment of the COI gene was sequenced from 56 specimens, representing all nine Australian *Chrysomya* and three calliphorid outgroups. The second ribosomal transcribed spacer (ITS2) was sequenced from some species to verify results obtained using COI. The COI sequence divergences were calculated using the Kimura-two-parameter distance model, and a bootstrap neighbour-joining (NJ) tree was generated to provide a graphic display of the patterns of divergence among the species. We found the COI barcode to be successful for the identification of Australian *Chrysomya,* with all species resolved as reciprocally monophyletic groups on the NJ tree, with strong bootstrap support. The only exception was a specimen identified as *Ch. saffranea*, which was recovered on the NJ tree with its sister species, *Ch. megacephala*. Further morphological and molecular evidence led to the conclusion that the specimen was a hybrid, and thus it was not included in further analyses. Intraspecific sequence divergences averaged 0.097% (range = 0-0.612%), while interspecific divergences averaged 6.499% (range = 0.458-9.254%). The overlapping sequence divergences for *Chrysomya* is attributable to the low sequence divergence (mean = 0.484%) between *Ch. megacephala* and *Ch. saffranea.* We found no

difference in species delineation when we compared the NJ tree with more complex Bayesian analyses of the dataset.

Key Words: *Chrysomya*, COI, DNA barcoding, forensic entomology, identification

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Economic importance of Agricultural Diptera and their control strategies

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During the last few decades, some dipteran insects have expanded their distribution and become economically important pests in many nations. For example, the Tephritid fruit flies have become an obstacle to international or interregional trade of agricultural products. Therefore, eradicating programs have been implemented in many nations, and through sterile insect technique (SIT) complemented with other measures partial or complete success has been achieved. Agromyzid leaf miners such as *Liriomyza* spp. have also expanded their distribution as a result of an increasing international trade of ornamental and vegetable crops. Farmers have had no options but applying many agricultural chemicals against the leaf miner. However, since the leaf miners have developed high resistance to many agricultural chemicals, biological control has been developed, focusing on commercially mass-reared parasitoid wasps. This leads to introduction of exotic natural enemies that may affect native fauna and thus, as argued by many authors, in some cases biological control is no longer ecologically safe

In this lecture, focusing on the current situation of *Liriomyza* leaf miners in Japan, I will discuss the effectiveness of a new biological control strategy with naturally occurring parasitoid wasps as an alternative for greenhouse vegetables. According to literature, many parasitoid wasps attacking the leaf miner have wide host range. Generally it is considered that introducing parasitoids with wide host range may cause an adverse effect on non-target species and thus ecosystems. However, if native parasitoid fauna with wide host range are used to suppress the *Liriomyza* spp., it makes the biocontrol sound and ecologically safer. In contrast to chemical-based IPM, biocontrol-based IPM will provide us with an effective and sustainable control strategy. Some of the economically

important dipteran insects will become minor or negligible pest in agricultural lands.

Key Words: leaf miner, *Liriomyza*, garden pea, biological control, conservation

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Local differences in the frequency and temporal pattern of re-invasion of *Bactrocera dorsalis* complex (Diptera: Tephritidae) in Okinawa, southwestern Japan: Implications for different invasion pathways

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Since the *Bactrocera dorsalis* complex was eradicated from Okinawa Prefecture in 1986, the fruit flies have frequently re-invaded that area. Re-invasions sometimes caused outbreaks of the fruit flies and we have had to eradicate them again and again (e.g., Matsui, 1991). We compared the frequency and temporal pattern of re-invasion of the flies between two major island groups within Okinawa, i.e., Sakishima Islands (SI) and Okinawa Islands (OI), which are geographically distant (>300km). Adults were more frequently captured in SI by traps baited with a male-attractant, while outbreaks (detections of larvae infesting fruits) occurred more frequently in OI. Annual trap catches tended to increase in SI, but not in OI. In SI, adults were captured most frequently in summer (June), which corresponds to adult seasonal occurrence in the neighboring countries such as Taiwan. In contrast, peak catches in OI were observed in autumn (November); this pattern has never been found in other areas. These data demonstrate that the frequency of trap catches is not related to the frequency of outbreaks, and that the temporal trapping pattern in OI is independent from that in SI. The results are concordant with the hypothesis that re-invasions of the flies to SI and OI are caused mainly by natural factor(s) and human-induced factor(s), respectively. Considering the proximity of SI to Taiwan (minimum distance 111km), the higher trapping frequency and its summer peak in that area may be explained by long-range dispersal of adult flies. OI is exposed to higher risk of human-induced invasion of the flies because it holds the center of international trade and tourism in Okinawa Prefecture. Such a human-induced invasion, especially via transportation of infested fruits, might have increased the

chance of outbreaks in OI and made the temporal trapping pattern independent from that in SI and other countries.

Key Words: male annihilation, methyl eugenol, oriental fruit fly, re-invasion warning program, Ryukyu archipelago

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Host alternation by the *Paederia* flower bud gall midge, *Asphondylia* sp. (Diptera: Cecidomyiidae), with phenological information on its emergence and oviposition season

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Skunk vine, *Paederia foetida* (Rubiaceae), has recently been introduced into southeastern USA from Asia. It has overgrown on native vegetation and has caused serious damage. To control skunk vine, USDA has been considering use of biological control agents and we have been involved in this project since 2003. In Japan, an *Asphondylia* segregate, the *Paederia* flower bud gall midge (Diptera: Cecidomyiidae), has been known to induce flower bud galls on *P. foetida* during summer and autumn, but it has not been identified because of morphological similarity to some other congeners and lack of information on its life cycle except the summer-autumn season on *P. foetida*. We analyzed region of the cytochrome oxidase subunit I (COI) and 12S gene of mtDNA for the *Paederia* flower bud gall midge and other *Asphondylia* congeners on different host plants in Japan in order to identify the segregate, because recent studies revealed that some *Asphondylia* species are alternate host plants seasonally. The molecular sequencing data indicated that the segregate might be identical with the *Hedera* fruit gall midge. So, we considered that the gall midge utilizes fruit of *Hedera rhombea* (Araliaceae) during winter and flower buds of *P. foetida* during summer and autumn. Phenological data indicated that the gall midge might use another unknown host plant before coming to *Paederia* in summer after emergence from *Hedera* in May.

Key Words: host alternation, *Paederia* flower bud gall midge, *Asphondylia*, Cecidomyiidae, phenological information

Anhydrobiosis in the Sleeping Chironomid, *Polypedilum vanderplanki*

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Life and death are mutually exclusive states. But some organisms showing no sign of living due to complete desiccation are nevertheless able to resume active life after rehydration. Organisms in this peculiar biological state are highly resistant to dehydration in a condition referred to as “cryptobiosis “ or “anhydrobiosis” (Keilin, 1959). Larvae of the Sleeping Chironomid *Polypedilum vanderplanki*, lives in temporary rock pools in semi-arid areas on the African continent and is able to achieve anhydrobiosis. When the rock pools dry up, the larvae become dehydrated but can revive within about an hour after water becomes available upon the next rain (Hinton, 1958). This larva is the largest of all animals to achieve anhydrobiosis. Many anhydrobiotic animals accumulate large amounts of the disaccharide trehalose, which serves as a compatible solute thought to protect desiccating tissues by replacing the primary water of hydration and possibly through sugar glass formation. Anhydrobiotic *P. vanderplanki* larvae accumulate trehalose to levels of about 20% of their dry weight (40 µg/individual). Using a classical insect endocrine technique we also demonstrated that even larvae without a brain and thoracic ganglia could synthesize trehalose and enter anhydrobiosis successfully. Those observations indicated that induction of anhydrobiosis in *P. vanderplanki* is not under cerebral control, in spite of the fact that the brain has a significant role in regulating both induction and termination of insect diapause, in general. We also found that tehalose synthesis could be induced by exposuring larvae in 1% NaCl solusion for 1 day even without dehydration, which suggests that an increase in internal ion concentrations might be the trigger synthesizing trehalose. Several genes expressed upon desiccation were isolated from *P. vanderplanki,* and their possible functions were investigated.

Key Words: anhydrobiosis, desiccation tolerance, trehalose, *Polypedilum vanderplanki*

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Cranefly Citation Database

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The online Catalogue of the Craneflies of the World (CCW; http://ip30.eti.uva.nl/ccw/) covers the more than 15.000 species, including synonyms, distributions, etc. of the Dipterous families Pediciidae, Limoniidae, Cylindrotomidae and Tipulidae.
The catalogue is online since 2004 and was well received by workers on these families and others.
A new initative is to include for every species or subspecies an overview of all citations from the recent literature. Almost all references worldwide from 2000 to 2005 have been processed, resulting in a database with some 5300 citations.
For each citation the author, year, and pages are given, a keyword-like overview as well as a short summary of the content.
This database can be consluted directly from the CCW, at the species level. For example, a search for *Tipula helvola* gives 21 citations, none of them about systematics or immature stages, all including localities, 7 including habitat information, etc.
The database can also be consulted independently, to search for a certain topic. For example, a search on *Quercus* results in some 40 citations for 27 species.

Key Words: citations, Pediciidae, Limoniidae, Cylindrotomidae, Tipulidae

Review of the cryptic taxa within the genus *Anopheles* in Iran, with particular reference to the main malaria vectors

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Despite decades of control success and a competent network of country-wide health infrastructure, malaria remains an important health threat in rural of southeast corner of Iran. Members of 3 anopheline species complexes, *Anopheles maculipennis*, *A. culicifacies*, and *A.fluviatilis*, and also biological forms of *A.stephensi* and *A.superpictus*, are considered to be primary malaria vectors in the country. Representatives within the taxa are difficult or impossible to separate morphologically from one another, and insufficient information exists about population genetics between sibling species and vector status. This review looks at the status of the Iranian cryptic taxa using either nuclear rDNA ITS2 or mtDNA COI-COII sequences which are widely used to diagnosis of cryptic taxa. Analysis of sequence data on representatives of *A.maculipennis* complex revealed three genetically distinct species of the complex: *A.maculipennis* Meigen, *A.sacharovi* Favre and a new species named as *A.persiensis* sp.n. The sequence data of ITS2 regions of *A.fluviatilis* samples showed that from three known members of the complex only species T exists in Iran. Ongoing studies on members of the *A.culicifacies* complex in the country confirmed presence of species A and at least one of the other four (B,C,D, and E) members of the complex in Iran. Studies on *A.stephensi* showed the occurrence of all three known biological forms: ‘type”, “intermediate” and “mysorensis” in the country. Sequence analysis of *A.superpictus* specimens confirmed a new group species containing at least two members (A and B) within the taxa. The new sibling species is the first species and sibling species within *Anopheles* genus which was characterized and named principally on the basis of DNA evidence. This approach has been crucial to understanding the biology of the vectors and to discriminate among the major vectors, lesser vectors and non-vectors of ubiquitous anopheline

sibling species and could have a major impact on effective vector control programs.

Key Words: *Anopheles*, species complex, Iran, malaria

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Mitochondrial sequence variation of *Aedes albpoictus* (Diptera: Culicidae) in Japan

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Aedes albopictus (Skuse), a mosquito vector of the dengue fever virus, is originated in the Oriental region, and has been reported in more than 25 countries of various continents. In Japan, *Ae. albopictus* is widely distributed except for the northern part, though its range is expanding northwardly. To survey the genetic structure of *Ae. albopictus* in Japan, we analyzed mitochondrial DNA sequence variation in 421 base pairs (bp) of cytochrome oxidase subunit 1 (CO1) and in 406 bp of NADH dehydrogenase subunit 5 (ND5) among 240 individuals from 12 cities of Japan. Ten variable sites were found in the CO1 region, and all the variations were synonymous changes. Seven variable sites were found in the ND5 region, and 3 of the variations were nonsynonymous changes. Based on the variable sites, 22 haplotypes were identified. Although previous studies showed that populations of *Ae. albopictus* in Asia had low level of variation in mitochondrial DNA and shared a common haplotype, composition of the haplotypes varied among the cities of Japan, suggesting that gene flow is moderate between populations in Japan.

Key Words: *Aedes albopictus*, population, genetic variation, Japan, mitochondrial DNA

Flesh fly phylogeny - more meat to the bone

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The phylogeny of Sarcophagidae is ready to be upgraded into comprehensive, testable, scientific hypotheses. The monophyly of the three flesh fly subfamilies Miltogramminae, Paramacronychiinae and Sarcophaginae is well corroborated, and in contrast to the other oestroid families, the phylogenetic relationship between the constituent subfamilies is well supported. Data from larval morphology is accumulating particularly for the subfamily Miltogramminae, providing valuable information that complements adult morphology and brings clues to the major cladistic groupings within this subfamily. The small subfamily Paramacronychiinae contains several relict genera and species, and while some phylogenetic resolution is emerging, the first cladistic splits are still an entirely open issue. The large subfamily Sarcophaginae is characterized by extensive uniformity in external larval and adult morphology, and the current classification is heavily dependent on the complex structures of the distiphallus and acrophallus. Thorough documentation of these structures is leading to re-interpretations of homologies and increasing support for certain generic groupings, but widespread morphological homoplasy leaves most branches on the subfamily phylogeny with low support values. Molecular data is rapidly accumulating from both mitochondrial and nuclear genes, adding support to the already well-corroborated sister-group relationship between Paramacronychiinae and Sarcophaginae and giving much new data relevant to the phylogenetic topology of the vast genus *Sarcophaga* (*sensu lato*).

Key Words: Sarcophagidae, phylogeny, adult, larva, morphology, DNA

An overview of the Diptera of Thailand

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Thailand was not a colony, and it was not a target for extensive collecting activities on Diptera. The old material is scattered, the "classical" works on the flies of the Oriental Region contain rather few occurrence data, and Thailand (formerly "Siam") has been the type locality of a relatively low number of dipterous species.

The publication of the Catalog of the Diptera of the Oriental Region (Delfinado & Hardy 1973, 1975, 1977) was an important action in the faunistic survey of the Oriental flies, yet we estimate that more works and more first records of species were published in the last three decades than formerly. Unfortunately, neither a summary of Thailand Diptera, nor a history of the Diptera survey in Thailand has hitherto been published. So far there was no national collection of Diptera, which would serve as a solid base for a broad faunistic survey. Most recently, such a collection is under development at the National Science Museum, Bangkok.

Results of the Diptera identifications in the materials (nearly 15.000 individuals) collected by the workers of the Hungarian Natural History Museum (HNHM, Budapest) in Thailand in 2003 and 2004 are reported (supplemented by a collection in 2000 of the MHNG, Geneva). Twenty-four families are reported for the first time from Thailand, by which representatives of 99 Diptera families are known from this country. Three new genera, a new subgenus and 29 new species have been described.

The Diptera fauna of Thailand is rather unevenly known. There are families, e.g. Culicidae, Tabanidae, Strongylophthalmyiidae and Muscidae, where the majority of the extant fauna has already been made known. On the other hand, there are species rich dipterous families, e.g. Mycetophilidae, Sciaridae, Hybotidae, Empididae, Dolichopodidae, Syrphidae, Chloropidae, Sphaeroceridae, etc., in which only a minor proportion has been surveyed yet.

Key Words: taxonomy, Diptera, collecting, collection, faunistics

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The phylogeny of the Hippoboscoidea (Diptera: Calyptratae).

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The Hippoboscoidea are a superfamily of Diptera that contains the Glossinidae or tsetse flies, the Hippoboscidae, and two families of batflies, the Streblidae and the Nycteribiidae. Recently published analyses based on DNA sequences have not been able to clarify the relationships within the superfamily. Also, with the exception of the Nycteribiidae, the monophyly of the constituent families remained unsupported. Here, we present the results of a phylogenetic analysis of the Hippoboscoidea using sequence data from four genes: 28S (part), 16S, CO1 (part) and CAD (part) and a morphological data partition. Our results confirm the monophyly of the superfamily as well as that of the Hippoboscidae, the Nycteribiidae, the Glossinidae and several subfamilies and species groups. In addition, the monophyly of the "Pupipara" (Hippoboscidae+Nycteribiidae+Streblidae) is confirmed. However, our results also indicate paraphyly of the Streblidae, although this is poorly supported. Overall, the proposed phylogeny confirms Hennig's views on the relationships of the Hippoboscoidea.

Key Words: Hippoboscoidea, phylogeny, morphology, DNA

Maxillary palpal sensilla of the lower Diptera with an emphasis on the intrafamiliar variation within the Tipuloidea (Diptera)

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Scanning electron microscopy was used to examine the external morphological structure and variation in composition of the sensilla located on the apex of the larval maxillary palpus of Tipuloidea genera. The palpal sensilla of other lower Diptera families (Axymyiidae, Blephariceridae, Chironomidae, Ptychopteridae, Scatopsidae, Sciaridae, Simuliidae Tanyderidae, and Trichoceridae) were studied to aid in determining homologies between individual sensilla. The numbers of sensilla on each palpus were variable, ranging from 5-14. Five predominant sensilla (E_1, E_2, A_1, A_2, and A_3) were observed on all Tipuloidea genera and could be homologized with those in other lower Diptera. The sensilla of the maxillary palpus were typically arranged in a single cluster for out-group Diptera and for the majority of Tipuloidea genera. The families Scatopsidae and Chironomidae, and the Tipuloidea genera *Gonomyia* Meigen, *Hexatoma* Latreille, *Pilaria* Sintenis, and *Dicranota* Zetterstedt showed a split in the palpal sensilla cluster, one containing E_1 and A_1, and one with E_2, A_2, and A_3. The split in Tipuloidea genera was associated with an elongation or enlargement of the maxillary palpus and is thought to be an adaptation to predatory feeding behavior.

Key Words: Diptera, Tipuloidea, sensory receptors, maxillary palpus, crane fly

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Phylogenetic analysis of the superfamily Tipuloidea (Diptera) based on combined morphological and molecular characters

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The phylogenetic relationships of the lower Diptera have been highly contentious because of the incongruence in placement of many understudied taxonomic groups. Of these, the placement of crane flies (Diptera; Tipuloidea) within the lower Diptera has been highly problematic, the group having been placed equivocally as the most basal to one of the most highly derived clades. While well understood in terms of richness (> 15,000 species), the phylogenetic relationships of the Tipuloidea are still largely unknown. A cladistic analysis utilizing a character matrix comprised of both morphological (larval, pupal, and adult) and molecular (28s rDNA and CAD) characters was conducted in order to: (1) resolved the intrafamiliar phylogenetic relationships of the Tipuloidea, (2) provide stability in taxonomy within this group, and (3) aid in their placement within the Diptera. Independent and combined morphological and molecular analyses were largely congruent and showed monophyletic Cylindrotomidae, Pediciidae, and Tipulidae clades. The Pediciidae are seen to represent the basal most crane fly group and are a sister-group to the Tipulidae/Limoniidae/Cylindrotomidae clade. The subfamilies of Limoniidae (Chioneinae, Limnophilinae, and Limoniinae) were only weakly recovered and the group as a whole was recovered as a paraphyletic group in respect to the Tipulidae/Cylindrotomidae clade.

Keywords: Diptera, Tipuloidea, crane fly, Tipulidae, Limoniidae

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How Diverse are Empididae and Hybotidae (Diptera, Empidoidea) in New Zealand

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Empididae and Hybotidae species diversity in New Zealand were estimated by extrapolation of (a) systematic sampling data and (b) an assessment of published and other taxonomic accounts.

(a) Flight interception trap data from South Island forest sites at Kaikoura, Hope River (Ewers *et al.* 2002) and a less intensive survey of Stewart Island revealed 35 described and 22 new taxa and 24 'morphotypes' (forms not reliably identified but possibly new). Extrapolation of the ratio of new to described forms over the whole New Zealand fauna suggests that the 148 species currently known might be increased by 62-134% (239-346 species). Any extrapolation is qualified by the lack of other intensive studies in different biotopes and the likely differences in local endemicity between and within the islands of New Zealand.

(b) Taxonomic revisions have enumerated broadly similar increases in species diversity across a wide range of empidoid taxa. Studies of Hemerodromiinae for example (Plant, 2005; 2006 in prep) indicate the subfamily is 2-3 times as species rich as previously thought. Undescribed forms may account for 170% of *Hilara* Meigen and 50% *Hilarempis* Bezzi species in museum collections (I. G. Andrew *pers. com.*) and in *Ceratomerus* Philippi an estimated 26 undescribed forms (Sinclair, 1998) represents an increase of 200% over the 13 species currently known. Taxonomic revisions are usually based on material collected by general methodologies and it is likely that even greater diversity will be revealed through intensive and focused sampling protocols; for example, despite a recent revision (Plant, 1999), the number of species in the hybotid genus *Isodrapetis* Collin was increased by 50% during the present study.

The total number of Empididae and Hybotidae in New Zealand is likely to be 300-450 species; double or triple the current number. Accurate quantification will require further taxonomic revisions and the adoption of systematic sampling methods to fully interrogate all available biotopes.

Key Words: Empididae, Hybotidae, New Zealand, diversity

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Videotaped feeding behaviour of some Dolichopodidae

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A movie dealing with feeding behaviour of some Dolichopodidae (*Dolichopus*, *Hydrophorus*, *Campsicnemus* and *Sciapus*) will be shown. The observations were made in the central part of European Russia (Oksky Nature Reserve). A wide variety of food resources is used by the dolichopodids. Videotaping also provides ample details that can be used for analysis of feeding mechanisms and behaviour.

Key Words: Dolichopodidae, feeding behaviour

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Black flies (Diptera: Simuliidae) and their Diptera predators

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Black flies are attacked in all their life stages by a wide variety of organisms, ranging from birds and fishes at one end of the scale to protozoans and nematodes at the other. Some act as internal parasites, attacking mainly the larval stages. Others are predators and scavengers, and attack egg, larval, pupal and adult stages.

Insects from at least 9 orders are known to feed on black flies. The most important of these are undoubtedly the caddis flies (Trichoptera). Equally important, but under-estimated and certainly under-investigated, are the Diptera, many of which are obligate predators as larvae or adults or both.

Our research activities based on literature searches and fieldwork over the last few years have shown that there are 15 families of Diptera that prey on black flies. Some of these associations are undoubtedly fortuitous or opportunistic, but others indicate a significant and close association between black flies and their predators. Contrary to what is generally written and accepted about predation, not all predators are promiscuous in their choice of prey. It is clear that there are some very specific associations between certain Diptera predators and black flies, and this is particularly clear in the families Empididae and Muscidae which include the most significant Diptera antagonists of black flies.

Within the broad context of the "management" of black fly populations, the Diptera predators undoubtedly have a role to play. Our work has shown that this is not an insignificant role, and our ongoing investigations of both larval and adult predators are not only expected to confirm this and to reveal additional associations, but will also provide base-line information on the natural regulatory mechanisms of black fly populations.

Key Words: Simuliidae, Diptera predators

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Comparative phylogeography of the black flies (Diptera: Simuliidae) in Thailand based on mitochondrial DNA sequences

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Population genetic structures of three black fly species, namely, *Simulium tani*, *S. nakhonense* and *S. quinquestriatum*, were determined using 720 base pairs of the cytochrome oxidase I (COI) gene of mitochondrial DNA. All of these black flies had similar patterns of population genetic structure and diversity. Populations from the northern region have greater diversity and are highly structured within this region as well as being genetically differentiated from populations in other regions. Both geographical (e.g. mountain ranges) and ecological conditions of the habitat seem to be important factors in limiting gene flow and allowing populations to genetically differentiate. The greater diversity and higher genetic structure of the northern populations is likely due to the longer history of populations in this region. In contrast, populations from the south were colonized recently from a subset of the haplotypes from the lower north or central regions approximately 100,000 to 200,000 years ago followed by population expansion. The absence of genetic structure in the southern populations is most likely due to the recent history of populations in this region rather than a high level of gene flow between populations. The similar pattern of genetic structure and diversity among geographically co-

distributed species observed here reflects the shared contemporary ecological or historical (e.g. due to Pleistocene climatic change) conditions of the region. The similarity of pattern of genetic structure and diversity between *S. nakhonense* and *S. quinquestriatum* revealed by mitochondrial DNA could also be due to mitochondrial introgression.

Key Words: *Simulium*, phylogeography, population structure, population history

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Fauna and Abundance of Non-Chironomid Dipterans (Insecta: Diptera) in the Littoral Zone of Small Lakes in Northwestern Russia

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Faunal composition, habitat distribution and abundance of Diptera excepting Chironomidae were studied in the upper littoral zone of six small lakes (from lower border of the eulittoral zone to depth 1-1.5 m). The lakes constitute three pairs: northern (66°21'N 33°35'E), central (60°18'N 29°17'E), and southern (56°12'N 28°40'E).

The study first combined quantitative assessment (numbers and biomasses) of immatures in all families during the season, and reliable identification based on mass rearing to adults using three methods (rearing from separate larvae and pupae, laboratory rearing from substrata collected in eulittoral zone, and field emergence traps; over 2500 adults were reared).

A total of 59 species in 13 families develop within the littoral zone of study lakes. The numbers of species and families increase more than twice from northern to southern lakes.

Larvae of 4 families, Ceratopogonidae, Limoniidae, Tabanidae and Ephydridae were abundant and occurred in most habitats. Non-chironomid Diptera are represented mainly by insectivorous predators (all lakes), detritivores (northern and southern lakes) and phytophages of emergent macrophytes (central and southern lakes). However, Palpomyiinae (Ceratopogonidae) were only non-chironomid dipterans abundant in all lakes. All taxa except Ceratopogonidae and *Dicranota bimaculata* are confined only to stands of emergent macrophytes. A tendency to the decrease of species number from oligotrophic to eutrophic waterbodies, as well as with pH decreasing, was not expressed.

Two peculiar habitats are formed by dense stands of emergent macrophytes in southern lakes, dense turf of monocotyledones’ roots and the layer near the water surface filled with plant remains. These habitats are populated,

respectively, by turf-dwelling larvae (*Palpomyia tibialis* and root-piercing larvae: *Erioptera squalida*, *E. flavata*, *Chrysops rufipes*, *Melanogaster aerosa*, and *Notiphila* spp.) and by semiaquatic larvae typical of eulittoral zone (*Helius longirostris, Oplodontha viridula*, and *Hybomitra ciureai*).
According to literature, almost all species in study waterbodies are not confined to lakes but develop in diverse shallow-water and semiaquatic habitats.
In each lake, mean biomass varied greatly between habitats reaching maximum on sites with the least slope of bottom and low wave action. Higher biomass is typical for the following conditions: northern and central lakes, macrophyte stands or soft bottom covered with detritus; southern lakes, only dense stands of emergent macrophytes whose roots create organic-rich turf. In these conditions, mean biomass increased from northern (0.05-0.3 g/m^2) to southern lakes (1-4 g/m^2).

Key Words: littoral zone, small lakes, rearing, larvae, habitat distribution

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‘Size matters!’- Mating success determined by male-to-female size ratio in *Sepsis dissimilis*

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Here, I investigate the mating behaviour and morphology of *Sepsis dissimilis*. I describe the male courtship behaviour and use mating trials to investigate which male and female features determine mating success. The mating behaviour is characterized by seven very distinct male behavioural elements (e.g., ‘hind leg curl’, ‘mid leg wave’, ‘surstylus stimulation’, ‘wing flick’) and two female behaviours (‘female shake’ and ‘abdomen lowering’). There is intraspecific variation in the degree to which these elements are displayed, but the general sequence of events remains fairly constant. Interestingly, most of the male behaviours are stimulatory in nature and often non-contact. In order to test which morphological structures influence male mating success, I measured 13 morphological traits and use a principal component analysis (PCA) for analyzing the data (females: head width, scutum length, wing length; males- head width, scutum length, wing length, length of fore, mid and hind legs, length and angle of bent for longest femoral spine; length and width of the male surstylus). I find that mating success is positively correlated with larger male-to-female size ratio rather than actual male size. None of the sexually dimorphic features had a significant effect on mating success. The current literature emphasizes male traits, but my results suggest a need for considering female variables.

Key Words: Sepsidae, sexual selection, mating behaviour, size ratio

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The Tree of Love: The Evolution of Mating behaviour in Sepsidae (Diptera)

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Sepsid flies are well known for strongly modified male fore legs, which are used to grasp the female wing base during mounting, and genitalia that are remarkably diverse. Here, we document how these structures are actually being used during mating. We describe the behavior of sixteen species across the family in order to investigate if morphological structures change in response to changes in mating behaviours. We find that sepsid mating behaviour is amazingly diverse with each species having its own profile and we describe more than 40 different behavioural elements across the family. A detailed morphological study using SEM shows that most of the structures involved in male behaviours are not sexually dimorphic and at times even more or less unmodified between species. We also find that when we map the male fore leg interaction with the female wings onto the tree, the different types of armature have different evolutionary origins. In order to investigate the evolution of mating behaviour, we code the behavioral elements as characters and trace them on the phylogenetic tree for the family. Most characters show much homoplasy thus indicating that courtship behaviour in Sepsidae is evolutionarily labile. Our results demonstrate that studying behaviour in line with morphology provides valuable additional insights and adds meaning to reconstructing the tree of life for Sepsidae.

Key Words: Sepsidae, mating behaviour, morphology, evolution

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Responses of *Ceratitis malgassa* (Diptera Tephrititidae) female to Torula Yeast and Tri lure

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In view to implement the different methods of an IPM to control the Malagasy fruit fly *Ceratitis malgassa*. We tested and evaluated the response of this fruit fly to Torula yeast and Tri Lure. Test was carried out in two sites at different season: first during rain season (November, December and January) in temperate fruit orchard and the second time at the beginning of winter in citrus orchard. Both type of attractant were effective for capture of Ceratitis malgassa but Tri lure was more attractive than Torula yeast.

Key Words: *Ceratitis malgassa*, Torula yeast, Tri lure, attraction

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A cladistic study of the Limnophilinae (Limoniidae) using adult male characters: some light shed on the evolution of Tipulomorpha

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The Tipulomorpha, including Cylindrotomidae, Pediciidae, Tipulidae, Limoniidae, and maybe Trichoceridae, is one of the largest groups of Lower Diptera. The phylogenetic relationships among Tipulomorpha subgroups at different levels remains poorly understood. Although the monophyly of Pediciidae, Cylindrotomidae and Tipulidae seems more defensible based on existing morphological evidences, the same is not true for the Limoniidae and many of its subgroups. Among the subfamilies of Limoniidae, the Limnophilinae is perhaps the most inclined to be the big “taxonomic trash can” in the Tipulomorpha. Synapomorphic features are lacking and the group can be paraphyletic not only with respect to the other subfamilies of Limoniidae, but also to some of the other Tipulomorpha families as well. A cladistic study was conducted focused on the interrelationships among extant Limnophilinae genera and subgenera, but with a taxonomic sample of other Tipulomorpha subgroups that in some extension allowed a study of its phylogeny at higher levels. The analysis was based on 80 characters from the adult male morphology, scored from 91 species of Limoniidae (77 species in 53 genera/subgenera), Pediciidae (2 species, 2 genera), Tipulidae (4 species, 4 genera), Cylindrotomidae (4 species, 4 genera), Trichoceridae (2 species, 2 genera), Tanyderidae (1 species), and Mecoptera (1 species). In general, the results reinforce the paraphyly of Limonophilinae with respect to the other subfamilies of Limoniidae. Different solutions for the position of Pediciidae, Cylindrotomidae, Tipulidae and subgroups of Limoniidae were obtained depending on different analytical procedures and a posteriori weighting methods. Although a high level of homoplasy was encountered, the data set based on the adult male morphology has shown enough phylogenetic

signal for the recovering of completely resolved topologies. Although preliminary, the study brings new light for the understanding of the interrelationships among major crane fly lineages. Questions of relevance for future studies are presented and discussed.

Key Words: phylogeny, Diptera, Tipulomorpha, Limoniidae, Limnophilinae

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Molecular phylogeny of Mycetophilidae

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Our present knowledge about the phylogeny and classification of the Mycetophilidae is exclusively based on morphological characters, mainly from the study of adult males. Some larval characters have been used as well, but are currently of restricted value as immature stages are unknown for the majority of taxa within Mycetophilidae.

Based on resent phylogenies it has been suggested that previously recognized subfamilies and tribes are not monophyletic, but no consensus about the systematics of the group have been reached.

The present study applies molecular markers in an attempt to solve these questions. Both mitochondrial and nuclear genes are utilized. A phylogeny is proposed and the relationships within the family Mycetophilidae are estimated.

The work has been supported by funding from the "National Centre for Biosystematics" (Project nr. 146515/420), University of Oslo, Norway.

Key Words: Sciaroidea, Mycetophilidae, molecular phylogeny

Protozoan parasite *Ascogregarina* spp.: a fundamental study in the light of using the parasite for the biological control of dengue vector mosquitoes.

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Dengue and dengue haemorrhagic fever (DHF), an important re-emergent disease, has become a serious health problem recently in terms of both mortality and morbidity to humans in tropics and subtropics. In view of the necessity to develop a new vector control strategy, the consideration of *Ascogregarina* spp, the apicomplexan parasite of dengue vector mosquitoes might sound promising in the near future. In this context a comprehensive bio-molecular study on *Ascogregarina taiwanensis* and *Ascogregarina culicis* the parasite of *Ae. albopictus* and *Ae. aegypti* respectively, have been undertaken to search for the suitability and applicability of these two protozoan parasite to consider for the biological control of dengue vector mosquitoes. The study revealed some interesting biological properties in the developmental process and the dryness resistance of the oocysts, and their phylogenetic relationship with each other basing on small subunit ribosomal DNA (SSU rDNA) sequences as well. In addition, the promoter region of Heat shock protein 70 (HSP 70) gene could be successfully cloned. All the findings of the present study will serve as baseline information to use the *Ascogregarina* spp. for the biological control of the vector mosquitoes of dengue and dengue haemorrhagic fever.

Key Words: *Ascogregarina taiwanensis*, *A. culicis*, dryness resistance, small subunit ribosomal DNA, heat shock protein 70

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Availability of the puparium as a DNA source

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In forensic practice, fly puparia are often found on a corpse or coverture such as clothing even when the body is in advanced decomposition. These insect remains can provide important forensic information, if their species can be properly identified, based on their ecological characteristics: e.g., seasonal dominance, period of activity/diapause, habitat, etc. However, it is often difficult even for entomologists to accurately identify insect species from the morphology of such shells. On the other hand, a molecular biological technique that is simple and time-saving has recently been applied to identify the species of insects. We attempted to extract DNA from the puparia of two blowfly species (*Lucilia sericata* and *Calliphora vicina*) and evaluated the availability of the puparium as a DNA source. The blowflies were reared in a laboratory and the species were identified by the male genitarial shape of emerging adult flies. The puparia were collected from a rearing container and the DNA were extracted using a DNeasy Tissue Kit (QIAGEN, Hilden, Germany). The 348 base pairs of the polymerase chain reaction (PCR) products of mitochondrial cytochrome oxidase gene subunit I (*COI*) were sequenced. The DNA was successfully extracted and amplified from the puparia collected under dry rearing conditions. The mtDNA sequences of the PCR products extracted from the puparia were identical to those of the adults. Therefore, it was suggested that the puparium would be useful for a DNA source. However, caution should be taken in preserving the puparia specimens, and avoiding DNA contamination by other organisms,as with other forensic DNA samples for practical use.

Key Words: puparium, mitochondrial DNA, species identification, postmortem interval, forensic entomology

Asio-Nearctic disjunct distribution in Diptera

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Although Asia and North America are separated by the Bering Strait, some groups of Diptera are distributed exclusively in both temperate Asia, particularly eastern Asia, and North America. This Asio-Nearctic disjunct distribution was first pointed out for flowering plants by Asa Gray (1860), and the origin of this distribution is mostly explained as a relict of the Arcto-Tertiary flora, which survived during the Pleistocene in glacier–free areas in eastern Asia and North America but destroyed in Europe. This distribution pattern was then detected in several groups of insects including Diptera and other arthropods (Esaki, 1932, Linsley, 1963, etc.). In this presentation, I list the groups of Diptera that show the Asio-Nearctic disjunct distribution, divide it into several subtypes according to their range, and also to taxonomic level. In Diptera at least the following groups show an Asio-Nearctic disjunct distribution (In some groups limit of range in Asia extends to N. W. Himalayas and the Altai; some have a few exceptional representatives in Europe): Tipulidae (*Cladura*), Trichoceridae (*Paracladura*), Tanyderidae (*Protoplasa*), Ptychopteridae (*Bittacomorphella*), Axymyiidae, Cramptonomyiidae Keroplatidae (*Robsonomyia*, *Fenderomyia*), Ditomyiidae (species gp. of *Symmerus*), Mycetophilidae (*Loicia*, *Aglaomyia*, *Acomoptera*, some gps. of *Boletina*), Blephariceridae (*Agathon*, *Philorus*, *Bibiocephala*), Deuterophlebiidae, Thaumaleidae (*Trichothaumalea*, *Androprosopa*), Chironomidae (*Chasmatonotus*), Rhagionidae (*Dialysis*, *Litoleptis*), Xylophagidae (*Glutops*), Dolichopodidae (*Diostracus*), Empididae (*Megagrapha*, *Euhybus*, *Hoplocyrtoma*, *Hesperempis*, *Trichoclinocera*, *Proclinopyga*, *Ochterohilara*, subgen. *Calorhamphomyia*, the *arakawae* gp. and *unbilicata* gp. of *Rhamphomyia*). The immature stages of most of these groups are either aquatic or sylvicolous, living in soil or rotten wood. The above list does not include any group of Brachycera (Muscomorpha). It is important to clarify in the future the origin of this distribution through

detailed analyses of their phylogenetic relationships using both morphological and molecular characters – focusing particularly on the time of differentiation of the counterparts of the disjunct distribution.

Key Words: biogeography, Asio-Nearctic disjunct distribution, Arcto-Tertiary flora, Diptera

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Torrenticolous Empididae from northern Argentine Patagonia

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Through a recent field survey of torrenticolous empidids in northern Argentine Patagonia, eight species representing five genera, three known and two undescribed, were found. The monotypic genus *Dipsomyia* Bezzi is represented by an undescribed species that differs from the type species, *Dipsomyia spinifera* Collin known only from Chile, by yellow mesonotal bristles and more symmetrical fork of R4 and R5. Two males of *Proagomyia torrentium* Collin were found near its type locality. *Asymphyloptera* hitherto unknown from Patagonia is represented by an undescribed species that has a unique combination of four scutellars, incomplete fringe along posterior margin of basal area of wing and the presence of humeral crossvein, and belongs to neither the New World group nor the Australian group (Sinclair, 1995). An undescribed genus containing 4 moderately large undescribed species is similar to *Dipsomyia*, and has bare compound eyes, elongated, stout and recurved proboscis bearing setal brushes on apical portion of epipharynx, porrect maxillary palpi, setose laterotergites and broadly flattened 5th tarsomeres laterodistally produced into short processes. The genus appears to be a member of the *Ragas*-group (Sinclair, 1999), and it is extremely diversified in male genitalia, female terminalia and wing shape, vestiture and markings. They feed on small insects on wet stones in mountain brooks. The other undescribed genus somewhat similar to the former contains a small undescribed species characterized by flagellomeres incorporated into an elongate segment with tiny apical seta or style, drooping maxillary palpi and simple 5th tarsomeres.

Key Words: torrenticolous Empididae, *Ragas*-group, *Asymphyloptera*, *Dipsomyia*, Argentine Patagonia

Wing base structure of Diptera

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The interpretation of vein CuP in Diptera was simultaneously changed by Saigusa (1989) and Wooton and Ennos (1989) mainly based on the comparative morphology of wing venation between Diptera and Mecoptera. As a result of these works, vein CuP, vein A1 and anal cell in hitherto widely used terminology were interpreted as a thickened cuticular line (pseudovein), vein CuP and cell CuP, respectively. The new interpretation was supported by the comparative study of wing base structure between the two orders (Saigusa, 1993). However, the new interpretation is not widely used in current descriptive taxonomy. In this presentation I forward a plesiomorphic condition of the wing base in Diptera, propose a new terminology of detailed parts of wing base structure for the convenience of future comparative morphological work of the wing base, and criticize published works on the wing base of Culicidae (Harback & Knight, 1980), Drosophilidae (Ferris, 1965), and Calyptratae (McAlpine, 1981). The wing base structure of Diptera has the following characteristics: (1) the basicostale is reduced in size, and located below base of vein C, (2) the basisubcostale is distally enlarged forwards, where it is approximated to upper part of base of vein C, and its proximal end has loose articulation with anterior process of 1st axillary, (3) the vein Sc has a weakened membranous area on anteroventral part near its base, (4) the basiradiale is posteriorly separated from 2nd axillary by a narrow membranous slit, and its proximal end is closely articulated with basal part of anterior process of 1st axillary, (5) basal swelling of clavus is prominent, and the middle portion of its anterior margin is articulated with posterior margin of vein R stem, (6) a longitudinal internal ridge develops between veins A1 and A2, (7) the jugal area composed of bending cuticle lacks in any vein.

Key Words: comparative morphology, wing base, Diptera, CuP, anal cell

A novel Japanese isolate of *Bacillus thuringiensis* with strong larvicidal activity against mosquitoes of Culicidae

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A novel mosquitocidal isolate of *Bacillus thuringiensis*, recovered from fresh water in Japan and designated B282, was characterized and compared with the reference strain of *B. thuringiensis* serovar *israelensis* (H14). There was no significant difference between the strain B282 and the *israelensis* strain in the level of larvicidal activity against *Culex pipiens molestus*, *Anopheles stephensi* and *Aedes aegypti*. When examined with SDS-PAGE, parasporal inclusions of the strain B282 contained three major proteins of 28, 70, and 80 kDa, but lacked a 130-kDa protein present in parasporal inclusions of *israelensis*. A marked difference was also evident between B282 and *israelensis* in plasmid profiles. PCR experiments with the primers specific for the five existing genes of *israelensis* showed that the strain B282 is positive for *cry11*, *cyt1*, and *cyt2* genes, but negative for *cry4* and *cry10* genes. PCR products, amplified with primers of *cry11* and *cyt1*, were >95% homologous to the genes *cry11* and *cyt1*, respectively.

Key Words: *Bacillus thuringiensis,* Culicidae, mosquitocidal activity, *cry11*, *cyt1*

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Comparison of genetic structure between individuals re-invading Okinawa and Taiwanease natural populations of *Bactrocera dorsalis* complex using microsatellite markers: Evidence for invasion sources other than Taiwan.

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Since the *Bactrocera dorsalis* complex was eradicated from Okinawa prefecture in 1986, the fruit flies have re-invaded that area every year except one. However, there is little information on invasion sources of the fruit flies, which is important for preventing re-colonization of the flies on Okinawa. Taiwan has been believed to be a major source of the flies to invading Okinawa because of its geographical proximity (minimum 111km). We compared microsatellite variation (Dai *et al.*, 2004) between individuals of *B. dorsalis* complex that re-invaded Okinawa prefecture from 2000 to 2005 and those collected from several localities in Taiwan. Four to eight allele were found from each of six loci of the 314 individuals examined. One allele was unique to re-invaded Okinawa individuals. Though we determined alleles of 214 individuals from almost the whole area of Taiwan, this allele was not found. This is one indication of an invasion source other than Taiwan. The second indication is the difference in allele frequency between Taiwanese populations and re-invaded Okinawa individuals, when Okinawa individuals were subdivided into six groups that differ in collection year and/or localities (Okinawa Islands and Sakishima Islands). Pairwise Fst values were significant in most group pairs ($p < 0.05$). Okinawa Island populations were well separated from Taiwanese populations. In a dendrogram constructed using the Fst values, two groups from Sakishima Islands (2002, 2005) were included in a cluster together with Taiwanese populations, but three groups from Okinawa Islands (2000, 2001, 2002) and one group from Sakishima Islands (2000) formed a different cluster. This result suggests that invasions from outside of Taiwan occur more frequently in Okinawa Islands than in Sakishima

Islands. Since the center of trade is in Okinawa prefecture, there may be many opportunities for infested fruits to be brought in from outside Taiwan.

Key Words: *Bactrocera dorsalis*, oriental fruit fly, Okinawa, invasion source, microsatellite, allele frequency, Fst.

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A revision of the world *Japanagromyza* species (Agromyzidae)

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The genus *Japanagromyza* Sasakawa, 1958, was erected for a small group of species, belonging to the genera *Agromyza* Fallén and *Melangromyza* Hendel, in Japan. Later, it was found to be well represented in the Oriental-Pacific and Neotropical Regions. It is intermediate between the above-mentioned genera in the chaetotaxy: there are two pairs of dorso-central bristles as in *Melanagromyza* and normally a pair of strong prescutellar bristles as in *Agromyza.* Also, it is provided usually with a lateral bristle on fore tibia, although this character is found in some *Melanagromyza* species, and membranous tubulose distiphallus. A peculiar characteristics are the variability in colour of the halteres, development of the hypandrial apodeme and paraphallus, and number of the larval posterior spiracular openings. The halteres are uniformly yellowish white or dark brown, or variegated on knobs. The hypandrial apodeme and paraphallus are lacking or variegated in form. The larval posterior spiracular openings are three or more, or three main branches each subdivided into minute openings.

This is a predominantly tropical genus and declines northwards in the Holarctic Region. Seventy-one species are now known to occur in the world, of which 27 species from the Neotropical Region, 17 from the Oriental Region, 10 from the Australian Region, remainder 9 in the Palaearctic Region, 4 in Nearctic and Ethiopian Regions, respectively. In Japan, there are eight species, of which four are widespread in the Oriental and Australian Regions.

The larval host-plants are only known of 23 species. Of these, 19 are leaf miners, mainly on the Fabaceae, 3 gall inducers and 1 flower-bud miner. Pupation takes place in the soil. It is surprising that the mature larvae of *J. quercus*, produced further speciation of the *Quercus*-miners, jump out of the mines to a distance of maximal 61 mm in a horizontal plane.

Key Words: Agromyzidae, *Japanagromyza*, revision, world species

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Tabanid flies and other blood sucking flies as possible blood suckers of wild chimpanzees at the Mahale Mountains National Park, Tanzania

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Mahale Mountains National Park, Tanzania (6°07'S, 29°44'E), is a biogeographically interesting region; its animals and plants show affinities to those of western rather than eastern Africa, while remnants of older faunas and floras are also being preserved in the area. Mahale can be regarded as a "forest-island" in the midst of the *Miombo* woodland which extends over a vast area of western Tanzania and eastern Zaire (Congo). Surveys targeting blood sucking flies associated with wild chimpanzees have been carried out at the park, during the November-December rainy season of 1995, 1996 and 2004. A total of 14 species belonging to 4 genera of tabanid flies have been collected. In addition, the tabanid fly specimens have been stored to be examined in the Center for African Studies at Kyoto University, I found 3 genera and 3 species to be newly recorded and have been added to the list. Collected tabanid flies are mainly *Haematopota* species. The predominant species is *Haematopota fasciatapex*. From this research, *Haematopota nigripennis, H. unicolor* and *H. theobaldi* are newly recorded in Tanzania. Two tsetse species, *Glossina morsitans morsitans* and *G. longipennis*, have been collected in the vicinity of chimpanzee populations. The blood meals of *G. longipennis* are determined to be primate origin in high rate by the ELISA method. Two genera and 9 species of stomoxyn biting flies have been collected as well. Those flies are captured mainly at the grassland sites in the short period of time after the chimpanzees visited. From this research, *Haematobosca wooffi, Stomoxys omega, S. pallidus* and *S. transvittatus* are newly recorded in Tanzania. According to the results, the tabanid fly and other blood sucking flies fauna are also characteristic of central and western Africa, rather than eastern Africa together with animals and plants.

Key Words: tabanid flies, tsetse flies, Stomoxyninae, chimpanzee, Mahale Mountains National Park

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The use of acute and marked wings in the courtship behavior of *Hercostomus* sp. (Dolichopodidae)

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Modifications or ornamentations of the wings have been described as secondary sexual characters of the males in numerous species of Dolichopodidae. They provide good characters for the identification of species and may stimulate considerations about a correlation between these morphological characters and courtship behavior (Lunau, 1992; Zimmer et al., 2003).

A new species of *Hercostomus* found by K. Masunaga and the author in Southern Japan was observed on the surface of leaves or rocks on the banks of rivers. The males have the most curious wings among the known Japanese dolichopodid flies. The wings are acute and elongated toward the tip which bears a black and white spot on a small circular area. Although it should be expected that wing modifications are restricted by the requirements of flight, the present modifications do not only affect the outline of the wing surface and its coloration. The small circular tips are twisted and crossing each other above the abdomen in the resting position. The coloured and twisted wing tips are very conspicuous when viewed from behind the fly, together with contrasting black bands on the yellow hind femora.

Courtship was observed exclusively on leaves in the shade. The sequence of the male's behavior is usually performed in the following order; 1) flight display, 2) position behind female, 3) wing-opening in vertical posture, 4) wing-fanning display in vertical posture, 5) wing-fanning display in horizontal posture, 6) wing-fanning display at a slow speed in vertical posture and 7) try to copulation. The small circular tips are displayed beside the potential mate's eyes in wing-fanning display in horizontal posture. This observation confirms that the wing modifications of this species are actually used in its courtship behavior. Continued field observations may help to assess the role of signal enhancement in the view from behind.

Key Words: mating behavior, wing modification, *Hercostomus*, Dolichopodidae

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Findings of two new *Mikiola* species (Diptera: Cecidomyiidae) that induce leaf galls on *Fagus crenata* (Fagaceae) in Japan and their phylogenetic relationships with *M. fagi* in Europe

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In Japan, at least 26 sorts of midge gall have been known to occur on the leaves of *Fagus crenata* (Fagaceae). Because gall shape and galled position are species-specific of gall midges in many cases, we have considered that the 26 sorts of gall are induced by different gall midge species (Diptera: Cecidomyiidae). However, most of them have been left unidentified due to difficulties in rearing adults from larvae that overwinter in cocoons or in fallen galls on the ground. Among the 26 sorts, we have noted that two different sorts of acorn-shaped gall on *F. crenata* leaves are similar to that induced by *Mikiola fagi* on the leaves of *Fagus sylvatica* in Europe. Recently, we succeeded to rear adults of the gall midges from the acorn-shaped galls. Based on morphological features of mature and immature stages as well as the gall shape, we considered that the gall midges belong to the genus *Mikiola*, which has been represented by only two species in the world: *Mikiola fagi* in Europe and *Mikiola orientalis* inducing leaf galls on *Fagus* sp. in Asia Minor. Morphological differences between the Japanese gall midges obtained from the two different acorn-shaped galls were relatively obscure, but partial sequences of the cytochrome oxidase subunit I (COI) gene of mtDNA indicated that they are different from each other. Both species are also morphologically quite different from *M. fagi*. NJ-tree based on DNA sequencing data indicated that the two Japanese species are closely related to each other, but distantly located from *M. fagi*. The univoltine life history pattern of the Japanese species is similar to that of *M. fagi*, overwintering as pupae, which is rather uncommon in major genera of gall-inducing cecidomyiids.

Key Words: Cecidomyiidae, *Mikiola*, gall, *Fagus*, phylogenetic relationships

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Revision of the New World species of *Mesembrina* Meigen (Muscidae) with remarks on the Old World fauna

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In spite of their large size and striking appearance, flies of the genus *Mesembrina* are poorly known, and biological and taxonomic information on the New World fauna of *Mesembrina* is especially scarce. Consequently, the Nearctic fauna has been revised and the first Neotropical species described. The Nearctic *Mesembrina solitaria* (Knab) was found to be a junior synonym of M*esembrina decipiens* Loew, previously known only from the Palaearctic region and the synonymy of *Mesembrina alascensis* (Townsend) with *Mesembrina latreillii* R.-D. was supported. To place the New World fauna in context, a key to the twelve world species of *Mesembrina* has been written and a brief discussion of the intricacies of the *Mesembrina resplendens* Wahlberg complex is presented.

Key Words: Muscidae, *Mesembrina*, New World fauna, taxonomy

Diversity of Oriental *Elaphropeza* (Hybotidae, Tachydromiinae): species groups, morphological characters and distribution

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Oriental *Elaphropeza* are revised based on the old species described by de Meijiere (Indonesia), Senior-White (India), Bezzi (Taiwan), Melander (Philippines) and Smith (Nepal). In addition a large set of fresh material from Singapore, Malaysia, Northeast Thailand and Cambodia, was studied. The current status of *Elaphropeza* versus *Drapetis* is discussed on the basis of morphological analysis of the male genitalia and external characters. A number of species groups in *Elaphropeza* are recognized based on abdominal and genital structures. In addition to a varied distribution of the glands and the squamiform setae on the tergites, an enigmatic structure was found on the abdomen.

During the present study we found 47 species in Singapore. Ten species are represented by singletons, four by doubletons. This suggests that still a large number of unknown species is expected to occur in Singapore and Southeast Asia on the whole. Geographical analysis shows that few widely distributed species occur in Southeast Asia. Although the main habitat is terrestrial in *Elaphropeza*, nearly one third of the species are only found in mangrove habitats.

Key Words: Hybotidae, Oriental *Elaphropeza*, new species groups, morphology

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Molecular identification of some forensically important blowfly species (Diptera: Calliphoridae) from India

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Rapid and accurate identification of an insect specimen collected from a cadaver is of prime importance in forensic entomology based investigations. Traditionally, the identification is performed using the diagnostic morphological characters of the insect. However, these characters may bear striking similarity especially in the immature stages of different species. Moreover, the availability of only the fragmented adults and larvae of the insects, on the crime scene may further complicate the identification. Mitochondrial DNA (mtDNA) analysis seems to be a logical solution in such cases. The present study comprised of the sequencing of a short segment of 480 bp from the mitochondrial gene for cytochrome oxidase subunit I (COI) to identify some blowflies of forensic importance from India. The sequences were obtained for 21 specimens belonging to subfamilies Chrysomyinae, Luciliinae and Calliphorinae. The phylogenetic analysis of the data revealed groupings according to the genus. The present sequence database will provide a baseline data for further molecular studies in India.

Key Words: identification, Calliphoridae, forensic entomology, MtDNA, COI gene

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Diptera (flies) associated with stored products in Mahabad (urban and rural): their importance, biology and control

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Diptera, the two-winged or true flies. About 804 species have been described in approximately 108 families in Iran and new ones are being added at a rapid rate. Members of this order are involved in the transmission of more pathogens of diseases of men and animals than any other group of Arthropods; hence medical, urban and stored-products entomology must be extensively familiar with the Diptera. It is necessary to combat this flies because of their economic and Hygiene importance. This project was carried out to survey of this insect group. Samples were taken by random selection of 75 silos, storage houses, mills, bins, bakelies…etc. In the Mahabad area in this research 5 species belonging to 4 families were collected and identified, one beneficial species reported for the first time. In the area surveyed all storage and food processing buildings except silos and government storage houses are in poor construction .The private storage houses, mills, bins, bakeries were constructed from sun dried mud bricks, mud and wooden roofs were much more infested. Diptera were collected are:
Family Calliphoridae (blow flies)
1- *Calliphora vicina* R.-D. (=*erythrocephala* Meigen)
2- *Calliphora vomitoria* (L.)
The adults begins oviposition 5-9 days after emergence at 28 c°. The egg period varies according to the age of the egg when laid out the temperature and humidity most commonly 10-14 h. both species also deposit living newly hatched larvae on bacon, fish, cooked meat, meat, ham ,smoked meat or fish, cheese, jombon and sausage .
Family Piophilidae
1-*Piophila casei* (L.) the cheese skipper

The larva of the cheese skipper living on softer and riper varieties of cheese.The flies will infest proteinaceous foods such as ham, smoked meat or fish, jombon and sausage.

Family Drosophilidae

1- *Drosophila melanogaster* Meigen

The females lay from about 450-950 eggs at the rate of 15-30 per day. The larvae hatch and burrow in to the breeding material. It feeds on fig, date and dried vegetable materials.

Family Omphralidae

1- *Omphrale fenestralis* (L.) window pane fly

The white thread like worm sometimes attains a length of about three-fourths of an inch. Not injure grain or cereal products but is a predator on other insects found in mills and war houses.

Key Words: Diptera, Calliphoridae, Piophilidae, Drosophilidae, Omphralidae

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Larval competition of *Chrysomya megacephala* and *C. rufifacies* (Diptera: Calliphoridae), and its implication for forensic entomology

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Chrysomya megacephala and *C. rufifacies* are two dominant necrophagous species in Taiwan. Larvae of the latter can prey on other maggots including that of their own species as facultative foods. This facultative characteristic of *C. rufifacies* enhances its competition strength to other maggots, and could also change the situation of the other coexisted colonies. In this study, these two species were colonized in the laboratory, and the main objective is trying to understand the effect of competition on the development of larvae. According to our results, the intra-specific competition mostly occurred in competing for food; increasing the rearing density, larvae pupated earlier and resulted in lighter adult dry weight. The tendencies are similar in both species, but *C. megacephala* could develop smaller viable adults and have higher survivorship under high density. Although *C. rufifacies* could use food resource by cannibalism, its survivorship is still low. On the other hand, under inter-specific competition, the 1st instar larvae of *C. rufifacies* will invade the maggot mass of *C. megacephala* to feed together. And the 3rd instar larvae of *C. rufifacies* could expel *C. megacephala* larvae from their foods by using the surface fleshy protrusion, and the *C. megacephala* will be forced to pupate earlier by shortening their larval stages. Under mixed-specific rearing of different ratio, the larval duration of *C. rufifacies* increase as the ratio increases, but this result did not appear in *C. megacephala*. In general, under mixed-specific rearing in different temperatures and densities, both species decreased the larval duration, adult dry weight and the survivorship. However, our results did not agree with the previous studies, and we suspect the difference is probably caused by the different experimental designs. Duration of the larval stages of both species would decrease up to 54 hrs in the single-specific rearing when food is limited. The effects on the larval duration by inter-specific competition were mainly happened on

the 3rd instars and the postfeeding larvae of *C. megacephala* and on the 2nd instars of *C. rufifacies*. The largest reduced amount, ca. 25 hrs in *C. megacephala* and 34 hrs in *C. rufifacies*, of larval duration is caused by inter-specific competition under high larval density. In conclusion, competition decreased the larval duration of these two species up to 2 days; and this also draw the attention to justify the PMI estimation by using larval developmental data when larval competition is existed.

Key Words: forensic entomology, Calliphoridae, larval competition, postmortem interval

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Diptera collections in Japan

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Diptera collections in Japan are rather scatteringly housed in universities or museums. Here are introcuded some large collections of Diptera in Japanese institutes.

Hokkaido University, Sapporo, has one of the biggest insect collections in Japan. Matsumura collection contained many types of Diptera in early entomological study of Japan. Others are Shiraki collection (Syrphidae, et al.), Takano collection (Tachinidae, Sarcophagidae) and Suwa collection (Anthomyiidae and muocoids, many types); rather big general collection of Diptera are sorted into familes; general collection of Nepales insects also contains many Diptera.

National Institute of Agro-environmental Sciences, Tsukuba, houses the type specimens of Syrphidae by Shiraki and other general collection of Diptera which are sorted into to families.

National Science Museum, Natural History, Tokyo, recently took over big Diptera collections: Chironomidae of Sasa collection (mainly from Japan), Drosophilidae and some some other acalypterate Diptera of Okada collection (from Japan, Oriental and Oceanian regions), Muscidae, Sarcophagidae and Calliphoridae of Kano, Shinonaga and Kurahashi collections (mainly from Japan, Oreintal and Oceania regions, some from Afrotropical); these collections were well studied and contain many type species.

Osaka Museum of Natural History, Osaka, has recently received two big collections: Agromyzidae and some other Acalypterae of Sasakawa collection and Brachycera of Nagatomi.

Ehime University, Matsuyama, has collections of Brachycera and general acalyptrate and calyptrate Diptera in the Entomological Laboratory.

Kyushu University, Fukuoka, has big insect collections in Entomologial Laboratory and Biosystematics Laboratory; the former

houses types of Tipuliae (from Japan) by Alexander and Tokunaga, Dixiidae (from Japan) by Takahashi, Chironomidae and some other Nematocera by Tokunaga and Yamamoto; Biosystematics Laboratory has Tachinidae of Shima (mainly from Japan and Oriental region, some from Pacific area), Sciomyzidae and Clusiidae (Japan), and Sepsidae, Spaheroceridae, Fannidae, Muscidae, Sarcophagidae, and Calliphoridae from Nepal; there are also unsorted Diptera collection from Nepal.

Key Words: Japanese Diptera collection, Japanese entomological institutes, type specimens

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Tachinid fauna of Fiji Islands

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The Fijian Bioinventory Arthoropoda Project yielded (and is still yielding) more than 3,500 tachinid specimens collected by malaise traps in Fiji. I am systematically studying this collection together with Fiji tachinid collections in Bishop Museum, Honolulu, and Kyushu University, Fukuoka. Fijian tachinids have been known from 30 species including 7 introduced species for biocontrol purpose (excluding 4 uncertan misidentified species) (Cantrel & Crosskey, 1983; Shima, 1998). Ten of them, including 4 introduced species, were not found in the present collections, but 45 species were newly added, now totally 75 species of Tachinidae being known from Fiji: more than 20 species are undescribed and 2 (or 3) are unassignable to any known genera. Some of these species apparently have their relationships with Australia or New Guinea, such as *Paropsivora* sp. (Exoristinae, Blondeliini), *Anagonia* sp. (Blondeliini), *Voriella* sp. (Tachininae, Neaerini), *Donovanius transfuga* (Dexiinae, Rutilliini), *Rasiliverpa vicinella* (Dexiinae, Dexiini) and *Leverella* sp. (Phasiinae, Parerigonini), but many others appear to belong to genera of mainly known from the Oriental Region. Among this rather small number of Fiji tachinids, Leskiini appear to be diverse and include about ten endemic species of two or three genera, *Cavillatrix* and unknown ones. Siphonini comprise 3 genera of 7 species, 3 of them appearing endemic. *Pales* (Goniini) is characteristic, comprising 7 endemic species, *bezziana*, *poecilochaeta* and 5 undescribed ones. *Pales* is known from some ten species in New Zealand and the phylogenetic relationships of these species are very interesting. It is also interesting that eryciine *Palexorista,* most species of which are widely distributed over the tropical and subtropical Asia and Oceania, comprises 3 species including 2 endemic and undescribed.

Key Words: Fiji Islands, Tachinid fauna, geographical distribution

Invasion of solanum fruit fly, *Bactrocera latifrons* (Diptera: Tephritidae) on Yonaguni Island, Okinawa

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The solanum fruit fly *Bactrocera latifrons* was first discovered in cherry tomato plants on Yonaguni Island in 1984, during oriental fruit fly *Bactrocera dorsalis* eradication. This is the first record of this species in Japan. In successive host fruit surveys between 1985 and 1986, a large number of *B. latifrons* emerged from some host fruits. However, in the following 12 years (1987 to 1998), *B. latifrons* was not detected on Yonaguni Island in periodic surveys of host fruits. In 1999, *B. latifrons* was again found in bell peppers and egg plants on the Island, and subsequent surveys to 2004 revealed that *B. latifrons* was detected in large numbers year to year and was distributed all over the Island. We concluded that *B. latifrons* has already been established on Yonaguni Island. This report will summarize host fruit surveys from October 1999 to July 2004 because in this period we intensively collected solanaceous fruits of the main hosts and detected *B. latifrons*. Fruits infested by *B. latifrons* were egg plants, tomatoes, cherry tomatoes, bell peppers, red peppers, *Solanum americanum* Mill. in solanaceous plants, and *Diplocyclos palmatus* in cucurbitaceous plants. *B. latifrons* appeared from spring to autumn and was most frequent in summer. In winter, *B. latifrons* almost disappeared. *B. latifrons* has not been detected on the other islands of Okinawa Prefecture so far, though we collected numerous fruits of the hosts. At present, the distribution of *B. latifrons* is restricted to Yonaguni Island. We will discuss the possibility of invasion into the other areas including mainland of Japan. Controlling *B. larifrons* on Yonaguni Island by the sterile insect technique will then be considered.

Key Words: *Bactrocera latifrons*, invasion, host fruit, seasonal occurrence, Yonaguni island

Comparison of the adult chironomid fauna caught by light traps in Nishina Three Lakes

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Lake Aoki, Nakatsuna and Kizaki are called Nishina Three Lakes and connected in the same water system. The trophic level of each lake has been differed. These Lakes is one of the most intensively investigated lakes in Japan. But adult chironomid study is little. Asakawa (1977) only reported 40 species of adult chironomid around the Lakes. This study was conducted to clarify the species composition in Nishina three Lakes. The abundance of adult chironomid was monitored using light traps in May, August and October 2005, and February 2006. The light traps captured a total of 97 species (the total chironomid individual numbers 13,180). The dominant species was *Tanytarsus mendax* in Lake Aoki (2,394 individuals) and Lake Kizaki (693 individuals), and *Polypedilum kyotoense* in Lake Nakatsuna (1,377 individuals). The individual number and species composition showed seasonal change and differed in each lake.

Key Words: adult chironomid, different trophic level, light trap, species composition, seasonal change

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Distributional patterns of Lauxaniidae species (Diptera, Schizophora) along the Atlantic Forest, Brazil

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The Atlantic Forest used to extend along the entire Brazilian eastern coast until the end of the 19th century. Even today, this forest holds a huge biodiversity, mostly unknown. This study is part of a Project that intends to use material collected with standardized methods along the Atlantic Forest to delimit areas of endemism of Diptera groups and to apply phylogenetic and biogeographic methods of analysis to study congruence among their patterns. In this particular project, we are analyzing the geographic distribution of the Lauxaniidae, trying to verify if there is congruence between the patterns shown by species of the family and patterns from other dipteran and non-dipteran groups, known to be associated with the geological history of South America. This is a key-point because the lauxaniids could serve as indicators for the biogeographic evolution of the Acalyptratae. A pre-Cretaceous diversification of the acalyptrates would imply that their presence in the Neotropics would be due to Gondwanian origin; a more recent origin would imply in large dispersion events of clades within families along the Cretaceous or early in the Tertiary to the Region. The Lauxaniidae are one of the biggest Schizophora families – presently 57 genera and 358 species have been assigned for the region. In the present paper we consider the diversity of lauxaniids collected using sweeping in five Brazilian states, Sergipe, Bahia, Espírito Santo, Rio de Janeiro, and São Paulo. We identified 25 genera, six of which are widely distributed in the sampled area; 16 genera show a distribution restricted to two contiguous states; and three genera have a disjunctive distribution. At least 42 species have been recognized, 21 of which are new to science. Data from Malaise and Möericke traps will be added to define a more detailed picture of the Lauxaniidae distribution in the Atlantic Forest.

Financial support: FAPESP (Proc. 03/10274-9).

Key Words: Neotropical region, Lauxaniidae, geographic distribution, Atlantic Forest, endemism

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The New World species of the genus *Clinocera* (Diptera: Empididae: Clinocerinae)

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The New World species of *Clinocera* Meigen, comprising some 64 species, are divided into six species groups (three endemic to the Nearctic Region). In North America, 40 species are represented, comprising three Holarctic species (*C. stagnalis, C. nivalis, C. aucta*), three species are restricted to the East, six species are transcontinental, and 30 species are restricted to the western Cordillera. South of Mexico, only two species groups exist, with five species from Central America, five species from Brazil, 10 species confined to the western mountains from Venezuela to Tierra del Fuego and four species from the Juan Fernandez Islands. The relationships of species and species groups will be discussed.

Key Words: Empididae, *Clinocera*, Nearctic, Neotropics, taxonomy

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The morphology, higher-level phylogeny and classification of the Empidoidea (Diptera)

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A cladistic analysis of the Empidoidea and basal lineages of the Cyclorrhapha, based on morphological characters, confirms the monophyly of both groups as well as that of the Eremoneura. The resulting final trees are used to revise the classification of the Empidoidea to include the following five families: Empididae, Hybotidae, Atelestidae (including Nemedininae), Brachystomatidae (comprising the subfamilies Brachystomatinae, Ceratomerinae and Trichopezinae), and Dolichopodidae *s.lat.* The family Microphoridae is not recognized, and the Microphorinae and Parathalassiinae are assigned to the Dolichopodidae *s.lat.* The Dolichopodidae *s.str.* includes 15 subfamilies that were previously recognized within the family. Within the Empidoidea we found support for Atelestidae as the sister group to the Hybotidae and for the monophyly of Parathalassiinae + Dolichopodidae *s.str.* The Empididae remains poorly defined and the genera *Homalocnemis* Philippi, *Iteaphila* Zetterstedt, *Anthepiscopus* Becker, and *Oreogeton* Schiner are classified as *incertae sedis* within the Empidoidea.

Key Words: dance flies, long-legged flies, Empidoidea, phylogeny, cladistics

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Nocturnal larviposition by flesh flies (Diptera: Sarcophagidae)

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Immature stages of sarcophagids are often encountered on dead bodies and they may be important forensic indicators to determine the post-mortem interval (PMI). Perusal of literature reveals that forensic importance of flesh flies is often underestimated, especially if immature stages of blow flies are found on the dead body. Nevertheless the larvae of sarcophagids showing association with the carrion can play significant forensic role if their age can be determined accurately. As put forth by Greenberg (1990) and Singh and Bharti (2001), the conventional belief that these carrion breeding flies do not lay eggs at night can interfere with the correct estimation of association of their maggots with the dead body. Though night oviposition by Calliphoridae is a foregone conclusion now, nothing is known about the sister family Sarcophagidae. It has been established during the present studies that flesh flies deposit their larvae during night time as well. The methodology of Singh and Bharti has been followed to prove active attraction of flesh flies towards carrion during night.

Key Words: nocturnal larviposition, flesh flies

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Combined effect of *Bacillus sphaericus* and *Achyranthes aspera* on *Culex quinquefasciatus* Say

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In the present investigation an attempt has been made to evaluate on the methanolic extract of *Achyranthes aspera* and *Bacillus sphaericus* on the larval pupal toxicity against *Culex quinquefasciatus*. *A. aspera* at different concentrations had an impact on the different larval instars and pupal stages of *C. quinguefasicatus*. Similarly, *B. sphaericus* was also tested on the different larval instars and pupae of mosquito. Combined treatment had significant larval and pupal toxicity against mosquito than on alone treatment. The increased toxicity of plant extracts and bacterial larvicide's (Bs) may be due to the synergistic/additive effect of active compound from *Achyranthes aspera* and Bt toxins.

Key Words: *Achyranthes aspera, Culex quinquefasciatus, Bacillus sphaericus,* synergistic

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Phylogeny of the Lower Cyclorrhapha (Diptera)

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A key area of the brachyceran phylogeny that has posed ongoing problems involves the basal cyclorrhaphan lineages. Several conflicting morphological hypotheses exist. These conflicts are based partly on differences in interpretation of homology and character evolution. Molecular data should provide an independent approach to examining these relationships but up until now no molecular data have been focussed on this problem (although related studies have focussed on Empidoidea and Syrphoidea). In the present study, we attempt to synthesize morphological evidence, add new morphological characters, and focus efforts of molecular data collection on this part of the phylogenetic tree. Forty-two Eremoneura exemplars and two outgroup taxa were chosen to represent the Eremoneura diversity. Molecular data were obtained for three genes: 632 base pairs from 12s mitochondrial rDNA, 818 base pairs from the 3' end of 28s nuclear rDNA, and 4469 base pairs of the nuclear gene CAD were utilized. The results of analyses of all datasets will be presented.

Key Words: Diptera, phylogeny, lower cyclorrhapha, total evidence, ‘Aschiza’

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DNA barcodes reveal cryptic species in Costa Rican *Belvosia* (Diptera: Tachinidae)

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Insect parasitoids, including tachinid flies (Diptera: Tachinidae), are a major component of global biodiversity and affect population dynamics of their hosts. We used the cytochrome *c* oxidase DNA barcode to test the taxonomic integrity of 20 species of *Belvosia* reared from Lepidoptera hosts in the Area de Conservación Guanacaste in Guanacaste Province, Costa Rica. DNA barcodes corroborated all 20 morphospecies that were recognized, but within 3 of the morphospecies additional cryptic species were discriminated by the DNA sequence data. The 3 morphospecies that turned out to be species complexes were somewhat polyphagous as initially recognized, but the cryptic species that were revealed are highly host-specific. These results, if found to be general for other parasitoid groups, will increase estimates of global species richness and imply that tropical host-parasite interactions are more complex than expected.

Key Words: Tachinidae, *Belvosia*, species richness, DNA barcodes, cryptic species

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Phylogenetic patterns of the Andean Reinwardtiini (Muscidae) genera *Brachygasterina*, *Dalcyella*, *Psilochaeta* and *Palpibracus*

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The genera *Brachygasterina*, *Dalcyella*, *Palpibracus* and *Psilochaeta* (Reinwardtiini) are endemics to the Andean Region. Recently, the phylogenies of *Palpibracus* and *Brachygasterina* were proposed and new species of these genera were described, along with the suggestion that *Psilochaeta* is paraphyletic. Also, a new species in *Brachygasterina* extends its concept and indicates that *Psilochaeta* may, in fact, be *Brachygasterina*. To examine these relationships, we performed a cladistic analysis on all available species of those four genera (37 species, using 57 characters). The analysis resulted in two equally parsimonious cladograms of 265 steps, consistency index of 32 and retention index of 63, and two main clades. The first clade places *Palpibracus* as a monophyletic unit, supported by a strong prealar setae and the yellow thorax with a brown dorsal stripe and yellow humeral callus and yellow scutellum. The main clades within *Palpibracus* (already recognized) are supported, however the two new species changed the internal topology. The second clade includes *Philornis aitkeni* and *Synthesiomyia nudiseta*, *Psilochaeta*, *Brachygasterina* and *Dalcyella*. The target genera were supported by the weakly dilated flagellomere (also found in *Palpibracus*), males are holoptic with a greater interocular distance, prealar setae and notopleural anterior setae equal in length, and two anterior catepisternals setae. The species are as follows: (a) *Psilochaeta chlorogaster*, (b) a new *Brachygasterina* species, (c) a clade containing the other three *Psilochaeta* species, (d) three new *Brachygasterina*, not as a monophyletic group, with characters belonging to both *Psilochaeta* and *Brachygasterina*, (e) *Dalcyella veniseta* and (f) an apical clade, containing *Brachygasterina strictu sensu*, supported by the presence of a strong dilated palpus. Here, our analysis supports the inclusion of *Psilochaeta*, as well as the inclusion of *Dalcyella*, in the genus *Brachygasterina latu sensu*.

Key Words: cladistic analysis, phylogeny, taxonomy

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Phylogenetic relationships and male foreleg evolution in Sepsidae.

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The Sepsidae are a family of acalypterate flies in the Sciomyzoidea, with about 300 species in 30 genera. Here, we reconstruct the phylogenetic relationships of the Sepsidae as well as trace the evolution of male fore leg morphology on the tree. The phylogenetic relationships of Sepsidae were reconstructed based on 74 species from 20 genera, using molecular data. We sequenced 11 gene fragments totaling about 10 kbp, including nuclear (28S, 18S, EF1α, H3, AATS, CAD) and mitochondrial genes (12S, 16S, COI, COII, Cytb). Sensitivity analyses were carried out to test which weighting regime improved inter-partition congruence in the data and assessing several different alignment techniques. We re-establish that the Sepsidae are monophyletic, but with respect to the relationships within the family, there is major topological conflict between the available molecular and morphological data. The males of many sepsid genera have strongly modified fore legs bearing large spines and protuberances, while the female fore legs are relatively unmodified. Here, we study male fore leg evolution by mapping fore leg characters onto the sepsid tree. We confirm that the armature has evolved multiple times independently.

Key Words: Sepsidae, molecular phylogeny, morphology, evolution

Discovery of new species of *Pelidnoptera* Rondani and related new genus from Asia and their implications to the basal lineage of Sciomyzidae.

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With the recent discoveries of unusual feeding behavior in sciomyzid flies, it has become necessary to reconstruct their phylogenetic and taxonomic relationships. Such information is needed for further understanding of the evolutionary scenarios of sciomyzoid parasitoids and predators of gastropods, finger-nail clams, millipedes, and oligochaetes. The genus *Pelidnoptera* Rondani, 1856, includes a millipede-killing species, *P. nigripennis* (Fabricius), among the three known species from the western Palaearctic sub-region. It was hitherto considered that predation on millipedes, together with a few diagnostic adult and larval morphological characters, supported the placement of this sole genus in the family Phaeomyiidae. However, information on the phylogeny of the superfamily Sciomyzoidea is limited and most past studies have not focused on developing evolutionary scenarios for sciomyzoid parasitoids and predators. Moreover, autapomorphies and the systematic position of *Pelidnoptera* have not been tested. In this paper, we tested the monophylies of *Pelidnoptera* and the family Sciomyzidae (including the subfamilies Huttonininae and Sciomyzinae, and *Salticella* Robineau-Desvoidy, 1830, of Salticellinae), and sister-group relationships between *Pelidnoptera* and other sciomyzid genera, using adult morphological characters from fossil and living species of Sciomyzoidea, using a cladistic method. We also discussed the significance of using *Pelidnoptera* species to gain an understanding of the evolution of the Sciomyzidae. During our study of *Pelidnoptera* and while searching for out-group taxa for a cladistic analysis, two new genera and species of Sciomyzidae and a single new species of

Pelidnoptera were discovered from far eastern Russia, Japan, and Nepal. These discoveries included the first record of *Pelidnoptera* from the eastern Palaearctic sub-region. The family status of Phaeomyiidae for the sole genus *Pelidnoptera* is here considered doubtful since it appears to be an obligate parasitoid of millipedes, which is in contrast to the malacophagous feeding behaviors of most Sciomyzidae (except for two Afrotropical predators of oligochaetes).

Key Words: *Pelidnoptera*, Sciomyzidae, phylogeny, Asia, taxonomy

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Research of marine chironomid from Japan on taxonomy and ecology

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Chironomid is an aquatic insect that has a lot of species, and there is a part of species lives seawater region. Taxonomy is not advanced yet, and it is not understood how much species exist in sea region. Then, we provide information on the taxonomy and ecology of marine midges in Japan. The larval samples clarified habitat by making attention to a zonation of the intertidal zone, collecting from each layer. A past report was added, number of marine midges was 16 genus 34 species. Two new species are included in that. It was listed to have added information of habitats. The seasonal variation was investigated in the Kamagari island, the Kurahashi island and Cape Ashizuri every month. *Dicrotendipes enteromorphoe*, *Tanytarsus pelagicus* and *Semiocladius endocladiae* occurred more frequently in summer. On the other hand, genus *Clunio*, genus *Telmatogeton* and *Thalassosmittia nemalione* occurred in season from autumn to spring. Moreover, to investigate the regional distribution, it sampled in 21 points in West Japan. *Thalassomyia japonica* and *Telmatogeton pacificus* lived in the open sea coast (the south region). Occurrences of *Ainuyusurika tuberculatum* and *Yaetanytarsus iriomotensis* showed in region from the north to the south. It was clarified for a lot of species of marine midges lived changing the season within the wide range in Japanese coast.

Key Words: chironomid , marine, taxonomy, ecology, intertidal

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Scathophagidae: Molecular phylogeny and larval natural history evolution of a calyptrate family

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The 60,000 described species of calyptrates have an unusual diversity in larval life history traits which range from saprophagy over phytophagy to parasitism and predation. The relatively small family in the calyptrates, the Scathophagidae, displays with its 250 described species in 50 genera a wide variety of breeding and feeding habits which range from dung-feeding over leaf-mining to predation on caddisfly eggs. Here, we present the results of a cladistic analysis based on 63 species from 22 genera based on DNA sequences from the mitochondrial genes 12S rDNA, 16S rDNA, Cytochrome b and the nuclear genes 28S rDNA, Elongation factor 1-alpha and RNA polymerase II. The results of the cladistic analysis confirm the monophyly of the Scathophagidae. The two subfamilies Scathophaginae and Delininae are sistergroups and most genera are well supported. We also find that Scathophagidae+Anthomyiidae form a strongly supported clade within the Muscoidea superfamily of the Calyptratae. In addition, we have also subjected this dataset to an extensive sensitivity analysis in order to compare the performance of different alignment techniques (Clustal, manual and direct optimization). Based on our tree, phytophagy in the form of leaf mining seems to be the ancestral larval feeding habit. The species in the phytophagous genera (*Cordilura, Nanna, Norellia, Gimnomera*) are generally host-specific for particular monocot and/or dicot host plants where their behavior can range from boring in culms and damaging immature flowering heads to feeding on seed capsules and ovules. From phytophagy, two shifts to saprophagy have occurred. Most species of *Scathophaga* are coprophagous, with the larvae of a few species

being specialized for feeding on decaying seaweed. Predation has evolved at least twice in the family.

Key Words: Scathophagidae, Calyptratae, natural history, phylogeny, alignment techniques

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Forensic entomology cases in northern Thailand in 2000-2006

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This review reported northern Thai forensic entomology cases that were transferred for investigation to the Department of Forensic Medicine, Faculty of Medicine, Chiang Mai University, from 2000-2006. In the 26 corpses infesting with fly specimens obtained, the most common insects found were blow flies (family Calliphoridae) consisting of the species *Chrysomya megacephala, Chrysomya rufifacies, Chrysomya villeneuvi, Chrysomya nigripes, Chrysomya bezziana, Chrysomya chani* and *Lucilia cuprina*, and one unknown blow fly species. Flies of the family Muscidae (*Hydrotaea spinigera, Synthesiomyia nudiseta*), Piophilidae (*Piophila casei*), Phoridae (*Megaselia scalaris*), Sarcophagidae (*Parasarcophaga ruficornis* and unidentified species) and Stratiomyidae (*Sargus* spp.) were also collected from the human remains. The beetle, *Dermestes maculatus*, belonging to the family Dermestidae, was found in some cases. *Chrysomya megacephala* and *C. rufifacies* were the most common species found in varied ecological death scenes; both urban and forested areas; while *C. nigripes* was commonly discovered in forested places. *Synthesiomyia nudiseta* was collected only at an indoor death scene.

Key Words: forensic entomology, Thailand

Clearing technique to identify fly puparia: application in forensic entomology

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In many cases of forensic investigations, the immature stage of the fly (egg, larva or puparia) can be used as entomological evidence at death scenes, not only to estimate the post-mortem interval, but also may indicate the movement of a corpse in homicide cases. In order to achieve efficient use by forensic entomologists, identification of fly specimens found in a corpse is primarily needed. Typically, puparia of flies, particularly those of forensic importance, are similar in general appearance, being coarctate and light brown to black in color. In this study, we reported the clearing technique used to pale the integument of fly puparia, thereby allowing observation on some important puparial features (i.e. the posterior spiracle, integument or intersegmental spine between the prothorax and mesothorax), which are used for identification. We used puparia of the blow fly, *Chrysomya megacephala*, as the model species in this experiment. Being placed in 20% potassium hydroxide solution daily and then mounted on clearing medium (Permount®), the profile of the posterior spiracle and intersegmental spine of *C. megacephala* puparia could be clearly examined under light microscope beginning on the 5th day; whereas the number of papillae in the anterior spiracle was counted easily starting from the 9th day. Puparia of other blow flies (*Chrysomya nigripes, Chrysomya rufifacies, Chrysomya villeneuvi* and *Lucilia cuprina*) and a house fly (*Musca domestica*) were illustrated, focusing on the profiles of the posterior spiracle, integument and intersegmental spine between the prothorax and mesothorax.

Key Words: technique, puparia, fly, identification, forensic entomology

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Ecological study of the multivoltine sciarid fly *Ctenosciara japonica* (Diptera, Sciaridae) in a forest in Yokohama, Japan

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Knowledge of the ecology of wild sciarid fly populations is limited, mainly due to difficulty in the identification and quantitative sampling of these flies. Only one previous study has been conducted, by Steffan (1973), in which the author described the phenology of *Ctenosciara hawaiiensis* (Hardy, 1956) in Hawaii. Here I report on the ecological seasonality of *C. japonica* Sutou & Ito, 2003. Larvae of this species are phytosaprophagous and live in soil humus. Study sites were a broadleaved forest dominated by *Castanopsis cuspidata* (site 1) and a coniferous forest dominated by *Pinus taeda* (site 2) in Yokohama, Japan (35˚28'N 139˚35'E, 60 m alt.). Adults of *C. japonica* were collected by net sweeping from April 2002 – March 2003 and April 2005 – March 2006. Sampling occurred twice per month, once during the first half, and once during the second half; each sampling consisted of 90 minutes of sweeping at each site. Throughout 2 years of sampling, I collected 607 adults at site 1 and 1001 adults at site 2. At both sites, the phenology of this species showed five peaks per year: May, early July, late August, October, and December; with the highest peak recorded in May. The sex ratio of collected specimens differed markedly between early summer and autumn: females comprised 72% and males comprised 28% of the samples in May, whereas females and males comprised 30% and 70%, respectively, in October. The seasonal variation in adult body size was minimal in summer and maximal in winter–spring. The longevity of newly emerged adults was measured in May, August, and December 2005, and it was lowest in August<May<December. Seasonality of this species was compared to monthly mean soil temperatures at site 1 and litterfall input at sites 1 and 2. A negative correlation between body size and soil temperature was found.

Key Words: Sciaridae, *Ctenosciara japonica*, ecology, phenology, Japan

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Immature stages of three species of the genus *Sciara* Meigen (Diptera, Sciaridae)

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The family Sciaridae is a large family that includes approximately 1800 described species worldwide. Recently, phylogenetic analyses of the genera of this family and that of the superfamily Sciaroidea were conducted based on the adult morphology (Menzel & Mohrig, 2000; Vilkamaa & Hippa, 2004; Hippa & Vilkamaa, 2005). Ecological studies have reported high abundance of sciarid larvae in terrestrial ecosystems, suggesting their functional importance in leaf litter decomposition in temperate forests (Hövemeyer, 1999; Sutou & Ito, 2005). To date, knowledge of the immature stages of sciarid flies is very scarce. The examination of the larval and pupal morphology of these flies will contribute to both the systematics and ecology of this family. The present study reports on the detailed morphology of final-instar larvae and pupae of three species of *Sciara*: *S. hemerobioides* (Scopoli, 1763), *S. humeralis* Zetterstedt, 1851, and *S. helvola* Winnertz, 1867. These species were originally described in Europe and were newly recorded in Japan by Sutou *et al*. (2004). Sciarid larvae are normally devoid of body processes or setae, and the taxonomic importance of the structures of the head capsule and spiracles (prothoracic and seven pairs of abdominal spiracles) are emphasized here. Eight sensory pits of the frontal apotome and ten sensory pits of the genae of the larval head were numbered for comparison. The arrangement of these pits shows several differences among the three species. Each spiracle consists of a crescentic scar and a circular opening with no differences among species. Sciarid pupae are also hairless. Characters of the head, legs and spiracles were examined, and the sexual differences in their habitus are noted. Application of molecular identification by COI gene sequencing is proposed for these larvae. Finally, a photo of a newly discovered "army worm" from Japan (sciarid larvae, probably *Sciara* sp.) is presented.

Key Words: Sciaridae, *Sciara*, larva, pupa, taxonomy

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Some peculiar species of Anthomyiidae in Japan

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In Japan 222 species of Anthomyiidae have been recorded. Most of them are widely distributed in the Palaearctic or the Holarctic region, or have their allies in the region. Some are, however, very different from the northern elements and have a lot of allies in southern China or the Himalayan ranges, being exemplified by *Pegomya chinensis* Hennig, 1973, *Pegomya nigra* Suwa, 1974, *Phorbia asymmetrica* Suwa, 1974, etc. Some others have a few allies disjunctly distributed outside Japan, being exemplified by *Chirosia asymmetrica* Suwa, 2006, *Hydrophoria japonica* Suwa, 2002, *Hyporites shakshain* Suwa, 1974, and so on. The members of the former group are understood to be descendants of lineages originated in mountainous ranges of southern Asia from the ancestors with northern origin. On the other hand, the members of the latter group might be interpreted as relics descended from the ancestors distributed in northern ranges. The anthomyiid fauna of Japan basically composed of northern Palaearctic elements is enriched with southern elements and relics.

Key Words: Anthomyiidae, Japan, fauna, peculiar species, origin

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Calyptrata flies in pig carrion in Central Europe - forest habitats

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A study concerning insect succession on animal models in various forest habitats resulted in 3006 adult specimens of Calyptrata flies belonging to 34 species. Most abundant and species rich were Muscidae (2234 adult specimens and 23 species) dominated by *Thricops simplex* (Wied.) and the predaceous *Hydrotaea* spp. (492 specimens, 8 species). Among blowflies most abundant (both adults and third instar larvae) were *Calliphora vomitoria* (L.), *Phormia regina* (Meig.), and *Lucilia caesar* (L.). Three other species of Calliphoridae as well as Anthomyiidae, Scathophagidae and Sarcophagidae were represented only by few specimens. High abundances of adult *Thricops simplex* (Wied.) and *Hydrotaea* spp. are correlated with very low abundances of their larvae. Possible reasons for the high abundance of Muscidae and assumed links between particular species and carrion decomposition are discussed. Frequency spectra of the most abundant Calliphoridae and Muscidae are presented.

Key Words: succession, pig carrion, Calyptrata, Central Europe, forensic entomology

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Morphology of the first instar larvae of satellite flies (Diptera: Sarcophagidae: Miltogramminae)

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Satellite flies show unusual morphological variability of the first instar larvae among oestroid flies. Using a combination of light and scanning electron microscopy, we are studying the morphology of the cephaloskeleton as well as the general external morphology. Variability concerns the shape of antenna, maxillary palpus and other sensory organs of the pseudocephalon, deep modifications of the first thoracic segment, various types of cuticular swellings and ridges on the integument, occurrence of prolegs and various types of lateral papilla on abdominal segments and modifications of the anal division. This morphological variability corresponds probably to the cleptoparasitic life-history and appears to be the result of the existence of a free-living first instar larva in this taxon. Many larval characters carry phylogenetic information and might be used for an improved classification within the subfamily. In the light of these findings concerning the morphology of the first instar larvae the systematic position of selected genera is discussed.

Key Words: morphology, first instar larva, Sarcophagidae, Miltogramminae, SEM

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Positive indirect effects of deer browsing on dwarf bamboo for the abundance of gall midge

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To examine the indirect effects of deer browsing for the abundance of gall midge, we investigated density of the bamboo culm gall midge (unidentified, tribe Oligotrophini) in- and outside of the deer exclosures. The gall midge studied here forms bean-shaped galls on culm of the dwarf bamboo (*Sasa nipponica* Makino et Shibata), the major forage for Sika deer (*Cervus nippon* Temminck). Field study was conducted at Mt. Ôdaigahara, in west-central Japan from 1997 to 2004. Gall and larval density was ordinary low (both area and plant level) at inside of deer exclosures where the bamboo culms were longer and the density of bamboo shoot were low due to their escape from browsing. On the other hand, at outside of deer exclosures, bamboo culms were shorter but dense by compensation growth of bamboo against deer browsing. Although gall and larval density was low inside of deer exclosures, midge females selected large one as oviposition site in the choice experiment of large and small bamboo sprout. This result suggests that large bamboo sprouts have some resistance for the gall formation because large bamboo sprouts would be oviposited more eggs in the field. In summary, deer browsing produce small and galling-susceptible bamboo and causes positive indirect effect for the abundance of gall midge.

Key Words: community ecology, indirect effect, Cecidomyiidae, Gramineae, Cervidae

Phylogeny of the tribe Exoristini based on morphological and molecular data (Diptera, Tachinidae)

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The tribe Exoristini has approximately 250 species belonging to 21 genera in the world. This is one of oviparous tribes in the family Tachinidae, where females lay the unincubated eggs directly on their hosts. This reproductive strategy is considered to be primitive within this family (Herting, 1960). In morphological analysis the monophyly of the Exoristini has been so far suggested by many researchers (e.g. Herting, 1957; Wood, 1972; Tachi & Shima, 2006). Stireman (2002, 2005) showed that the tribe was monophyletic using the nuclear genes (28S rRNA and elongation factor 1-alpha). However, only five species of three genera were used in his analyses.

To elucidate the monophyly of the Exoristini and the phylogenetic relationships within the tribe, we conducted phylogenetic analyses with the mitochondrial DNA (16S rRNA and ND 5), nuclear DNA (18S and 28S rRNA) and morphology. Based on the mitochondrial data analysis, the monophyly of the Exoristini is weakly supported and a few generic relationships within Exoristini are shown, though detailed affinities are still unclear. On the other hand, the nuclear data suggests that the Exoristini is not monophyletic, forming that *Phorinia* and *Ctenophorinia* being clustered with members of the Blondeliini.

In this presentation, we show phylogenetic relationships within Exoristini based on the morphological and molecular data, and discuss the differences in the generated trees.

Key Words: parasitoid, systematics, mitochondrial DNA, nuclear DNA

Species Information Database KONCHU on Japanese, East Asian and Pacific Insects

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A publically available entomology database KONCHU is a general database name which includes six files at present, such as bibliographical (KONCHUR), checklist (MOKUROKU), dictionary (DJI), image (HANABACHI=bees; TOBIKOBACHI=encyrtid wasps) and type specimen (ELKUType) databases. The KONCHUR is based on main Japanese entomological journals (19 journals at present) and includes many East Asian and Pacific insect records as well as the Japanese ones. The MOKUROKU and DJI are the check list of the Japanese insects and a dictionary of the Japanese insect names which includes all the Japanese species. The HANABACHI and TOBIKOBACHI are the image databases of the Japanese bees and encyrtid wasps including various parts of the body. The ELKUType is a type specimen database based on the Type Collection of the Entomological Laboratory, Kyushu University, Fukuoka, Japan. The records of KONCHU are written mainly in English, and in Japanese with katakana and kanji characters. The KONCHU is administered by a text database management system SIGMA. The KONCHU has been opened to the public via the INTERNET. A user can access to the KONCHU by retrieving the following URL: http://konchudb. agr.agr. kyushu-u.ac.jp/. Outline, usage and examples of use of the KONCHU are presented.

Key Words: entomology database, species information, Japan, East Asia, Pacific area, image

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***Wolbachia* infection in *Liriomyza trifolii* and its potential as a tool in insect pest control**

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In Japan, the leafminer Liriomyza trifolii is an important insect pest. We detected the Wolbachia strains in L. trifolii populations and investigated the effect of *Wolbachia* infection on the host *L. trifolii*. An uninfected female never produced offspring on mating with an infected male, implying that *Wolbachia* induced strong cytoplasmic incompatibility against *L. trifolii*.

Kaspi and Parrella (2003) developed a new method for controlling *Liriomyza* populations. They considered the simultaneous use of a natural enemy (*Diglyphus isaea*) and sterile *L. trifolii* treated by radiation. A *Wolbachia*-infected male acts as a sterile male when mated with an uninfected female and is useful against uninfected populations. It is convenient to use infected strains because unlike the irradiated strains, infected strains do not need to irradiation for subsequent generations to function as sterile males.

Only few populations of *L. trifolii* were infected with *Wolbachia* in Japan, and *Wolbachia* infections have never been reported in other countries. Moreover, *Wolbachia* strains possibly transfect other host species such as *L. sativae* or *L. huidobrensis*. Thus, *Wolbachia* strains that infect *L. trifolii* can be used as a tool in insect pest control.

Key Words: *Liriomyza*, *Wolbachia*, cytoplasmic incompatibility, sterile insect technique

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Current situation of maggot therapy in Japan

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Maggot therapy is one of the effective medical procedures to treat chronic wounds, such as diabetic foot ulcers, arterial and venous ulcers, pressure ulcers and so on. The number of the patients treated by maggot therapy has been increasing these several years in Japan. The larvae of *Phaenicia sericata* (classified by some as *Lucilia sericata*) have been successfully used. However, there are still some problems to be solved, such as prejudice of dirtiness, lack of evidences of effectiveness, difficulty of commercialization and etc. We will report the current situation of maggot therapy in Japan, and discuss views on the future of this treatment.

Key Words: maggot therapy, *Phaenicia sericata*, *Lucilia sericata*, chronic wounds, commercialization

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Clinical and microbiological studies on the use of medicinal maggots in the management of diabetic foot ulcers

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The management of diabetic foot ulceration remains problematic despite advances in treatments. Recently, the use of maggot therapy for treating chronic wounds has been revived and is now increasing worldwide. We investigated the clinical and antimicrobial efficacies of medicinal maggots of *Lucilia sericata* in the treatment of nonhealing diabetic foot ulcers irresponsive to conventional therapies and surgical intervention. A cohort of 10 patients with 13 diabetic foot ulcers at the Diabetic Foot Unit of Alexandria Main University Hospital was selected for this study. The ulcers had an initial mean surface area of 23.52 cm² (range 1.32-63.13 cm²). Necrotic tissue represented a mean of 68.77% (range 29.97-100%) of size of ulcers. Nineteen biochemically different bacterial isolates were identified from the ulcers. All ulcers exhibited mixed bacterial populations ranged from 2 to 6 isolates. Initial bacterial burden of ulcers varied from 3.7×10^5 to 8.2×10^9 CFUs/g of ulcer fluid. One cycle of maggots was applied each week; each cycle lasted 3 days. Ulcers were examined for healing up to 12 weeks. Maggot therapy was associated with rapid removal of necrotic tissue, enhancement of healing, and marked antimicrobial activity. All ulcers completely debrided during a mean period of 2.62 weeks (range 1-8 weeks) and through a mean of 2 cycles (range 1-4 cycles). A mean of 38.16% decrease in size of necrotic tissue per week was recorded. The mean surface area of ulcers was significantly decreased ($P = 0.001$) within a mean period of 8.10 weeks (range 2-12 weeks). A mean of 11.09% decrease in size of ulcers per week was noticed. Eleven wounds (84.62%) completely healed during a mean period of 7.36 weeks (range 2-

10 weeks). After the first cycle, the bacterial burden of each ulcer was dramatically reduced to less than the 10^5 bacterial count threshold which permits healing.

Key Words: maggot therapy, *Lucilia sericata*, diabetic foot ulceration, wound management, chronic wound bacteriology

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Report of flies on the Lesser mouse eared bat (*Myotis blythii*) from Kermanshah, Iran

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Various groups of animals such as insect, acarina, invertebrates and amphibians have been reported from deep cave and also on the bat lives in the cave of various parts of the world. In this study we collected flies included two families (Streblidae and Nycteribiidae) on the Lesser mouse eared bat (*Myotis blythii*) in cave close to Kermanshah city. This city is the centre of Kermanshah province which is located in west of Iran neighboring with Iraq. We found eight flies of two bats, comprising three males of Streblidae and two females and three males of Nycteribiidae families. This is the first report on presence of Streblidae and Nycteribiidae families in Iran. Results of this study could be used in epidemiological studies of vector borne disease transmitted by flies.

Key Words: fly, Streblidae, Nycteribiidae, *Myotis blythii*, Iran

Malaria Vector Control after 40 Years Malaria Eradication in Taiwan

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Malaria is documented to have been prevalent throughout much of Taiwan in the 19te and 20th centuries. As a result of the effective strategy by using indoor residual house spraying with DDT (0.5-2.0 g of active ingredient per m2), the WHO declared Taiwan free from malaria in 1965. However in 2003, the reporting of 2 locally acquired malaria cases in a rural area causes a concern about malaria control. Among the 15 Anopheline species that are currently found in Taiwan, Anopheles minimus L is regarded as the principal malaria vector. Other potential species, Anopheles sinensis Wiedemann, An. maculatus Theobald, An. ludlowae Theobald, An. tessellatus Theobald, An. jeyporiensis Koidzumi, and An. annularis Van der Wulp have been implicated in malaria transmission in other countries but are not considered to be important in Taiwan.

The principal risk factors for malaria transmission in Taiwan were to sleep outdoors in hillside areas during the hot months and the raising of animals in proximity to the home. However, because of the extremely low parasite-human-vector contact, effective surveillances on malaria patients as well as mosquito vectors and protection from mosquito bites were more important than vector control itself. Therefore, the prevention should be focus on screening of the houses, the monitoring of malaria *Plasmodium* carrier movement in the high-risk areas (i.e. the areas with the presence of *Anopheles minimus*), and personal protection to reducing mosquito bites in outdoor night activities. No *Anopheles* mosquitoes were collected inside the 100 houses from 12 villages in a 2005 study; indoor residual house spraying with insecticides is no longer an effective method to control malaria in Taiwan. Hence, if locally acquired malaria is confirmed, an outdoor spraying was recommended.

Key Words: malaria vector control, *Anopheles minimus*, Taiwan

Morphological and Molecular Identification of Forensically Important Sarcophagidae (Diptera) in Taiwan

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By the analysis of the species found on a corpse and the record of the ambient temperature, investigators are able to estimate the date of death. Here we report the forensically important Sarcophagid flies in Taiwan. Forty-seven samples of Sarcophagid flies were collected from different area of Taiwan. The species identifications were based on morphology and DNA analysis of the cytochrome b oxidase subunit I mitochondrial gene. Six species, *Parasarcophaga crassipalpis, Parasarcophaga misera, Parasarcophaga dux, Parasarcophaga ruficornis, Boettcherisca pergrina, Seniorwhitea princeps* were initially identified by morphology. Then the DNA analysis results showed that the COI sequence variation within the intraspecies of *Parasarcophaga dux* is 1-2%. We suspected that there were three groups within the populations of *Parasarcophaga dux* in Taiwan area. Re-examine the specimens of dux found that they are morphologically very similar to each other, but there are somewhat difference among these three groups. Each group is not region specific, but can be collected from different region.. We also found that the DNA sequence variation between the individual of *Boettcherisca pergrina* ranging from 1 to 3%. The re-examine of the morphology difference is performing. The variation in the *Parasarcophaga dux* and that of *Boettcherisca pergrina* will be discussed in the paper.

Key Words : forensic entomology, Sarcophagidae, mitochondrial DNA, intraspecies

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Developmental velocity and the time of emergence in a day for *Diadiplosis hirticornis* (Diptera: Cecidomyiidae) attacking *Planococcus kraunhiae* (Homoptera: Pseudococcidae)

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A mealybug, *Planococcus kraunhiae* (Kuwana) (Homoptera: Pseudococcidae), is one of the most serious insect pests of persimmon in Japan. Frequently we have observed predatory larvae of *Diadiplosis hirticornis* (Felt) (Diptera: Cecidomyiidae) feeding on the mealybug. To establish control measures against the mealybug with *D. hirticornis* as a biological control agent, we need to gather basic information on the ecological and behavioral attributes of *D. hirticornis*. As the first step, we investigated its developmental velocity at 20, 22.5, 25, 27.5, and 30℃ and the time of emergence in a day. The developmental threshold for male and female was estimated to be 9.6℃ and 10.2℃, respectively, and temperature accumulation required for the development from egg to adult was calculated to be 250 day-degrees. The time of emergence differed between sexes. The males emerged exclusively between 6:00 and 12:00 in the morning, while most females emerged between 10:00 and 18:00.

Key Words: *Diadiplosis hirticornis*, *Planococcus kraunhiae*, predator, developmental velocity, developmental threshold, day-degree accumulation, time of emergence

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Mosquitocidal effect of *Murraya Koenigii* Spreng. against *Anopheles stephensi* Liston

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In the present investigation a study has been made to evaluate the effect *of Murraya koenigii* leaf extract against malarial vector, *Anopheles stephensi.* Methanolic extracts treatment considerably affected on the larva and pupa of mosquito. *M. koenigii* extract brought out higher larval and pupal mortality. Lethal concentrations (Lc50 and Lc90) values were also included on the treatment of plant extracts against 4th instars larva and pupa of mosquito. Plant extracts at lower dose treatment also exhibited growth inhibitory effect and also showed anti-emergence activities. Plant extract also possess repellent activities against mosquito species. The mosquitocidal properties of plant extract mainly due to the active chemical compounds in the plant and it has been discussed on the practical mosquito control programme in the drinking water system.

Key Words: *Anopheles stephensi*, *Murraya koenigii*, larvicidal, repellency

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Maggots to the Rescue: Using maggot therapy for wounds in hospice patients

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Introduction: Wounds are a problem that affect over 1/3 of hospice patients (Tippett, AW. Wounds at the End of Life. Wounds, April 2005), and often these wounds are severe, with various causes: ischemic, pressure, diabetes, trauma and surgical. Many times debridement of the wounds is indicated, due to infection, sepsis, pain, necrosis, or gangrene, but patients usually are not candidates for surgical debridement, including amputation of limb. Often other debridement forms such as wet to dry, or enzymatic, are not appropriate due to issues of pain, cost, or time constraints (e.g. infection with sepsis needs urgent debridement). Sometimes debridement is not seen as consistent with palliative care. This paper presents a selection of case studies of the use of *Phaenicia sericata* larval therapy (maggots) for wound debridement in hospice patients.

Methods: A selection of case studies from wound treatment of hospice patients over a three year period to illustrate wound types, problems, and outcomes are presented. The cases were selected to be representative of the types of wounds encountered that could benefit from maggot therapy.

Results: In all cases goals of therapy were achieved. Results included: resolution of sepsis, prevention of amputation, elimination of infection, reduced pain and odor, and in some cases, wound healing. Therapy was well tolerated in all cases.

Conclusions: Maggot therapy is a very viable option for treating complex wounds in hospice patients when debridement is indicated. Maggot therapy is rapid, inexpensive, nearly painless, simple, quite gentle, and consistent with goals of palliative care. Standard protocols are published and easy to follow (Sherman, R. Maggot Laboratory. www.ucihs.uci.edu/com/pathology/sherman/). Families and patients are very involved, and grateful for such innovative therapy, with newfound respect for one of nature's often maligned creatures.

Key Words: maggot, debridement, wound, hospice

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Fallen leaves revitalized by a gall midge

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Many biologists have paid special attention to plant-herbivore relationships for studying biological interactions and coevolutionary processes. Among herbivores, galling insects are notable in that they manipulate plant tissues in a sophisticated manner to induce specific plant morphology for their own sake. Here we report a gall midge, *Contarinia* sp. (Diptera: Cecidomyiidae), that induce leaf galls on *Styrax japonica* and shows a striking ability to regulate the survival, growth, and multiplication of host plant cells. While larvae of other *S. japonica*-associated gall midges mature quickly and leave their leaf galls before summer, the *Contarinia* species remained as first instar in the galls throughout summer. The larvae started to develop into second and third (=final) instars in September, when many galled and ungalled host leaves had already fallen. Coincident with the larval development, flat subglobular galls started to grow into globular shape, even when the galls were on fallen leaves. On the fallen leaves, the number and size of the plant cells in the gall tissue significantly increased during September. Even when the ungalled portion of fallen leaves had already died, the galled portion was fresh until the midge larvae left the galls in October. In an attempt to understand the underlying mechanism of the phenomenon, we analyzed the chlorophyll fluorescence and carbon fixation reflecting the photosynthesis activity of the gall tissue, and the C:N ratio of the gall tissue during the gall development on the fallen leaves. We also investigated the performance of gall midge larvae in the galls on the fallen leaves under manipulated environmental conditions: e.g. different light conditions; attached to, half-detached from, or completely-detached from the surrounding leaf tissue; etc. Based on these results, we discussed possible mechanisms as to how the gall midge controls the cellular growth and division in plant tissue of the fallen leaves.

Key Words: Cecidomyiidae, *Contarinia*, gall, green island formation, plant-herbivore interaction

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Occurrence of *Contarinia* sp. (Diptera: Cecidomyiidae) infesting cultivated roses in Japan

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In recent years, an unidentified species of *Contarinia* (Diptera: Cecidomyiidae) inducing leaf-fold galls on cultivated roses has been found at various localities in Japan. Because similar gall midges have never been reported from cultivated roses in other countries and from native roses in Japan, whether the *Contarinia* species is native to Japan or not is uncertain at the moment. In general, galling cecidomyiids are considered to have narrow host ranges, but recent studies have revealed that some gall midge species exhibit polyphagous habit. For example, *Contarinia maculipennis*, known as a pest of orchids, infests flower buds of other plant species across seven families. In order to identify the *Contarinia* species infesting cultivated roses in Japan, we compared its morphological features with *C. maculipennis* and other congeners and analyzed partial sequences of mitochondrial DNA cytochrome oxidase subunit I region for the *Contarinia* species collected from cultivated roses in Japan. As a result, the *Contarinia* species was morphologically distinguishable from *C. maculipennis*, some other pest species of *Contarinia*, and known native Japanese species of *Contarinia*. By molecular phylogenetic analysis, we detected several haplotypes in the *Contarinia* species collected from cultivated roses, which seem to reflect geographical variations, suggesting that each haplotype might derive from a native gall midge population in the respective localities. In addition, we examined ecological traits of the *Contarinia* species in the greenhouses and under laboratory conditions. Based on these results, we discuss the taxonomic position and possible origins of the *Contarinia* species infesting cultivated roses in Japan.

Key Words: Cecidomyiidae, *Contarinia*, gall midge, leaf-fold gall, *Rosa*

Seasonal prevalence and species composition of *Liriomyza sativae* Blanchard, *L. trifolii* (Burgess), and *L. bryoniae* (Kaltenbach) (Diptera: Agromyzidae) on commercially grown tomato plants in Kyoto Prefecture.

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In Japan, the vegetable leafminer, *Liriomyza sativae* Blanchard, was found for the first time in Okinawa, Yamaguchi, and Kyoto prefectures in 1999 (Iwasaki et al., 2000), and it is now distributed in western Japan (Tokumaru et al., 2002; Tokumaru and Abe, 2003). The American serpentine leafminer, *L. trifolii* (Burgess), was found for the first time in Japan in 1990, and has spread rapidly throughout the country (Saito, 1992). In Kyoto Prefecture, this fly was recorded for the first time in 1995 (Saito, 1997). The tomato leafminer, *L. bryoniae* (Katenbach), was known to be an important pest of eggplant, tomato, (Sasakawa, 1966), potato (Haruki and Tomioka, 1962), and melon (Ikeda and Oishi, 1987).

From August to December 1999, *L. sativae* coexisted with *L. trifolii* and *L. bryoniae* on commercially grown tomato plants and these three species had different peaks in a greenhouse in Muko City, Kyoto Prefecture (Abe and Kawahara, 2001). In the present study, to document the relative abundance of the three *Liriomyza* species after invasion by *L. sativae*, the seasonal prevalence of *L. sativae*, *L. trifolii*, and *L. bryoniae* infesting commercially grown tomato plants was surveyed in two greenhouses in Kyoto Prefecture from 2000 to 2002.

Only *L. bryoniae* was found from April to July 2000 and 2002, but from August to December 2000 and 2002, *L. sativae* was predominant. Throughout 2001, *L. sativae* was predominant with a few *L. bryoniae*. In 2001 and 2002, *L. trifolii* was not found at all. After invasion by *L. sativae*, *L. trifolii* population decreased suddenly throughout the year, and *L. bryoniae* population decreased after August.

Key Words: *Liriomyza sativae*, *Liriomyza trifolii*, *Liriomyza bryoniae*, seasonal prevalence of occurrence, species composition

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Solving basal phylogeny and some taxonomic problems within family Ceratopogonidae (Diptera) using 16S rDNA sequences

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The family Ceratopogonidae is a diverse and interesting family of biting flies containing vectors of viruses, protoza and nematodes as well. Sequences from the mitochondrial 16S rDNA gene were analysed for 16 species of the family Ceratopogonidae representing 6 genera of 3 subfamilies. Phylogenetic reconstruction by NJ, MP and MP methods gave a strong support to the monophyly and the recent systematics of the family. The analysis of the 16S rDNA sequences supported the separation of the family to the subfamily and tribe level. We documented also the ability of 16S rRNA gene sequences to distinguish species within a genus. Obtained results in general confirmed the intrageneric classification and helped to resolve some taxonomical problems, i.e. supported the validity of species *Dasyhelea saxicola*, *D. versicolor* and *D. septuosa*, which are very variable in their morphological characters and difficult to identify on the basis of their morphology. The only phylogenetic study based on molecular data analysed sequences of the *cox*2 gene and supported the monophyly of the family as well as the recent classification based on morphological

characters (Beckenbach & Borkent 2003). However, *cox*2 gene was not tested for its usefullnes on interspecific level.

First, we used the mitochondrial 16S rRNA gene sequences to analyse a molecular phylogeny of the family and compared the generic relationships with the established phylogeny of this group based on morphology and fossil records. Second, we tested the usefullnes of 16S gene marker on the genus and species level and by using these sequences we tried to revise the validity of problematic taxa from the genus *Dasyhelea*.

The study was financially supported by the PhD Research Fellowship of Ministry of Education GA ČR 524/05/H536 and grant MSM No. 0021622416 of the Masaryk University.

Key Words: Ceratopogonidae, 16S, phylogeny, Diptera, *Dasyhelea*

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Predation by *Crossopalpus hirsutipes* Collin (Diptera: Empididae) on adult *Liriomyza sativae* Blanchard (Diptera: Agromyzidae)

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The fly species *Crossopalpus hirsutipes* Collin (Diptera: Empididae) was found to be an important predator of adults of the leafminer *Liriomyza sativae* Blanchard (Diptera: Agromyzidae) infesting vegetables in Hochiminh city, Vietnam. We successfully reared the predator in the laboratory for 15 generations by using the earthworm *Perionyx excavatus* Perrier (Oligochaeta: Lumbricidae) as food for the larvae, and adult *L. sativae* flies, adult *Drosophila melanogaster* (Diptera: Drosophilidae) flies and nymphs, and adults of the leafhopper *Empoasca flavescens* Fabricius (Homoptera: Cicadellidae) as prey for the adults. All cultures were held and all experiments were done at 27°C, 12L:12D photoperiod and 65% RH. The average time from oviposition to adult emergence of *C. hirsutipes* was 22 days. The mean adult longevity was 41 days for females and 36 days for males, and the mean lifetime fecundity was 23.5 eggs per female. Single adults preyed on 14-20 (mean: 17.3) *L. sativae* adults per day, and males and females ate the same amount. When offered four different species as prey in no-choice predation experiments, *C. hirsutipes* fed more frequently on adult *L. sativae* than on adult *D. melanogaster* and nymphs and adults of *Empoasca* sp., and least frequently on adult *D. radicum* (Diptera: Anthomyiidae)

Key Words: earthworms, laboratory rearing, leafminers, life history

Effects of temperature on the immature development of the stone leek leafminer *Liriomyza chinensis* (Diptera: Agromyzidae)

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The effect of seven constant temperatures of 15, 17.5, 20, 22.5, 25, 27.5 and 30°C on development of the stone leek leafminer, *Liriomyza chinensis* (Kato) (Diptera: Agromyzidae), on Japanese bunching onion, *Allium fistulosum* L., was studied in the laboratory. Total developmental times from egg to adult emergence decreased from 69.6 to 17.1 days for temperatures from 15 to 30°C, with pupae requiring more time for development than the combined egg and larva stages. Both linear and nonlinear (Logan equation VI) models provided a reliable fit of development rates versus temperature for all immature stages. The lower developmental thresholds that were estimated from linear regression equations for the egg, first, second and third instars, total larva, egg-larval, pupa, and total combined immature stages were 12.1, 10.6, 13.6, 8, 9.6, 11.3, 11.2 and 11.4°C, respectively. The degree-day accumulation was calculated as 312.5 for development from egg to adult emergence. By fitting the nonlinear models to the data the upper temperatures for egg, larva, pupa and total immature stages were calculated as 39.9, 38.5, 36.7 and 37°C, and optimal temperatures for egg, larva, pupa and total immature stages were 33.7, 30.3, 30.8 and 31°C, respectively. These data are useful for predicting population dynamics of *L. chinensis* under field conditions and determining the maximum proportion of susceptible individuals for facilitating improved timing of application of control measures.

Key Words: *Liriomyza chinensis*, temperature, development, threshold, degree-day

Phylogeny of the Bombyliidae

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The Bombyliidae are among the largest and most diverse asiloid families. Their striking diversity contributes to the complexity of determining their evolutionary relationships by using comparative morphology alone. Our current molecular study aims to confirm, test and further resolve the higher-level classification within the Bombyliidae. We sequenced 28S ribosomal DNA and the entire nuclear gene CAD for more than 80 taxa, representing all of the major subfamilies. Based on parsimony and bayesian analysis, we assess support for the monophyly and placement of currently recognized subfamilies, including the enigmatic Mythicomyiinae.

Key Words: Bombyliidae, Asiloidea, phylogeny, molecular systematics

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***Bactrocera invadens*: taxonomy and some biological aspects in Sri Lanka (Diptera: Tephritidae)**

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Bactrocera (*Bactrocera*) *invadens* belonging to *B. dorsalis* species group has only been known from Sri Lanka in Asia and has recently invaded African countries. I have made fruit fly surveys in Sri Lanka from 1993 to 1999 and have conducted taxonomic study based on the collected material. Drew et al. described *B. invadens* in 2005. As *B. dorsalis* has been recorded from Sri Lanka in previous catalogues (Delfinado & Hardy, 1977; Norrbom *et al*., 2000), it is neccessary to revise *B. dorsalis* species group in Sri Lanka. Therefore I examined 11 species collected from Sri Lanka including *B. invadens*, *B. kandiensis* and *B. paraverbascifoliae* which are methyl eugenol responding species and *B. dorsalis* mainly collected from Taiwan. The results of morphological, ecological, and biological studies show that the taxon recorded as *B. dorsalis* in Sri Lanka is referred to *B. invadens*. Information on hostplants, distribution, seasonal abundance and parasite (braconid wasp) of *B. invadens* in Sri Lanka is additionally presented.

Key Words: *Bactrocera invadens*, Sri Lanka, Dacini, *Bactrocera dorsalis*, taxonomy

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Morphological diversity of male genitalia in *Bactrocera dorsalis* species group (Diptera: Tephritidae)

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Bactrocera dorsalis species group contains significant plant quarantine pests and is most frequently intercepted at airport inspection in Japan. Identification of species in this group is very difficult when based only on general external morphological characters. Primary purpose of this study is to find new characters for identification of this group. In my taxonomic study of Dacini in Sri Lanka, I examined male genitalia of 34 species as follows: *Bactrocera* (*Afrodacus*), *B*.(*Bactrocera*), *B.(Hemigymnodacus*), *B. (Javadacus)*, *B*.(*Paratridacus)*, *B*. (*Parazeugodacus)*, *B. (Zeugodacus)*, and *Dacus* (*Callantra*), and *D*. (*Didacus*). I found the shapes of acrophallus and epandrium and lateral surstyli are useful for identification for some related species in *B. dorsalis* species group, such as *B. kandiensis* and *B. fernandoi*, while those of *B. caryeae*, *B. invadens*, *B. kandiensis*, and *B. paraverbascifoliae* are very similar to each other and difficult to distinguish. Further investigation based on 37 Asian and 14 Australian species revealed that the structure of acrophallus is invariable in *B. dorsalis* species group, while the shapes of acrophallus and epandrium and lateral surstyli are variable as shown in most of the Sri Lankan species. The significance of shapes of acrophallus and epandrium and lateral surstyli as taxonomic characters is discussed.

Key Words: *Bactrocera dorsalis* species group, male genitalia, morphology, Asia, Australia

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Screening of natural medicines used in Vietnam for larvicidal activities against *Aedes albopictus* (Diptera: Culicidae) and *Paratanytarsus grimmii* (Diptera: Chironomidae) Part 2

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Insect vectors, especially mosquitoes are responsible for spreading serious human diseases like malaria, Japanese encephalitis and dengue fever, and *Aedes albopictus* (Diptera: Culicidae) act as a vector for dengue virus. We screened acetone extracts of 34 natural medicines used in Vietnam for their larvicidal activities against target species *Ae. albopictus* and non-target species *Paratanytarsus grimmii* (Diptera: Chironomidae) at a concentration of 1 mg/ml within 2 days. As the result, the extracts of *Adenosma caeruleum* R. Br. (Scrophulariaceae), *Mentha arvensis* L. (Labiatae), *Zingiber officinale* Rosc. (Zingiberaceae) and *Pogostemon cablin* (Blanco) Benth. (Labiatae) showed high mortalities against mosquito larvae at a concentration of 250 μg/ml. In particular, the extract of *M. arvensis* still showed high larvicidal effect at a concentration of 100 μg/ml 1). Next, we tested major constituents of *M. arvensis* and *Z. officinale, i.e.* menthol, menthone, gingerol and shogaol, for their larvicidal activities against mosquito larvae. The LC_{50s} of these compounds were 155.23 μg/ml, 291.72 μg/ml, 133.98 μg/ml and 41.45 μg/ml, respectively. Shogaol exhibited 56% of mortality against mosquito larvae, however it showed perfect mortality against chironomid larvae at a same concentration of 50 μg/ml.

Furthermore, other acetone extracts of 19 natural medicines used in Vietnam were tested for their larvicidal activities against mosquito and chironomid larvae. Larvicidal activities were clearly found in the acetone extracts of 7 natural medicines, *i.e. Chenopodium ambrosioides* L. (Chenopodiaceae), *Sophora flavescens* Ait. (Leguminosae), *Prunus armeniaca* L. (Rosaceae), *Orthosiphon stamineus* Benth. (Labiatae), *Notopterygium incisum* Ting (Umbelliferae), *Erythrina indica* Lam. (Leguminosae) and *Oldenlandia corymbosa* L. (Rubiaceae) against mosquito larvae. Especially, the extracts of *O. stamineus* exhibited 64% of mortality against mosquito larvae at a concentration of 100 µg/ml, while it showed only 4.8% of mortality against chironomid larvae at a concentration of 500 µg/ml.

1) N. Uchiyama *et al*., International Conference on Biodiversity of Insects: Challenging Issues in Management and Conservation (BIMC, 2006), India.

Key Words: Vietnam, natural medicine, larvicidal activity, *Aedes albopictus*, *Paratanytarsus grimmii*

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A new species of the genus *Orseolia* (Diptera: Cecidomyiidae) on *Zoysia* (Poaceae) in Okinawa, Japan and its phylogenetic relationships to other congeners

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The genus *Orseolia* (Diptera: Cecidomyiidae) contains 27 species and is distributed in Palaearctic, Afrotropical, and Oriental regions. All *Orseolia* species are associated with Poaceae and induce galls at the growing point of culm. There are some serious pests, such as the Asian and African rice gall midges, *Orseolia oryzae* and *Orseolia oryzivora* that attack rice, *Oryza sativa* and *O. glaberrima*, respectively. In Japan, so far only *Orseolia miscanthii* that induces galls on *Miscanthus sinensis* has been recorded. Recently, we found another species that induces galls on *Zoysia tenuifolia* in Okinawa, Japan. In this presentation, we report this species with its gall, morphological, ecological, and genetic information. We also compare this species at the molecular level with some other congeners that were collected from Southeast Asia: *O. oryzae* from Thailand, Indonesia, and Viet Nam, *O. javanica* on *Imperata cylindrica* from Indonesia, and on *Cynodon dactylon* from Viet Nam.

Key Words: gall, *Orseolia*, Poaceae, *Zoysia*, Okinawa

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Phylogenetic relationships among Palearctic species of the genus *Asphondylia* (Diptera: Cecidomyiidae) that induce galls on fabaceous plants.

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Because some species of the genus *Asphondylia* (Diptera: Cecidomyiidae) are morphologically quite similar, molecular sequencing data have been used in recent years to determine inter- and intraspecific relations. We analyzed a region of the cytochrome oxidase subunit I (COI) gene of mtDNA for Palearctic *Asphondylia* species that induce galls on fabaceous plants in order to investigate their phylogenetic relationships. We also used some European and Japanese *Asphondylia* gall midges on different host families as outgroup taxa. A NJ-tree based on the molecular sequencing data of the COI region indicated that all Fabaceae-associated European species examined, except *A. gennadii*, were included in one clade, which was supported by a 91.3% bootstrap value. Based on the tree and morphological studies, we concluded that *A. ulicis* and *A. jaapi* are identical species, but they are different from *A. coronillae* although *A. jaapi* was once synonymized with *A. coronillae*. We considered that the remaining three species, *A. pilosa*, *A. sarothamni*, and *A. cytisi* are independent species. A Japanese species, *A. yushimai*, as well as *A. gennadii*, was not included in the clade of European *Asphondylia* on Fabaceae. It is remarkable because both *A. yushimai* and *A. gennadii* are polyphagous species alternating host plants seasonally, which may imply they came to Fabaceae from other host plant families.

Key Words: Palearctic *Asphondylia*, Cecidomyiidae, gall, Fabaceae, phylogeny

Evidence and error in current interpretations of the brachyceran male genitalia

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As a contribution to understanding the homologies of the major sclerotized parts of the male genital segment in Eremoneura, the published data on the skeleto-muscular apparatus were compared in lower brachycerans and Empidoidea. Ovtshinnikova's proposal (1993) that the paired muscle moving the surstylus in Cyclorrhapha is her M21, is applicable to the Empidoidea too. The muscle appears, however, to have shifted its point of insertion in the Empidoidea, which would imply that the surstyli may not be homologous in both groups. If the epandrial hypothesis is adopted for the Empidoidea, another two pairs of muscles, both inserted on the hypandrial [= gonocoxal] apodemes, can be homologized without constraint, namely, the muscles 3 and 6 in Ulrich (1972) with $M5^1$ and $M5^2$ in Ovtshinnikova (1989 etc.), respectively. The apparent homologies of the three muscles are taken as support to the epandrial hypothesis. Some current interpretations of individual parts are rejected, however; they concern epandrial processes mistaken for surstyli and an alleged sheath of parameral origin around the aedeagus. It is argued that establishing homologies of complicated and highly variable organ systems like the male genitalia demands consideration of the three-dimensional construction of the cuticular skeleton, its kinetic properties, and the muscles that move the skeletal parts.

Key Words: male genitalia, Brachycera, homology, epandrial hypothesis, endophallus

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Evaluation of the efficacy of food baits for trapping the tomato fruit fly, Neoceratitis cyanescens (Bezzi) (Diptera: Tephritidae) in Mauritius

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Management of *Neoceratitis cyanescens* and *Bactrocera cucurbitae* is a major concern for tomato and cucurbit growers in Mauritius. The former is controlled by insecticides only while the latter with a developed IPM package.

This paper presents a first attempt at (1) identification of an appropriate food bait to lure and kill adult tomato fruit flies and (2) study on the economic importance of *N. cyanescens* with the developed trapping system along with fruit damage assessment.

Two types of traps (plastic bottle (1.5 L) and Mc Phail) with food bait (10% molasses) were tested in tomato fields. There was no significant difference in fruit fly catches between traps.

Plastic bottle traps were used in field trials to determine the efficacy of five food baits (molasses, wine, protein hydrolysate, mashed banana and mashed tomato) in attracting fruit flies. Wine bait solution attracted significantly highest numbers of *N. cyanescens* ($p<0.01$), *Ceratitis rosa* ($p< 0.05$) and *B. cucurbitae* ($p< 0.01$). Catches were female bias (60 %-65%)

The tomato fruit fly was more prevalent during summer period (about 26 °C). The average number of fruit flies/trap/day was 0.5 and fruit damage 3.8 %. During winter (about 22 °C), catches were not significant (≤ 0.08 adults/trap/day) and fruit damage was also negligible (0.05%). Catches were strongly correlated with fruit damage ($r=0.8$) and temperature ($r=0.87$).

Key Words: *Neoceratitis cyanescens*, *Bactrocera cucurbitae*, *Ceratitis rosa*, traps, food bait

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Control of nuisance flies in Australian cattle feedlots

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Temporal and spatial distributions of nuisance fly species have been determined in Australian cattle feedlots. The prevalence and impact of natural enemies, such as parasitic wasps, entomopathogenic fungi and mites, were also established.

The impact of different under-the-fence-cleaning regimes and of a larvicide treatment on fly production was quantitatively assessed in a feedlot. Shorter cleaning intervals resulted in substantially suppressed *Musca domestica* populations.

A local field strain of the parasitic wasp *Spalangia endius* was mass reared with several production parameters being investigated. Laboratory experiments and field releases of *S. endius* were carried out to determine their impact on fly production.

Isolates of the entomopathogenic fungi, *Metarhizium anisopliae* and *Beauveria bassiana* isolated from flies and soil, have been characterised

and their optimum growth temperatures and sporulation characteristics determined. Bioassays have demonstrated the effectiveness of selected isolates against adult and immature flies.

This knowledge will subsequently be applied to designing and implementing measures for controlling nuisance fly populations in feedlots with minimal chemical use.

Key Words: Muscidae, *Musca domestica, Stomoxys calcitrans*, cattle feedlots, biocontrol agents.

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Classification of Japanese robber flies (Diptera: Asilidae) based on molecular evidence

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The family Asilidae is one of the remarkably large and abundant families of the Diptera, and distributed through out all biogeographic regions of the world. More than 500 genera and some 7,000 species are known from the world (Geller-Grimm, 2005), and 34 genera and 72 species have been recorded from Japan (Hirashima, 1989). The family Asilidae is a taxonomically unified group. However, there are various opinions on the higher classification of Asilidae at the subfamily or tribe level (Lavigne, 2000). Various authors have been carried out a comparative morphology work (Macquart, 1838; Osten-Sacken, 1884; Hull, 1962; Papavero, 1973; Wood, 1981; Lehr, 1969, 1996) and the classification of Asilidae has been stabled. However, those classifications by the various authors have been based on intuition rather than a quantitative phylogenetic analysis. Recently Bybee *et al*. (2004) presented the first analysis of phylogenetic relationship among the subfamily of Asilidae, based on molecular data sets. It indicated an inconsistency between the former systematic based on comparative morphology and systematic based on molecular phylogeny.
In this study, phylogenetic analysis among the Asilidae, based on three genes: 16S rDNA, 18S rDNA, and 28S rDNA was carried out. Thirty ingroup taxa from Japan representing 9 of the 10 described subfamilies were used. From the results of the phylogenetic studies, classification of Japanese Asilidae species based on molecular phylogeny is provided.

Key Words: Asilidae, molecular phylogeny, classification

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A Motion-picture film on Sciomyzidae

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The 20-minutes, Color film was produced and narrated by the late Professor C. O. Berg (1912-1987) in about 1975 at Cornell University (U.S.A.). The film shows aspects of the life cycle, including striking footage of aquatic predators attacking snails, parasitization and emergence of wasp natural enemies, etc. The presenter gives a brief, illustrated biographical check of Prof. Berg following the film.

Key Words: Sciomyzidae, Mollusca, life cycle, biology, biocontrol

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Overview of Sciomyzidae

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An overview of some major aspects of Sciomyzidae is given. It is based on a book, by these authors, on all aspects of the family, to be published by Cambridge University Press in 2007. The relationships of Sciomyzidae to other Sciomyzidea and the taxonomy of the family; diversity of the 535 species in the 61 genera; range of terrestrial to aquatic habitats; and distribution in all major zoogeographic regions are noted. Hosts/prey – freshwater, brackish water marine littoral and terrestrial snails, snail eggs, slugs, fingernail clams, freshwater oligochaetes and millipedes (latter by Phaeomyiidae) are displayed in relation to a cladogram of genera of Sciomyzidae. A cladogram of all families of Gastropoda is linked to-the behavioural groups, based on saprophagous-predatory-parasitoid behavior, hosts/prey, and microhabitat are shown in comparison to a cladogram of the genera. A few examples of experimental studies on host/prey preference, predation, competition, populations, survival, etc are presented. The seven phenological groups, based on voltinism, overwintering stage, and generations per year, with a new group for tropical species, are diagrammed. Some natural enemies and stereoscan photos of a few key morphological features are illustrated, e.g. presence of float hairs in terrestrial larvae, fine structure of cross-section of eggs. Evolution of diverse feeding behaviour and associated adaptations is encapsulated. With increasing importance of slugs as agricultural pests, and aquatic snail habits due to development of new dams (S.E. Asia, Africa) along with resistance to anti-helminthic drugs, renewed prospects for use of Sciomyzidae as biocontrol agents, supported by extensive recent and current research, is considered.

Key Words: Sciomyzidae, Mollusca, biology, evolution, biocontrol.

Artificial neural networks for insect identification

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ANN have already been very rarely applied for identifying of insects. We developed, tested and applied the ANN methodology at three different insect orders:

I. Diptera – Tachinidae: The objects were primarily photographed, then digitalized; consequently the picture was scaled. The variables used were length of wing veins and widths of antennal segments. There were 17 characters studied, particularly in males and females (*Tachina*), or in right or left wings (*Ectophasia*). Right and left wings data are interchangeable and data from one wing are sufficient. Additionally, the sex of the studied specimens was included. It was shown that classification using ANN was possible assuming sufficiently high number of specimens of each species in the “training set”.

II. Thysanoptera – Thripidae: The three species of *Dendrothrips* were characterized by 20 quantitative and three binary characters, and by sex. The optimum ANN architecture was found from the data set containing 74, 75, and 14 specimens. It enabled a 100% correct classification. The prediction of unknown species was 99-99.8%. Thus, reliable characters were found and the model provided a fast identification tool.

III. Hemiptera – Psylloidea – Phacopteronidae: Adults of up to ten species of the genus *Pseudophacopteron* were measured (17 characters on forewings, antenna, head and hind legs), and sex as the 18th variable were used. In spite of a limited number (7-14) of specimens of each species, the

ANN model performed well on the data set and unambiguously classified unknown samples.

ANN classification of three different insect orders is possible and quite general. It can be applicable for objects where appropriate database can be created. After ANN "learning" (training) the species identification is fast and reliable. In contradiction to "manual" identification, all characters are simultaneously taken into account over the complete database. This approach is non-destructive unlike e.g. molecular analyses. Where the identification appears difficult or it is e.g. sp.n., ANN can indicate the situation. Study is supported by MSM 0021622416 and GACR 524/05/H536 projects.

Key Words: Artificial Neural Networks, insect identification, Tachinidae–Diptera, Thripidae–Thysanoptera, Phacopteronidae–Psylloidea

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Bionomics of malaria vector, *Anopheles d'thali* (Diptera: Culicidae) in a malarious area, Bandar Abbas, Hormozgan province, southern Iran

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Ecology of *An.d'thali* was studied in Bandar Abbas county, where there is indigenous malaria. This species plays as a secondary malaria vector in the region. Adult and larvae were collected from different habitats. Susceptibility tests were carried out according to WHO methods to a diagnostic dose of 10 insecticides. The irritability to 4 pyrethroids by WHO insecticides impregnated papers were determined. Four larvicides were used at the diagnostic dose. All the concentrations were provided by WHO. *An. d'thali* is active throughout the year in mountainous area with two peaks of activity. This species usually rests outdoors. It has different larval habitats. Insecticides susceptibility tests on adult females exhibited susceptibility to all insecticides recommended by WHO. LT_{50} for the currently used insecticide, lambdacyhalothrin, is measured less than one minute. The irritability tests to pyrethroid insecticides showed that permethrin and lambdacyhalothrin had more irritancy compared to deltamethrin and cyfluthrin. Larval bioassay using malathion, chlorpyrifos, temephos and fenitrothion did not show any sign of resistance to these larvicides at the diagnostic dose.

Although the Hormozgan province had been sprayed with DDT since 1952 and subsequently with malathion from 1968, but *An.d'thali* remained susceptible to DDT 4% and dieldrin 0.4%. Furthermore, this species is highly susceptible to organophosphate, carbamate and pyrethroid insecticides. This insecticides can be used for malaria vector control in the region.

Key Words: ecology, *Anopheles d'thali,* malaria, Iran, resistance

Entomological survey on sandflies (Diptera- psychodidae) in a new focus of zoonotic Coetaneous leishmaniosis (ZCL) in Sarakhs, Khorassan province of Iran2003

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Introductions:

Leishmaniosis, is the most important health problem in Iran. So, we have to study biology and ecology of sand fly and epidemiology of coetaneous Leishmaniosi for every years and prepare our prophylaxis programs based on it. *Sarakhs* is a near by borderline rural place in east of Iran.

Material and methods:

A total of 2982 sand-flies representing six species were collected using sticky (oiled) paper traps in *Sarakhs* rural places which was three villages, one in desert, another in steps and the other in mountain situation. Sand-flies were collected and carried to lab for fixing and identification.

Results:

from May 2003 to Sept 2003, *Phlebotomus papatasi* was the predominant species. The average indoor resting density of *P. papatasi* ranged from 11 (May 2003) to 131 per 10 traps (September 2003). The average indoor resting density of this species varied between 9.–120 per 10 traps in May and September, respectively in 190. The activity of *P. papatasi* starts from late April or early May and extends to mid October with two peaks, one in mid or late June and the second one in early September. Natural leptomonad infection was found in *P. papatasi* and *Sergentomyia sintoni*.

Discussion:

Due to our study and others in this area, *P. papatasi* could be a vector of humans and gerbils and it is placed in gerbils hole and some aimals breading houses and it was susceptible to propxore.

Key Words: Leishmaniosis, Psychodidae, sandflies, Sarakhs, Khorasan, Iran

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Phylogeny of fossil and extant Sciaroidea

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Phylogeny of fossil and extant Sciaroidea was studied with parsimony analysis. A cladistic analysis with representative genera of all known family group taxa as well as genera without current family affiliation, including three undescribed taxa in the ingroup, produced one most parsimonious cladogram. The new result differs from our earlier hypothesis especially by placement of many of the fossil taxa, e. g. Mangasidae and Antefungivoridae appear now at the base of the cecidomyiid clade instead of belonging to the *Diadocidia* clade. A monophyletic *Heterotricha* group includes even *Colonomyia* + *Ohakunea*. A new Cretaceous fossil genus (two species) from Alava amber is the sister group of *Colonomyia* + *Ohakunea*, and a new extant genus from Madagascar is the sister of all these four taxa. *Starkomyia* belongs to the Mesosciophilidae clade. The Mesozoic *Thereotricha* is in the mycetophilid clade and appears as the sister of *Freemanomyia* + *Archipleciomima*.

Key Words: phylogeny, Sciaroidea, fossils

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Evolutionary affinities of New Zealand blowflies (Calliphoridae)

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Recent work has clarified the evolution of the Calliphoridae of the Australasian region using molecular markers. To date, the focus has been on Australian carrion-breeding endemics and related introduced species. Application of a molecular clock approach to these data suggests divergence of the major subfamilies Calliphorinae and Luciliinae around 19 mya. The most recent analysis, presented here, includes representatives from New Zealand, targeted because of this country's special evolutionary history. New Zealand has a relatively depauperate blowfly fauna, with especially limited diversity at the subfamily level. Most endemic species probably have their origins not in Gonwandan elements, but rather in considerably more recent introductions.

Six species of endemic and introduced species of Calliphorinae from New Zealand (representing four separate genera) were analysed to reveal their relatedness, based on mitochondrial DNA sequences, to blowflies from Australia. DNA sequences were analysed using parsimony and maximum-likelihood Bayesian techniques. The analysis places all species firmly within the subfamily Calliphorinae. *Calliphora quadrimaculata*, *Ptilonesia* and *Xenocalliphora* form a monophyletic group, seemingly most closely allied to *Calliphora nigrithorax* and *Calliphora ochracea* from Australia. However, *Calliphora vicina* is the sister taxon to all Australian + New Zealand calliphorines. These molecular data therefore do not support separate generic status for *Ptilonesia* and *Xenocalliphora*, despite the morphological distinctiveness of these taxa.

Key Words: *Calliphora*, mtDNA, New Zealand, *Ptilonesia, Xenocalliphora*

Effectiveness of combination with malaise and box traps for survey of tabanid flies（Tabanidae）

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Use of a trap has been widely performed for investigation of the tabanid flies.

I have also used canopy or box traps with carbon dioxide (CO^2) for the survey of *Hirosia iyoensis*. Although these traps were suitable for capturing the small size tabanid flies which attack the ventral of the domestic animals, it was unsuitable for capturing the large size tabanid flies which attack the back of them. On the other hand, the malaise trap without carbon dioxide has the advantage, which can capture various tabanid fly species including large size horseflies. However, malaise trap was unsuitable for capturing the large number of tabanid flies. Then, it was considered that both traps were combined using the advantage of box and malaise traps. Combination traps were created to investigate the tabanid fly fauna and its population dynamics of a certain study point.

The effectiveness of this combination trap was tested in summer of 2005. The commercial malaise trap (Townes style) and the self-making box trap (80~90cm length/width, 40cm height, 70cm leg) were combined. The traps were set from the middle of July to the end of September. The recovery of captured tabanid flies was carried out every week around 15:00 on Wednesday. Dry-ice 2kg was put on the boundary line ground of both traps.

As a result, it was observed that the combination traps compared with the box trap only captured more species and individual numbers. These experiments will be continued in 2006, and the report will also announced.

Key Words: tabanid flies, combination trap, malaise trap, box trap, species composition

Biology of necrophagous flies and its application to forensic science and maggot therapy

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Cyclorraphan larvae are the primary invertebrate consumers of terrestrial vertebrate carrion. Perhaps most notable are the large and ubiquitous Calliphoridae and Sarcophagidae. These are among the most familiar of insects because they are often closely associated with human activity. Many carrion flies can be reared in the laboratory and manipulated in the field, and these animals have long been extensively studied by physiologists and ecologists. Therefore they have substantially contributed to our basic knowledge of scientific topics such as insect diapause and population regulation.

Although some calliphorids and sarcophagids are medical or veterinary pests, like most insects they are largely benign or beneficial. In addition to their environmental role in recycling nutrients, carrion flies also serve forensic and medical science. Although these functions are not new, in recent years both forensic entomology and maggot debridement therapy have noticeably expanded and matured as scientific and professional disciplines. Specialized professional societies now provide venues for the recruitment of young practitioners, the greater exchange of ideas concerning experiments and funding, and for the establishment of best practice standards. Examples of recently scientific developments include the greater use of molecular genetics and computer models by forensic entomologists, and the application of maggot therapy in veterinary situations in addition to human health care.

Key Words: forensic science, medicine, Calliphoridae, Sarcophagidae

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DNA-based identification of Forensically Important Diptera

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It has become relatively easy and inexpensive to generate a molecular genotype for many of the insect species used as forensic evidence. It seems likely that DNA-based methods can be used to identify a specimen, thus overcoming the current lack of diagnostic characters for many immature forms. For this advance to occur, greater attention should be paid to the logic of experimental design and method validation. In many ways the situation is analogous to constructing a morphological key. The reference database must include a taxon sample that is useful for a real death investigation, the reference specimens must be properly identified, and replication must be sufficient to estimate intraspecific variation and population genetic structure. The popular GenBank/EMBL/DDBJ sequence database, although extremely convenient, is well known to contain many erroneous records. Therefore careful consideration should be given to judging the reliability of a published genotype. Often a polymorphic locus that is a candidate for distinguishing closely related species is not monophyletic. Validation of a cytochrome oxidase I (COI) data set for identifying forensically relevant Chrysomyinae (Calliphoridae) in North America was successful, with hundreds of specimens supporting concordance between morphologically defined species and haplotype lineage. In contrast a global sample of Luciliinae (Calliphoridae) uncovered widespread COI paraphyly, and our conclusions based on earlier smaller samples were in error. In summary, many loci and genotyping methods are potentially useful for DNA-based identification of carrion insects, but the utility of a given method cannot be known prior to empirical validation. The binomial confidence interval is proposed as a way to estimate a useful sample size.

Key Words: DNA, Calliphoridae, molecular systematics, forensic

Taxonomic Studies of the genus *Protocalliphora* (Diptera: Calliphoridae) in North America

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Protocalliphora are obligate bloodsucking parasites of nestling birds. Adults are rarely encountered in museum collections; however, these flies and their immatures commonly infest birds' nest. This paper reviews developments in the taxonomy of the group and methods to facilitate their reliable identification. Two main areas are addressed.

1. The taxonomic status of the genus in North America was unclear until it was revised by Sabrosky, Bennett and Whitworth (1989). In that work my colleagues and I identified 15 new species of the genus by rearing specimens from bird nests and matching males, females and puparia. I outline here the approaches taken in this work and our current taxonomic understanding of the genus.

2. Since empty puparia are readily collected in old bird nests, such puparia can potentially expand our knowledge of the group. To this end, since 1995, I have solicited networks of birders via the internet to send me nests. To date, I have received over 6000 nests, in addition to over 2000 nests that I have collected myself. About one-half the nests were infested with *Protocalliphora* thus providing a large quantity of material for study.

A variety of useful puparial characters have been identified from these specimens including size, shape, and distribution of spines and ridges in the stigmatal, dorsal and ventral regions. By comparing specimens from many geographic areas I was able to create a puparial key to 27 species; three new species have also recently been described.

Key Words: Calliphoridae, *Protocalliphora*, puparial keys, bird nests

New molecular phylogenetic evidence on relationships of the 'true' Empididae (s.s.)

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The high species and morphological diversity of empidoids has made it difficult to achieve consensus on a higher-level phylogeny-based classification. Recent morphological and molecular studies have added significant new support to family-level groups. Despite this important progress, definition and support for a ‘true’ Empididae and for its constituent subfamilies remains weak --especially in molecular data sets. In nearly all studies published to date, support is limited or contradictory for establishing relationships among Hemerodromiinae, Empidinae, Clinocerinae and Brachystomatinae, Multiple hypotheses have been presented for genera that have previously been placed in subfamilies Oreogetoninae and Trichopezinae. Here, we present new phylogenetic evidence and propose a monophyletic definition of ‘true’ Empididae (s.s) from a combined analysis of multiple nuclear genes. In particular, we focus on molecular evidence for the placement composition and relationships among the traditional empidid subfamilies. Fossil and phylogenetic evidence supports a scenario of rapid radiation for these clades suggesting that, in several key lineages, combination of morphological and molecular evidence may be critical for increased understanding of the evolutionary history of dance fly diversity.

Key Words: Empidoidea, Empididae, dance fly, molecular phylogeny

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A molecular phylogeny of the Asiloidea

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We present molecular phylogenetic evidence in support of family-level relationships among asiloid families and their placement within the infraorder Muscomorpha. Relationships among the asiloid families have been controversial or poorly resolved due to differing interpretations of morphological character evolution and a general lack of definitive characters. In the current study, we combine data from multiple genes, including CAD and the 28S ribosomal RNA gene (28S rDNA), for 50 taxa representing all asiloid families. Parsimony and Bayesian likelihood analyses provide support for the monophyly of the superfamily and for its constituent families. Molecular evidence for the position of enigmatic taxa, including Hilarimorphidae, Evocoidae, and *Apystomyia* are also discussed in light of newly emerging morphological data.

Key Words: Asiloidea, molecular systematics, phylogeny, Brachycera

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The position of Diptera in the Holometabola: Evidence from multiple nuclear genes

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Phylogenetic relationships among the holometabolan orders has been one of the most controversial and difficult questions in modern insect systematics. Morphological data support placement of Diptera in the Antliophora along with Mecoptera and Siphonaptera, but convincing evidence for the exact sister group of the Diptera has been elusive. Support for the Neuropteroidea and resolved placement for Hymenoptera has been equally confounding. Elucidation of the closest relatives of Diptera and the phylogeny of other holometabolan orders is critical for outgroup comparison, for a more explicit understanding of key morphological transformations, and for the development of robust groundplans for Diptera and other holometabolan lineages. Molecular phylogenetic data have contributed significantly to recent re-analyses of order-level insect relationships, but have also added the possibility that the Strepsiptera are a potential close relative of flies. Building on data generated in the NSF-ATOL FLYTREE project, and from several newly completed insect genome sequences, we present new evidence from proteins and protein coding genes on the phylogeny of Holometabola and the sister-group of the Diptera.

Key Words: Holometabola, phylogeny, Diptera, Strepsiptera, genes

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The environmental requirements of Sciomyzidae (Diptera) on turloughs in the west of Ireland with particular reference to the role of mollusc host/prey communities.

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Turloughs which are temporary water bodies unique to Ireland, are listed as a priority habitat in the European Union Habitats Directive (1992). Recent work has focused on carabids, but less attention has been paid to Diptera on turloughs. Fifty-two species of the family Sciomyzidae (Diptera), all of which have malacophagous larvae, occur in Ireland. Skealoghan turlough was selected to determine within-site variation of sciomyzid species across a range of vegetation zones. Ten sweeps (5m) in each of six homogeneous vegetation zones were taken weekly (2/6/04 – 29/9/04) in addition to a number of environmental variables. The univoltine *Ilione albiseta* was dominant, but species displaying a range of life history traits were also present. Results suggest that sciomyzid communities are specific to particular turlough zones with even adjacent zones having different communities. Key environmental determinants of sciomyzid community composition and abundance appear to be vegetation height and hydroperiod of the zone. A wider study on 24 zones across ten turloughs was conducted to determine between-site variation. Sampling methods followed those of the intensive single-site study, with the addition of mollusc surveys, which were undertaken at the same sampling locations during the flooded winter period to elucidate the role of host/prey communities. Again, *Ilione albiseta* dominated the catch and the importance of vegetation structure and hydrology was evident, suggesting that flooding regime and grazing during the dry phase are of major importance. Additionally, a method for partial regression analysis of spatial, environmental and larval resource variables for the most abundant species is presented.

Key Words: Sciomyzidae, turlough, Mollusca, hydrology, vegetation structure

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Communities of Diptera restricted to high altitudes in the Australian Wet Tropics are vulnerable to climate change

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The Australian Wet Tropics World Heritage Area (WHA) contains a number of highland vertebrates predicted to face extinction due to a warming climate, but little is known about risks to invertebrates, which are vital to ecosystem function. This study investigates the distribution and abundance patterns of the schizophoran Diptera along an altitudinal transect in the Carbine Uplands of the WHA using malaise traps. The season of peak abundance changed with altitude, with highland abundance peaking in October, and lowland abundance peaking in April. There was a high level of species turnover with altitude, and some evidence for distinct low-, mid-, and high-elevation assemblages, with the high-elevation assemblage containing the most restricted species. We would expect this high-elevation assemblage to be at risk of local extinction with 2-3°C of warming, and the mid-elevation assemblage to be at risk with 4-5°C warming. Both these levels of warming are well within conservative forecasts over the next 100 years. Future work should continue sampling to confirm patterns presented here and to monitor range shifts with climate change. A highland species *Helosciomyza ferruginea* (Helosciomyzidae) has potential as an indicator species for such monitoring.

Key Words: Australian Wet Tropics, climate change, indicator species, rainforest, Schizophora

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Molecular phylogeny of the superfamily Opomyzoidea (Diptera: Acalyptratae)

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The superfamily Opomyzoidea as currently recognized (sensu J.F. McAlpine) includes fifteen families of small acalyptrate flies, the phylogenetic affinities of which have historically been uncertain or controversial. DNA sequence data (approximately 3500 bases) was obtained from twenty-four species representing twelve families of opomyzoids, comprising portions of the 28S ribosomal DNA and CAD (rudimentary) genes. Outgroups used for the analysis were from five other acalyptrate superfamilies. Results did not support the monophyly of the Opomyzoidea, and support values for interfamilial relationships were generally low, though most confamilial taxa clustered together with high support. Results suggest that the Stenomicrinae may correctly be placed with Aulacigastridae, as earlier favored by Hennig. Possible sister-group relationships of the Agromyzidae, with implications for the origin of phytophagy, are discussed.

Key Words: phylogeny, Opomyzoidea, acalyptrate

Phylogeny, diversification, and host use evolution of *Phytomyza* and *Chromatomyia* leaf mining flies (Diptera: Agromyzidae)

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The importance of shifts to novel host plant groups for diversification in phytophagous insects has been the subject of much discussion, but little formal analysis. The leaf-mining fly genera *Phytomyza* and *Chromatomyia* (Diptera: Agromyzidae) together form a monophyletic group well-suited for such analyses. These genera are comprised of about 640 described species which can mostly be placed in species groups defined by similar genitalic morphology and the tendency to feed on a specific host plant family. A phylogeny estimate was obtained using over 3000 bases of DNA sequence data from 100 species of *Phytomyza* and *Chromatomyia* and from additional species in four related genera as outgroups. Results confirm the monophyly of most recognized species groups, and underscore the importance of host conservatism at the family level. Species feeding on Ranunculaceae, a primitive herbaceous plant family, show the most genetic and morphological diversity, suggesting a significant early radiation onto hosts in this family. However, later shifts to herbaceous asterid plant families have also resulted in significant radiations. The genus *Chromatomyia* is not monophyletic, with one major group feeding on Asteraceae and Poaceae, and another on herbaceous and woody hosts in several plant families; both are nested within *Phytomyza*. Morphology of representative species was also examined and compared to descriptions of remaining species in the taxonomic literature to confirm monophyly of species groups and to estimate the number of species belonging to each. Along with relative divergence times estimated from the molecular data, this allowed comparison of relative diversification rates across species groups and higher lineages. Possible correlates of increased diversification rate in this group are discussed.

Key Words: Agromyzidae, *Phytomyza*, phylogeny, diversification, host shifts

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Evolution of the Therevoid clade (Diptera: Asiloidea) with special emphasis on Window flies (Scenopinidae): a total evidence approach

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A robust estimate of Asiloidea phylogenetic relationships has proven elusive, with numerous differing hypotheses of relationships between the constituent families. Whilst Therevidae and Scenopinidae have historically been associated as sister groups based on larval characteristics, descriptions of two additional and closely related families (i.e. Evocoidae and Apsilocephalidae) has blurred our understanding of evolution of what has become known as the therevoid clade. A well-supported total evidence phylogeny of the Therevoid clade is presented based on DNA sequence data (CAD, 16S, COI, 18S) and over 100 morphological characters. Relationships of the four families are discussed, as well as subfamilial and generic relationships of Scenopinidae and Therevidae and implications for the higher-level classification of these families.

Key Words: Therevidae, Scenopinidae, systematics, Evocoidae, Apsilocephalidae

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The future is multimedia: electronic and internet resources for Asiloidea research

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Communication of research is a basic responsibility of scientists, and for taxonomists, provision of identification or diagnostic tools (e.g. published keys) is one such base responsibility. In developing identification tools, many new generation taxonomists are taking advantage of new technologies such as digital photography, interactive keys, java language and XML programming and relational databases. These are often consolidated into web pages (World Wide Web) of various levels of sophistication, thus taxonomic resources on Diptera and Asiloidea on the internet are increasing rapidly in number. A summary of the electronic and internet resources for the study of asiloid flies is presented and discussed in light of the future directions of taxonomic and Diptera research.

Key Words: Asiloidea, electronic media, internet

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Long term monitoring the vector's density as the Dengue control program in Liuchiu, Taiwan

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The results of 17 years study, from 1989 to 2005, for long term density monitoring and water sources reduction of *Aedes* mosquito in Liuchiu, Taiwan, showed that significant drop of the Breteau index from 60 to 0-2. In 1989 surveillance, the ratio of occurrence of *Aedes aegypti* and *Ae. Albocaptius* was 87.1:12.9 inside the house, and 71.4:28.6 outside the house, respectively. After the eradication program funded by Environmental Protection Administration, in 1995, the occurrence ratio of the *Ae. aegypti*, mainly found in Benfu, Chungfu and Yufu villages dropped below 20% in 1995 and further down to 10% in 1996. The results of surveillance, from 2001 to 2005, indicated *Ae. aegypti* was only found outside the houses located in Benfu and Chungfu villages only, After 17-years efforts of monthly monitoring and breeding site cleaning up of mosquitoes, the few mosquito individuals in colony collected from the field can't even be set up in the laboratory. The risk of Dengue caused by vector's transmission was greatly decreased by the long term monitoring program. Also, in order to prevent the occurrence of the Dengue fever, cooperating with Taiwan CDC, the measure of promoting and encouraging the volunteers in village to clean up the vector breeding sites in the dengue fever breaking out areas has been conducted since 2004. The effect is excellent by this approach, the Breteau index is keeping lower than 9 due to the weekly activities of whole village participation for source reduction in Pingtung area. Obviously, remove the breeding sources and control the mosquito larva is indeed can prevent the dengue fever. No domestic Dengue disease has occurred nowadays in Liuchiu area, since 1987 when the Dengue outbreak severely. The successful control might be owing to

the efforts of long term monitoring and breeding site eradication and thus lowering the density of mosquito vectors below the critical levels.

Key Words: long term monitoring, the Breteau index, breeding site eradication, eradication program, dengue

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Looks yellow but green － the chromatic cues for attracting the orientation fruit fly, *Bactrocera dorsalis*

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The oriental fruit fly, *Bactrocera dorsalis*, is one of the destructive tephritid fruit flies in Pacific Rim. Numerous methods had been developed to monitor and control this pest, and the so-called ‘yellow colored traps’ were generally considered as effective devices to lure it. Since color is very subjective and using color name would not give accurate information about the visual cues, the attractive cues should be identified in terms of visual physiology. To reveal which wavelengths are most attractive to the fly, we firstly measured the spectral sensitivity of the fly’s photoreceptors intracellularly. There were five types of photoreceptors were recorded: four with single peak wavelengths at 370, 380, 490, and 510 nm, and one with dual peaks at 350 and 490 nm. Based on the peak wavelengths, six colored papers with special reflectance spectrum were chosen to test the color preference of the fly. Our results showed that two wavelength ranges, 300 ~ 380 nm and 500 ~ 570 nm, were attractive to the fly. However, wavelengths between the two ranges, i.e. 380 ~ 500 nm, diminished the attractiveness.

Key Words: oriental fruit fly, *Bactrocera dorsalis*, spectral sensitivity, color preference

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Unique emergence tube induced by a gall midge (Diptera: Cecidomyiidae) on flower galls in syconia of *Ficus microcarpa* (Moraceae)

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We found two new gall midges (Diptera: Cecidomyiidae) that induce female flower galls in syconia of *Ficus microcarpa* (Moraceae) on Okinawa Island, Japan. Here, we report a unique emergence behavior by one of them. A single larva develops and pupates in each gall. A little before adult emergence, the bottom of each gall elongate to form a tube, which develops, through the skin of syconium, up to 5-6 mm in height within about 7 hours. The pupa crawls out of the gall half way through the tube, or pushes up the bottom of tube with its head and comes out of the gall directly from the base of the tube. Such tube induction has never been observed at the time of emergence by other inhabitants of the syconium, such as species of Agaonidae, Pteromalidae, and Torymidae (Hymenoptera). To observe tube tissues, we kept tubes in acetic acid alcohol (glacial acetic acid : 99.5% ethanol = 1 : 3) for 2-3 days at -15 ℃ and transferred into 99% ethanol in a refrigerator. After dehydrated by 45% acetic acid, the tubes were dyed with aceto-carmine solution. Under a binocular microscope, we observed a mass of small square cells at the base and tip of the tube. Exfoliative tissue or layer was not observed at the tube bottom. In the middle part of the tube, long cells were arranged regularly. To confirm if a kind of plant hormone is responsible for the rapid tube development, a small amount of gibberellin’s paste was applied to the bottom of three galled and three ungalled syconia, but no tubes were induced. Further investigations are needed to conform which tissue (or layer) of the female flower develops and what kind of chemicals are responsible for the rapid tube development prior to the gall midge emergence.

Key Words: Cecidomyiidae, emergence tube, gall midge, *Ficus microcarpa*, Okinawa I.

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Colonization and biology of *Phlebotomus papatasi* (Diptera:Psycodidae), the main vector of zoonotic cutaneous leishmaniasis from an endemic focus of Iran

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One hundred and thirty *Phlebotomus papatasi* were collected by CDC miniature light traps and aspirator from indoors in Badrood, central Iran, and this sand fly species was colonized successfully for the first time as a laboratory strain. The fly has been maintained by the procedures of Modi & Tesh (1983) with minor modifications for 7 generations. Minimum and maximum rate of productivity was calculated to be 8.5 and 56.1 in F7 and F3 respectively and significant difference was observed among productivity of some generations ($P<0.001$). The sex ratio ranged between 70 (F1) and 101.8 (F6). The mean duration of egg to adult emergence varied between 47.21±4.46 and 52.6±7.85 days. The life cycle was completed in 34.4 to 60 days at 26±1ºC. Using larval diet without liver powder is recommended. The blood of white hamster for the sand fly vector blood feeding was preferred to golden hamster and guinea pig at the insectary.

Key Words: *Phlebotomus papatasi*, sand fly biology, leishmaniasis, vector colony, Iran

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Some taxonomic characters of the so-called *Einfeldia* (Diptera, Chironomidae)

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Einfeldia dissidens is now placed under a member of the subgenus *Lobochironomus* of the genus *Chironomus* as well as *Chironomus longipes* by some workers. Recently Jon Martin emphasized that *dissidens* should be removed from *Lobochironomus* to the genus *Benthalia* Lipina based on the chromosomal and DNA evidence (personal communication). His conclusion is coincident with my opinion led from the morphological study of imagines (antepronota) and immatures (larval maxillae). The so-called *Einfeldia* including *Chaetolabis* (*macani*) is separable from *Chironomus* by having the median suture (median commisure; Hansen and Cook, 1976) on the antepronotum.

Six species identified as *Einfeldia* are distributed in Japan, i.e., *dissidens* (Walker), *thailandicus* (Hashimaoto, as *Chironomus*), *ocellata* Hashimoto, *kanazawai* Yamamoto, *pagana* (Meigen) and *chelonia* Townes. These species are classified into 3 species groups based on the features of adult thoraces and laraval maxillae.

1. *ocellata*-group: two antepronotal lobes fused medially and weakly produced anteriorly; scutal tubercle distinct, acrostichals normally developed; larva *anthracinus*-type, chaetulae of palpiger as in *Chironomus*. *ocellata* Hshimaoto, *kanazawai* Yamamoto?
2. *dissidens*-group: anteprotonum and scutal tubercle as those of *ocellata*-group, acrostichals reduced in number (0-3); larva with one pair of ventral

tubules, chaetulae of palpiger composed of 2 different types of chaetulae *dissidens* (Walker), (*dystenus* Kieffer?), *thailandicus* (Hshimoto)
3. *pagana*-group: antepronotum distinctly divided at middle by a conspicuous V-shaped notch, scutal tubercle indistinct, acrosthichals normally developed; larva with one pair of ventral tubules, chaetulae of palpiger rather long compared with those of *Chironomus*. *pagana* (Maigen), *chelonia* Townes?

Key Words: Chironomidae, Chironominae, *Einfeldia*, external morphology, taxonomy

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Systematic study of the subgenus *Tripodura* Towns of the genus *Polypedilum* Kieffer (Chironomidae) in Iriomote Island, the Ryukyus, Japan

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The Chironomidae are one of the hugest families in Diptera, occurring in all zoogeographical regions including the Antarctica. In Japan, more than 70 species of the genus *Polypedilum* Kieffer, 1912 in the subfamily Chironominae have been recorded (cf. Sasa & Kikuchi, 1995; Kondo et al, 2001). The subgenus *Tripodura* Towns, 1945 belonging *Polypedilum* is characterized by the superior volsella that is broad, pad-like and covered entirely by microtrichia, with 1 to several long posterior setae and without bare distal or inner process and/or tergite IX often with projections lateral to each side of anal point (Sæther et al., 2000). As a result of several-years survey, we recognized five newly recorded species, including two new species, from Iriomote that is one of main islands of the Yaeyama islands located in the subtropical region in southernmost part of Japan, between Taiwan and Okinawa Island, and have been noted by the distribution of some endemic plants and animals.

In the present study, we newly recorded *P.* (*T.*) *sagitteferum* (Tokunaga, 1938), *P.* (*T.*) *unifascium* (Tokunaga, 1940) and *P.* (*T.*) *tananense* Sasa et Hasegawa and recognized two new species, *P.* (*T.*) sp.1 and *P.* (*T.*) sp.2, from Iriomote Island, the Ryukyus. *Polypedilum* (*T.*) sp. 1 is similar to *P.* (*T.*) *subovatum* Freeman, 1957 in the general habitus of male genitalia, but from which it can be distinguished by the superior volsella with a distinct long seta and the anal point being gradually expanded toward apex. *Polypedilum* (*T.*) sp. 2 is allied to *P.* (*T.*) sp.1 in having the distinct long seta of superior volsella, but it is separable from it by the presence of the lateral tooth.

Key Words: Chironomidae, *Polypedilum*, *Tripodura*, Iriomote island, Japan

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Importance of *Culicoides* biting midges as vectors for bovine arboviruses in Japan

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The genus *Culicoides* belongs to the family Ceratopogonidae and includes species that suck blood from mammals and fowls. Several *Culicoides* species transmit variety of virus, protozoa and nematode, including important pathogens in medical and veterinary fields.

In southern Japan, outbreaks of bovine congenital malformation caused by infection with Akabane, Aino (the genus Orthbunyavirus: the family Bunyaviridae) and Chuzan (the genus Orbivirus: the family Reoviridae) viruses have been reported frequently. Febrile illness in cattle, which is caused by infection of Ibaraki (the genus Orbivirus) virus, is known to occur at 5-10 years interval. The beef and dairy industries have been greatly affected by these diseases in this region. It is considered that these viruses are arthropod-borne (arbo-) viruses which are mainly transmitted by *Culicoides* biting midges.

To determine possible vector species involved in the epidemic, entomological surveillance for bovine arboviruses has been conducted in Kagoshima, located in the most southern part of the main islands of Japan since 1985. *Culicoides* biting midges were collected in a cowshed by light traps and were tested for virus isolation. Overall, 85 isolates of six different viruses, Akabane, Aino, Chuzan, D'Aguliar (the genus Orbivirus), Ibaraki and one unclassified viruses, were obtained from the collected midges. Of 13 collected species, the viruses were most frequently isolated from *Culicoides oxystoma,* indicating that this species is a potential vector of bovine arboviruses in this region. Another collection of *Culicoides* biting midges was carried out in Okinawa, which extends southwestward from the main islands, between 2001 and 2004. A strain of Bluetongue virus (the genus Orbivirus) was isolated from *C. brevitarsis* which is incriminated as a vector species of bovine arboviruses in Australia. These studies will improve to elucidate the role of *Culicoides* biting midges in the transmission of bovine arboviruses in Japan.

Key Words: *Culicoides*, Ceratopogonidae, biting midges, arbovirus, voctor

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Some photosynthetic pigment-protein complexes are lifetime deficient in two cecidomyiid galls derived from *Machilus thunbergii* leaf.

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Two cecidomyiid galls at young, greening and mature developmental stages, derived from *Machilus thunbergii* Sieb & Zucc leaves were collected from the Yang-Ming Shan National Park at northern Taiwan. Their biochemical composition of photosynthetic pigment-protein complexes located in thylakoid membranes were analyzed by using of the Thornber and MARS electrophoretic fractionation systems. Both galls were found to be totally deficient in pigment-protein complexes CPI, and A1, AB1, and AB2, respectively, through the whole period of gall formation. Immunoblotting of antibody against LHCIIb apoprotein confirmed this lifetime deficiency, which never recovered under any condition. Electron microscopy demonstrated that even at the early developmental stage the galls still have thylakoid morphology as normal as leaf. However, it is unknown how the cecidomyiid insects cause the deficiency of some pigment-protein complexes in gall chloroplasts and whether the unique phenomenon is ubiquitous or just a special case.

Key Words: cecidomyiid gall, LHCIIb, *Machilus thunbergii*, pigment-protein complexes

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The expression of the cecropin genes in *Armigeres subalbatus*

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Five cecropin genes, *AsCec 1*, *AsCec 2*, *AsCec 4*, *AsCec 6*, *AsCec 7*, were expressed in the adult mosquito, *Armigeres subalbatus*, by inoculating heat-killed *Escherichia coli*. Most expressed genes were inducible except *AsCec 6*. However, an interesting phenomenon observed in *AsCec 6* was the constitutive expression in both adult and larval stages, which was not affected by the microbial challenge as that of *Staphylococcuc aureus, Nomuraea rileyi*, and *E. coli*. A novel gene-expressed profile was also observed in *AsCec 6* that the expression of *AsCec 6* declined 1 hr after pupation and then disappeared till 48 hr, but expressed again at 72 hr after pupation. During the early period of pupae, *AsCec 6* was inducible and persistently expressed until 18 hours with *E. coli* treatment, then gradually decreased to lowest at 36 hr, and finally rise again from 48 hr till emergence. Furthermore, the gene function of *AsCec 6* was verified by using the RNAi technique. Silencing of *AsCec 6* resulted in the failure of emergence or morphological abnormal of adult legs. The results reveal that *AsCec 6* may serve as peptide antibiotics as well as play an important role in the emergence of *Ar. subalbatus.*

Key Words: cecropin, *Armigeres subalbatus*

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Comparison of synaptic organization of the mushroom body calyx with the lateral horn neuropile in the brain of *Drosophila melanogaster*.

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Projection neurons (PNs) of the antennal lobe, a primary sensory neuropile, serve to integrate sensory information of different modalities and to transfer information to other areas of the insect brain. Presumed cholinergic PNs in the brain of *Drosophila melanogaster*, immunoreactive to choline acetyltransferase (ChAT-ir), convey olfactory information between the antennal lobe and the conspicuous neuropiles, mushroom bodies (MBs), and finally terminate in an area called lateral horn (LH). The MB is regarded as a high-order integrative center required for olfactory learning and memory. The LH is a prominent but poorly investigated diffuse neuropiles that have so far remained blank area in the insect brain. We investigated the texture and synaptic connections of ChAT-ir PNs in the LH and, comparatively, in the MB calyces by immuno-electron microscopy. We especially looked for differences in the patterns of cholinergic fiber innervation between these two neuropiles, and for general difference in the design of their neural circuits.

The ChAT-ir PN terminals establish an array of large boutons (diameters 2-7μm) throughout MB calyces. The ChAT-ir boutons form the core at each glomerulus, and are encircled by tiny dendrites of the local intrinsic interneurons, as well as by a number of GABAergic terminals. The cholinergic calycal boutons are the largest identified cholinergic synapses in the *Drosophila* brain. In the LH, the ChAT-ir PNs boutons accumulate in the lateral margins of the LH, where the more proximal LH exhibits less intense immunolabeling. Synapses of ChAT-ir fibers appear predominantly as divergent synaptic boutons (diameters 1-3μm), connected to unlabeled postsynaptic profiles, or alternatively as a minority of tiny postsynaptic spines (diameters 0.05-05μm) among unlabeled profiles. The synaptic circuits of the LH are far more complex than the synaptic organization of the MB calyces. The differences in the basic design of neural circuits in these complex neuropiles will be discussed.

Key Words: cholinergic projection neurons, synaptic bouton, choline acetyltrasferase, mushroom body, lateral horn

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Apystomyia, Evocoidae and the therevoid clade: What do we know about the relationships of the asiloid flies?

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The asiloids represent the first major radiation of brachyceran flies, containing well over 15,000 species, and much of their early evolution has been linked to angiosperm diversification in the early Cretaceous. Recent progress in our understanding of the relationships between the asiloid families have been driven by the following three major developments: (1) the discovery of an entirely new family in the southern hemisphere, (2) the reinterpretation of the relationships of enigmatic lineages, and (3) the results from analyses of new molecular datasets. I report here on a reanalysis of asiloid family-level relationships in the context of the Lower Brachycera and Eremoneura. Particular attention will be focused on the anatomy and relationships of the new Chilean family Evocoidae, and its placement in the therevoid clade near the Scenopinidae. The relationships of the enigmatic genus *Apystomyia* is reassessed based on a large series of specimens recently collected at the type locality in the San Bernadino Mountains of California. Family status is warranted for *Apystomyia*, which is more closely related to Eremoneura than the asiloids. Future research directions, including character systems worthy of more detailed study, will be discussed in the light of recent molecular analyses.

Key Words: Asiloidea, *Apystomyia*, Evocoidae, phylogeny

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Evolution of obligatory cecidophagy in the genus *Wagnerinus* Korotyaev (Coleoptera: Curculionidae)

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Obligatory cecidophagy is a unique insect-plant interaction, because it is an indirect host plant utilization through galls induced by a third organism. Obligatory cecidophages are rarely found among herbivorous insects, such as Lepidoptera and Coleoptera. A weevil *Wagnerinus costatus* (Hustache, 1916) (Coleoptera: Curculionidae) is known to inhabit the axillary bud galls induced on *Weigela* species (Caprifoliaceae) by a Japanese gall midge species *Asphondylia baca* Monzen, 1937 (Diptera: Cecidomyiidae). Females of *W. costatus* lay their eggs in the midge galls, and hatched larvae feed exclusively on gall tissues. At the 5th Asia-Pacific Congress of Entomology in 2005, we presented that the genus *Wagnerinus* Korotyaev, 1980 could be classified into two species groups and further divided into 16 species from Northeast Asia including twelve undescribed species. At the same time, we reported that *Wagnerinus* species are associated with *Weigela* or *Abelia* species (Caprifoliaceae) and exhibit different ways of host plant utilization, feeding on flower buds, seed capsules, or midge galls at their larval stage. Considering its species and ecological diversity, *Wagnerinus* is a good target to study the evolutional mechanism of obligatory cecidophagy. However, the evolution of host plant utilization pattern within *Wagnerinus* has not yet been studied owing to the lack of a phylogenetic hypothesis of this genus. In addition, associated plants and/or larval food sources of several species are still uncertain. This has prevented progress in evolutionary studies of the cecidophagous habit of *Wagnerinus* weevils. Therefore, a phylogenetic study combined with field surveys to gather fundamental ecological data is needed to promote future studies. In this study, we gather additional ecological data and investigate phylogenetic relationships among *Wagnerinus* weevils including

undescribed species to consider the evolution of host plant utilization pattern within this genus, using molecular phylogenetic analyses based on sequences of the mitochondrial 16S and COI genes.

Key Words: *Asphondylia*, axillary bud gall, *Weigela*, weevil, cecidophagy

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Effects of early abscission of galled organs on population dynamics of gall midge species (Diptera: Cecidomyiidae)

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In order to find regulation mechanisms of gall midge population density, we have been studying, since 1970, population dynamics of several univoltine gall midge species (Diptera: Cecidomyiidae) that inhabit forests of broad-leaved evergreen trees in southern parts of Japan. In various gall midge–host plant systems, we observed that early abscission of galled organs affected gall midge populations density-dependently in some cases and density-independently in other cases. The longevity of heavily galled leaves was shortened in the systems of *Pseudasphondylia neolitseae–Neolitsea sericea* (Lauraceae), *Illiciomyia yukawai–Illicium anisatum* (Illiciaceae), and *Masakimyia pustulae–Euonymus japonicus* (Celastraceae). Such an earlier drop of galled leaves operated as a density-dependent mortality factor on the gall midge populations. In contrast, heavily galled leaves did not drop earlier than ungalled leaves in the systems of *Daphnephila machilicola–Machilus thunbergii* (Lauraceae) and *Lasioptera camelliae–Camellia japonica* (Theaceae) because of toughness of the host leaves. Some galled and ungalled leaves of *Elaeocarpus sylvestris* (Elaeocarpaceae) naturally drop to the ground a little before the emergence season of *Pseudasphondylia elaeocarpini*, which causes the death of the gall midge when the fall of galled leaves occurred before pupation. In the system of *Asphondylia sphaera–Ligustrum japonicum* (Oleaceae), abortion of flower buds and young fruit caused the death of the gall midge larvae, but it was not density-dependent. In addition to these observations, we evaluated other bottom-up effects that are related to gall density, such as production of plant organs available for oviposition in the following generation.

Key Words: early abscission, gall, population dynamics, Cecidomyiidae, mortality factor

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Study on the Tribe Blondeliini (Diptera, Tachinidae) from China

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The tribe Blondeliini (Tachinidae, Exoristinae) from China are studyed, and 69 known species (two newly recorded) and 3 undetermined species of 23 genera (one newly recorded) are recognized, viz, *Admontia* sp. from Sichuan, *blanda* (Fallén), *cepelaki* (Mesnil), *continuans* Strobl, *gracilipes* (Mesnil), *grandicornis* (Zetterstedt); *Biomeigenia auripollinosa* Chao *et* Liu, *flava* Chao, *gynandromima* Mesnil; *Blondelia siamensis* (Baranov), *inclusa* (Hartig), *nigripes* (Fallén); *Compsilura concinnata* (Meigen); *Compsiluroides communis* Mesnil, *flavipalpis* Mesnil; *Dolichocoxys* Townsend, newly recorded for China and *Dolichocoxys* sp. from Mêdog, Tibet; *Drinomyia hokkaidensis* (Baranov); *Eophyllophila elegans* Townsend, *includens* (Walker); *Istocheta altaica* (Borisova), *bicolor* (Villeneuve), *brevichirta* Chao *et* Liang, *brevinychia* Chao *et* Zhou, *graciliseta* Chao *et* Zhou, *grossa* (Chao), *leishanica* Chao *et* Sun, *longicauda* Liang *et* Chao. *ludingensis* Chao *et* Zhou, *nigripedalis* Yang *et* Chao, *nyalamensis* Chao *et* Liang, *nyctia* (Borisova), *rufipes* (Villeneuve), *subrufipes* (Borisova), *shanxiensis* Chao *et* Liu, *tricaudata* Yang *et* Chao, *zimini* (Borisova); *Leiophora innoxia* (Meigen); *Ligeriella aristata* (Villeneuve); *Lixophaga fallax* Mesnil, *latigena* Shima, *parva* Townsend; *Medina collaris* (Fallén), *fuscisquama* Mesnil, *malayana* (Townsend), *melania* (Meigen); *Meigenia* sp. from Jilin, *dorsalis* (Meigen), *majuscula* (Rondani), *nigra* Chao *et* Sun, *tridentata* Mesnil, *velutina* Mesnil; *Opsomeigenia orientalis* Yang; *Oswaldia eggeri* (Brauer *et* Bergenstamm), *illiberis* Chao *et* Zhou, *issikii* (Baranov), *muscaria* (Fallén); two new records for China, *glauca* Shima from Shanxi and *hirsuta* Mesnil from Heilongjiang; *Prodegeeria chaetopygialis* (Townsend), *japonica* (Mesnil),

javana Brauer *et* Bergenstamm, *villeneuvei* (Baranov); *Steleoneura minuta* Yang *et* Chao; *Trigonospila ludio* (Zetterstedt), *transvittata* (Pandellé); *Urodexia penicillum* Osten-Sacken; *Uromedina atrata* (Townsend), *caudata* Townsend; *Vibrissina debilitata* (Pandellé), *turrita* (Meigen); *Zaira cinerea* (Fallén). And keys to the species and genera of Chinese Blondeliini are presented.

Key Words: Tachinidae, Blondeliini, key, new recorded, China

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The search for a sister group: First results on the phylogeny, taxonomy and biogeography of the genus *Germaria* (Diptera, Tachinidae)

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The author is in the process of revising the phylogeny, taxonomy and biogeography of the poorly-known Holarctic tachinid genus *Germaria* Robineau-Desvoidy, 1830. This genus currently contains 11 rarely collected species of which 8 have been described in the last 50 years. A further 3-4 undescribed species have been found by the author in the course of his current investigations. The only species of the genus to have a relatively wide distribution are the Holarctic *G. angustata* and the possibly transpalaearctic *G. ruficeps*. The other species are found only in the southern Palaearctic eremial belt. This region – the former Thetys – has a climate that is becoming progressively more dry and has been separate from the rest of the Palaearctic region since the Tertiary. This region is thought to be the centre of origin of the genus *Germaria*. At least 6 species occur in the Mediterranean subregion, and three of these are also found in parts of the adjacent Irano-Turanian subregion to the east, where, together with at least eight further species that occur there, they form a centre of diversity.

By adapting to hosts that are difficult to access, the species of *Germaria* have come to occupy a very special niche. Their hosts are Lepidoptera larvae that live in the soil or which are borers in plants, the families Phycitidae and Sesiidae. As the female flies do not have a specialised ovipositor, the first-instar larvae have to act independently to seek out their concealed hosts, and they have adaptations for this. On the other hand, the characters of the third larval instar are predominantly plesiomorphous.

Adults are characterised by their elbowed and thickened arista and by their broad frons, for which reason the species were placed in the genus *Gonia* in the time of Meigen and Zetterstedt. However, these similarities to not indicate a common descent but are rather the result of convergence – as is so often the case in Tachinidae. The systematic position of *Germaria* is not clear at present. It has been thought to be related to the most diverse genera, but recent authors are in agreement that it belongs to the subfamily Tachininae. This presentation will discuss different hypotheses concerning the sister-group of the genus *Germaria* in the light of the characters of the immature stages, biology and historical biogeography.

Key Words: Tachinidae, *Germaria*, biogeography, taxonomy, phylogeny, larvae

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The Diptera Collection at INBio, Costa Rica: a fully accessible collection

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INBio was established in 1989, and has accumulated a collection of insects from Costa Rica, which at present includes 371,115 specimens of Diptera. At present 96 families, 806 genera, 1,170 valid species, and 767 morphospecies had been recorded. 52,291 specimens had been identified to species, and 15,000 to morphospecies.

This collection if fully digitalized and each and every specimen is represented in INBio´s biodiversity information management system, called Atta, by a record containing at the minimum its collecting data (specific collecting site, elevation, geographic coordinates, date, and collector) and each bears a unique identifier in the form of a barcode label which codify for a serial number, in addition to the locality label. When a specimen, or a series of specimens, are identified at different levels, the taxonomic information is enter in the Taxonomy Module of Atta and then the specimens just need to be scanned, this way the system generates a list of serial numbers which then, in just one step, are associated or linked with the chosen taxon, and the information updated in the DB System. Interested users can access all this information through the WWW at www.inbio.ac.cr, or at the mirror web site www.inbio.eas.ualberta.ca/en /default.html

Distribution maps (collecting localities maps) can be generated on-line for any species and/or morphospecies with associated specimens in the collection.
Multiple searchable fields are grouped in five categories: taxonomic information, geographic information, collecting event information, specimen information, and identification information. Up to 15 fields can be combined in a single query.

The Atta system can be queried for political units (province, county, district), protected area (national park, wildlife refuge, forest preserve), specific sites or localities, elevation ranges, watershed, dates, taxon, status, collector, et cetera. Taxon-associated images and links to species web pages are also available at this web version of Atta.

Key Words: biodiversity, databasing, Atta system, neotropical fauna, inventoring

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Dipterological research by the National Centre for the Study and Conservation of Forest Biodiversity (CNBF), Verona – Bosco della Fontana (Italy)

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During the last ten years, the National Centre for the Study and Conservation of Forest Biodiversity of Verona – Bosco della Fontana (Italy) has been involved in a series of faunistic and ecological studies in Italy, including two LIFE-Nature projects and the CONECOFOR programme (part of the ICP Forests network for long-term monitoring of forest ecosystems). The first LIFE project (1999-2003) was focussed on the study of the ancient oak-hornbeam forest Reserve of Bosco della Fontana (Mantova), and resulted in the finding of over 500 Diptera species, over 50 of which new for Italy, as well as of two Mycetophilidae (*Leia padana* Chandler, *L. fontana* Chandler) and one Phoridae (*Megaselia mantuana* Gori) new to science. A study of the Apennine beach-wood belt in 2000-2001 yielded over 850 Diptera species, including 200 new records for Italy and 5 Hybotidae new to science (*Platypalpus pseudoalter* Raffone, *P. pseudostroblii* Raffone, *P. submaculus* Raffone, *P. subpectoralis* Raffone, *Tachypeza subnubila* Raffone). Many interesting faunistic records and several species new to science (e.g. the Tachinidae *Pales abdita* Cerretti, *P. marae* Cerretti, *Pseudogonia metallaria* Cerretti), some of which still awaiting description, were found during a two-year monitoring scheme (2003-2005) in 12 Italian CONECOFOR permanent plots. In a second LIFE project, currently being carried out in a riparian forest at Vincheto di Celarda (Belluno, NE Italy), tree-crown dipteran communities are being investigated with aerial Malaise traps. With an agreement protocol recently stipulated between the Nature Protection Department of the Italian Ministry for the Environment and the Italian State Forestry

Service, the CNBF has been put in charge of monitoring the state of Natura 2000 and CONECOFOR sites in Italy: a network of six entomological labs (CORIN) is being established for this task. Dipterologists wishing to take part in these schemes are kindly invited to contact the CNBF.

Key Words: Diptera, Italy, faunistic surveys, monitoring

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Towards a better knowledge of *Sarcophaga (Heteronychia)*

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The subgenus *Heteronychia* Brauer & Bergenstamm, which currently contains approximately 100 valid species, is one of the three largest subgenera of *Sarcophaga* Meigen, together with *Liosarcophaga* Enderlein (approx. 90 species) and *Sarcorohdendorfia* Baranov (approx. 60 species). It is widespread across the Palaearctic Region, with high species richness in both the Mediterranean area and Central Asia. The only records of *Heteronychia* species from other biogeographical regions refer to Oriental parts of China and Japan, and to Pakistan. Prior to the recenty re-adopted widened concept of *Sarcophaga* s.l., *Heteronychia* was usually subdivided into several genera and subgenera. More or less well-outlined definitions of these taxa, as well as definitions embracing most species now listed under *Heteronychia*, have been provided by several authors. However, a clear definition of the current concept of *Heteronychia* does not exist in the literature, and relationships within and among species-groups remain largely uninvestigated. A 3-year Ph.D. project has been initiated, the two principal aims of which are: a) to review the taxonomy of *Heteronychia* under its present, wide concept; b) to carry out a phylogenetic analysis of the subgenus based on a morphological character matrix. The latter objective will be tackled by using mainly features of the adult morphology, and many characters are expected to be found in the highly complex structures of the male terminalia. During a recent visit to the Zoological Museum, Copenhagen, the genital structures of over 50 species of *Heteronychia* and 3 species of the closely related subgenus *Discachaeta* Enderlein were documented using SEM microscopy. These images represent a great increase in our knowledge of structures such as juxta, harpes, vesica, median and lateral styles, and contribute to a more precise definition of the subgenus. A phylogenetic analysis of the group, based also on these newly documented characters, will bring further insight into

relationships between species and relationships between *Heteronychia* and *Discachaeta*.

Key Words: Sarcophagidae, *Sarcophaga*, *Heteronychia*, definition, taxonomy, phylogeny

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