

Seventh
International Congress
of
Hymenopterists

20-26 June 2010

Programme and Abstracts
List of Participants

Editor: George Melika

Kőszeg
HUNGARY



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Note: This publication is not intended to form part of the permanent scientific record; it is therefore not a valid publication for the purposes of biological nomenclature.



Programme

(presenter in bold)

Sunday 20 June 2010 Arriving and Registration

Monday 21 June 2010

8:30 - 8:45 James B. Woolley, George Melika

Welcome and Opening

Symposium I. A Myriad of Morphology

8:45 - 10:05 Chair: **Matthew J. Yoder**

08:45 **Matthew J. Yoder** – Introduction

08:50 **Lars Vilhelmsen**, Perrichot, V. & Shaw, S.R. -- Past and present diversity and distribution in the parasitic wasp family Megalyridae

09:05 **Hannes Baur**, Doczkal, D. & Schweizer, M. -- Morphological and molecular analysis of *Vanhornia leileri* Hedqvist (Proctotrupoidea, Vanhorniidae), a neglected European parasitoid of eucnemid beetles

09:20 **Zoya Yefremova**, Mishchenko, A. & Yegorenkova, E. -- Biology and morphology of immature stages of some species of Eulophidae (Hym.: Chalcidoidea), parasitoids associated with leafminers (Lep.: Gracillariidae and Gelechiidae)

09:35 **István Mikó**, Vilhelmsen, L.B. Gibson, G.A.P., Yoder, M.J., Seltmann, K., Bertone, M. & Deans, A.R. -- Towards a compendium of Hymenoptera muscles

09:50 **Deepak D. Barsagade** -- Surface ultra-sculptural studies on the antenna, mouth parts and external genitalia of the Carpenter ant, *Camponotus compressus* (Hymenoptera: Formicidae)

10:05 - 10:30 Coffee and Tea Break

10:30 - 12:00 Chair: **Katja Seltmann**

10:30 **Ekaterina Shevtsova** & Hansson, C. -- Structural colours in Hymenoptera wings

10:45 **Seán G. Brady** -- The importance of morphology in the age of molecular hymenopteran phylogenetics

11:00 **Gérard Delvare** -- Looking inside the head capsule of Chalcididae provides informative characters to infer their phylogeny

11:15 **Matthew J. Yoder**, Mikó, I., Bertone, M.A., Seltmann, K. & Deans, A.R. -- Four years later: the Hymenoptera Anatomy Ontology, an overview and call for participation II

11:30 **Katja Seltmann**, Bertone, M.A., Yoder, M.J., Mikó, I., Macleod, E.S., Ernst, A. & Deans, A.R. -- Building the Hymenoptera Anatomy Ontology through exploration of the Journal of Hymenoptera Research

11:45 **Group Discussion.** Morphology's role in the future of hymenopteran research

12:00 - 13:30 Lunch



Symposium II. Scientific publication, informatics and DNA barcoding

13:30 - 14:45 Chair: **Donat Agosti**

- 13:30 Yu Dicky & **Michael Sharkey** -- BracBank – a specimen and taxon-based program to facilitate taxonomic research
- 13:45 **Donat Agosti**, Catapano, T. & Penev, L. -- The future of taxonomic communication and publishing
- 14:00 **James B. Woolley** & **Michael Sharkey** -- Group Discussion: A new model for the Journal of Hymenoptera Research
- 14:30 Smith, M.A., **José Fernández-Triana**, Achterberg van K., Goulet, H., Hallwachs, W., Hrcek, J., Huber, J.T., Janzen, D.H., Miller, S., Quicke, D.L.J., Rodriguez, J., Sharkey, M.J., Ward, D., Whitfield, J.B., Zaldivar-Riverón, A., & Hebert, P.D.N. -- An inordinate fondness for parasitoid wasps: DNA barcoding data from a global array of projects
- 14:45 Chesters, D., Vogler, A.P., Smith, M.A., Janzen, D., Hallwachs, W., Fernández Triana, J., Laurence, N.M., Zaldivar-Riverón, A., Shaw, M.R., Broad, G.R., Klopstein, S., Shaw, S.R., Hrcek, J., Hebert, P.D.N., Miller, S., Rodriguez, J., Whitfield, J., Sharkey, M.J., Sharanowski, B., Gauld, I.D. & **Donald L.J. Quicke** -- Beyond the barcode to the tree: Ichneumonoid phylogeny and the importance of taxon sampling density and strategy

15:00 - 15:30 Coffee and Tea break

Symposium III. Biological Control and Economic Entomology

15:30 - 17:30 Chair: **Andrew D. Austin**

- 15:30 Muirhead, K.A., **Andrew D. Austin**, Sallam, N. & Donnellan, S.C. -- Biosystematics of the *Cotesia flavipes* species complex (Hymenoptera: Braconidae): Towards the effective control of mothborer pests in Australia
- 15:45 **Robert A. Wharton**, Condon, M., Scheffer, S. & Lewis, M. -- Species diversity of neotropical tephritid fruit flies and their braconid parasitoids
- 16:00 Scheffer, S., Wharton, R.A., Norrbom, A. & **Matthew L. Buffington** -- Proposed world wide molecular survey of tephritid-parasitoid associations using fly puparia: a new approach to understanding host associations, systematics, and ecology in complex tritrophic communities
- 16:15 **John T. Huber** & Fernández-Triana, J.L. -- Parasitoids of *Choristoneura* spp. (Lep.: Tortricidae) in the Nearctic region
- 16:30 **Stephan M. Blank**, Hara, H., Mikuláš, J., Csóka, G., Ciornei, C., Constantineanu, R., Irinel Constantineanu, I., Roller, L., Altenhofer, E., Huflejt, T. & Véték, G. -- East Asian pest of elms (*Ulmus* spp.) now invading Europe: the zigzag sawfly, *Aproceros leucopoda* (Hymenoptera, Argidae)
- 16:45 **Erhan Koçak** -- Entomophagous complex associated with the insects on *Heracleum platytaenium* (Apiaceae) in Turkey, with new records
- 17:00 **Hosseinali Lotfalizadeh**, Delvare, G. & Rasplus, J.-Y. -- The almond seed wasp, *Eurytoma amygdali* Enderlein (Hymenoptera: Eurytomidae) of Iran, morphological and molecular aspects
- 17:15 **M. Reza Mehrnejad** -- Impact of secondary-parasitoids on population density of *Psyllaephagus pistaciae* in pistachio plantations of Iran

19:30 Welcome Reception



Tuesday 22 June 2010

Symposium IV. Cynipoids and gall communities

8:30 - 10:15 Chair: **George Melika**

- 08:30 **Matthew L. Buffington** & Seán G. Brady -- Divergence estimates and new insights into the early evolution of cynipoid wasps (Hymenoptera)
- 08:45 **Mattias Forshage** -- "The Kieffer syndrome" - endogenous taxonomic impediments in poorly known groups, as exemplified by the taxonomic history of Eucilinae (Cynipoidea: Figitidae)
- 09:00 **Johan Liljeblad**, Nieves-Aldrey, J.L., Melika, G. & Naser, S. -- A remarkable new species of gallwasp (Hymenoptera: Cynipidae) from South Africa, placed in a new tribe
- 09:15 **Katherine N. Schick**, Potter, D. & Shorthouse, J.D. -- A preliminary study of molecular relationships within *Diplolepis polita* (Hymenoptera: Cynipidae)
- 09:30 **Giovanni Bosio**, Quacchia, A., Piazza, E., Ferracini, C., Brussino, G., Melika, G. & Alma, A. -- *Dryocosmus kuriphilus* Yasumatsu in Europe: current distribution, associated parasitoids and biological control (Hymenoptera: Cynipidae)
- 09:45 **Chang-Ti Tang**, Yang, M.-M., Melika, G. Nicholls, J.A. & Stone, G.N. -- Gallwasp diversity of Taiwan: testing the Asian Origin hypothesis for the Cynipini (Hymenoptera, Cynipidae)
- 10:00 **James A. Nicholls**, Tang, C.-T., Yang, M.-M., Abe, Y., DeMartini, J.D., Melika, G. & Stone, G.N. -- Global patterns of host-plant association and phylogeography in the oak gallwasps

10:15 - 10:45 Coffee and Tea Break

10:45 - 12:15 Chair: **Graham N. Stone**

- 10:45 **Karsten Schönrogge** -- An introduction to gall formation
- 11:00 **Jack Hearn**, Stone, G.N., Blaxter, M., Shorthouse, J. & The GenePool -- Investigating the genetic control of gall induction in Cynipid gallwasps
- 11:15 **Frazer Sinclair**, Schönrogge, K., Stone, G.N. & Cavers, S. -- Oak Provenances on Trial: the distribution of gall forming wasps at an experimental oak plantation in Northwest France
- 11:30 **Juli Pujade-Villar**, Rodriguez, C., Stone, G.N., Melika, G., Penzès, Z., Ben Jamâa, M. L., Ouakid, M., Adjami, Y., Bouhraoua, R., Boukreris, F. & Arnedo, M.A. -- Evolutionary history and phylogeography of western Mediterranean *Synophrus* inquiline gallwasps (Hym., Cynipidae: Synergini)
- 11:45 **Jose Luis Nieves-Aldrey** & Medianero, E. -- Taxonomy and phylogeny of inquiline oak gallwasps of Panama, with description of eight new species of *Synergus* (Hymenoptera, Cynipidae, Synergini)
- 12:00 **Graham N. Stone**, Melika, G., Ács, Z., Challis, R., Bihari, P., Blaxter, M., Hayward, A., Csóka, G., Péntes, Z., Pujade-Villar, J., Nieves-Aldrey, J.L. & Schönrogge K. -- Phylogeny and DNA barcoding of inquiline oak gallwasps (Hymenoptera: Cynipidae) of the Western Palearctic

12:15 - 13:30 Lunch



Symposium V. Taxonomy and Systematics

13:30 - 14:45 Chair: **Gavin R. Broad**

- 13:30 **Gavin R. Broad** & Wharton, R.A. -- Phylogeny and re-classification of the genera of the ctenopelmatine tribe, Perilissini (Hymenoptera: Ichneumonidae)
- 13:45 **Mehmet Faruk Gürbüz** & Özdan, A. -- Hotspots of Ichneumonidae (Hymenoptera) Fauna in Natural Protection Areas of East Mediterranean Region in Turkey
- 14: 00 **Marla D. Schwarzfeld** & Sperling, F.A.H. -- *Ophion* (Ichneumonidae) of western Canada: molecules, morphology and species delimitation in a taxonomically challenging genus
- 14:15 **Alejandro Zaldívar-Riverón**, De Jesús-Bonilla, V.S.; Rodríguez-Pérez, A.C., Ceccarelli, F.S., Reséndiz-Flores, A. & Smith, M.A. -- DNA barcoding the parasitic wasp subfamily Doryctinae (Braconidae) from the Chamela-Cuixmala Biosphere Reserve, Mexico
- 14:30 **Anu Veijalainen**, Erwin, T.L., Sääksjärvi, I.E., Wahlberg, N., Broad, G., Gómez, I. & Longino, J.T. -- Presenting an on-going PhD project: Aspects to consider when estimating the diversity of Neotropical Ichneumonidae (Hymenoptera)

14:45 - 15:15 Coffee and Tea Break

15:15 - 16:15 Chair: **Jose L. Fernández-Triana**

- 15:15 **Jose L. Fernández-Triana** & Whitfield, J.B. -- Challenges, opportunities and future strategies in the study of Microgastrinae (Braconidae)
- 15:30 **Julia Stigenberg** -- Phylogeny and systematics of the tribe Meteorini (Braconidae)
- 15:45 **Neveen S. Gadallah**, Ahmad, R.S., El-Heneidy, A. & Mahmoud, S.M. -- Ichneumonidae collected from the Suez Canal and North Sinai regions, Egypt (Hym.: Ichneumonoidea)
- 16:00 **Inanc Özgen** & Beyarasan, A. -- Contributions to the Braconidae (Hymenoptera) Fauna of Turkey
- 16:15 **Péter Bihari**, Sipos, B., Melika, G., Somogyi, K., Stone, G.N. & Péntes, Z. -- Western Palearctic phylogeography of an inquiline gallwasp: *Synergus umbraculus* Olivier 1791 (Hymenoptera: Cynipidae, Synergini)

Wednesday 23 June 2010

Symposium VI. Biology, Behavior, Relationships with Hosts or Prey

8:30 – 10:00 Chair: **James B. Woolley**

- 08:30 **Richard R. Askew**, Ribes Escolá, A. & Rizzo, M.C. -- Chalcidoidea associated with seed capsules of *Asphodelus*
- 08:45 **Alex V. Gumovsky** -- Evolution of solitary and gregarious development in parasitoids: what we can learn from *Entedon* wasps (Chalcidoidea: Eulophidae)
- 09:00 **James B. Woolley**, Hopper, K.R. & Heraty, J.M. -- Evolution of host use in cryptic species of aphid parasitoids
- 09:15 **Pablo Fuentes-Utrilla**, Nicholls, J.A., Bihari, P., Ernst, J., Marsan, C. & Stone, G.N. -- When morphology is not enough: are generalist chalcid parasitoids aggregates of cryptic sibling species?
- 09:30 **Yoshimi Hirose** -- Evolution of egg parasitism under water in parasitoid Hymenoptera



- 09:45 **Rikio Matsumoto** -- Host manipulation by spider parasitoids of the *Polysphincta* group (Pimplinae, Ichneumonidae)
- 10:00 - 10:30 Coffee and Tea Break
- 10:30 - 12:00** Chair: **Serguei Triapitsyn**
- 10:30 **Serguei Triapitsyn** -- Egg parasitoids (Hymenoptera: Aphelinidae, Mymaridae, and Trichogrammatidae) of Proconiini leafhoppers (Hemiptera: Cicadellidae: Cicadellinae) in the New World and Oceania: recent discoveries and a glimpse into future research
- 10:45 **Münevver Kodan & Gürkan, M.O.** -- Biology of egg parasitoids *Trissolcus semistriatus* Nees and *Trissolcus grandis* Thomson (Hymenoptera: Scelionidae) on *Graphosoma lineatum* L. (Hemiptera: Pentatomidae) in laboratory conditions
- 11:00 **Simon van Noort**, Masner, L., Popovici, O.A., Taekul, C., Johnson, N.F. & Austin, A.D. -- The maritime parasitoid wasp *Echthrodesis lamoralis* Masner (Hymenoptera, Platygasteridae, Scelioninae)
- 11:15 **Mark R. Shaw** -- Biology of some parasitoids of *Apoda limacodes* (Lepidoptera: Limacodidae) in Europe
- 11:30 **Keizo Takasuka & Matsumoto, R.** -- Oviposition behaviour and infanticide by *Zatypota albicoxa* (Hymenoptera, Ichneumonidae), an ectoparasitoid of a theridiid house spider
- 11:45 **Vladimir E. Gokhman** -- Recent advances in the chromosomal studies of the superfamilies Cynipoidea and Chalcidoidea
- 12:00 – 13:30 Lunch
- Symposium VII. Taxonomy and Systematics**
- 13:30 - 14:45** Chair: **Barbara J. Sharanowski**
- 13:30 **Barbara J. Sharanowski & Deans, A.R.** -- A salute to the ensign wasps: molecular phylogenetics of Evaniidae
- 13:45 **Patricia L. Mullins**, Sharanowski, B.J., Mikó, I. & Deans, A.R. -- Molecular and morphological revision of *Evania* (Hymenoptera: Evaniidae) of Costa Rica
- 14:00 **Norman F. Johnson & Musetti, L.** -- Progress in taxonomy and systematics of Platygastroidea: new taxa, tools, and troubles
- 14:15 **Charuwat Taekul**, Johnson, N.F. & Valerio, A.A. -- Molecular evolution of the subfamily Telenominae (Hymenoptera: Platygasteridae)
- 14:30 **Elijah J. Talamas**, Masner, L. & Johnson, N.F. -- Phylogeny and taxonomic status of the *Paridris* (Platygasteridae) complex
- 14:45 - 15:15 Coffee and Tea Break
- 15:15 - 16:00** Chair: **Kees van Achterberg**
- 15:15 **Kees van Achterberg & Saure, C.** -- Revision of the Western Palearctic Gasteruptiidae (Hymenoptera)
- 15:30 **Andrew Ernst**, Mikó, I., Sharanowski, B.J. & Deans, A.R. -- Revision of the subfamily Megaspilinae (Hymenoptera: Ceraphronoidea)
- 15:45 **Gary A.P. Gibson** -- *Calosota* Curtis (Chalcidoidea: Eupelmidae) — pulling the proverbial thread of knowledge
- 16:00 - 18:00** Poster Session



Thursday 24 June 2010 All day excursion – Fertő-Hanság National Park

- 08:00 Assembly – Sandwich bag lunch for everyone will be served by the hotel
08:30 Departure
18:30 Grill Party (BBQ) in the Kőszeg mountains

Friday 25 June 2010

Symposium VIII. Biogeography and Systematics

8:30 - 10:00 Chair: **Simon van Noort**

- 08:30 **Simon van Noort**, Eardley, C. & Robertson, H. -- Hymenoptera of the Afrotropical region: diversity assessment and identification guide proposal
08:45 **Denis J. Brothers** & Lelej, A.S. -- Re-evaluation of phylogeny and higher classification of Mutillidae (Hymenoptera)
09:00 **Arkady S. Lelej** -- Biogeography of the mutillid wasps (Hymenoptera, Mutillidae) in the Palaearctic region
09:15 **Konrad Lohse**, Sharanowski, B.J. & Stone, G.N. -- Quantifying the Pleistocene history of the oak gall parasitoid *Cecidostiba fungosa* using twenty intron loci
09:30 **Astrid Cruaud**, Jabbour-Zahab, R., Genson, G., Couloux, A., Yan-Qiong Peng, Da Rong, Y., Ubaidillah, R., Santinelo Pereira, R. A., Kjellberg, F., van Noort, S., Kerdelhué, C. & Rasplus, J.-Y. -- Phylogeny and historical biogeography of Sycophagine non-pollinating fig wasps (Hymenoptera, Chalcidoidea)
09:45 **Serguei V. Triapitsyn** -- Remediation and curation of the University of California, Riverside collections of Aphelinidae and Encyrtidae (Hymenoptera: Chalcidoidea) on slides: problems and solutions

10:00 - 10:30 Coffee and Tea Break

10:30 - 12:00 Chair: **Stefan Schmidt**

- 10:30 **Stefan Schmidt** & Walter, G.H. -- Breaking the bonds of Gondwana – adaptive radiation of the Gondwanan pergid sawflies (Hymenoptera, Symphyta, Pergidae)
10:45 **Lars Krogmann** & Austin, A.D. -- Australian spider wasp systematics (Hymenoptera: Pompilidae) – Clearing up more than 200 years of confusion and misclassification
11:00 **Stefanie Krause** & Ohl, M. – Basics First – The Phylogeny of the Brood Parasitic Nyssonini (Hymenoptera: Apoidea)
11:15 **Volker Lohrmann** & Ohl, M. -- Taxonomy, systematics and biogeography of Rhopalosomatidae with special reference to macropterous forms (Hymenoptera: Vespoidea)
11:30 **Villu Soon** -- What do we know about *Chrysis ignita* (Hymenoptera: Chrysididae)?
11:45 **Takuma Yoshida**, Romel, Q., Muller, F., Perrard, A. & Villemant, C. -- The Yellow-Legged Hornet *Vespa velutina* (Hymenoptera: Vespidae): a new invader in France

12:00 - 13:30 Lunch

13:30 - 14:45 Chair: **Justin O. Schmidt**

- 13:30 **Yasemin Güler**, Aytekin, A.M. & Dikmen, F. -- Wild Bee Diversity of Sweet Cherry Orchards in Sultandağı Reservoir (Turkey)
13:45 **Nil Bağrıaçık** & Büyükkakış, S. -- Nest materials and some physical characteristics of the nest of *Vespa orientalis* Linnaeus, 1771 (Hymenoptera: Vespinae) in Turkey



- 14:00 **Sándor Csősz** & Majoros Gábor -- Ontogenetic origin of mermithogenic *Myrmica* phenotypes (Hymenoptera, Formicidae)
- 14:15 **Justin O. Schmidt** -- Defense in honeybees: can bees determine how much is at risk?
- 14:30 **Kurt M. Pickett** & Carpenter, J.M. -- The poverty of partitioned analyses and character-type chauvinism

14:45 - 15:15 Coffee and Tea Break

Symposium IX. Higher-level phylogeny of Hymenoptera

15:15 - 16:45 Chair: **Michael J. Sharkey**

- 15:15 **Ralph S. Peters**, Meyer, B., Krogmann, L., Borner, J., Niehuis, O., Schütte, K. & Misof, B. -- Daring the impossible - a phylogenomic 2000 species approach to Hymenoptera phylogeny
- 15:30 **James M. Carpenter**, Agosti, D., Azevedo, C.O., Brabant, C.M., Brothers, D.J., Dubois, J., Kimsey, L.S., Lohrmann, V., Ohl, M., Packer, L. & Schulmeister, S. -- Phylogeny of the Aculeata: Results of the Hymatol Taxonomic Working Group
- 15:45 Heraty J.M., Burks, R., Munro, J., Liljeblad, J., Yoder, M. & **Elizabeth Murray** -- Relationships of Chalcidoidea: a Molecular and Morphological Approach
- 16:00 **Michael J. Sharkey**, Carpenter, J.M., Vilhelmsen, L., Heraty, J.M., Ronquist, F., Deans, A.R., Dowling, A.P.G., Hawks, D., Schulmeister, S. & Wheeler, W.C. -- Morphology and molecules, the first comprehensive, total evidence, phylogenetic analysis of the Hymenoptera

16:45 - 17:00 Short Break

17:00 ISH Business Meeting

19:00 Congress Dinner

Saturday 26 June 2010 -- Departure and Collecting day 1 – vicinity of Kőszeg

Sunday 27 June 2010 -- Collecting day 2 – near Balaton Lake. Lunch in the forest

Monday 28 June 2010 -- Collecting day 3 – Őrség, south of Hungary. Lunch in the forest

Tuesday 29 June 2010 -- Departure



List of Posters

(presenter in **bold**)

- Alizadeh** Esmacil & S.E.Sadeghi -- Population dynamics of alfalfa weevil parasitoids in West Azarbaijan (Iran)
- Barkan** Nezahat Pınar & A.M. Aytekin -- Comparing wing shapes of the subspecies *Bombus (Thoracobombus) sylvarum citrinofasciatus* and *Bombus (Thoracobombus) sylvarum daghestanicus* (Hymenoptera: Apidae: *Bombus* Latreille) using landmark based geometric morphometrics
- Bertone** Matthew A., I. Mikó, M.J. Yoder, K. Seltmann & A.R. Deans -- Aligning insect anatomy ontologies: identifying congruence between Hymenoptera and Diptera
- Boyadzhiev** Peter S., A.D. Donev & T.S. Gechev -- A new mechanical modification of an insect manipulator
- Breitkreuz** Laura & M. Ohl -- Bizzare Wasps on the Island New Caledonia – A Revision of the Genus *Arpactophilus* (Hymenoptera: Apoidea)
- Budrienė** Anna, Ž. Nevronytė & E. Budrys -- Body weight change during the development of solitary wasp *Symmorphus allobrogus* (Hymenoptera: Vespidae: Eumeninae)
- Budrys** Eduardas, A. Budrienė & Ž. Nevronytė -- Dependence of brood cell length on nesting cavity width in xylicolous solitary wasps of genera *Ancistrocerus* and *Symmorphus* (Hymenoptera: Vespidae: Eumeninae)
- Budrys** Eduardas & A. Budrienė -- Assessment of anthropogenic impact at landscape scale using trap-nesting wasp and bee community in Europe
- Dias Filho** Manoel Martins, M. Geraldo, A.M. Penteado-Dias & A.F. Herrera Flórez -- Hymenoptera parasitoids of immature stages of Geometridae (Lepidoptera), associated with plants of a sub-native forest in the state of São Paulo, Brazil
- Early** John W., L. Masner & D.F. Ward -- Parasitic wasps of the Proctotrupoidea, Platygastroidea and Ceraphronoidea in New Zealand: review and analysis
- Falco-Gari** Jose Vicente, M.T. Oltra-Moscardo, F.J. Peris-Felipo & R. Jimenez-Peydro -- Exotic fig pollinators and associates (Chalcidoidea: Agaonidae) of *Ficus* trees in Europe
- Falco-Gari** Jose Vicente, M.T. Oltra-Moscardo, F.J. Peris-Felipo & R. Jimenez-Peydro -- Diversity of Heloridae (Proctotrupoidea) in a protected natural area in Spain
- Fusu** Lucian -- Tracing the geographical origin of *Eupelmus vesicularis* and a molecular taxonomic analysis of the *Eupelmus vesicularis* species-complex
- Fursov** Viktor N. -- The importance of morphological characters in the taxonomy of egg-parasitoids of the family Trichogrammatidae (Hymenoptera, Chalcidoidea)
- Fursov** Viktor N. -- Life-cycle of a fig wasp *Blastophaga psenes* L. (Hymenoptera, Agaonidae) as obligate pollinator and gall-former in *Ficus carica* L. (Magnoliopsida) in Crimea, Ukraine
- Gess** Sarah K. & Gess Friedrich W. -- Flower visiting by sand wasps in southern Africa
- Gokhman** Vladimir E. -- Chromosomes of *Xyela julii* (Xyelidae) and karyotype evolution in the order Hymenoptera
- Gómez J.F., R.R. Askew & Jose Luis **Nieves-Aldrey** -- Foodweb structure and diversity of parasitoid communities (Hymenoptera, Chalcidoidea) of herb gallwasps (Hym., Cynipidae) inducing galls on Lamiaceae



- Gómez J.F., R.R. Askew & Jose Luis **Nieves-Aldrey** -- Larval morphology of Pteromalidae (Hym., Chalcidoidea) parasitoids of gallwasps (Hymenoptera, Cynipidae) in Europe
- Gratiashvili** Nana, B. Seifert & S. Barjadze -- Diversity and distribution of the *Formica* species in Georgia (Hymenoptera: Formicidae)
- Guz N., Erhan **Kocak**, A.E. Akpinar, M.O. Gürkan & A.N. Kilincer -- First record of *Wolbachia* in *Trissolcus* species (Hymenoptera: Scelionidae)
- Haghighian, F. & Seyed Ebrahim **Sadeghi** -- Some biological aspects of a seed pest wasp, *Bruchophagus astragali* (Hym.: Eurytomidae), in rangelands of Chaharmahal & Bakhtiary province of Iran
- Hilszczański** Jacek -- New data on the occurrence of stephanids (Hymenoptera, Stephanidae) in Turkey and Greece
- Holy** Kamil -- Research of the family Ichneumonidae in the Czech Republic
- Hu** Hongying -- The resources of Trichogrammatidae and Mymaridae and their utilization in biological control in Xinjiang, China
- Izquierdo Moya** Isabel, J.M. Cano & C.M. Albadalejo -- *EOS, Revista ibérica de Entomología*, soon available online
- Izquierdo Moya** Isabel -- Contribution of *EOS, Revista Española de Entomología*, (1925-1994) to the knowledge of the Hymenoptera
- Janšta** Petr -- Updates to the evolution of torymids (Hymenoptera: Torymidae)
- Japoshvili** George -- Morphometrics and host information for the support of phylogenetic relations in genera *Microterys* Thomson and *Aschitus* Mercet (Hymenoptera: Encyrtidae)
- Jiao** Tian-Yang & Hui Xiao -- Preliminary Investigation of Chalcidoidea in Hainan Island, China
- Karlsson** Dave -- The Swedish Malaise Trap Project. One step further!
- Kirpik** Mehmet Ali -- Field observations on the defense and hunting behaviour of Pompilidae (Hymenoptera: Insecta) species
- Kirschey** Lukas & M. Ohl -- A review of the wasp genus *Lyroda* from Thailand (Hymenoptera: Apoidea)
- Klopfstein** Seraina, D. Quicke & C. Kropf -- The evolution of antennal courtship in parasitoid wasps of the subfamily Diplazontinae (Hymenoptera, Ichneumonidae)
- Kolesova** Natalia S. -- Trophical links of Bumblebees (Hymenoptera: Apidae, *Bombus*) in Vologda Region of Russia
- Konishi** Kazuhiko -- Taxonomy of the genus *Eurypterna* with biological notes on *E. cremieri* (Ichneumonidae, Hybrizontinae)
- Kos** Katarina, Ž. Tomanović, A. Petrović, J. Jakše & S. Trdan -- The separation of cereal aphid parasitoids, *Aphidius rhopalosiphi*, *A. uzbekistanicus* and *A. avenaphis* (Hymenoptera: Aphidiinae), using mt-DNA (COI) sequences
- Krogmann** Lars & R.A. Burks -- Rare giants – A review of Leptofoeninae (Chalcidoidea: Pteromalidae) and discovery of the first *Doddifoenus* from Indomalaya
- Loffredo** Ana Paula da Silva, A.M. Penteado-Dias, J.F. Sobczak & M. de Oliveira Gonzaga -- Contributions to knowledge of Pimplinae wasps (Hymenoptera, Ichneumonidae) from Brazil
- Lohrmann** Volker, L. Kirschey, S. Krause, M. Schulze & M. Ohl -- TIGER wasps – a preliminary review of the apooid wasp diversity in Thailand



- Lotfalizadeh** Hosseinali & M.-H. Kazemi -- Hymenopterous parasitoids of safflower fruit flies (Diptera: Tephritidae) in Iran
- Masnady-Yazdinejad** Ashkan -- The first braconid species record of subfamily Charmontinae from Iran: *Charmon extensor* (L.) (Hym., Braconidae, Charmontinae)
- Masnady-Yazdinejad** Ashkan -- The ichneumonid parasitoids (Hym., Ichneumonidae) of *Yponomeuta malinellus* Zeller (Lepidoptera: Yponomeutidae) in Iran
- Masnady-Yazdinejad** Ashkan -- Two newly recorded ichneumonid species as parasitoid wasp of Codling Moth (*Cydia pomonella* L. (Lepidoptera: Tortricidae) from Iran
- Matsuo** Kazunori, M. Tokuda, K. Kiritani, M. Mishima & J. Yukawa -- Comparison of parasitoid communities between insular and mainland populations of *Pseudasphondylia neolitseae* (Diptera: Cecidomyiidae) in the Izu district, Japan
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- Mete** Özlem & A. Demirsoy -- A preliminary study on the gallwasp fauna of Kemaliye (Turkey), with a new record for Turkey (Hymenoptera: Cynipidae)
- Mitroiu** Mircea-Dan -- A second European species of *Netomocera* Bouček (Hymenoptera: Pteromalidae: Diparinae), with notes on other diparines
- Mottern** Jason L. & J.M. Heraty -- Calesinae: morphological examination and molecular phylogenetics of an enigmatic chalcidoid taxon
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- Nevronytë, Ž., Eduardas **Budrys** & A. Budrienė -- The effects of prey abundance on nesting behavior of solitary wasp *Symmorphus allobrogus* (Hymenoptera: Vespidae: Eumeninae)
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- Noyes** John S. -- An inordinate fondness of beetles? Even more fond of microhymenoptera!
- Österblad** Ika & N.R. Fritzén -- Rare in collections, common in the forest – the occurrence of the pimpline spider parasitoid *Reclinervellus nielseni* in Finland
- Özgen** İnanç & H. Bolu -- The chalcidoid parasitoids of Coccoidea in southeastern Anatolia Region of Turkey
- Paretas-Martínez J., C. Restrepo-Ortiz, M. Buffington & Juli **Pujade-Villar** -- New systematics of Australian Thrasorinae (Hymenoptera: Cynipoidea: Figitidae) with a description of two new genera and a new subfamily
- Penteado-Dias** Angélica M. -- New records of Braconidae (Hymenoptera) genera from Brazil in the state of São Paulo
- Penteado-Dias** Angélica M. & M.M. Dias Filho -- What is “the news” about the institute of studies on parasitoid Hymenoptera from southeastern Brazil – *HYMPAR-SUDESTE* ?
- Peris-Felipo** Francisco Javier, J.V. Falcó-Garí, M.T. Oltra-Moscardó & R. Jiménez Peydró -- Diversity of Alysiinae (Hymenoptera: Braconidae) in protected areas from the Comunidad Valenciana, Spain
- Peris-Felipo** Francisco Javier, J.V. Falcó-Garí, M.T. Oltra-Moscardó & R. Jiménez Peydró -- Habitat distribution patterns of Alysiinae community (Hymenoptera: Braconidae) in a forest reserve in Spain



- Peters** Ralph S. & R. Abraham -- Little known facts about a well known hymenopteran: on the field life history of *Nasonia vitripennis* (Walker, 1836) (Chalcidoidea: Pteromalidae)
- Popescu** Irinel E. -- Confirmation of the species rank of *Torymus macrurus* (Föerster, 1859) (Hymenoptera: Chalcidoidea: Torymidae)
- Popovici** Ovidiu A. -- The maxillo-labial complex in scelionid wasps (Hymenoptera: Platygastroidea)
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- Rahemi, S., S.E. **Sadeghi**, E. Rakhshani, S. Moharramipour, M. Shojai & S. Zeinali -- Parasitoids wasps reported on willow aphids in Iran
- Reshchikov** Alexey -- New species of the genus *Lathrolestes* (Hymenoptera, Ichneumonidae) from the World
- Sadeghi** S. Ebrahim, Melika, G., Stone, G.N., Assareh, M.A., Askary, H., Tavakoli, M., Yarmand, H., Azizkhani, E., Zargarani, M.R., Barimani, H., Dordaii, A.A., Aligholizadeh, D., Salehi, M., Mozafari, M., Golestaneh, R., Zeinali, S., Mehrabi, A. -- Oak gallwasp fauna of Iran (Hymenoptera, Cynipidae, Cynipini)
- Shayesteh** Nouraddin -- Study on the biology and efficiency determination testes of *Habrobracon hebetor* Say (Hymenoptera: Braconidae) on larvae of *Plodia interpunctella* Hübner (Lepidoptera: Pyralidae)
- Shevtsova** Ekaterina & C. Hansson -- Structural colours in Hymenoptera wings
- Sparks K.S., Andrew D. **Austin**, A.N. Andersen, S.O. Shattuck, & S.C. Donnellan -- The ant genus *Monomorium* in Australia: morphological plasticity or cryptic diversity?
- Szabó** Gyula, R. Horváth, E. Zakar, L. Kozák, S. Lengyel -- The effect of grassland restoration on bee communities – a preliminary study in Hortobágy National Park, Hungary
- Stojanova** Anelia, H.S. Civelek, B. Yörük, S. Sarı & T. Atahan -- Turkish Eurytomidae and Torymidae (Hymenoptera, Chalcidoidea): published data and new records
- Talamas** Elijah J. -- Montage Ultra: High Resolution Imaging of Parasitic Hymenoptera
- Tavakoli** Majid, G. Melika, S.E. Sadeghi, R.R. Askew, G.N. Stone, H. Barimani, D. Aligholizadeh, Ali asghar Dordaii, H. Yarmand, M.R. Zargarani & S. Mozafarian -- Parasitoid communities (Chalcidoidea) of oak gallwasps of Iran (Hymenoptera: Cynipidae)
- Tavakoli** Majid, G. Melika, S.E. Sadeghi, R.R. Askew, G.N. Stone, H. Barimani, D. Aligholizadeh, Ali asghar Dordaii, H. Yarmand, M.R. Zargarani & S. Mozafarian -- Oak cynipid gall inquiline of Iran (Hymenoptera: Cynipidae: Synergini)
- Triapitsyn** Serguei V. -- Remediation and curation of the University of California, Riverside collections of Aphelinidae and Encyrtidae (Hymenoptera: Chalcidoidea) on slides: problems and solutions
- Turčinavičienė J., A. Budrienė, Eduardas **Budrys** & R. Radzevičiūtė -- Mitochondrial COI gene sequence in European Eumeninae wasps (Hymenoptera: Vespidae): intra-specific diversity and applicability for DNA barcoding
- Turrisi** Giuseppe F. & D.R. Smith -- Systematic and phylogeny of the endemic south-eastern Asiatic *Pristaulacus comptipennis* species group (Hymenoptera Evaniidae: Aulacidae)
- Vårdal** Hege -- The gallwasp venom apparatus
- Wachi** Nakatada & Y. Abe -- Taxonomic notes on the oak gall wasp *Callirhytis hakonensis* Ashmead (Hymenoptera: Cynipidae), with description of the sexual generation



Yarmand Hamid, S.E. Sadeghi, V.-R. Moniri -- Seed affecting wasps of none-legume forage plants in Iran

Yousuf Mohammad -- Record on Indian species of *Trichogramma* Westwood, along with two new species, their host range and application against forest insect pests

Zimmermann Dominique & J. Schmidl -- Hymenopterans on tree barks along climatic and altitudinal gradients in Ecuador



ABSTRACTS OF PAPERS

(* = presenter)

Revision of the West Palaearctic Gasteruptiidae (Hymenoptera)

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The Gasteruptiidae are worldwide distributed but with more species in tropical than in temperate areas. The family contains six valid genera with about 500 valid species, mostly belonging to the subfamily Gasteruptiinae. Gasteruptiidae first devour the egg or young larva of the solitary host bee (Apidae s.l.) and develop mainly on the bee food. Solitary wasps (Vespidae-Eumeninae and Crabronidae) are also reported as hosts, but the reports concern double nests. The subfamily Gasteruptiinae contains three Neotropical genera and the cosmopolitan genus *Gasteruption* Latreille. *Gasteruption* is still unknown from Polynesia and Hawaii and it is apparently most diverse in the Australian and Afrotropical regions. The world species are monographed by Kieffer (1912) and catalogued by Hedicke (1939). Useful are the following keys to part of the European species: Šedivý (1958; Czechoslovakia), Oehlke (1984; Germany), Madl (1988; Sardinia) and Pagliano & Scaramozzino (2000; Italy). The distribution and the synonymy of European species (excluding Caucasus) are given by Madl (2004). In the West Palaearctic region we have only the genus *Gasteruption* Latreille. According to the FE database (Madl 2004) there are 30 European valid species, but our revision revealed 18 new synonyms, two species with new status and one extension of an Asian species. It results in a provisional total of 28 described valid species of *Gasteruption* in Europe. Up to now three undescribed species have been found in Europe and in addition several undescribed species in Asiatic Turkey. A short overview of the first results of the revision will be presented.

The future of taxonomic communication and publishing

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Publishing taxonomic work has multiple functions, not least to communicate and share results, get credit for scientific discovery and document the progress in the knowledge in the domain. The printed work in respective scientific journals, accessible through a ubiquitous library system as part of our scientific infrastructure has been its cornerstone, supplemented by an exchange of reprints by mail.

The advantage of having a printed record dating back to 1758 is today hugely outdated by its deficiencies compared to what the digital world now has to offer: immediate access, discoverability, linkage to underlying data and other external resources, data mining over large amount of documents, the use of shared vocabularies and archiving. This all moves these publications and in fact the underlying science much closer to the scientific criteria of



reproducibility: essentially every body could have access to all the data, including protocols and programs to reproduce and challenge a piece of research.

In this lecture aspects of state of the art and future developments concerning taxonomic publishing will be discussed. A first part will discuss efforts to digitize legacy publications, enhance it with semantic mark-up and links to external databases such as Zoobank, the Hymenoptera Name Server, Hymenoptera Anatomy Ontology, individual collections through Life Science Identifiers or equivalent, GenBank, and how it's access is improved by applications allowing to harvest specific elements from these publications. An assessment of the costs and benefits will lead to the second part, prospective publishing. At center will be the National Library of Medicine Document Tape Definition (NLM DTD) for publishing and archiving that has been customized for the taxonomic domain (taxpub). Its use in a journal production workflow will be explained that is being developed in collaboration with Pensoft, the future publisher of our Journal of Hymenoptera Research. This includes the generation of a manuscript to its dissemination as peer reviewed journal article, the linking to external resources such as Zoobank, image banks, GenBank etc.

Finally this change of paradigm from an emphasis of print/archive to digital/access, and its implication for our taxonomic infrastructure, such as access to databases, shared vocabularies or ontologies, its dissemination and reuse, open access, and not least the social changes that this might imply, will be explained.

The lecture is based on the experiences from building antbase and its pdf repository for ant taxonomic publications, Hymenoptera Name Server, the fledgling Zoobank, Plazi, Taxpub and Taxonx XML schemas, developing of Zookeys as a taxpub XML based online journal and Journal of Hymenoptera Research that is under development.

Chalcidoidea associated with seed capsules of *Asphodelus*

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Seeds of *Asphodelus* (Liliaceae) were known, prior to the present study, to be infested by a single species of Eurytomidae, *Eurytoma asphodeli* Hedqvist, and by parasitic species in the tetrastichine genus *Puklina*. In our research *E. asphodeli* was the chalcid reared most commonly from the seeds and at first it was thought to be phytophagous. However, it belongs to the robusta-group of species, the great majority of which are entomophagous, and the structure of the occipital surface of the head with a strong postgenal carina and complete postgenal groove, is correlated with larval entomophagy. Probable hosts of *E. asphodeli* are some undescribed species of Eurytomidae, provisionally attributed to *Bruchophagus*. These species have an occiput that is characteristic of phytophagous Eurytomidae, lacking a postgenal carina and with an incomplete postgenal groove. *E. asphodeli* can have at least two generations a year, adults emerging both in the calendar year of seed formation and after overwintering, but the *Bruchophagus* species are predominantly univoltine, almost all individuals emerging in spring after overwintering inside the seeds as fully grown larvae.

The pteromalid *Pteromalus tethys* Gijswijt and a eupelmid in *Eupelmus urozonus* Dalman agg. have also been reared from asphodel seeds, *P. tethys* as an ectoparasitoid of eurytomid larvae and *E. urozonus* as a secondary parasitoid of *P. tethys*. A species of *Puklina*, perhaps *P.*

depilata Graham, was reared in large numbers as a gregarious parasitoid of Eurytomidae in *A. cerasiferus* seeds, and other slightly different *Puklina* but possibly only variants of *P. depilata*, emerged in smaller numbers from seeds of other asphodel species.

Microlepidoptera larvae, probably Tortricidae but not yet identified, are common in asphodel seed capsules in which they consume the seeds. They are attacked by Ichneumonidae, Braconidae, *Hyssopus nigrifolius* (Zetterstedt) (Eulophidae), and by *P. tethys* and *E. urozonus* agg. which may also develop on the Eurytomidae.

Species of Eurytomidae and *Puklina* encountered in this study appear to be associated only with asphodels, and there is evidence that different *Asphodelus* species support differing faunas of Eurytomidae and *Puklina*. The *Bruchophagus* in *A. ramosus* (*aestivus* auct.) seeds in Sicily has six segments in the female antennal funicle, five in the male, whereas in specimens reared from *A. albus* in the French and Spanish Pyrénées the clava in both sexes has more or less 'captured' a funicle segment, and wing pilosity is white. The form of *E. asphodeli* in seeds of *A. cerasiferus* is larger and has more extensively red legs than *E. asphodeli* from *A. ramosus* and *A. albus*, and the *Bruchophagus* in *A. fistulosus* seeds is a species distinct from that found in other species of asphodel.

Nest materials and some physical characteristics of the nest of *Vespa orientalis* L., 1771 (Hymenoptera: Vespinae) in Turkey

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The species of Vespinae use pulp gathered from nearby environment to make their nest by chewing and mixing it with their saliva. In the plant material choice of social wasps, there is a significant variation: worn or fresh wood fiber, plant feathers, short plant scrapings, inorganic materials, etc. *Vespa* prefers dead parts of live trees and worn woods, and tree bark as their nest material. In addition to plant fiber, they also add soil and mud to their nests. According to the characteristics of nest location, there might be inorganic materials in *Vespa orientalis*'s nests. The selected material, the amount of saliva and chewing duration determine the physical features of the nest. In this study, we aim to determine the nest material and its physical features of a nest of *Vespa orientalis* in Niğde/Turkey.

The nest surface was monitored by stereomicroscope and Scanning Electron Microscope. The thickness of plant fibers was measured. An EDX analysis was carried out in order to determine the presence of structural organic and inorganic elements and their amount. The percentage of plant material and saliva in the structure of the nest was measured. The water absorption capacity of the nest was calculated and the relationship between the fiber thickness and the water absorption capacity was statistically analyzed.

Vespa orientalis constructed the nest inside the wall made by soil. At the nest, there was no envelope. At the comb, there are beige, yellowish and brownish linings. The plant fibers were observed to be short and thick at the images taken by Stereo Microscope and Scanning Electron Microscope. There are inorganic materials, especially soil, between the fibers. The average thickness of the fiber is 13,47 µm. It is founded in EDX analysis that the concentration of nitrogen is 18,75 % and of silicon higher than the other elements. The percentage of the fiber was calculated to be 20%, saliva 80%, and the water absorption



capacity 91%. Conclusively, no statistically significant relationship was observed between the nest's water absorption capacity and the thickness of fiber.

Surface ultra-sculptural studies on the antenna, mouth parts and external genitalia of the Carpenter ant, *Camponotus compressus* (Hymenoptera: Formicidae)

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The antenna in all polymorphic forms of carpenter ant, *Camponotus compressus* (Fabricius) (Hymenoptera: Formicidae) is of a genniculate type. The antenna consists of a basal scape ball, pedicel and various numbers of flagellomeres. The SEM study shows the scape ball covered with three types of basiconical sensilla, SB- I, SB- II and SB- III in all castes of adults. The scape shaft contains sensilla trichoidea (ST) in all polymorphs.

On the pedicel sensilla trichoidea are commonly distributed in female, male and worker antenna while sensilla basiconica has been noticed only in the female. In female and workers, flagellum content ten numbers of flagellomeres while eleven flagellomeres in the antenna of male. On the flagellum in female and male, sensilla trichoidea curvata, sensilla trichoidea, sensilla basiconica and sensilla chaetica while in worker sensilla trichoidea curvata and sensilla trichoidea are found. The mouth parts are adopted for grasping the prey and feeding. The labrum is the fringe, plate like consists of ST and SB in female and male but only ST in workers. The mandibles are large and powerful. The dorsal surface of mandibles consists of sensilla trichoidea, DT-I, DT -II and DT-III while on the ventral side VT-I, VT-II and ventral basiconica (VB) in female and workers, while VB absent in male. Each mandibles consists four incisors and three molar teeth in female and worker while two incisors teeth in male. The ST present on cardo, stipes and palps while papillae are present on anterior part of galea of maxillae in male, female and worker. The maxillary palps covered with ST. Three types of ST are present on the mentum and submentum of labium. The glossa is large tongue like structure in the worker, covered with SB-I, SB-II and acanthae. On the labial palp, ST-I, ST-II and sensilla trichoidea curvata (STC) are found on all segment while, microtrichia MT- I and MT- II are present on first segment in workers only.

The male genitalia consist of a basal plate apically. A pair of outer gonocoxites, a pair of middle volsellae and inner penis wall is extended at the long appendicular structure. The gonocoxites consists of basal segments basimere and distal region telomere. The female external genitalia is greatly reduced in queen and worker ants. The IX terga and sterna covered with trichoid sensilla differentiated in to DT-I, DT-II on dorsal surface and VT-I, VT-II on ventral surface. The cuticular wall of anus consists of variable numbers cuticular setae radiating peripherally with a retractile sting.

Morphological and molecular analysis of *Vanhornia leileri* Hedqvist (Proctotrupoidea, Vanhorniidae), a neglected European parasitoid of eucnemid beetles

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The small, enigmatic family Vanhorniidae (Proctotrupoidea) comprises only three described species in two genera, *Sinicivanhornia quizhouensis* Jun-Hua & Ji-Ming, 1990 from China, *V. eucnemidarum* Crawford, 1909 from North America, and *V. leileri* Hedqvist, 1976 from in Southern Sweden. While *V. eucnemidarum* is relatively well studied morphologically and genetically, *S. quizhouensis* and *V. leileri* remained in obscurity because of the paucity of the material. Their descriptions were based on very few specimens and no new specimens were recorded since their description. The holotype female and single paratype male of *V. leileri* were reared from eucnemid beetles. The rediscovery of *V. leileri* in Central Switzerland (Trimbach, canton Olten) by the entomologist Georg Artmann in 2002 was thus rather surprising. Later, another specimen from the Savoy Alps in France (near Geneva) could be traced among miscellaneous material in the Hymenoptera collection of the Natural History Museum Geneva. Finally, D. Doczkal recently collected several specimens in Germany (Baden-Württemberg) using malaise traps. This new material was studied morphologically and compared with the holotype female of *V. leileri* as well as specimens of *E. eucnemidarum*. One specimen was also available for molecular analysis, whereby sequences of 16S, 28S and COI were generated. The morphological analysis revealed numerous further characters for separation of the two *Vanhornia* species. These characters were extensively documented with a digital imaging system and concern shape of head and body and sculpture of the integument. In the molecular analysis *V. leileri* is also clearly distinct from *V. eucnemidarum* though the two species came out as sister groups. However, their position remained ambiguous with respect to various genera of Proctotrupoidea (taxon sampling according to Dowton & Austin 2001), depending on the markers used.

**Western Palaearctic phylogeography of an inquiline gallwasp:
Synergus umbraculus Olivier 1791 (Hymenoptera: Cynipidae, Synergini)**

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The vast majority of gallwasps (Hymenoptera: Cynipidae) induce galls mainly on *Quercus* species (Cynipidae), however, around 10-15% of known species have lost their ability to induce galls (Synergini), and they develop as inquilines inside galls of other cynipids. In contrast to the gall inducers, we know little about inquilines, though they are abundant and supposed to play an important role in the community.

We used DNA sequences to study the diversity of *Synergus umbraculus*, a widespread and polyphagous inquiline gallwasp in the Western Palearctic. Our aims were to investigate (i) genetic structure on two spatial scales, and (ii) effect of gall hosts on the distribution of lineages.

Based on DNA sequences of two mitochondrial and one nuclear loci a remarkable degree of genetic differentiation was detected. Considering the analogous sequences of other *Synergus* species, *Synergus umbraculus* can not be regarded as one uniform species. At least four cryptic species were found.

Using 239 cytochrome *b* sequences we identified eight haplogroups within the “typical

umbraculus clade”, which overlap in distribution. Significant phylogeographic pattern was revealed in the Western Palearctic and a close connection between the Carpathian basin, Italy and North-Western Europe. Multiple colonisation events from different sources result in the high diversity of the Central European region where an endemic haplogroup was also found. These results imply the significance of this region in phylogeographic context.

Within the “typical umbraculus clade”, no pattern has been detected in variability related to the most common gall hosts, which suggests that *Synergus umbraculus* does not depend on a particular host association.

**East Asian pest of elms (*Ulmus* spp.) now invading Europe: the zigzag sawfly,
Aproceros leucopoda (Hymenoptera, Argidae)**

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At least since 2003, an invasive sawfly (*Aproceros leucopoda* Takeuchi, 1939) originating from East Asia, has colonized elms in Austria, Hungary, Poland, Romania, Slovakia and the Ukraine. In Europe, the larvae can completely defoliate native and non-native elm trees and may cause at least partial dieback. Field observations indicate that elms are infested independent of their age and site characteristics. Young larvae cause characteristically zigzag-shaped feeding traces on leaves. The life cycle of *A. leucopoda* is described based on material reared in Hokkaido, Japan. Parthenogenetic reproduction, short life cycle of summer generations and the ability to produce four generations per year result in the production of numerous progeny. The evolution of a seasonal dimorphism in head morphology, a simple cocoon that is attached directly to the host plant and a short period spent in cocoon stage during summer, are putative apomorphies shared by *Aproceros* Takeuchi, 1939 and *Aprosthemis* Konow, 1899. These traits reduce developmental costs and contribute to the proliferation of *A. leucopoda*. No specialized parasitoid is known effectively reducing outbreaks of this species.

The initial occurrence of *A. leucopoda* in Europe cannot be reconstructed. Presumably, it was introduced passively with elm plants used in horticulture or forestry. Transport of cocoons

with other merchandise is also possible. Passive dispersal along with traded material might be a major way in which this species rapidly extended its distribution over great distances within Europe, but active dispersal is also to be expected, since the imagines are strong flyers. It is likely that this pest will spread into central and south-western Europe. Further monitoring of *A. leucopoda* is required to assess future range extensions in Europe, its exacerbating effect on Dutch elm disease and to find a suitable biocontrol agent. In a forthcoming publication (European Journal of Entomology, in press), details on identification of larvae and imagines, current distribution in Europe, development and damage caused have been summarized.

***Dryocosmus kuriphilus* Yasumatsu in Europe: current distribution, associated parasitoids and biological control (Hymenoptera: Cynipidae)**

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The oriental chestnut gallwasp *Dryocosmus kuriphilus* Yasumatsu (Hymenoptera: Cynipidae), native of China but now present in Japan, Korea, Nepal and USA, was found for the first time in Europe in Piedmont, north-western Italy in 2002. The pest was probably introduced in Europe some years before, through import of chestnut scions for genetic improvement of chestnut stands in Piedmont. Official surveys carried out in 2002 showed that infestation already involved hundreds of chestnut woods' hectares, so attempts to eradicate were not feasible. In the following years, *D. kuriphilus* began to spread into many Italian regions, threatening chestnut fruit production. The pest is now reported in other neighbouring countries: France, Slovenia, Switzerland and Hungary. Chestnut trees are widely spread in Europe and especially in Italy. The fast diffusion of the chestnut gallwasp is probably due to the trade of young infested plants and to the flight of females, emerging from the galls during the summer. The huge development of an exotic pest's population is favoured by the lack of its natural enemies in the new environment. Considering the presence of many other oak gallwasps in Italy, a shift of parasitoids from numerous species of oak cynipid galls to the new host on chestnut was expected. Since 2002 about 25 chalcidoid parasitoid species have been reared from *D. kuriphilus* galls which belong to 6 Chalcidoidea families: Eurytomidae, Pteromalidae, Torymidae, Eulophidae, Ormyridae, Eupelmidae. Among these species, Eupelmidae and Torymidae are playing the major role. Many of them were already reported as *D. kuriphilus* parasitoids from other countries. Parasitoid studies evaluated in different regions of Italy during 2002-2009 showed a low impact of this parasitoid complex onto the population dynamics of the chestnut gallwasp, so they can't probably naturally control the pest. On the basis of this consideration and the lack of any other effective techniques [pesticide treatments produced nearly no positive effect], following the successful Japanese experience, the torymid ectoparasitoid, *Torymus sinensis* Kamijo, was introduced into Piedmont to control the pest. Chestnut galls, potentially parasitized by *T. sinensis*, were sent by Dr. S. Moriya (National Agricultural Research Center, Tsukuba, Japan) to the Entomology Department of the Agriculture Faculty of University of Turin during 2002-2008. The first *T. sinensis* releases in open field were made in three localities of Cuneo province in 2005.



Surveys in the following years have revealed that the exotic parasitoid is well established in the new environment and is under active reproduction.

The importance of morphology in the age of molecular hymenopteran phylogenetics

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Molecular data are eclipsing morphology as the primary source of phylogenetic characters for many hymenopteran groups. Molecular data also increasingly impact other areas of systematics such as species discovery and identification. In general, the study of morphology is becoming increasingly marginalized in the genomics era. I discuss case studies from own work on ants and bees that illustrate the continued importance of morphological data for molecular phylogenetics. These examples include incorporating fossils into phylogeny, inferring divergence dates, studying rare taxa, establishing independent sources of phylogenetic data, corroborating novel molecular clades, and creating diagnostic morphological keys based on molecular phylogeny. This is far from an exhaustive list of how morphology can impact molecular phylogenetics. As hymenopteran systematists embrace the vast potential offered by genetic and genomic data, we also have much to gain in continuing to forge new advances in morphological systems. The more that we as a community explicitly demonstrate to our colleagues the positive interplay between morphology and molecules, the better this perspective can be realized.

Phylogeny and re-classification of the genera of the ctenopelmatine tribe, Perilissini (Hymenoptera: Ichneumonidae)

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The ichneumonid subfamily Ctenopelmatinae is a heterogeneous assemblage of genera that are endoparasitoids of sawfly larvae and are more or less unsatisfactorily classified in up to nine tribes. Some of these tribes are very poorly defined, including the Perilissini. As part of a larger, PEET-funded initiative on the phylogeny and classification of Ctenopelmatinae, we have been concentrating on scoring the genera of Perilissini for a wide spectrum of morphological characters. We aim to (1) provide a re-definition of the Perilissini based on apomorphic characters; (2) re-classify those genera erroneously placed in Perilissini (e.g. *Perilimicron*); (3) produce a (hopefully relatively robust) phylogeny of the genera of Perilissini; (4) define the genera of Perilissini; and (5) re-classify the various species groups of the species-rich and vague genera, *Lathrolestes* and *Perilissus*. We present preliminary phylogenetic trees and an exploration of various character systems. Some novel characters are introduced (such as the shape of the upper division of the metapleurum) that have proved very useful in defining large groups of genera.



Re-evaluation of phylogeny and higher classification of Mutillidae (Hymenoptera)

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Brothers (1975) produced the first phylogenetic analysis and higher classification of Mutillidae (velvet ants) on a world-wide basis, using 43 characters and groundplans for the taxa. Seven subfamilies (Myrmosinae, Pseudophotopsidinae, Ticoplinae, Rhopalomutillinae, Sphaerophthalminae, Myrmillinae and Mutillinae) and several tribes and subtribes were proposed. In 1997 Lelej & Nemkov published an analysis (using 89 characters, many different from those previously used at this level, and similar methods) and proposed ten subfamilies (Myrmosinae, Kudakrumiinae, Pseudophotopsidinae, Ticoplinae, Rhopalomutillinae, Ephutinae, Dasylabrinae, Sphaerophthalminae, Myrmillinae and Mutillinae), reflecting several differences in inferred relationships. Slight expansion and reanalysis by Brothers in 1999, taking Lelej & Nemkov's results into account, produced essentially the same results as he had obtained in 1975, however.

In order to clarify the reasons for the above differences, and in an attempt to derive an improved classification, Brothers invited Lelej to collaborate on a more extensive analysis.

Methods: More than 50 genera (rather than assumed higher taxa), including varied species for each where possible, were individually scored for all morphological characters previously considered in such analyses as well as others used at the genus level, a total of about 190 characters. Four outgroup genera representing those families previously found to be most closely related to Mutillidae were similarly scored. Parsimony analyses were performed, using various options involving additivity of character states and implied weighting of characters.

Neither Brothers's nor Lelej's previously proposed phylogenies were fully supported. Several "taxa" were found probably to be paraphyletic. Different analytic assumptions produced considerable differences in branching patterns.

Recognition of a series of higher taxa somewhat intermediate between the earlier schemes proposed by Brothers and Lelej may be justified. However, the inclusion of several characters polymorphic within genera, and the fact that such variation in state expression appears to differ in extent in different parts of the trees found, has undoubtedly confounded the situation; such factors, and the possibility of using species rather than genera as terminals, need further exploration before firm conclusions can be reached.

Divergence estimates and new insights into the early evolution of cynipoid wasps (Hymenoptera)

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The Cynipoidea, generally known as the gall wasps, possess a broad range of biological attributes, ranging from primary and hyper parasitization, to gall induction and inquillinism. We explore the early phylogenetic branching patterns of the cynipoids, and in the process,



estimate non clock-like divergence times for all the major lineages. Recent work on fossil cynipoids has provided calibration points for our analyses. Our results estimate the median age of the branch leading to the root of the Cynipoidea to be 130 million years old, the branch leading to the true gall wasps (Cynipidae) to be 54 million years old, and the branch leading to the entomophagous Figitidae to be 105 million years. Given these dates, and the estimated divergence estimates for the hosts of cynipoid wasps (both plants and other insects), we build on previous hypotheses that the gall wasps are a derived, phytophagous lineage nested within the largely parasitic Cynipoidea, and that major lineages of Figitidae chronologically 'tracked' the divergence times of their hosts.

Phylogeny of the Aculeata: Results of the Hymatol Taxonomic Working Group

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The first phylogenetic analysis based on combined morphological and molecular data for all families of Aculeata is presented. The morphological characters are modified from those used in previous studies by the authors, and are scored for more than 80 species terminals; they consist of more than 200 variables. The molecular data are from four genes (16S, 18S, 28S and COI), and comprise more than 4000 sites. Cladistic analysis using ichneumonoid outgroups resolves Chrysidoidea as monophyletic, and the sister-group of Apoidea and Vespoidea. Apoidea is monophyletic, but Vespoidea is not supported. Most families with multiple representatives are supported as monophyletic.

Beyond the barcode to the tree: Ichneumonoid phylogeny and the importance of taxon sampling density and strategy

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The enormous sequence database of cytochrome *c* oxidase subunit 1 (CO1) being assembled from various DNA barcoding projects as well as from independent phylogenetic studies provides an almost unprecedented amount of data for molecular systematics in addition to its original species delimitation role. Here we explore the phylogenetic trees that can be reconstructed from the available species-level sequence data in the enormously diverse, cosmopolitan parasitoid wasp superfamily Ichneumonoidea. Out of approximately 78 currently recognised subfamilies and 58,000 described species, data for the barcoding region of CO1 were assembled for over 3500 putative species-level terminals (many undescribed), representing all but 3 of the recognised subfamilies. Phylogenetic trees were reconstructed from the whole data and from variously rarefied subsets, using both parsimony and rapid likelihood techniques. The probable phylogenetic accuracy of each analysis was assessed using the taxonomic retention index (tRI) and a new Simpson Diversity Index-based metric (tSD) of the morphologically recognised families, subfamilies and genera on the resulting trees. We implemented concurrent but independent sampling and scoring of the 680 genera and 74 subfamilies within the Ichneumonoidea with the aim of giving accuracy scores in the context of a variable, large scale phylogenetic treespace. We find that a subset of taxa show consistent monophyly, regardless of the number or identity of sequences used in the resampled data set. However, for the majority of taxonomic groups, maximisation of the measures of phylogenetic accuracy is dependent upon the numbers of terminals sampled, with increased sampling of a given taxon leading to a reduction in polyphyly and paraphyly both of the taxon itself, and the local phylogenetic environment (deeper taxonomic nodes). Further, we find improvements to accuracy are enhanced when sampling shifts from a single biogeographic zone to multiple zones. Finally, we find accuracy associating with particular tree characteristics, especially maximum branch length. The results suggest minimum parameters for taxonomic and geographic coverage if COI is to be used as a primary means of phylogenetic assessment and indicate the relationship between higher taxonomic group association and the interaction between taxonomic coverage and rates of COI evolution.

**Phylogeny and historical biogeography of Sycophagine non-pollinating fig wasps
(Hymenoptera, Chalcidoidea)**

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Figs (*Ficus*, Moraceae) are exploited by rich communities of often host-specific phytophagous and parasitoid wasps. Among them, non-pollinating Sycophaginae (Hymenoptera, Chalcidoidea) may share a common history with *Ficus* and their mutualistic pollinators (Agaonidae). Therefore they could be used as an additional tool to unravel the biogeographical complexities of the fig system. We investigate here, for the first time, the phylogeny and the biogeographical history of Sycophaginae at a world level and compare the timing of radiation and dispersion of major clades with available data on *Ficus* and fig pollinators. Maximum likelihood and Bayesian analyses were conducted on 4267 bp of mitochondrial and nuclear DNA to produce a phylogeny of all genera of Sycophaginae. Two relaxed clock methods with or without rate autocorrelation were used for date estimation. Analyses of ancestral area were also conducted to investigate the geographical origin of Sycophaginae.

The phylogeny is well resolved and supported. Our data suggest a post-Gondwanian age of Sycophaginae (50-40 Ma) and two independent out-of-Australia dispersal events to Continental Asia. Given paleoclimatic and paleogeographic records, the following scenario appears the most likely. The ancestor of *Idarnes*+*Apocryptophagus* migrated to Greater India through the Ninetyeast Ridge (40-30 Ma). The ancestor of *Anidarnes*+*Conidarnes* dispersed later via Sundaland (25-20 Ma). *Idarnes* and *Anidarnes* subsequently reached the New World via the North Atlantic Land Bridges during the Late Oligocene Warming Event. *Apocryptophagus* reached Africa 20 Ma ago via the Arabic corridors and returned to Australasia following the expansion of Sundaland tropical forests (20-10 Ma). We recorded a good coincidence of timing between dispersal events and continental connections. Furthermore the timing of radiation and dispersion of Sycophaginae is concomitant with the timings estimated for *Ficus*, pollinators and fig dispersers. Therefore, our study highlights the power of phylogenetic multiple dating of interacting groups to reconstruct the historical biogeography of these associations.

Interestingly *Sycophaga* renders *Apocryptophagus* paraphyletic. Both *Sycophaga* and *Apocryptophagus* possess similar males with a unique suite of synapomorphies: the long peritremata of the abdominal spiracles, the flat scape of the antenna and the rectangular head.

Males of *Platyneura* and *Sycophaga* cannot be separated on tangible morphological characters. However females of *Sycophaga* are strongly differentiated and exhibit several morphological adaptations to crawl into the ostiole of the figs (flattened and elongated head, short fore tibiae, spurs on the hind tibia, absence of any sculpture on the mesosoma) that make them easy to identify on morphology. Our results show that for Sycophagine fig wasps 1) the ability to enter the fig through the ostiole took about 30Ma and 2) in the next 15 Ma the female wasps evolved several morphological adaptations to crawl through the bracts so that females of *Sycophaga* and *Apocryptophagus* seem to belong to different genera.

Ontogenetic origin of mermithogenic *Myrmica* phenotypes (Hymenoptera, Formicidae)

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Entomopathogen parasites typically induce alternative "parasitogenic" phenotypes in ants and other insects. However, the basis of generated developmental changes is poorly understood. Parasitic mermithid nematodes also cause the formation of three discrete and aberrant morphologies within *Myrmica* ants. These have been called "worker-like" ("mermithergate"), "intermorphic" ("gynaecoid mermithergate") and "gyne-like" ("mermithogyne") and their formation has been attributed to infection of worker- and queen-presumptive larvae, respectively. In order to better understand the developmental mechanisms that lead to the formation of these alternative parasitogenic phenotypes we observed allometric patterns of parasitogenic *Myrmica gallienii* phenotypes in comparison with uninfected workers and gynes from the same nests. It was revealed that the three discrete morphologies of parasitogenic female phenotypes did not differ significantly from each other in their scaling indicating that these were trapped in the same developmental pathway. Infected individuals scaled according to basically gyne-like allometry, however significantly differed from workers in their scaling. Based on the observed scaling patterns we herein raise an alternative explanation according to which both "mermithergate", "gynaecoid mermithergate" and "mermithogyne" *Myrmica* phenotypes develop from the same type of larvae, namely from the queen-presumptive larvae and their formation, therefore, is rendered as a diverging process. According to the mechanism we propose effect of nematodes may turn out to be the determining factor in the formation of alternative parasitogenic morphologies.

Looking inside the head capsule of Chalcididae provides informative characters to infer their phylogeny

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Chalcididae are a well characterized family of chalcidoid wasps. Nevertheless, using molecular data, the family is never retrieved monophyletic. On the other hand, looking to the back of the head provided informative characters for the inference of their phylogeny in Eurytominae. In Chalcididae this region – postocciput, postgena and hypostoma – is quite variable and the homologies across the different recognized subfamilies or tribes were difficult to assess. Therefore the examination of the internal structures – tentorial arms,

postoccipital apodemes – postgenal bridge – was considered the only way to solve the question. This examination, across the family and some extra groups (Torymidae, Leucospidae, Pteromalidae Cleonyminae and Pteromalinae, Eurytomidae Heimbrinae, Buresiinae and Eurytominae), provided 24 characters which, combined with 138 other ones, allowed us to infer the phylogeny of the family, retrieved monophyletic with a high support. The Heimbrinae are the sister group of the Chalcididae. Within the family, the Cratocentrini, which otherwise exhibit very special derived states – this is the only lineage having a true postgenal bridge – branch on a basal node. The Epitraninae and Dirhininae are sister groups while *Smicromorpha* shares a strong synapomorphy with the Haltichellinae.

Revision of the subfamily Megaspilinae (Hymenoptera: Ceraphronoidea)

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Megaspilinae is a diverse group, yet the limits of the seven genera are poorly known. They are parasitoids and hyperparasitoids of at least five orders of insects. Generic concepts have never been tested by any phylogenetic analysis. To test these generic concepts, we used both morphological and molecular characters. Our results hypothesize that some genera are monophyletic and some are in need of redefinition (*Dendrocercus* and *Conostigmus*). In examining morphology of *Trassedia*, we discovered a suite of morphological characters, including the presence of the waterstone evaporatorium, that suggest the genus *Trassedia* should be transferred from Megaspilidae to Ceraphronidae. All sources of data are managed using MX, an online database for systematists. Such comprehensive management of data is a novel and useful method for revisionary work such as this.

Challenges, opportunities and future strategies in the study of Microgastrinae (Braconidae)

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Microgastrine wasps are the single most important group of Lepidoptera parasitoids, with significant importance in biological control programs worldwide. Here we highlight present and future developments in the study of the subfamily, discussing major challenges and opportunities. We estimate the actual diversity of Microgastrinae (currently around 2,000 described species) to be between 15-30,000 species, based on two extrapolation methods and supplemented by the study of collections from all major biogeographical regions and barcoding data from over 15,000 specimens from about 60 countries. The problems of understanding such an extraordinary diversity are further complicated by the rapid evolutionary radiation of the group, the presence of numerous cryptic and morphologically similar species, the lack of comprehensive taxonomic reviews for the largest genera, and scarce and/or inaccurate information on hosts. Among the factors that might facilitate the study of the group are the availability of comprehensive databases, types concentrated in relatively few institutions, a rather organized taxonomy at supra-specific level (with some

unresolved controversies), thousands of fresh specimens collected or reared, new techniques to unravel host records, DNA barcoding efforts, numerous molecular- and morphology-based phylogenetic studies, and (in a few recent efforts) the combination of several of the abovementioned approaches. We discuss strategies to take advantage of these opportunities in future research on Microgastrinae on a worldwide basis.

"The Kieffer syndrome" - endogenous taxonomic impediments in poorly known groups, as exemplified by the taxonomic history of Eucoilinae (Cynipoidea: Figitidae)

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It is well known that so-called taxonomic impediments are manifold. Infrastructural limitations and lack of funding in science are important external factors. In many poorly known groups, the unaccounted diversity in itself as well as technical difficulties in studying the animals may be considered an endogenous factor.

An impediment sometimes presented by taxonomy itself is the work of previous careless taxonomists, which may leave groups in states far worse than ignorance. Enthusiasm over apriori characters and superficial variation, and lack of concern for type studies, phylogenetic questions and nomenclatural principles, can create entirely artificial classifications that take generations to tidy up. A roaring lack of knowledge can be concealed in a rigid pragmatic system and a wealth of names.

I will give a brief history of the taxonomic history of the Eucoilinae, one of those groups where the fluctuation between absence of taxonomic research and very ambitious but mostly misleading taxonomic work highlights some of the basic questions of taxonomy, and present some recent efforts at taking up this challenge. We seem now to have reached up to 88% adequacy of available names in the group, compared to the all-time low of 14% after Jean-Jacques Kieffer's total revision. I will also discuss criteria for considering groups "poorly known".

When morphology is not enough: are generalist chalcid parasitoids aggregates of cryptic sibling species?

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Species within many insect groups are known to be hard to identify based solely on morphological characters, especially within speciose groups such as chalcid wasps. However, DNA sequences provide an alternative suite of characters to assist in species identification. This so-called DNA barcoding can be particularly useful for discovering cryptic species or ecotypes within generalist natural enemies, whereby molecular data reveal that a single generalist morpho-species actually consists of multiple more specialised genetic species – a pattern consistent with theory describing the evolution of stable foodweb interactions. Such cryptic diversity needs to

be explored in order for any study of ecological interactions to be placed into the correct context. Within the community of wasps associated with cynipid oak galls, many chalcid parasitoid natural enemies have very broad host ranges and in some cases genetic data have revealed the presence of previously unknown cryptic species. Here we investigate whether two chalcid parasitoids of oak galls, *Ormyrus pomaceus* (Ormyridae) and *Eupelmus urozonus* (Eupelmidae), contain cryptic genetic lineages. Both these species have particularly broad host ranges; *O. pomaceus* is known to attack at least 95 species of cynipid gall inducer, while *E. urozonus* is exceptionally polyphagous, attacking both at least 87 oak gall species and a wide range of non-cynipid hosts. We used a multi-locus DNA barcoding approach, sequencing both the standard gene used for barcoding, the mitochondrial cytochrome c oxidase subunit I gene (COI), plus introns from multiple nuclear loci. Although levels of sequence variation are typically lower in nuclear genes, they are an essential tool when searching for cryptic species as nuclear corroboration for mitochondrial lineages provides strong evidence for the reproductive isolation of these lineages, and hence the delimitation of cryptic species. Bayesian methods were used to construct phylogenies for the two morpho-species, and host use (both the insect attacked by the parasitoid and the host plant of the attacked insect) was then mapped onto the phylogenies. Both morpho-species were found to contain multiple cryptic lineages supported by both the nuclear and mitochondrial genomes. Cryptic species within both species complexes did not appear to be ecological specialists either at the level of host taxon or at the lower trophic level of host plant, at least within the sampling obtained from cynipid oak galls. One lineage with the *E. urozonus* complex was sampled almost exclusively from leaf-mining caterpillars on oak trees, although one individual from this lineage was also sampled from an oak cynipid gall, indicating that the communities of natural enemies attacking leaf-mining caterpillars and cynipid galls occasionally exchange members. The presence of cryptic generalist parasitoids within the oak gall community highlights the need for further ecological study of these cryptic lineages to explain how multiple ecologically similar species co-exist within the same community and to describe impacts on trophic interactions mediated by increased numbers of apparently generalist natural enemies.

Ichneumonidae collected from the Suez Canal and North Sinai regions, Egypt (Hymenoptera: Ichneumonoidea)

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The present study is carried out to investigate and review the species of the family Ichneumonidae (Hymenoptera: Ichneumonoidea) attacking different pests of cultivated plants in Suez Canal (especially Ismailia) and N. Sinai (especially El- Arish) regions. Collection was done using the Japanese sweeping net and Malaise trap during the period 2007-2009.

A total of 31 ichneumonid species belonging to 23 genera and 10 subfamilies: Anomaloninae (2 genera, 3 species), Banchinae (1sp.), Campopleginae (7 genera, 10 species), Cryptinae (3 genera, 4 species), Diplazontinae (2 genera, 2 species), Ichneumoninae (2genera, 2 species), Metopiinae (1species), Ophioninae (2 genera, 3 species), Pimplinae (2 genera, 3 species) and Tryphoninae (1 genus, 2 species). Of these seven species are new records to the fauna of Egypt.



The collecting data of the ichneumonid species, their hosts as well as their previous records in Egypt is given. Almost all the listed species are not previously recorded from the two regions under study except for: *Venturia canescens* (Gravenhorst) and *Enicospilus ramidulus* (Linn.) were previously recorded from W. Rabdet (N.Sinai) and *Ophion obscuratus* Fab., previously recorded from Ismailia (Suez Canal Region) and El-Zaraniq (N.Sinai).

***Calosota* Curtis (Chalcidoidea: Eupelmidae) — pulling the proverbial thread of knowledge**

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Calosota Curtis (Chalcidoidea: Eupelmidae) is a comparatively small genus of parasitoid wasps that primarily attack woodboring beetles. Eight species have been included in the genus in the New World, including 3 from South America and 5 from North America, whereas 13 valid species are recognized in Europe. In 2009 specimens were received for identification that were reared from the goldspotted oak borer, *Agrilus coxalis* Waterhouse (Coleoptera: Buprestidae), a pest of oaks in California. Initial study suggested that these specimens represented a new species and the foolish promise to describe it because of its potential for biocontrol of the pest. Additional study to adequately characterize the new species quickly led to the discovery of other undescribed North American species in the CNC and a full revision of the genus for the region. This resulted in the discovery that some of the North American species extend further south into Central America and West Indies and enlarging the revision to include these regions. Study to ensure correct nomenclature also suggested that three of the five described North American species occur also in Europe under other names, which led to a "review" of the European species. The results of what started out as a single species description but ended up in a revision of the West Indies and North and Central American species, including the description of 7 new species, 7 new synonyms for North American and European names, the resurrection of 2 European species names, observations on 9 other European names, and the transfer of 2 South American species to other genera will be summarized.

**Recent advances in the chromosomal studies of the superfamilies
Cynipoidea and Chalcidoidea**

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Chromosomes of about 200 species of parasitic wasps that belong to 16 families of the Chalcidoidea and Cynipoidea have been studied up to now. Although overall karyotypic features of those groups are summarized in my recently published monograph, *Karyotypes of Parasitic Hymenoptera*, the described pattern must be updated with a number of new results. Specifically, these results confirm that the chromosome set containing eleven subtelocentrics or acrocentrics is likely to be ancestral for the superfamily Chalcidoidea. Moreover, modern karyotypic information blurs an apparent border between the so-called "high-numbered" and "low-numbered" families of the Chalcidoidea having $n = 8-12$ and $3-7$ respectively. Mymaridae, the most basal chalcid family, is the only taxon of its rank that has fully retained

a relatively high chromosome number, $n = 9$. In other groups of the superfamily Chalcidoidea that were supposed to be entirely high-numbered, i.e. Encyrtidae ($n = 8-12$) and Eurytomidae ($n = 9-10$), species with lower chromosome numbers have been recently detected. For example, $n = 5, 6$, and 7 were found in *Eurytoma compressa* (Fabricius), *Eu. serratulae* (Fabricius), and *Eu. robusta* Mayr respectively. These species are likely to form a well-supported clade within their genus. Another originally high-numbered chalcid family, Aphelinidae, also harbours groups with lower chromosome numbers, i.e. all Aphelininae and a few species of *Encarsia*. Species with higher n values (7 to 10) are now detected in the family Eupelmidae that generally has lower chromosome numbers ($n = 5-6$). In addition, $n = 10$ has been recently found in two species of the genus *Podagrion*, whereas $n = 4-6$ were detected in other Torymidae. Among the "low-numbered" families, $n = 6$ has been found in the first studied species of the family Agaonidae, *Blastophaga psenes* (Linnaeus). The karyotype containing five large metacentrics and a small subtelocentric or acrocentric is considered the ground plan feature of the common lineage that includes Torymidae, Ormyridae, and Agaonidae. The same karyotype structure is also found in *Euderomphale chelidonii* Erdős that belongs to Euderomphalini, the most basal tribe of the subfamily Entedoninae (Eulophidae). In the superfamily Cynipoidea that generally contains high-numbered species ($n = 9-11$), low chromosome numbers were detected in the genera *Andricus* (Cynipidae, $n = 5-6$) and *Leptopilina* (Figitidae, $n = 5$). Chromosomal characters can be used in species-level taxonomy of certain genera of parasitic wasps that belong to the Chalcidoidea and Cynipoidea. For example, *Metaphycus flavus* (Howard) and *M. luteolus* (Timberlake) (Encyrtidae) both have $n = 10$, whereas *M. angustifrons* Compere has $n = 9$, and *M. stanleyi* Compere has $n = 5$. Analogously, $n = 10, 9$, and 5 were found in *Leptopilina heterotoma* (Thomson), *L. boulardi* Barbotin, Carton et Keiner-Pillault, and *L. clavipes* (Hartig) respectively.

Evolution of solitary and gregarious development in parasitoids: what we can learn from *Entedon* wasps (Chalcidoidea: Eulophidae)

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Nominal difference between solitary and gregarious parasitoids concerns number of siblings developing in the same host. However, the ability to be gregarious may concern degree of tolerance between sibling larvae, rather than simply number of the eggs laid. Wasps of the genus *Entedon* are larval or egg-larval, gregarious or solitary endoparasitoids of Coleoptera (mostly weevils and bean beetles). Evolution of life history traits in this genus was reconstructed by phylogenetic analysis of nuclear ribosomal (D2 of 28S) and mitochondrial (COI and Cyt B) gene regions. The analysis suggests that gregarious parasitism originated more than once in larval and egg-larval parasitoids. Also, the egg-larval parasitism is rather common (or even predominant) parasitism in the genus. The preimaginal development also differs in solitary and gregarious parasitoids. The solitary parasitoids physically eliminate other rival larvae during their first instar, which is armed with sharp mandibles. In egg-larval gregarious parasitoids the active "fighting" first instar is omitted: it is embryonized and the early development of the larva takes place within an extraembryonic cellular membrane. The larva, which corresponds to the second instar of solitary *Entedon* species, is formed directly from the proliferating cells inside this extraembryonic membrane. This embryonization of "fighters" may be an approach to avoid killing of siblings by aggressive first instars.

However, larval gregarious parasitoids of *Entedon* have typical “fighter” first instars, which are just somewhat less mobile and molt quicker to the second instar, than in solitary parasitoids. So, the larval tolerance may be achieved in two ways: by losing of aggressive instars (egg-larval gregarious species of *Entedon*) or by lower mobility and faster development of these instars (larval gregarious species of *Entedon*).

Wild Bee Diversity of Sweet Cherry Orchards in Sultandağı Reservoir (Turkey)

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Many varieties of sweet cherry are self-incompatible. Therefore, sweet cherry orchards require a huge population of pollinator bees that would carry out the adequate amount of pollen transfer between the different varieties. In practice, the honeybee is the main pollinator used in sweet cherry orchards. But the wild bees are more efficient than the honeybee in unfavourable climatic conditions. This study was undertaken in the sweet cherry orchards in Sultandağı (Afyonkarahisar province) and Akşehir (Konya province) towns, Turkey. Bees were collected by Malaise trap from three sweet cherry orchards in the period between April-May in 2008 and 2009 to study the composition and richness of wild bee species. The traps were set in the bud swell period and lifted in the green fruit period. A total number of 1980 bee specimens, belonging to 86 species and five families (Andrenidae, Halictidae, Apidae, Antophoridae, Megachilidae) were collected. Although the abundance of bee populations varied from year to year and from orchard to orchard in the family level, the members of Halictidae presented the greatest species richness both in 2008 and 2009. The results of the study were evaluated by Shannon-Wiener (H) and Simpson (D) diversity indexes. Differences in bee diversity among three orchards were shown.

Hotspots of Ichneumonidae (Hymenoptera) Fauna in Natural Protection Areas of East Mediterranean Region in Turkey

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Halep Çamlığı, Kengerlidüz, Habib-i Neccar Natural Protection Areas which have different ecological characters chosen from East Mediterranean Region. This study was conducted between March-September for each site during 2007-2008 at day in monthly intervals. It is also one of the most remarkable regions of the world in terms of the biodiversity hotspots such that 3 of them have major extensions into Turkey: Caucasus, Irano- Anatolian, and Mediterranean Basin (Myers et al., 2000) Consequently, 54 species of Ichneumonidae were recorded; 20 species are belonging to Mediterranean Hotspot, 9 species are belonging to mediterranean - Caucasus Hotspots, 3 species Mediterranean - Caucasus - Irano-Anatolian Hotspots, 6 species Mediterranean - Irano-Anatolian Hotspots. 5 species did not found in these hotspots.

Insects prone to reaching to hotspots. *Banchopsis crassicornis*, *Syrphoctonus nigratarsus*, *Orthocentrus radialis* are found first of all in Mediterranean, after pasted time, these

parasitoids are found in Irano Anatolian hotspots. As a result, we can say that if these parasitoids are in two regions, may be they can arrive at Caucasus hotspot.

Lissonota lineata, *Pion fortipes*, *Syrphophilus bizonarius* spread three in hotspots. According to Yu *et al.*, 2006, these ichneumonids were found first in Mediterranean hotspot, second in Irano Anatolian hotspot and lastly in Caucasus hotspot. Consequently, we can say that these ichneumonids may have followed these routes.

Lathrolestes unguaricus, *Diaparsis nitida*, *Gelanes fuscus*, *Gelanes simillimus*, *Tersilochus nitens*, which are in Palearctic region, did not find in three hotspots. These species reach to Mediterranean hotspot.

Investigating the genetic control of gall induction in Cynipid gallwasps

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Cynipid gallwasps induce complex and morphologically diverse galls on highly-conserved host plants, the mechanism utilized is a long-standing entomological mystery. With the advent of new high-throughput sequencing technologies traits of non-model organisms with complex life-histories have become amenable to study. We are using a combination of Illumina GAIIx and Roche 454 sequencing to generate genomic data and expressed transcripts at key larval plus adult life stages to determine the genetic control of gall induction. Genomic data will be used for Cynipid genes of viral origin, analogous to virus-like-particle structural genes previously identified in some Polydnavirus utilizing Ichneumonoidea wasp genomes. It will also aid transcriptome assembly. Transcriptome sequencing of larvae during the initial gall induction phase will provide a set of candidate genes for control of gall-induction when controlled for by expression in other life-stage. A comparative approach using two species from different cynipid clades will test for a common conserved mechanism. The Palearctic oak apple forming *Biorhiza pallida* and the Nearctic rose galler *Diplolepis spinosa* have been selected for this purpose. Results from initial genome sequencing, assembly and analysis are presented as is the plan for transcriptome sequencing.

Relationships of Chalcidoidea: a molecular and morphological approach

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Chalcidoidea are economically and ecologically one of the most important groups of Hymenoptera. They are a hyperdiverse group of insects with more than 500,000 estimated species currently allocated to about 89 subfamilies in 19 families. Perhaps not surprisingly, there is little consensus on relationships in the group, and there has never been a comprehensive phylogenetic analysis of the superfamily. We address their relationships using two approaches. First, a molecular phylogeny of 720 taxa including 51 outgroups using a secondary structure alignment for partial 18S and 28S sequences. Second, a morphological



approach based on scoring 243 characters for more than 200 representative taxa using MX, an on-line content management system, with the help of numerous collaborators worldwide. Results of the independent and combined results will be presented in an attempt to resolve the family level relationships in the superfamily.

Evolution of egg parasitism under water in parasitoid Hymenoptera

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Parasitoid Hymenoptera are species-rich in nearly all terrestrial ecosystems, but the richness of hymenopterous parasitoids of aquatic insects is rather limited, given the species richness of potential aquatic hosts. Clearly, the aquatic habitat has been a barrier to parasitism by parasitoid Hymenoptera. However, subsurface egg parasitism of aquatic insects is not so rare. In the evolution of this type of egg parasitism, there are four reproductive strategies for parasitoid females that lack adaptations to dive and attack eggs of aquatic insects. Such parasitoids can exploit aquatic hosts in the following ways: (1) when the host's eggs are laid on plants and other substrates above water, (2) when the host's eggs are exposed above water at some point in their life cycle, (3) if the females walk down among the plants bearing these hosts under water (i.e., when the hosts are always under water), and (4) by swimming in search of hosts that are always under water. The last step is highly evolved, and is found in at least three families, Trichogrammatidae, Mymaridae and Scelionidae. Thus, females of species of some genera belonging to these families are well adapted to searching the hosts under water, but their searching by swimming might be largely limited to the hosts in ponds rather than those in streams. Such parasitoid females must have a difficulty in searching the hosts in flowing water because of their small size. Evolution of egg parasitoids also is under the ecological constraints of their small size since their hosts are usually smaller than those of larval or pupal parasitoids.

Parasitoids of *Choristoneura* spp. (Lepidoptera: Tortricidae) in the Nearctic region

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The genus *Choristoneura* (Lepidoptera: Tortricidae) includes several economically important pests in North America. The Eastern spruce budworm, *C. fumiferanae* is the most devastating pest of conifers in eastern North America but six others are also important in forestry (*C. biennis*, *C. conflictana*, *C. pinus*, *C. occidentalis*) or agriculture (*C. rosaceana*, *C. parallela*) in many parts of the continent. Decades of biological studies have resulted in literature records for 230 parasitoids in 106 genera from 11 of the 16 Nearctic species, including 50 species of Braconidae in 18 genera, 113 species of Ichneumonidae in 45 genera, 51 species of Chalcidoidea in 29 genera (9 families), 1 species of Bethyridae, and 15 species (13 genera) of Tachinidae. Illustrated identification keys to most of the species and all of the genera were produced over the past 15 years by four taxonomists (J. Huber, A. Bennett, J. O'Hara, J. Fernández-Triana) based at the CNC, Ottawa. An additional 36 species (14%) of parasitoids are erroneous associations.

Choristoneura fumiferanae has the highest number of parasitoids: 122 species (53%) of the total for Nearctic *Choristoneura*. Rearings from the pest species together account for 90% of the parasitoid species. Only 16 parasitoid species (7%) were reared from more than 5 *Choristoneura* species. The proportion varied considerably between Tachinidae, where 9 of 15 (60%) species attacked more than 5 hosts, and Hymenoptera, where only 7 of 215 (7%) species attacked more than 5 hosts. Half of the parasitoid species, including those that are hyperparasitoids, were reared from only one *Choristoneura* species. The number of apparently monophagous parasitoids (on *Choristoneura*) is probably artificially inflated because 20 chalcid hyperparasitic species were added to the number considered to have emerged from only 1 *Choristoneura* species. If they are ignored the number of apparent monophages is still 112 species (48.3%). The most common genera reared are *Glypta* spp. (Banchinae), *Apanteles* spp. (Microgastrinae), *Meteorus* spp. (Meteorinae), and *Macrocentrus* spp. (Macrocentrinae).

The only comparable taxonomic study to the four papers on Nearctic *Choristoneura* parasitoids is for Nearctic *Rhyacionia* (pine tip or pine shoot moths, Tortricidae). Yates (1967) reported 100 parasitoid species (53 genera) in 10 families, essentially the same ones as for *Choristoneura*. These were reported from 8 of the 11 species/subspecies of *Rhyacionia* (at the time 11 species were recognized; now 27 are). Most of the records came from only two species: *R. buoliana*, a European alien invasive species, and *R. frustrana*, a native species. Yates excluded another 27 species (27%) as erroneous associations.

The value of producing artificial identification keys to particular pest species or genera as opposed to 'natural' keys to taxa is discussed in light of the scarcity of parasitic Hymenoptera taxonomists relative to the size of the taxa they study.

Progress in taxonomy and systematics of Platygastroidea: new taxa, tools, and troubles

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The Platygastroidea PBI is a project focusing on elaboration of the knowledge of species and genera of the superfamily, including both alpha taxonomy, new collectings, and phylogenetic analysis of relationships. The results elaborated over the past three years are described, along with the cyberinfrastructural tools used to accelerate and increase the accuracy of the work. Prospects for the final two years of the project are discussed.

Entomophagous complex associated with the insects on *Heracleum platytaenium* (Apiaceae) in Turkey, with new records

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In this study, the entomophagous insect complex with hosts on endemic plant *Heracleum platytaenium* Boiss. (Apiaceae) were determined. For that, 17 parasitic hymenopters and 3 predators were reared from their host insects, Coleoptera, Hemiptera, Lepidoptera, and Diptera found in umbels, stems and branches of *H. platytaenium*. This plant contains furanocoumarins that are insect repellents and suppress growth in some species. Plant materials with insects were collected from Ankara and Bolu provinces in July-September

2007-2008. All parasitoids belonging to Hymenoptera obtained from egg batches of some hemipters are *Ooencyrtus telenomicida* (Vassiliev) (Encyrtidae), *Trissolcus grandis* (Thomson) and *Telenomus heydeni* Mayr (Scelionidae) from *Graphosoma lineatum* L. (Hemiptera: Pentatomidae); *Ooencyrtus kuvanae* (Howard) from *Dolycoris baccarum* (L.); *Gryon leptocorisae* (Howard) from predator *Rhynocoris punctiventris* (Herrich-Schaeffer) (Hemiptera: Reduviidae). The ectoparasitoids obtained from larvae of the weevil and moths are *Odontepyrus* sp. (Bethyridae) as from a moth larva in the branch, *Bracon piger* (Wesmael) and *Ascogaster quadridentata* (Wesmael) (Braconidae) from *Epinotia thapsiana* (Zeller) (Lepidoptera: Tortricidae) in the umbel; *Pristomerus vulnerator* (Panzer) and *Aritranis confusator* Aubert (Ichneumonidae) from *Lixus nordmanni* Hochhuht (Coleoptera: Curculionidae) (New host) in the branch. Also an endoparasitoid *Baryscapus crassicornis* (Erdős) (Eulophidae) was obtained from larvae of *L. nordmanni* (New host) in the stem and branch. As to the pupa parasitoids, *Didyctium brunnea* (Belizin) (Eucolidae) was reared from puparia of *Lasiambia albidipennis* (Strobl) (Diptera: Chloropidae) (New host); *Pronotalia carlinarum* (Szelenyi and Erdos) (Eulophidae) and *Homoporus febriculosus* (Girault) (Pteromalidae) from *Melanagromyza heracleana* Zlobin (Diptera: Agromyzidae) (new host), and *B. crassicornis* from *Lixus nordmanni* Hochhuht (Coleoptera: Curculionidae) (New host) in the stem and branches of the plant. *B. crassicornis* also emerged from adults of *L. nordmanni*. It is larval, larval-pupal, pupal and pupal-adult parasitoid, not directly adult. *Aphelinus mali* (Haldeman) were reared from the aphids (Hemiptera: Aphididae) on the plant. As predators, *R. punctiventris* (Hemiptera: Reduviidae), *Scaeva pyrastris* (L.) and *Eupeodes corollae* (F.) (Diptera: Syrphidae) on the plant, and spider hunters *Miscophus bicolor* Jurine and *Trypoxylon attenuatum* F.Smith (Crabronidae) in the stem were determined. The any parasitoids of flies *M. heracleana* and *L. albidipennis* were not known. So, these records are the first parasitoid records for the flies. Chloropidae is new host family for *D. brunnea* after Phoridae. In addition, *Aritranis confusator*, *Gryon leptocorisae*, *Didyctium brunnea* and *Homoporus febriculosus* are recorded from Turkey for the first time.

Biology of egg parasitoids *Trissolcus semistriatus* Nees and *Trissolcus grandis* Thomson (Hymenoptera: Scelionidae) on *Graphosoma lineatum* L. (Hemiptera: Pentatomidae) in laboratory conditions

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Egg parasitoids *Trissolcus* species (Hymenoptera: Scelionidae) are the most important natural enemies of sunn pest. In this study, biological parameters of *Trissolcus semistriatus* Nees and *T. grandis* Thomson such as parasitisation, emergence and sex ratios, development, oviposition and postoviposition periods, and longevity were determined using eggs of *Graphosoma lineatum* L. (Hemiptera: Pentatomidae) as host.

To find out biological parameters of *T. semistriatus* and *T. grandis* investigations were carried out at 25±1 °C temperature, 70±5% relative humidity and L:D 16:8 photoperiod in laboratory conditions. Three clusters of *G. lineatum*, which were 42 eggs, were offered to the females for parasitisation. Each day, parasitoids were transferred glass tube contained 42 host eggs, and this process was continued until female parasitoid death. Experiments were conducted to for each parasitoids species separately and 10 replicate.

At the end of the investigations; developmental times were determined as average of 13.62 ± 0.01 and 11.48 ± 0.13 days for female and male of *T. semistriatus*, respectively. Similar results were also obtained for *T. grandis*. Both of parasitoids species males emerged before two days than females. Females lived significantly longer than males. While the female of *T. semistriatus* parasited an average of 173.70 ± 10.69 eggs during longevity, it was found an average of 151.60 ± 14.66 eggs for the female of *T. grandis*. Emergence range of *T. semistriatus* and *T. grandis* were determined between 17.50- 93.04% and 31.66- 91.46% respectively. It was designated that sex ratio was in favour of female at first ten days of parasitoids life time and in favour of male with increasing parasitoids age. Effective mass rearing time for both of parasitoids was also carried by these data results.

Basics First – the phylogeny of the brood parasitic Nyssonini (Hymenoptera: Apoidea)

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In most species of apoid wasps, the females build their own nests and stock the brood cells with paralyzed prey. Remarkable exceptions are the Nyssonini, a poorly studied tribe of worldwide distribution: All of the more than 200 recent species are assumed to be obligate brood parasites. That is, they use the nests and larval food provided by females of other crabronid wasps for their own offspring. Obligate brood parasitism evolved several times independently in different groups of aculeates, for example within the Pompilidae and Sapygidae. However, within the apoid wasps, this alternative behavior probably evolved twice, in the genus *Stizoides* and in the Nyssonini. Despite their extraordinary mode of parental care, which spotlight the Nyssonini, their biology, evolution and even taxonomy are still only poorly understood. As an essential prerequisite for further research on this group, the current work aims to conduct a first cladistic analysis. The genus level analysis presented here is based on 43 morphological characters. It includes 34 terminal taxa, which represent the 18 nyssonine genera, as well as three outgroup-species belonging to the Alyssontini and Bembicini respectively. The result supports the monophyly of the Nyssonini and of most nyssonine genera. *Nursea* and *Nippononysson*, repeatedly described as basal genera within the Nyssonini, form a monophyletic group, which actually branches off early within the tribe. The monophyly of *Foxia* + (*Cresson* + (*Perisson* + *Antomartinezius*)), traditionally regarded as very close-knit group, is supported. It is found to be the sister taxon to the rather derived monophylum (*Hovanysson camelus* + *Brachystegus*) + (*Acanthostethus* + (*Zanysson* + (*Metanysson* + (*Idionysson* + *Losada*))))). The relationship between the disputable genera *Nysson* and *Synnevrus* remains unresolved. However, each of these two genera is shown to be not monophyletic. *Hovanysson* also constitutes an artificial group and needs to be revised.

Australian spider wasp systematics (Hymenoptera: Pompilidae) – clearing up more than 200 years of confusion and misclassification

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The first Australian spider wasp was collected during James Cook's famous exploration of Terra Australis and described by Fabricius in 1775. In the following two centuries Australian pompilids have received relatively little attention and were never comprehensively treated. The continent's fauna is huge with an estimate of more than 500 species, about 60% of which are still undescribed. The generic level classification is confusing and no identification keys are available for most of the fauna. Large numbers of Australian species have been misclassified by previous authors in European genera such as *Cryptocheilus* and *Priocnemis*, which do not occur in Australia. The subfamily Pepsinae is taxonomically most problematic as it comprises the poorest studied Australian genera. Many of these genera are endemic to Australia, have been described on the basis of single specimens and lack proper generic diagnoses. Numerous pepsine genera also exhibit a striking level of sexual dimorphism, which complicates sex associations. In many genera males have either remained undescribed (see Krogmann et al. 2008) or are classified in other genera, sometimes even in different subfamilies. A recent catalogue of Australian pompilids (Elliott 2007) summarizes the current taxonomic state of the fauna and highlights some of the major problems. Here we outline the results of a 4-year study that recognizes 44 genera of Australian pompilids, five of which are recorded from the continent for the first time. Most pepsine genera are reclassified resulting in dozens of new combinations and new synonymies. In addition we recognize a number of species groups that do not fit into existing genera and which will be formally described in future studies. Our generic synopsis also presents large amounts of new distributional data and new host records based on museum collections and recent fieldwork.

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Biogeography of the mutillid wasps (Hymenoptera, Mutillidae) in the Palaearctic region

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The Mutillidae is a large family of solitary wasps which currently numbers 208 genera and about 4200 described (c. 6000 estimated) species. Their greatest diversity occurs in the tropical and subtropical regions of the world. The Palaearctic fauna numbers 57 genera including 14 endemic ones and 506 species.

The distributions of 57 genera in seven biogeographical subregions, as well as the dispersal patterns of nine subfamilies and distribution of 302 species in 24 Palaearctic local faunas, were analysed. Faunal similarities between five biogeographical regions of the Palaearctic were evaluated by using Sørensen's coefficient of similarity. The similarity matrix resulting from pair-wise calculations was then presented by dendrograms, ordination, and Terent'ev pleiades.

The subfamilies Mutillinae (265 species, 30 genera), Dasylabrinae (103 species, five genera), and Myrmillinae (65 species, nine genera) are those most diverse in the Palaearctic region. Subfamilies Myrmosinae and Pseudophotopsidinae have Palaearctic origins. The greatest

diversity of the Mutillidae occurs in the Ancient Mediterranean Region (AMR) - 464 species and 47 genera, including 12 endemic and 18 unique genera. Among the subregions of the AMR, the Mutillidae are most abundant in the Mediterranean subregion (198 species, 34 genera) and Irano-Turanian superprovince (178 species, 31 genera) of the Sahara-Gobi subregion. The East Asian region numbers 48 species in 21 genera, including nine unique ones common with the Oriental region. Thirty eight species in 15 genera are distributed in the Boreal region, but no endemic or unique genera exist there.

The cluster analysis of the distribution of 57 genera among seven Palaearctic regions shows that the branch of East Asian fauna deviates at first (coefficient similarity 0.36) and then the branches of Central Asian and Sahara-Sind faunas. The Mediterranean and Irano-Turanian faunas of the AMR form a stable cluster (coefficient similarity 0.71, bootstrap 84). The Boreal region and Eurasian steppe subregion of AMR have the greatest similarity (coefficient similarity 0.84, bootstrap 96). The cluster analysis of the distribution of 302 species among 24 local faunas shows that the East Asian region is most distinct. The Mutillidae of the Boreal region forms a weak cluster with the Mediterranean subregion. The mutillid fauna of Georgia, Armenia, and Azerbaijan is transitional between the Mediterranean and the Irano-Turanian faunas.

The greatest diversity has AMR - 464 species, 47 genera including 12 endemic and 18 unique genera. On the generic level the Palaearctic fauna is the most similar to the Oriental (31 common genera) and Afrotropical (21 common genera) faunas. The mutillid fauna of the Boreal region is a less diverse and poorest. In spite of the small size of the East Asian mutillid fauna of the Palaearctic, it is closely connected with the Oriental region.

**A remarkable new species of gallwasp (Hymenoptera: Cynipidae)
from South Africa, placed in a new tribe**

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We describe as new a species in a new genus and new tribe. Larvae and adult females of the hitherto only known generation were collected from galls on the small tree *Scolopia mundii* (Eckl. & Zeyh.) Warb. (Flacourtiaceae). Diagnostic characters and a key to the tribes of the Cynipidae are included. With its unique South African distribution and seemingly plesiomorphic morphology, this taxon will be important for the future untangling of the early evolution of the microcynipoids.



Taxonomy, systematics and biogeography of Rhopalosomatidae with special reference to macropterous forms (Hymenoptera: Vespoidea)

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The family Rhopalosomatidae is still one of the least known hymenopteran groups. The oldest fossil representatives date back to the early Cretaceous. Whereas the family assignment of the known compression fossils tentatively placed in Rhopalosomatidae is rather controversial, the affinities of *Eorhopalosoma* from Burmese amber is fairly clear. The two amber specimens share most diagnostic features of the modern macropterous forms, such as the characteristic wing venation, the large ocelli, apical bristles on the first flagellomeres and the upcurved male parameres. Nevertheless, the presence of only one apical bristle on each basal flagellomere and a quadridentate mandible suggests that the amber fossils are intermediate between the enigmatic, brachypterous genus *Olixon* and the modern macropterous forms.

The recent fauna of the family currently consists of four genera, and its distribution is largely limited to the subtropics and tropics in all biogeographical regions. As far as is known, members of the family are ectoparasitoids of crickets. Although the family has been quite rare in collections for a long time, the number of specimens available for study has increased rapidly in the last 30 years as a result of the use of non-selective traps and several large-scale biodiversity inventory projects. As an example, this has resulted in over 300 specimens of the rhopalosomatid genus *Liosphex*, a genus previously known from two species and 15 specimens only. Based on the newly collected material, the genus in fact comprises at least 14 species worldwide. Based on a cladistic analysis of external morphological characters, a preliminary phylogeny of the world *Liosphex* is proposed. The results support a sister group relationship between *Liosphex* and a monophyletic clade consisting of *Rhopalosoma* and *Paniscomima*. Within *Liosphex*, the only Asiatic species, *L. trichopleurum*, is probably the sister taxon to all New World species, which together form a monophyletic group.

Quantifying the Pleistocene history of the oak gall parasitoid *Cecidostiba fungosa* using twenty intron loci

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The longitudinal spread of temperate organisms into refugial populations in Southern Europe is generally assumed to predate the last interglacial. However few studies have attempted to quantify this process in non-model organisms using explicit models and multilocus data. We used sequence data for 20 intron-spanning loci (12 kb per individual) to resolve the history of refugial populations of a widespread western Palearctic oak gall parasitoid *Cecidostiba fungosa* (Pteromalidae). Using maximum likelihood and Bayesian methods we assess alternative population tree topologies and estimate divergence times and ancestral population sizes under a model of divergence between three refugia (Middle East, Balkans and Iberia). Both methods support an 'Out of the East' history for *C. fungosa*, matching the pattern

previously inferred for their gallwasp hosts. However, coalescent-based estimates of the ages of population divides are much more recent (coinciding with the Eemian interglacial) than nodal ages of single gene trees for *C. fungosa* and other species. Our results suggest that similar methods could be applied to multiple species to test alternative models of parasitoid assemblage evolution.

The almond seed wasp, *Eurytoma amygdali* Enderlein (Hymenoptera: Eurytomidae) of Iran, morphological and molecular aspects

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The systematic studies of the almond seed wasp, *Eurytoma amygdali* Enderlein (Hymenoptera: Eurytomidae) were performed using morphological and molecular methods. Two different morphological types were identified, which appeared to be fitted with *E. amygdali* and *E. schreineri* characteristics. Two genetic markers COI and ITS2 were used. However, the molecular studies reject specific value of the second form and show two types belonged to *E. amygdali*.

Host manipulation by spider parasitoids of the *Polysphincta* group (Pimplinae, Ichneumonidae)

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The *Polysphincta* group is a monophyletic lineage of Ephialtini of Pimplinae and comprises koinobiont ectoparasitoids of active spiders. The female wasp stings and paralyzes the host spider and lays an egg on it. The spider recovers shortly after and continues normal life. The parasitoid larva remains on the host body, consuming body fluids of the host. In some species, it is known that the host spider weaves a modified “cocoon web” of quite different structure to the normal web when the parasitoid larva reaches its penultimate instar. As the web modifications do not occur until the parasitoid reaches the penultimate instar, and the parasitoid larvae are on active hosts at this stage, the modified webs are considered to be formed by the spider under the manipulation of the parasitoid larva.

Three types of host manipulation have been detected. 1) Weaving a modified web with durability: the larva of *Hymenoepimecis argyraphaga* induces its orb-weaving host, *Leucauge argyla*, to build a highly modified web with only radii and lines connecting them at the hub and lacking circular hub lines and sticky spirals, shortly before it kills the host. Similar modification in web structure of hosts has been observed for *Reclinervellus* spp. on *Cyclosa* spp., where the disappearance of most of the sticky spiral is recognized. The same kind of modification was observed in *Cyclosa fililineata* attacked by *Polysphincta janzeni*. Another modification providing durability for the web is also known in a parasitoid of the linyphiid spider, *Neolinyphia fusca*, forming a hammock-like sheet web between twigs. The cocoon of

Longitibia sp. is found in a modified web whose sheet is lost, and surrounded by densely and irregularly spun thick threads. 2) Weaving a modified web resistant against predators and scavengers: in the case of *Brachyzapus nikkoensis*, a parasitoid of *Agelena limbata* forming a funnel web, when the parasitoid larva is a penultimate instar, veils of very fine and dense threads covering the spider and parasitoid larva were observed in the tunnel of the funnel web. Removal of the veil indicated that penultimate instar larvae and pupae were more likely to fail to emerge in manipulated webs compared to the controls. The modified web seems resistant against predators and scavengers such as ants. 3) Arresting the growth of the host and detaining it in a more concealed site: the dome-like sheet webs of an immature *Turinyphia yunohamensis*, (Linyphiidae) are small and formed under leaves of the undergrowth. When the spiders mature, they move out to more exposed spaces to form larger webs. If the spider bears a larva of *Zatypota* sp., the growth and molt of the spider is arrested and the spider remains immature even when unattacked spiders become adults. Although reinforcement of webs was not detected in this species, this action of the parasitoid on the spider seems potentially adaptive for the parasitoid, which spins a cocoon on the web, because such small hidden webs are possibly resistant to damage.

Impact of secondary-parasitoids on population density of *Psyllaephagus pistaciae* in pistachio plantations of Iran

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The specific, solitary endoparasitoid, *Psyllaephagus pistaciae* Ferrière (Hymenoptera, Encyrtidae), is the most widely distributed biological control agent of the common pistachio psyllid, *Agonoscena pistaciae* Burckhardt & Lauterer (Hemiptera: Psylloidea), in Iran. The appearance of the first adult parasitoid in the field tended to coincide with the first psyllid nymphs emerging on the pistachio leaves. Thereafter, the parasitoid normally has no difficulty in finding its host, as all psyllid nymphal instars are available throughout the pistachio growing season. The parasitism rate of *A. pistaciae* was found low throughout spring, summer and early autumn, ranging from 1 to 5%, rising to about 11% in November, in orchards where chemical sprays were applied for pest control as usual each year. However, in orchards where no chemical was used for several years, the parasitism rate is also low from May through to September but increased to 65% in November. Of the 6159 wasps emerging from psyllids mummies, 26.6% were *P. pistaciae*, and the remaining 73.6% represented six species of hymenopterous hyperparasitoids, *Chartocerus kurdjumovi* (Nikol'skaja), *Marietta picta* (André), *Pachyneuron aphidis* (Bouché), *Pachyneuron muscarum* (Linnaeus), *Psyllaphycus diaphorinae* (Hayat) and *Syrphophagus aphidivorus* (Mayr). *Syrphophagus aphidivorus* was found as the dominant secondary parasitoid for the common pistachio psyllid. The presence of shared hyperparasitoids attacking both *A. pistaciae* and weed-infesting aphids in pistachio orchards was verified. The braconid wasp, *Lysiphlebus fabarum* Marshall, the parasitoid of *Aphis gossypii* Glover and *Aphis craccivora* Koch present on weeds was found to be an alternative host for three major hyperparasitoids of *A. pistaciae*. *Syrphophagus aphidivorus* was the most abundant hyperparasitoid for aphids in pistachio orchards. It is widely distributed in pistachio plantation areas. The weed-infesting aphids, along with their primary parasitoid, can act as a reservoir of *A. pistaciae* secondary parasitoids. Therefore, parasitized aphids allow populations of secondary parasitoids to increase and consequently to apply



higher pressure on *P. pistaciae*. Based on this information, the hyperparasitoid complex is an important factor affecting efficiency of *P. pistaciae*.

Towards a compendium of Hymenoptera muscles

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General knowledge on the muscle system is crucial for understanding the functional morphology of skeletal structures. Studying muscles is therefore indispensable both for the correct interpretation of morphological characters of any level of systematic research. The knowledge of the site of attachments of skeletal muscles delivers critical information for defining numerous traditionally used anatomical structures. Providing accurate definition for anatomical structures (i.e., classes) is perhaps the principle requirement for making hypotheses on homology. The Hymenoptera muscle compendium is an account of the complete skeletomusculature of the adult Hymenoptera. The muscles described in the compendium include those of the head, thorax, abdomen. The origin and insertion sites, definition and synonymous names used in Hymenoptera are proposed. The result of the trial for aligning Hymenoptera muscles with those of *Sophophora melanogaster* based on function is also reported.

Biosystematics of the *Cotesia flavipes* species complex (Hymenoptera: Braconidae): Towards the effective control of mothborer pests in Australia

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The *Cotesia flavipes* species complex of microgastrine wasps are economically important worldwide for the biological control of lepidopteran stemborer species associated with gramineous crops. The complex currently comprises four species: *C. flavipes* Cameron, *C. sesamiae* (Cameron), *C. chilonis* (Matsumura) and *C. nonagriæ* Olliff, which are morphologically very similar. The absence of clear diagnostic characters to separate the species and inaccurate identification have confounded past efforts to assess the impact of specific introductions. Moreover, geographic populations exhibit variation in host-parasitoid physiological compatibility and reproductive success. In addition, the species and populations in the complex harbour different strains of polydnviruses (PDV). These PDVs are integrated in the wasp genome and play an important role in host immune suppression and, in turn, successful parasitism and host range. Differences in PDV symbionts among populations have

potentially important implications for host utilisation and, thus, the diagnosis of appropriate strains for biological control against specific host species. We have employed a multi-gene approach to investigate genetic variation among worldwide populations of the *C. flavipes* complex and phylogenetic congruence between wasps and their PDVs. Our results provide a framework for examining phylogenetically distinct lineages, identification of potential cryptic species, and parasitoid-host evolution and compatibility.

Molecular and morphological revision of *Evania* (Hymenoptera: Evaniidae) of Costa Rica

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Evaniidae are large, unique, and relatively common predators of cockroach eggs. Despite many fascinating biological attributes, such as mimicry complexes and variable oviposition behaviors, evaniids have been largely ignored by systematists and ecologists. Currently, there are only 6 described species of Evaniidae in Costa Rica. We discovered several new morphospecies of *Evania* in Costa Rica and have tested these concepts with novel morphological and molecular techniques. We have developed multiple new loci from protein coding genes to use as independent tests against the barcoding region of COI. We have also discovered several new internal morphological characters used to delineate species.

Global patterns of host-plant association and phylogeography in the oak gallwasps

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Oak gallwasps (Cynipidae: Cynipini) represent a major radiation of herbivorous insects associated with oaks (genus *Quercus*) and their near relatives in the family Fagaceae. Information on the origins and patterns of species radiation within these gall inducing insects and their host plants provides insight into general questions relating to the co-evolutionary interactions controlling host shifts and co-radiations among herbivores and their host plants. Previous work on Western Palearctic members of this wasp group highlighted the strong co-evolutionary links between gallwasps and their host plants imposed by gall induction, with very few shifts between the two host oak sections present in this area. Here we test whether such extreme host-plant conservatism holds on a global scale, incorporating gallwasp taxa attacking all five major groupings within the genus *Quercus*, as well as species galling the related plant genera *Lithocarpus*, *Castanopsis*, *Notholithocarpus*, *Chrysopsis* and *Castanea*.

Specifically, we test whether on this global scale switching among host plant taxa is also rare. Within the Nearctic the major oak host lineages are more closely related than those occurring within the Palaearctic, with occasional hybridisation among them, so we test whether host switching within this region is more common. We also test whether deeper relationships among oak gallwasp lineages mirror the genus-level relationships of host plant lineages, supporting a hypothesis of very long-term co-radiation of these two ecologically-linked groups.

Such global sampling also allows testing of the origins of this speciose insect group. Current levels of species diversity led the famous gallwasp researcher Alfred Kinsey to propose that this group originated in the Nearctic with subsequent invasion into Asia and the Western Palaearctic (the “Out of America” hypothesis). Under this scenario, we would expect basal gallwasp lineages to occur in the Nearctic, while Asian and Western Palaearctic radiations should be derived. In addition, basal gallwasp groups should be associated with Nearctic oak groups, including the endemic lineages *Quercus* sections Lobatae and Protobalanus and the genera *Notholithocarpus* and *Chrysolepis*, while shifts onto Palaearctic sections and genera would be secondary. In contrast, oaks and closely related Fagaceous genera appear to have originated in Asia, so if oak gallwasps have tracked the evolution of their host plants this suggests an alternative “Out of Asia” hypothesis for oak gallwasp origins. Under this hypothesis we predict that basal gallwasp lineages will be Asian and associated with the endemic Asian oak and near-oak taxa (*Lithocarpus*, *Castanopsis*, *Quercus* subgenus *Cyclobalanopsis* and section Cerris), with derived lineages occurring in both the Nearctic and Western Palaearctic.

We test these hypotheses of origins and host plant associations using molecular data. We use DNA sequences from multiple genes (the mitochondrial cytochrome *b* gene, and two nuclear genes – the D2 region of the 28S rRNA gene and long-wavelength opsin) and Bayesian inference methods to reconstruct the phylogenetic history of the Cynipini. We then map host plant lineage and geographic region onto these phylogenies to examine phylogeographic origins and host plant associations within this group.

Taxonomy and phylogeny of inquiline oak gallwasps of Panama, with description of eight new species of *Synergus* (Hymenoptera, Cynipidae, Synergini)

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The poorly known gallwasp fauna of Panama is being inventoried and for the first time accurately sampled and studied. Knowledge of this fauna is interesting because it takes part of the southernmost distribution of the *Quercus*-associated Cynipidae in the Americas. In the frame of this project a taxonomical and phylogenetic study of the cynipid inquilines associated to oak gallwasps of Panama is here presented. The host gallwasp community sampled included sixty three gall morphotypes induced by cinipids associated with six species of *Quercus*, mainly *Quercus salicifolia* and *Q. bumelioides*. The inquiline fauna is composed of two genera *Agastoroxenia* Nieves-Aldrey & Medianero, 2010, with a single species, and *Synergus* including 10 species. *Synergus mesoamericanus* and *S. nicaraguensis* are firstly recorded for Panama while eight additional species are described as new. A key for the

identification of the inquilines of oak gallwasps of Panama is provided as well as accurate SEM based descriptions of all the studied species.

A preliminary morphological phylogenetic analysis of inquilines relationships is performed based in 14 exemplar taxa of inquiline oak gallwasps, including representatives of all the known species from Panama and three outgroups namely *Synergus colombianus* from Colombia, and *S. ibericus* and *Saphonecrus lusitanicus* from Europe. The morphological study results in 65 characters, 62 -- from external morphology, based on scanning electron and light microscopy images, and three from biology. Parsimony analysis indicated a well supported monophyly for the clades *S. mesoamericanus*+*S. sp. nova* and another composed by two undescribed *Synergus* species, while the relationships between the remaining Panamanian *Synergus* species are uncertain and weakly supported. The phylogenetic reconstruction found a clade of two inquilines species, provisionally identified as *Synergus* closer to *Saphonecrus* than *Synergus*, as well as *Agastoroxenia panamensis* as the sister group of the remaining *Synergus* species.

Contributions to the Braconidae (Hymenoptera) fauna of Turkey

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This study was carried out to determine the species of Braconidae found in vineyard, pistachio and almond orchards in Diyarbakır, Mardin and Siirt provinces in 2006-2009. In the study, the specimens were caught using light trap in pistachio and almond orchards and sweepnet in vineyards. The total of 16 species determined are *Orgilus (Orgilus) punctiventris* (Tobias, 1976), *Phanerotoma (Phanerotoma) leucobasis* (Kriechbaumer, 1894), *Phanerotoma (Bracotritoma) parva* (Kokujev, 1903), *Homolobus (Apatia) truncator* (Say, 1829), *Meteorus rubens* (Nees, 1811), *Bracon (Lucobracon) erraticus* (Wesmael, 1838), *Bracon (Hablobrcon) breviradiatus* (Tobias, 1957), *Macrocentrus collaris* (Spinola, 1808), *Heterospilus tadjhicus* (Belokobly, 1983), *Hormius moniliatus* (Nees, 1811), *Chelonus (Microchelonus) flavipalpis* (Szépligeti), *Mirax rufilabris* (Haliday), *Chelonus* sp., *Dorytosoma* sp, *Spathius* sp. and *Rogas* sp. Eight species are first records for the Turkish fauna. These species are *O. punctiventris*, *P. leucobasis*, *P. parva*, *H. truncator*, *B. breviradiatus*, *H. tadjhicus*, *H. moniliatus* ve *C. (Microchelonus) flavipalpis*.

Daring the impossible - a phylogenomic 2000 species approach to Hymenoptera phylogeny

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Countless molecular data of Hymenoptera species have been gathered over the last years, constantly growing in size and number. Our knowledge on Hymenoptera phylogeny is currently limited by the ability to combine these data in a fast, yet accurate and objective way. We present a novel approach to overcome this problem and to exploit what was published before and hence picture what we virtually already know. We used all molecular data of Hymenoptera taxa accessible through GenBank and put them in a single analysis. Our study combines approaches to several issues on different levels:

Firstly, we provide a methodical pipeline on how to acquire and prepare those enormous and variable data for the final tree reconstruction, including automatic download, orthologue search, sequence processing, quality management, alignment, partitioning, filtering ambiguous or randomly similar sites and eliminating heterogeneity.

Secondly, we present the methods of tree reconstruction that can be performed with very large datasets in a reasonable time and with high accuracy. Our method of choice is tree reconstruction with a super distance matrix (SDM). The super distance matrix is obtained by combining NJtrees of single genes with optimized branch lengths. Subsequently, the phylogenetic tree is reconstructed from the matrix with a neighbour-joining algorithm. The SDM method also provides a super variance matrix that allows identification and elimination of unplaceable taxa.

Thirdly, we show our results on Hymenoptera phylogeny. Open questions include systematic status and positioning of recognized superfamilies and of higher taxa, such as Aculeata, Proctotrupomorpha, and Evaniomorpha. Additionally to our contribution to understanding the origin and evolution of Hymenoptera these results allow us to point out open questions or weakly supported nodes to guide future studies in terms of taxon and marker selection.

Our dataset comprises more than 300 nuclear and mitochondrial genes and some 2000 Hymenoptera species from more than 70 families from all 22 superfamilies currently recognized.

The Hymenoptera are exceptionally numerous and diverse in terms of life history and feeding habits, i.e. include parasitoids, predators, phytophaga, eusocial and solitary taxa, and are known to be systematically challenging. This makes them an excellent exemplar clade for our approach. However, the presented approach is designed as a general approach and can be applied to all taxa following the presented pipelines of data preparation and analysis.

The poverty of partitioned analyses and character-type chauvinism

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Phylogenetic analyses of individual partitions of data (gene fragments, parts of the morphology, behavior, etc). sometimes give different results. This should be of no surprise, as even small amounts of data from the same partition will do the same. However, the common interpretation that is given is that morphology and molecules show fundamentally different patterns, leading researchers to simply pick the phylogeny from whichever data source they prefer, or to malign the utility of another data source entirely. Using social wasps and their close relatives as examples, we show that multiple different analyses that combine



all available data support traditional views of taxonomy much more than the individual analysis of partitions from any source.

Evolutionary history and phylogeography of western Mediterranean *Synophrus* inquiline gallwasps (Hymenoptera: Cynipidae: Synergini)

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Unlike most Cynipidae species, the tribe Synergini develops as obligate inquiline within the galls induced by other cynipids. The genus *Synophrus* stands apart from other Synergini genera by its remarkable abilities to enlarge and modify the structure of host galls. *Synophrus* has been recently the subject of a molecular phylogenetic analysis and taxonomic revision. The sampling of the western Mediterranean populations, however, was very sparse and left many questions unanswered. Reproductive patterns in *Synophrus hispanicus* are of special evolutionary interest. The Iberian populations of this species seem to be parthenogenetic, while both males and females have been reported in their North African counterparts. *Synophrus olivieri*, also present in the western Mediterranean, shows contrasting patterns of plant host association between its two disjunctive distribution areas. This species is found on *Q. suber* in North Africa, but it has been collected on *Q. brantii* and *Q. libani* in Iran. With the aim of providing a deeper understanding on the evolutionary history and phylogeographic patterns of *S. hispanicus* and *S. olivieri*, we are currently conducting a phylogenetic and population genetic analyses of a large sample of specimens collected along their distribution range using a combination of mitochondrial and nuclear markers. We will present preliminary results of these analyses, along with new information on hosts.

Proposed worldwide molecular survey of tephritid-parasitoid associations using fly puparia: a new approach to understanding host associations, systematics, and ecology in complex tritrophic communities

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Investigating dipteran-parasitoid interactions in complex communities is challenging. Often it is not possible to unambiguously associate a reared wasp with its fly host unless no other

potential hosts are reared from the same collection. Morphological identification of large numbers of reared fly or wasp specimens is limited by the availability/willingness of taxonomic specialists, and generally, in large studies, a nearly unmanageable number of undescribed species are discovered. In addition, pupal mortality during the rearing process may reach 40% resulting in a tremendous loss of fly-wasp association data.

We propose to use a novel molecular approach involving DNA-barcode data to unambiguously associate fruit-feeding tephritids and their parasitoids across a global framework of crop species and native plant hosts. This will be accomplished by more-or-less replicating the sampling design of Copeland, Luke, & Wharton's (2009) multiyear tephritid-parasitoid rearing project in Kenya with several modifications: 1) approximately 80% of pupae emerging from fruits will be immediately preserved for DNA-barcoding of both fly DNA and, if present, parasitoid DNA, 2) adult flies and wasps will be reared from the remaining 20% of pupae, and these specimens will be DNA-barcoded in order to associate adults with pupal samples, and 3) extensive sampling over three years (years 1-3) will simultaneously take place in 10-15 tephritid-rich regions of the world, and the processing, parasitoid screening, and DNA sequencing of the thousands of samples will take place over 4 years (years 2-5).

All of the data from this project will be immediately, publicly, and freely available via project-specific web portals and databases that link with established systems (GenBank, BOL, EOL, etc.). DNA-barcoded adult specimens will be immediately deposited into major museum collections. Aliquots of genomic DNA from DNA-barcoded specimens (both flies and parasitoids) will be made available, upon request, to researchers for use in their research programs. We hope that all scientists with interests in tephritid-parasitoid interactions will use any portions of the data to address questions involving taxonomy, cryptic species, systematics, biocontrol, phylogeography, food webs, specialization, host-shifts, etc. The science, scope and impacts of this project are unprecedented and will usher in a new era of understanding and managing complex global communities.

A preliminary study of molecular relationships within *Diplolepis polita* (Hymenoptera: Cynipidae)

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Diplolepis polita (Ashmead, 1890) is the most geographically widespread species of the genus *Diplolepis* (Hymenoptera: Cynipidae) in addition to having a surprisingly broad range of host plant species. Some distinct differences in adult morphology within one of the Canadian populations further suggest that this might be a species group and not just a single widespread species. As a preliminary test of the diversity within this species (or species-group) DNA was extracted from larvae of *Diplolepis polita* collected from populations in localities throughout Canada, Alaska and California. Extracted DNA was then amplified via PCR to examine one nuclear gene sequence (Long-Wave Rhodopsin), a ribosomal DNA sequence (28S rDNA), and two mitochondrial gene sequences (Cytochrome Oxidase I and Cytochrome B). We



discuss the usefulness of these particular gene sequences in cynipid phylogenetic analysis as well as implications for the validity of this species.

Defense in honeybees: can bees determine how much is at risk?

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Selection pressure acts simultaneously at several levels - including at the individual level and the colony level - to minimize risks while maximizing fitness. In honeybees, defense against large predators is risky and costly, and the ultimate reward for an individual successfully defending the colony is death from loss of the stinger into the potential predator. This success is also a cost both for the individual and the colony. The benefit of successfully stinging a threatening predator is an enhanced reduction in the probability of damage to, or destruction of, the reproductive unit: in this case, the honeybee colony of 3-60 thousand individuals. Defensive failure can have the ultimate cost to both the individual and the colony of failure to pass their genes to subsequent generations (fitness = 0). Given the extreme risks and costs of defensive behavior on one hand, and the potential benefit to individual and colony fitness on the other hand, individual defenders should optimally evaluate the risk-benefit ratio in executing defensive actions. The lower the potential harm level to the colony unit, the lower should be the risks taken by individuals. The opposite should apply to colonies having large potentials for harm. I hypothesize that risk of predation to a colony is proportional to the colony resources as measured by immature brood, honey, and pollen reserves, and that defending workers will be able to evaluate the risk to the colony and will tailor their defensive vigor accordingly. Data testing defensive responses of workers in colonies with little to lose and in others with much to lose will be presented and discussed.

Breaking the bonds of Gondwana – adaptive radiation of the Gondwanan pergid sawflies (Hymenoptera, Symphyta, Pergidae)

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The Pergidae show a Gondwanan distribution with the majority of species occurring in South America and Australia. They are the dominant sawfly family in Australia and one of the major families in the Neotropics. In Australia, three of the eight pergid subfamilies are associated exclusively with eucalypts and related Myrtaceae. These plants are characterised by high concentrations of potentially toxic essential oils (e.g. 1,8-cineole) and phytophagous insects that feed on them have developed specific mechanisms to deal with these oils. The two subfamilies Perginae and Pterygophorinae use different mechanisms to deal with the same toxic components in their respective host plants. Larvae of the Perginae have the inner surface of their mandibles equipped with soft brush-like structures for separating leaf oils from nutritive plant matter. Oil that, despite the filter mechanism, does reach the midgut is metabolised to hydroxycineole. The related Pterygophorinae also feed mainly on oil-rich Myrtaceae, but they do not sequester the oil and lack morphological structures on their mandibles. Pterygophorine larvae rely solely on chemical detoxification of the relevant plant

compounds. Both the Perginae and Pterygophorinae are, like their eucalypt host plants, endemic to Australasia. We assume that adaptive radiation of Australian sawflies that are attached to oil-rich Myrtaceae is closely associated with the aridification of the Australian continent and the adaptive radiation of the eucalypts and their allies during the Mid-Cenozoic. A phylogeny of the Pergidae based on morphological and molecular characters provides the basis for examining questions relating to the timing, specific environmental circumstances and preadaptations associated with this transition.

An introduction to gall formation

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The formation of insect galls on plants is one of the most fascinating, yet least understood examples of interspecies communication and manipulation. It is wide spread and many insect families evolved the ability to induce galls. Cynipid galls excel in the complexity of tissues and structures their galls display and one might expect the signaling to reflect this complexity. While the fundamental gall formation process is still unknown I will provide a short summary of past work on process and symptoms as an introduction to current work described in the following talk.

***Ophion* (Ichneumonidae) of western Canada: molecules, morphology and species delimitation in a taxonomically challenging genus**

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Ophion is a genus of large nocturnal Ichneumonidae in the subfamily Ophioninae. Whereas the Ophioninae are generally more diverse in the tropics, *Ophion* is most diverse in temperate regions, with an estimated 50 Nearctic species. Most species are internal parasitoids of medium to large-sized Lepidoptera larvae, especially Noctuidae. They are frequently collected at light traps, and are common in most habitat types. However despite their abundance, ease of collection and conspicuous size, the Nearctic *Ophion* remain very little studied. Only twelve species have been described, and most records are from eastern North America. *Ophion* are difficult to distinguish morphologically and have a great deal of intraspecific variability. Such species are often inaccurately or incompletely resolved with morphological analysis alone, and are thus well-suited to the use of molecular techniques. I am conducting a taxonomic study of Canadian *Ophion*, with an emphasis on western Canada, using a combined morphological and molecular approach. For the molecular analysis, I am sequencing both mitochondrial (COI) and nuclear (ITS2) regions. I have found that both of these regions are highly variable and informative within the genus, with sequence divergences of up to 14%. For the morphological analysis I am using characters that have been found to be informative in Ophioninae in other geographic regions, as well attempting to discover reliable characters that have not previously been examined. I will also be conducting a



morphometric analysis of wing venation, as a further tool to distinguish species. Preliminary results and implications of these analyses will be discussed.

Building the Hymenoptera Anatomy Ontology through exploration of the Journal of Hymenoptera Research

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The Hymenoptera Anatomy Ontology (HAO) project aims to capture the complex lexica used to describe hymenoptera anatomy. Our core data are extracted from the corpus of published works, particularly descriptions of new taxa. We reviewed the Journal of Hymenoptera Research (JHR) to extract new labels and ontological classes, explored the completeness of the present version of the HAO, and reflected upon community language trends. Three hundred and fifty three (353) Journal of Hymenoptera Research articles were parsed, accessed through the Biodiversity Heritage Library and vetted against the present ontology. New labels (2121) were collected during this process including about 650 adjectives used to qualify morphological features. Language trends were revealed in the process, showing the occurrence of anatomical labels used in the literature, possibly reflecting the character systems and qualifiers we most often use to describe novel taxa. Additionally the novel software used for text extraction is reviewed, outlining possible improvements and useful tools resulting from this effort.

A salute to the ensign wasps: molecular phylogenetics of Evaniidae

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Generic relationships among Evaniidae have been largely ambiguous in previous molecular analyses. Additionally, the phylogenetic relationships among members of Evanioidea and their relative position within Hymenoptera have never been satisfactorily resolved. Here, we examine phylogenetic relationships among genera of Evaniidae, as well as the position of the family within Evanioidea, using molecular data. We also make inferences regarding the phylogenetic position of Evanioidea relative to other superfamilies within the order. We present a robust, well-supported phylogeny of Evaniidae utilizing multiple molecular markers, several new to hymenopteran research. Furthermore we hypothesize evolutionary pathways concerning host usage and body size within Evaniidae, based on phylogenetic patterns.

Morphology and molecules, the first comprehensive, total evidence, phylogenetic analysis of the Hymenoptera

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The first comprehensive analysis of higher-level phylogeny of the order Hymenoptera is presented. The analysis includes representatives of all extant superfamilies, scored for 392 morphological characters, and sequence data for four loci (18S, 28S, COI and Efl α). Including three outgroup exemplars, 100 terminals were analyzed. Relationships within Apocrita are resolved. Well supported relationships include: Orussidae is sister to Apocrita; Evanioidea is monophyletic; Aculeata is sister to Evanioidea; Proctotrupomorpha is monophyletic; Ichneumonoidea is the sister-group of Proctotrupomorpha; Platygastroidea is sister to Cynipoidea, and together they are sister to the remaining Proctotrupomorpha; Proctotrupeoidea s.s. is monophyletic; Mymarommatoidea is the sister-group of Chalcidoidea; Mymarommatoidea + Chalcidoidea + Diaprioidea is monophyletic. Weakly supported relationships include: Stephanoidea is sister to the remaining Apocrita; Ceraphronoidea is sister to Megalyroidea, which together form the sister-group of (Trigonaloidea (Aculeata + Evanioidea)); Diaprioidea is monophyletic; Xiphydriidae is sister to Orussidae + Apocrita. Symphytan relationships are well resolved as follows: (Xyeloidea (Pamphilioidea (Tenthredinoidea (Cephoidea (Siricoidea (Xiphydriidae (Orussoidea + Apocrita)))))).

Biology of some parasitoids of *Apoda limacodes* (Lepidoptera: Limacodidae) in Europe

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The isolated family Limacodidae is represented in Europe by very few species, of which only two are widespread. The larger of these, *Apoda limacodes*, is regularly parasitised by five species of larval parasitoids. The biologies of the three most extreme specialists, one species each in the Braconidae: Rogadinae genera *Rogas* and *Triraphis* and the Ichneumonidae: Tryphoninae genus *Sphinctus*, are outlined.

Structural colours in Hymenoptera wings

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Compared to the colourful wings in butterflies wings in Hymenoptera are usually regarded as colourless. Typically monographs on Hymenoptera describe the wings as transparent or with pigmented patterns in different shades of brown, to black, but without any mention of more colourful tints. However, small Hymenoptera (≤ 3 mm) in particular actually display a multitude of colours on their wings, if viewed properly. These colours are distributed in a non-random pattern, and are frequently taxon-specific. We call this pattern WIP – Wing

Interference Pattern, and it is the result of thin film interference. The reflected patterns appear strong in live specimens and are perfectly preserved also in hundreds of years old dry museum specimens.

Most of the 17.000 species of butterflies can be distinguished by their wing colours alone. Our preliminary evaluation of WIP suggests that the same is the case for several groups of Hymenoptera. Especially in groups including small species with wing discs devoid of veins, e.g. the Chalcidoidea, the WIP could become a powerful tool for classification, species recognition and behavioural studies.

A Hymenoptera wing is composed of a single compressed double layer of transparent chitin, ideal for two-beam thin film interference, with beams reflecting from the upper and lower surfaces of the membrane respectively. The colour patterns are non-iridescent – dioptrically stabilized and reinforced by membrane corrugations, chaetotaxy, venation and pigmentation. These patterns reflect uneven thickness of the wing membrane, and if calibrated against a colour scale, the WIP colours can be used to calculate the thickness of different parts of the wing.

Membrane thicknesses, formation of membrane corrugations, chaetotaxy, all of which affect the WIP, are controlled genetically. Exactly how and by which genes this regulation occur remains to be established. However, comparing to investigations in Diptera where wing pigment patterns have been demonstrated to be formed and controlled by a set of spatiotemporal on/off switches for particular loci, similar regulating mechanisms are likely to be present in Hymenoptera.

The reflected colour sequence, which excludes red, fits the colour-vision in insects, strongly suggesting their biological significance for visual signalling. We therefore find it highly unlikely that the colourful WIP palette is merely an optical effect without biological significance. The production of WIPs is a highly cost-effective way to create visual signals. Unlike in the Lepidoptera, where colour patterns are made from scales – i.e. additional structures that cost energy to produce – the colour patterns in Hymenoptera do not need extra structures for their creation, and thus do not consume extra energy beyond, occasionally, the cost of pigment formation. Species-specific WIPs produced energy-efficiently may add a lot to e.g. speciation events through species recognition systems driven by visual pre-mating activities. Hymenoptera is a very successful insect group with very high species diversity. The majority of species are small, having the ideal size to display WIPs. All these things considered the WIP could be an important factor for the outstanding success of the Hymenoptera.

Oak Provenances on Trial: the distribution of gall forming wasps at an experimental oak plantation in Northwest France

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Recent climate change predictions suggest that by 2050, much of southern Britain will become unfavourable for native genotypes of several broadleaved tree species currently favoured in commercial forestry. A possible management strategy is to source seeds from sites in Europe where trees are currently adapted to the climatic conditions predicted for the

UK. However, work in the field of community genetics suggests that tree genotype can dramatically influence associated communities, and thus, the large-scale planting of non-native tree genotypes in the UK could have consequences for associated biodiversity. If communities are locally adapted to native tree genotypes then introduced genotypes should have a negative influence. If however communities are adaptable, then a combination of native and non-native genotypes may represent a broader niche and the influence could be positive. In this study, the influence of non-native tree genotypes is investigated using a model system of oak trees (*Quercus petraea*) and herbivorous gall wasps (Hymenoptera: Cynipidae) at an experimental provenance trial in Northwest France. Oaks are an important source of commercial timber in Europe, and they support the largest diversity of herbivorous insects of any European tree. At the provenance trial, the local populations of gallwasps are exposed to oaks from over 100 European populations (provenances). It is predicted that if these gallwasps are adapted to local oaks, then they will be most abundant on those provenances who are most genetically similar to, or whose phenotype most closely matches that of the local oak population. In spring and autumn 2008 and 2009, trees from 20 provenances were surveyed for gallwasps and the data were analysed in relation to host-tree provenance and host-tree phenotype. Initial results indicate that oak provenance dramatically influences the abundance of gallwasps, and that gallwasps are generally most abundant on provenances that are geographically close to the trial site. This supports the prediction that gallwasps are locally adapted to tree phenotypes/genotypes, and that introduced genotypes would have a negative influence on native communities. Ongoing work aims to address the further question of how host-tree provenance can influence the associations between gallwasps and their parasitoid natural enemies.

**An inordinate fondness for parasitoid wasps:
DNA barcoding data from a global array of projects**

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Parasitoid wasps are the largest group within Hymenoptera, comprising perhaps 10 % of the terrestrial eukaryote life. Most of its species are undescribed and there are considerable taxonomic difficulties and practical limitations in dealing with this enormous diversity. Here we present an overview of DNA barcoding projects on parasitoid Hymenoptera (mostly

Ichneumonoidea and Chalcidoidea) that are underway based on material from the Arabian Peninsula (Oman, UAE, Yemen), Canada (Arctic and Sub-Arctic), Democratic Republic of Congo, Madagascar, Meso-America (Area de Conservación Guanacaste, Costa Rica, and Mexico), Papua New Guinea, Sweden, Thailand, United States, and New Zealand. Vouchers specimens from which DNA extracts were obtained are deposited in the authors' institutions (listed above).

For every project we summarize results, including the cumulative number of species as defined by DNA barcoding. The species richness revealed in most of the projects was greater than expected, even for areas thought to contain low diversity. We tested the results of barcoding against traditional taxonomic data such as morphology, ecology and biology in several projects (especially Microgastrinae from Costa Rica and Canada; Orthocentrinae and Alysiinae from Churchill) and found that the results from both approaches are similar in more than 90 % of cases, except that barcoding reveals groups of unexpected species "hiding" within morphologically-defined species.

We conclude that DNA barcoding can provide a rapid and accurate overview of species richness within parasitoid Hymenoptera. The results are most robust when integrated with morphological and ecological data; however, barcode data alone will make a significant contribution to our understanding of this group.

What do we know about *Chrysis ignita* (Hymenoptera: Chrysididae)?

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Chrysididae is a cosmopolitan Hymenoptera family that includes about 3000 named species. The largest genus in the family, *Chrysis* Linnaeus is also the type genus for the family. *Chrysis* is divided into 70 species groups, of which the largest is the *C. ignita* species group, which includes *C. ignita* Linnaeus, 1758, the type species for the genus and the best studied species in the family. From numerous published sources we know that its distribution covers most of the Palearctic region from Macaronesian islands in the west to Japanese islands in the East. The life cycle of *C. ignita* is relatively well documented: it is one of only eleven cuckoo wasp species for which the mature larvae have been described, and even its oogenesis has been studied. The ecology of *C. ignita* is also well documented with the first identification of its hosts published in 1869. Currently more than 20 host species have been documented for this cuckoo wasp, suggesting that the species is not very host specific.

Despite its overall homogeneous morphology, *C. ignita* is known to exhibit considerable variation in minor morphological details. This has led to the establishment of numerous names, which are treated as synonyms, forms, varieties, subspecies or even separate species. The usage of these names varies from author to author, with the most conservative authors treating more than 30 names as synonymous with *ignita*. Since treatment of the *C. ignita* species group is so variable I aimed to delimit each of the taxa involved. Because morphological methods have been only partially successful, I focused on molecular methods and used mitochondrial DNA sequences for reconstructing the phylogeny of the European taxa within the group.

The results of my study demonstrated that many of the names often treated as synonyms of *C. ignita* in fact represent separate species. Furthermore, there appeared to be undescribed

cryptic species among the taxa usually grouped together into *C. ignita*. Therefore, the portrayal of *C. ignita* as a widespread variable species with wide host selection must be reconsidered. In this light, reliable understanding about its distribution, morphology and ecology becomes very limited since most published data cannot be associated with *C. ignita sensu stricto*. Indeed, the wide distribution area of the species is questionable, and I have only confirmed its occurrence in Europe, where it has actually become rare in recent years. Similarly, most, if not all, published host-parasite relationships of *C. ignita* must be considered as unconfirmed. Moreover, we cannot now be sure whether described details about the oogenesis and larval morphology of *C. ignita* could be associated with *C. ignita sensu stricto*.

Phylogeny and systematics of the tribe Meteorini (Braconidae)

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Parasitic wasps comprise a sizable portion of the animal diversity that remains to be described. Even the species that have names often remain very poorly known. In Sweden, parasitic wasps comprise roughly a quarter of the animal species for which the information is so scant that the Swedish populations cannot be judged according to the IUCN red-listing criteria (Gärdenfors 2000).

The Braconidae are one of the most diverse families of parasitic wasps. They develop as parasites of a wide range of insects and form an important component of most terrestrial food webs. The world fauna is estimated at 40 000 species (Gaston 1991), and the Swedish fauna may hold as many as 2 000 species (roughly 1 200 currently known). In terms of species richness, braconids are second only to the Ichneumonidae among families of animals. There is about 30 subfamilies of Braconidae, most of which occur in Sweden. Our research will focus on the Euphorinae, one of the most difficult and species-rich of the subfamilies. It is characterized by great diversity in host association accompanied by a similarly large morphological diversity. While most braconid subfamilies parasitize on a single host insect order, euphorines attack many: Orthoptera, Hemiptera, Psocoptera, Neuroptera, Coleoptera, Lepidoptera and Hymenoptera (Chen & van Achterberg 1997, Huddleston 1980, Shaw 1985). Many euphorines also attack adult insects, a trait that is extremely rare among the parasitic Hymenoptera. Outside the Euphorinae, adult parasitism is only found in the Aphidiinae and Neoneurinae among braconids. The Aphidiinae are entirely restricted to parasitism of aphids (Shaw & Huddleston, 1991) and the Neoneurinae attack and develop in the abdomen of adult formicine ants (Poinar 2004). Thus, the Euphorinae are unique in attacking a broad range of adult insects.

In recent work (still unpublished), I have used a combined morphological and molecular approach to study the systematics of one of the tribes, the Meteorini (by some authors recognized as a separate subfamily). About 178 specimens from 43 species have been sequenced. Previously, 35 species of the tribe Meteorini were recorded from Sweden. We have been able to add at least ten new species and four synonyms that will be presented as taxonomical changes. The user friendly key now includes almost 60 species from all of Europe with diagnostic descriptions. The phylogenetic analysis also revealed at several cryptic species and an interesting relation amongst the Meteorini. Especially the genera *Zelee*

seems to be included within the genera *Meteorus* rendering it paraphyletic. The host preference also shows interesting evolutionary steps.

Phylogeny and DNA barcoding of inquiline oak gallwasps (Hymenoptera: Cynipidae) of the Western Palaearctic

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We examine phylogenetic relationships within the *Synergus* complex of herbivorous inquiline gallwasps (Hymenoptera; Cynipidae; Synergini) associated with cynipid host galls on oak, a biologically diverse group whose genus-level morphological taxonomy has long been considered stable but whose species level taxonomy is problematic. We incorporate data for over 80% of recognised Western Palaearctic species in 5 morphology-based genera (*Ceroptres*, *Saphonecrus*, *Synergus*, *Synophrus*, *Ufo*), comprising sequence for two mitochondrial loci (*coxI*, *cytb*) and one nuclear locus (28S D2). In particular, we assess the evidence for monophyly of two long-established, morphology-defined sections within the genus *Synergus* that differ in a range of biological traits. To aid analyses of ecological interactions within oak cynipid communities, we also consider the utility of cytochrome oxidase I (*coxI*) DNA barcodes in the oak inquilines. In this assessment, we do not assume that species are delineated at a single threshold value of sequence divergence for a single gene, but examine concordance in the composition of molecular operational Taxonomic units (MOTUs) across a range of sequence divergences in each gene and across genes. We also assess the impact of sampling effort on MOTU stability.

Phylogenetic reconstructions for all three loci support monophyly for *Synergus* and *Synophrus*, but reject monophyly for *Saphonecrus* and for the two sections within *Synergus*. The suites of traits associated with the two sections of the genus *Synergus* are thus homoplasious. All three loci also reject monophyly for three *Synergus* species (*S. hayneanus*, *S. pallipes*, *S. umbraculus*). Sequences for each locus identify robust MOTUs that are largely concordant across loci for a range of cut-off values. Though many MOTU's correspond to recognised Linnean species, there is significant, multigene disagreement between groupings supported by morphology and sequence data, with both allocation of different morphospecies

to the same MOTU and allocation of the same morphospecies to multiple MOTUs, regardless of cutoff value. Our results imply that while DNA barcoding has considerable utility within this group, morphology-based identification needs major revision at both genus and species levels. Further, lifehistory traits currently attributed to single morphospecies probably confound attributes of multiple lineages. Revealing patterns of character state evolution in *Synergus* requires collection of new host association and life history data explicitly linked to DNA barcode data for the specimens concerned.

Molecular evolution of the subfamily Telenominae (Hymenoptera: Platygasteridae)

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The subfamily Telenominae is a cosmopolitan taxon with more than 870 described species. All telenomines are egg parasitoids of insects and are considered to be the most important group within the superfamily Platygastroidea in biological control for agriculture. A preliminary phylogenetic reconstruction was performed examining 6 genera of telenomines, including 3 species groups of the genus *Trissolcus* and 8 species groups within the genus *Telenomus*. The total number of in group taxa is more than 70 species from several localities around the world. Phylogenetic reconstruction was performed using Maximum Parsimony, Maximum Likelihood and Bayesian approaches, all of which were executed using three molecular markers: the mitochondrial cytochrome oxidase I and the 28S and 18S rRNA. The monophyly of the subfamily and its primary constituent genera and species groups are tested. The results set the stage for more in-depth analysis of these taxa; the formal classification will require significant revision. This work is part of the ongoing Platygastroidea Planetary Biodiversity Inventory.

Oviposition behaviour and infanticide by *Zatypota albicoxa* (Hymenoptera, Ichneumonidae), an ectoparasitoid of a theridiid house spider

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Zatypota albicoxa (Walker) of the *Polysphincta*-group (Pimplinae, Ephialtini) is a koinobiont ectoparasitoid of a common house spider, *Parasteatoda tepidariorum* (Koch) (Araneae, Theridiidae) in Japan. The web of *P. tepidariorum*, called an irregular, three dimensional web, is composed of a non-sticky frame threads and more or less vertical gumfoot threads bearing tiny sticky masses near the distal end. Preys of the spider such as ants are entangled with the sticky mass when passing under the web and lifted up by the spider.

The female wasp has evolved two modes of oviposition behaviour as an adaptation to the host spider hidden in such complex webs. In one, the wasp hangs on one of the vertical gumfoot

threads between a host spider and gumfoot, pulling the thread with its fore leg until the spider lifts it up or hangs motionlessly on the mid height of the web until the spider approaches (ambush-style). In the other mode, the wasp climbs the frame threads to gain access to the host spider directly (climbing-style). One of the wasps exhibiting ambush style under laboratory conditions, lay on back on the floor and grasped one of the vertical gumfoot threads with her legs touching the sticky mass directly. Any strategies succeed in paralyzation of the spider but the female wasps do not flutter inside the irregular, three dimensional webs.

As soon as paralyzation, the wasp rubbed the spider body with its ovipositor and tip of metasoma repeatedly for about ten minutes and finally laid an egg at the base of spider's abdomen. Throughout this process, the wasp remained hanging from the web by its hind tarsal claws and grasped the spider's abdomen with its fore and mid legs. The paralyzed spider recovered about ten minutes after oviposition and went back to initial position. As female wasps emerged from larger hosts and male wasps emerged from smaller ones, the ovipositing wasp apparently assesses the size of the spider prior to oviposition and chooses whether to lay a fertilized or an unfertilized egg. If paralyzed spider bore a previously attached larva or egg of the wasp, the female wasp always removed them from the body of spider by means of rubbing behaviour with its ovipositor, but the wasp did not kill them. Removal behaviour has evolved to remove the saddle so as to remove the larva because all larvae were removed by the 'saddle' attached to the ventral surface of the body, which plays a role in external attachment. The wasp has no way to discriminate her own progeny because she removed any pre-existing eggs, regardless of whether they were her own or others'. It is more time consuming for the female to remove medium second instar or large penultimate instar larvae than eggs because of the labor in unfastening the saddle. Removal of all previous occupants suggests that infanticide would be always advantageous, no matter how the costs to *Z. albicoxa*.

Phylogeny and taxonomic status of the *Paridris* complex

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Paridris is a cosmopolitan genus of cricket egg parasitoids; its morphology indicates close relationship with three other genera, *Tuora* (Eastern Palearctic), *Trichoteleia* (Malagasy region), and *Neoparidris* (Australia). *Trichoteleia* and *Tuora* are revised at the species level, resulting in an order of magnitude increase of species diversity. The concepts of all four genera are examined and updated in the context of a phylogenetic analysis of morphological and molecular data.

Gallwasp diversity of Taiwan: testing the Asian Origin hypothesis for the Cynipini (Hymenoptera, Cynipidae)

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Of the approximately 1400 known gallwasp species, the greatest richness (around 1000 species in 30 genera worldwide) is found in the monophyletic tribe Cynipini, which induce galls on oaks (*Quercus* L.) [mainly of the subgenus *Quercus*] and related Fagaceae (Csóka *et al.* 2005). The cynipid gallwasp fauna of the Eastern Palaearctic and Oriental region is poorly known: only 34 valid species are recognised from the Eastern Palaearctic, mostly from Japan and the Russian Far East (Abe *et al.* 2007), and only few oak gallwasp species have yet been described or mentioned as “cynipid gallwasp” for the Oriental region. However, a hypothesis suggested that the Eastern Asia should be the cradle for origin of oak gallwasps due to the evidence on phylogeny of gallwasps, the diversity and potential hosts in Eastern Asia, and recently suggested diversifying center of oaks in Asia (Stone *et al.* 2009). Taiwan located at the southeast corner of Asia, belonging to Oriental region, which is highly rich in the flora of Fagaceae. The family Fagaceae in subtropical Asia and Malesia represented by 4 genera which serve as hosts for oak gallwasps (Cynipini): *Castanopsis* (134 species; 8 species in Taiwan); *Lithocarpus* (= *Pasania* (Miq.) Oerst., usually united with *Lithocarpus* but in Asia remains accepted in some quarters where *Lithocarpus* s.l. is considered too heterogenous) (325 species; 15 species in Taiwan); *Quercus* L. subgenus *Cyclobalanopsis* (about 60 species; 13 species in Taiwan) and a moderate number of species from *Quercus* subgenus *Quercus* which are represented in Taiwan by 10 species (Govaerts & Frodin 1998; Lu *et al.* 2006). To date, eleven gall morphotypes attributed to cynipids have been described from Taiwan (Yang & Tung 1998), though none of the gall inducers have been described. Of these gall types, three are associated with *Quercus variabilis* Blume, though no associations have previously been recorded for *Quercus dentata* Thunb.; other 7 morphotypes were found on *Cyclobalanopsis* and one on *Lithocarpus* (= *Pasania*) (Yang *et al.* 2000).

Our survey so far explored a rich fauna of gallwasps. Galls on subgenera *Quercus* (Cerris and *Quercus* s.s. sections) and *Cyclobalanopsis* of *Quercus* were widely collected as well as on related host genera of Fagaceae, e.g. *Castanopsis* (Don) Spach and *Lithocarpus* (= *Pasania*). Up to date, we found: 12 types of unknown cynipid stem swelling-like galls on *Quercus variabilis* (Cerris section oaks), *Q. glauca* and *Q. globosa* (*Cyclobalanopsis* subgenus oaks), *Castanopsis carlesii*, and *Lithocarpus konishii*; 7 types of bud galls on *Q. variabilis*, *Q. glauca*, *Q. pachyloma*, *L. konishii* and *L. glabra*; 12 types of unknown leaf-galls on *Q. variabilis*, *Q. morii*, *L. glabra*, *L. hancei*, *L. konishii*, *L. amygdalifolius*; 5 types of catkin galls on *L. konishii* and *L. glabra* and one type of acorn gall on *Q. variabilis*.

Till now only three Eastern Palaearctic species were found on Taiwan, all on *Q. variabilis* (Cerris section oaks): *Cerroneuroterus vonkuenburgi* (Dettmer), *Trichagalma acutissimae* (Monzen) [earlier known from Japan only] and recently a new species, *Trichagalma formosana* Tang et Melika, was described from Taiwan, however, as an undescribed species was known earlier from Japan also (Melika *et al.* 2010). The first Oriental *Andricus* species, *Andricus formosana* Tang & Melika, known to induce multilocular leaf galls on *Q. dentata*, was also recently described from Taiwan (Tang *et al.* 2009).

Two new species of *Neuroterus* (as defined in Melika *et al.* 2010) recently found in Taiwan (*in press*) is of particular interest, since unlike all western palaearctic and nearctic *Neuroterus*, they induce galls not on section *Quercus* oaks but on *Q. hypophaea* (subgenus *Cyclobalanopsis* of *Quercus*), and on *L. konishii*, a plesiomorphic relative of *Quercus* within

the Fagaceae (Manos *et al.* 2001). This species may be an early offshoot in the diversification of Cynipini among oak sections, or another of the very rare examples of gallwasp switches between major hostplant lineages. The same possible alternatives apply to other recently discovered Taiwanese gallwasps, including a *Dryocosmus* galling *Castanopsis carlesii* (*in press*), and a *Plagiotrochus* galling *Q. glauca* (subgenus *Cyclobalanopsis*) (*in press*). Pleisiomorphic traits in the latter two species tentatively support their placement into *Dryocosmus* and *Plagiotrochus*, which also supports the Asian Origin hypothesis for the Cynipini.

Our work attempts to associate the alternate generations of gallwasps and to clarify the species diversity of Taiwanese cynipid fauna. Establishment of thorough fauna data will permit us further test the hypothesis on the Asian origin of gallwasps.

Diversity of egg parasitoids (Hymenoptera: Mymaridae, Trichogrammatidae, and Aphelinidae) of Proconiini sharpshooter leafhoppers (Hemiptera: Cicadellidae: Cicadellinae) in the New World and Oceania: recent discoveries and a glimpse into future research

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In the New World tropics and subtropics, an amazing diversity within the subgenus *Cosmocomoidea* of the fairyfly genus *Gonatocerus* (Hymenoptera: Mymaridae), most species of which are still undescribed, is attributed to the diversity and abundance of their hosts – leafhoppers from the tribes Proconiini (mostly) and Cicadellini (Hemiptera: Cicadellidae: Cicadellinae), which are commonly known as sharpshooters. The establishment of the glassy-winged sharpshooter, *Homalodisca vitripennis* (Germar), in California, USA, in 1990s prompted active research efforts aimed at classical and neoclassical biological control of this vector of the bacterium *Xylella fastidiosa* using hymenopterous egg parasitoids. Proconiini is a New World group that includes mostly large, xylem-sucking leafhoppers that lay eggs in clusters and often cover them with brochosomes. Recently, the glassy-winged sharpshooter also established in parts of Oceania (the Hawaiian Islands, French Polynesia, and Easter Island), so egg parasitoids were identified from there as well (both native and intentionally or unintentionally introduced).

Three main groups of chalcidoid egg parasitoids of Proconiini are identified: 1) Mymaridae, primarily numerous members of the *ater* species group of *Gonatocerus* (*Cosmocomoidea*) (45 described and perhaps more than 200 undescribed species, some of which may also attack eggs of Cicadellini), and also several members (most quite rare) of *Acmopolynema* (1 species), *Anagrus* (3 species), *Palaeoneura* (1 species), and *Polynema* (subgenus *Doriclytus*) (several undescribed species); 2) Trichogrammatidae: several species in the genera *Burksiella*, *Ittys*, *Oligosita*, *Paracentrobia*, *Pseudoligosita*, *Ufens*, and *Zagella*; and 3) Aphelinidae (3 undetermined, likely undescribed, species of *Centrodora*, extremely rare except for one species in Tahiti Island, French Polynesia). Taxonomic problems related to identification of these difficult groups are discussed, and their known host associations are indicated. Species composition of the egg parasitoids of Proconiini is different in various habitats: Mymaridae prefer humid areas but occur everywhere there are hosts, are dominant on trees and shrubs, rarely are host (insect or plant) specific, and their females are relatively fast searchers; Trichogrammatidae are more abundant in dry, semi-desert or desert areas, apparently are



more host (especially plant) specific, are more common on grasses, and their females are slow searchers. Members of *Gonatocerus* (*Cosmocomoidea*) are by far the most common egg parasitoids of Proconiini; they are mostly solitary (one wasp per host egg) except for one Nearctic species, *G. (Cosmocomoidea) fasciatus*, which is a gregarious parasitoid (several wasps per host egg). Known trichogrammatid egg parasitoids of Proconiini are all gregarious. Before the 1990s, only one publication existed that mentioned egg parasitoids of the sharpshooter leafhoppers (in Georgia, USA); from 1996 till present, the author contributed to 1 monograph, 27 refereed articles in scientific journals, and 37 other publications on the egg parasitoids of sharpshooters in the New World and Oceania. Possible directions of the future research are discussed.

**Remediation and curation of the University of California, Riverside collections of
Aphelinidae and Encyrtidae (Hymenoptera: Chalcidoidea) on slides:
problems and solutions**

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Two unprecedented projects at the Entomology Research Museum, University of California, Riverside (UCRC) have dealt with remounting of almost 20,000 specimens on slides from water-soluble solutions in a permanent mountant (Canada balsam), in two groups that are most important for biocontrol: Aphelinidae and Encyrtidae. Most of the specimens have valuable host data and are vouchers of past biocontrol projects, more than 50% had been poorly mounted in Hoyer's and were in various stages of decay, including numerous type specimens. Often several specimens or taxa were mounted on the same slide; other problems included poor labeling, old names, peeled off labels, etc. UCRC has arguably the largest collection of Chalcidoidea on slides in the world, including ca. 40,000 slides of Trichogrammatidae, ca. 25,000 slides of Aphelinidae, ca. 10,000 slides of Encyrtidae, and ca. 10,000 slides of Mymaridae. In the course of the previous project (May 1998 - April 2002), sponsored by NSF grant DBI-9728626, the world's largest collection of *Aphytis* (Aphelinidae) was curated: 7,292 specimens were remounted from Hoyer's in Canada balsam, labeled, and databased, including 309 primary types of 51 nominal species, 2,473 secondary types, and 4,626 non-type specimens of at least 70 species from more than 50 different countries. A catalog of the type material of *Aphytis* in UCRC was published.

The UCRC has ca. 60,000 specimens of Aphelinidae (of which ca. 35,000 specimens are species of *Aphytis*) and, besides the specimens mounted on slides, ca. 50,000 dry-mounted Encyrtidae (stored in 100 museum drawers). More than 20,000 non-*Aphytis* specimens of Aphelinidae were mounted in a temporary, water-soluble medium (Hoyer's) on 5,877 slides. More than 50% of these (3,874 slides) were in various stages of decay, of these the majority being completely or partially dry. Many specimens, including some types, have already been damaged. Material was mounted with an average of at least 5 specimens per slide. The scope of the current (5/1/2008 – 4/30/2011) project, sponsored by NSF grant DBI-0745496, involves remediation of at least 11,622 specimens (approximately 4,000 per year); the specimens are remounted individually, properly labeled, and databased (including georeferencing when possible, only ca. 83% of the slides have locality data). The total number of Aphelinidae other than *Encarsia* on slides in Hoyer's that needed immediate remediation was 2,672, among them represented are 13 genera and at least 70 determined species. In addition, there are 5,023 slides of *Encarsia* in Hoyer's (1,565 of them dry) from more than 50



countries. The total number of Encyrtidae slides in Hoyer's was 1,299 (1,202 of them, or about 90%, were completely dry); represented are 49 genera.

A database of the remounted specimens is now partially available online via GBIF and Discover Life websites. Such projects require skilled, motivated personnel and good funding – they are expensive but well worth the effort.

The maritime parasitoid wasp *Echthrodesis lamoralis* Masner (Hymenoptera, Platygasteridae, Scelioninae)

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The biology and behavior of *Echthrodesis lamoralis* Masner, an endemic South African egg parasitoid of spiders adapted to a life in the marine environment is recorded for the first time. Morphological evidence supports taxonomic affinities of *Echthrodesis* to *Opisthacantha*, another aquatic adapted genus. Similarities to Baeini and Embidobiinae appear to be a result of convergent morphological adaptation. A phylogeny based on 28S, 18S and C01 gene sequences is presented. Images of behavior and of both sexes of the adult wasp are provided. Biological adaptation of this parasitoid wasp to a marine environment is discussed.

Hymenoptera of the Afrotropical region: diversity assessment and identification guide proposal

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Family, generic and species richness of Afrotropical Hymenoptera is assessed and presented in a global context based on data synthesized for the web site www.waspweb.org. A concept for producing an identification guide to all genera of Afrotropical Hymenoptera in an electronic format, using interactive online keys, as well as in a printed version is presented.

Presenting an on-going PhD project: aspects to consider when estimating the diversity of neotropical Ichneumonidae (Hymenoptera)

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To get an in-depth picture of terrestrial community ecology, one can not ignore the biologically diverse and distinctive insect parasitoids. The parasitoid family Ichneumonidae (Hymenoptera) is possibly the largest animal family on earth, yet it is often regarded as having an anomalous diversity gradient (i.e. species richness decreases from temperate regions towards the tropics). Adequate data to justify this assumption, however, are badly lacking, particularly from Amazonia. Further, recent findings suggest that Ichneumonidae may actually be more diverse in the Neotropics – and especially in Amazonia – than previously imagined.

Here, I present my on-going PhD project that concentrates on a number of factors that need to be considered when estimating the diversity of Neotropical Ichneumonidae: canopy vs. ground-level fauna, cryptic species (DNA barcoding), beta diversity (geographical distance and local forest types), flight phenology, elevation, and bioindicators. The large data set that I am currently studying with my supervisors and collaborators consists of samples from northern, northeastern and southern Peru, eastern Ecuador, and Guatemala. In addition to presenting an overall outlook of the project, I report the subfamily composition of each of the sites and give some preliminary results on our studies.

Past and present diversity and distribution in the parasitic wasp family Megalyridae

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The small parasitic wasp family Megalyridae comprises approx. 50 described extant species predominantly distributed in the southern hemisphere. The family has a substantial fossil record extending well back into the Mesozoic. Curiously, all described fossil taxa are restricted to the present day Northern hemisphere having no current overlap with the extant taxa. Recently, a number of new fossil genera from both the Cretaceous and early Tertiary were described in a monographic treatment of extinct Megalyridae (Perrichot 2009). To evaluate the status of the newly described fossil taxa and more stringently delimit the family,

the phylogenetic relationships of extant and extinct Megalynidae are analysed at the genus level. The data set comprises seven outgroup taxa, all eight extant genera and a number of extinct taxa that have been associated with Megalynidae. Included are also two genera from the Maimetshidae as well as *Cretodina*; both are Cretaceous taxa whose affinities with the Megalynidae are uncertain. Analytical results are unstable because some of the fossil taxa have many missing entries, and Megalynidae as a clade are not strongly supported. The most stable results are produced when the maimetshid taxa and *Cretodina* are excluded. When included, these taxa frequently fall outside crown group Megalynidae, the maimetshid taxa often being the sister of *Orthogonalys* (Trigonidae), and *Cretodina* sometimes being retrieved among the outgroup taxa as well. The remaining fossil taxa usually fall in two distinct clades inside crown group Megalynidae, one comprising the Cretaceous taxa and the other the Eocene taxa. The classification of Megalynidae is revised according to the results of our analyses. When comparing past and present distributions of Megalynidae with the results of the phylogenetic analyses, it is evident that both extant and extinct genera radiated in the Mesozoic, and the family as a whole was much more widespread then. The present day distribution is essentially relictual, range contraction since the early Tertiary probably being caused by climate deterioration resulting in the contraction of tropical forest ranges throughout the Palearctic.

Species diversity of neotropical tephritid fruit flies and their braconid parasitoids

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Plants, phytophagous insects, and their insect parasitoids form complex tritrophic interactions. Specialist herbivores, such as many of the fruit-infesting Tephritidae, are ideal groups for testing hypotheses about the generation and maintenance of biodiversity via such mechanisms as cospeciation, host tracking, and host shifts. These mechanisms may also apply to diversification of tephritid parasitoids, but there is limited evidence for this to date. Members of the neotropical tephritid genus *Blepharoneura* attack and develop exclusively in plants of the family Cucurbitaceae. Prior work on a clade of *Blepharoneura* specific to two closely related cucurbit genera (*Gurania* and *Psiguria*) revealed an extraordinary diversity of 30 species, only partly explained by host plant and host plant part specificity. Each *Blepharoneura* species develops in a specific part of these dioecious plants: either male flowers, female flowers, or seeds. These fly species in turn are attacked by members of at least three different lineages of opiine Braconidae: *Utetes*, *Bellopius*, and *Thiemanastrepha*. *Bellopius* includes 11 valid species, only two of which had host-associated data prior to our studies. These two have been reared from one or more polyphagous species of tephritid pests in the genus *Anastrepha*. We provide evidence that within the *Blepharoneura*/*Gurania* cucurbit system, the species of *Bellopius* diversify as host plant and host plant part specialists just as their tephritid hosts do.

Evolution of host use in cryptic species of aphid parasitoids

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Parasitic Hymenoptera (parasitoids) are extremely diverse and parasitize a wide variety of host species. Differences in ability to use different host species may have provided strong selection for specialization, divergence, and thus speciation in parasitoids. We report here on the evolution of host specificity in a complex of cryptic species of aphid parasitoids. We address these questions: Does the pattern of host use differ among species in this complex? If so, when we map host use map onto a molecular phylogeny of the complex, is host use phylogenetically conserved, so that speciation is rarely associated with changes in host use, or are host use changes associated with cladogenesis, as expected if changes in host use have driven speciation? To answer these questions, we measured host use by six species from eight populations in the *Aphelinus varipes* complex (Hymenoptera: Aphelinidae), mapped their host use onto a molecular phylogeny, and tested the relationship between genetic distance and distance in pattern of host use. We measured parasitism of seven aphid species in five genera and two tribes on four host plant species. The pattern of parasitism of aphid species varied greatly among parasitoid species and somewhat between parasitoid populations. For most parasitoid species, some aphid species were heavily parasitized and others were parasitized either rarely or not at all. Neither host plant species nor taxonomic proximity of aphid species delimited which aphids were parasitized. Although sister species of parasitoids showed similar parasitism of some aphid species, they showed very different parasitism of other aphid species. The differences in host use between these closely related species suggests that changes in host use may have sometimes been involved in speciation. In addition, some members of the complex appear to be specialists on particular aphid species, while others are generalists or at least have a wider host range. Understanding the evolution of host use in parasitoids, and the degree to which parasitoid species are specialized in their ability to utilize host species, are important in biological control, for example, in predicting the potential impact (or non-impact) of introduced species on non-target hosts.

**Biology and morphology of immature stages of some species of Eulophidae
(Hymenoptera: Chalcidoidea), parasitoids associated with leafminers
(Lepidoptera: Gracillariidae and Gelechiidae)**

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Objects of research are two ectoparasitoids gregarious *Minotetrastichus frontalis* (Nees, 1834) (Tetrastichinae) and solitary *Pnigalio soemius* (Walker, 1839) (Eulophinae) and one endoparasitoid *Chrysocharis laomedon* (Walker, 1839) (Entedoninae). Species proved to be a larval-pupal parasitoid of *Phyllonorycter issikii* (Gracillariidae), which is associated with *Tilia* sp. and of *Chrysoesthia sexguttella* (Gelechiidae), associated with *Chenopodium album* L. A total number of observations were 1170. The fact the eggs of both ectoparasitoids might be laid beside host larva was documented for the first time. The biology and morphology of early larval instars are described in detail. First instar larva of ectoparasitoid with protuberances on II – IV thoracic and VI, VIII, X and XII abdominal and XIII anal segments from both sides and with long hairs are described. The larva uses these protuberances with hair for moving in the leaf mine and jumps onto the surface of the host. Second instar larva has lost the long hair on the protuberances. The larva is passive and can parasitize host larvae of the fourth-fifth instar or prepupae. Third instar larva has small protuberances with short trichoid setae that

may have a sensory function. The larva is feeding on haemolymph and the soft cuticle of the host. Fourth instar larva also has protuberances with trichoid seta. We observed active process of histogenesis at the end of this instar. Pupa of *M. frontalis* and *P. soemius* attaches to the leaf by filament in mine of host. Four larval instars and three moults in *M. frontalis* and *P. soemius* was discovered. The total development of gregarious *M. frontalis* is 11.2 days and of solitary *P. soemius* is 20.6 days. Gregarious parasitism exhibited by brood of larvae of *M. frontalis* (2-5 individuals). We have observed siblicide behavior between third instar larva and fourth instar larva of *P. soemius*. Hyperparasitism was discovered in second instar larva of *M. frontalis* on pre-pupa of *Ph. issikii*. Multiparasitism is also present.

Solitary endoparasitoid *Chrysocharis laomedon* has three larval instars and two moults. The larva of the first-third instars have segmentation are not clearly discernable visible. The larvae feed on the haemolymph. The size of the last instar is 3 times as long as the first instar. Third instar larva pupates completely free of host larva. The pupa is without filament and may be found beside the remnants of the host. Total development is 20.5 days. Hyperparasitism was not observed.

M. frontalis and *C. laomedon* are subjected to the same environment inside the mine, with the same temperature and humidity. *C. laomedon* has changed from the typical behaviour of endoparasitoids and its larva and pupa develops external, i.e. on the skin of the host larva. Developing inside the mine of *P. issikii*, ectoparasitoids and endoparasitoids have similar behaviours but a different strategy of parasitism; the first allow the host to develop, the second stop it from developing. The solitary endoparasitism that was discovered during our investigation is evolutionarily more primitive than gregarious ectoparasitism and its larval stages have a long period of development.

Four years later: the Hymenoptera Anatomy Ontology, an overview and call for participation

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The Hymenoptera Anatomy Ontology (HAO) is introduced. We overview the core data to be collected and integrated into the HAO and the justification for our approach. The existing data in the HAO includes over 3500 labels, 1500 ontological classes (tied together with over 1600 logical relationships), and 950 references. Gaps in the present coverage (e.g. venation) and other complex issues (e.g. unifying references to sculpture) are overviewed. The day-to-day utility of the HAO, i.e. how our ontological data can be accessed by hymenopteran researchers, is discussed. We introduce several new mechanisms, both presently realized and planned, by which the hymenopterist community can interact with the HAO, including methods for annotating existing data and proposing new additions, integrating the HAO into taxonomic publications, and constructing data subsets for personal use.

The Yellow-Legged Hornet *Vespa velutina* (Hymenoptera: Vespidae): a new invader in France

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The Yellow-Legged Asian Hornet, *Vespa velutina* (Hymenoptera: Vespidae) is an invasive species recently introduced in France. Within a few years, this hornet spread throughout a great part of south-west France and became rapidly famous, because of its large nests usually located in tree tops as well as its propensity to prey on honeybees in front of hives.

Since the first record of this species in France in 2004, the invasion is monitored, mainly through nest recording. After six years, the hornet appears to be well acclimated to the French ecosystems, invading both natural and urbanized environments.

The Yellow-Legged Asian Hornet that is originally widespread across South-east Asia, from Pakistan to China and Indonesia, presents a large range of color variations. The population introduced to France belongs to the *nigrithorax* form, which is distributed from Pakistan to South and East China. The most probable hypothesis of its introduction, (through importation of bonsais from East China) is being tested using genetic markers. A first predictive model using climatic data from the native and invaded areas suggests that *V. velutina* could acclimatize to a large part of Europe as well as various other countries around the world.

The genetic diversity of the invasive population, the colony development and the predation behavior of the hornet are being studied as well as the defense of French honeybees against this new enemy. Honeybees, however, are not the only preys of this invader. A diet study based on the flesh pellet brought back to the nest by the workers revealed a very wide prey spectrum, from social Hymenoptera and flies to dead vertebrate flesh. First results showed that honeybee ratio varies among preys according to habitats, reaching about 1/3 in rural areas and up to 2/3 in urban areas. The impact of *V. velutina* on local biodiversity is being investigated by evaluating the biomass of preys required to feed a colony.

Although its presence in France has no significant impact on public health, the Asian hornet locally significantly threatens beekeeping. The eradication of the hornet being no longer possible, effective and selective trapping methods are being developed in order to protect beehives at best.

BracBank – a specimen and taxon-based program to facilitate taxonomic research

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The goals of BracBank are twofold. 1. To make specimen-based data and images available through a continuously updated taxonomic frame-work. 2. Use the data to generate descriptions, diagnoses, interactive illustrated keys, distribution maps, and nomenclatorial summaries; in short all of the elements necessary for revisionary publications. BracBank is still in development but many functionalities are now operating and colleagues are invited to use it as a platform for their taxonomic research. The system allows individuals anywhere in the world to enter and edit information while password protection prevents misuse. The taxonomic frame-work is a crucial part of the system, as it removes the need for taxonomic editing and prevents spelling errors. All 24,936 braconid names at all taxonomic levels are incorporated.



DNA barcoding the parasitic wasp subfamily Doryctinae (Braconidae) from the Chamela-Cuixmala Biosphere Reserve, Mexico

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The Doryctinae represents one of the largest braconid subfamilies, mostly comprising idiobiont ectoparasitoids of xylophagous and bark boring Coleoptera larvae, and containing a number of speciose, morphologically heterogeneous genera. Here we show the preliminary results of an ongoing DNA barcoding study of the doryctine fauna from the Chamela-Cuixmala Biosphere Reserve in Mexico, a region mostly composed of tropical dry forest. DNA barcoding sequences from 407 specimens collected during three field trips were analysed using the general mixed Yule-coalescent (GMYC) model approach and the single threshold optimisation in order to delimit species from DNA sequences alone. Use of the above approach resulted in a total of 186 putative species that were assigned to 22 genera, 114 of which belong to the highly diverse, polyphagous genus *Heterospilus*. Sequences of the D2-D3 domain region of the 28S nuclear rDNA gene were also obtained for all the specimens in order to confirm the species boundaries indicated by the mtDNA marker. The results obtained helped to clarify cases where the indiscriminate use of highly homoplastic morphological characters led to the erection of non-monophyletic genera. This study highlights the urgent necessity of carrying out diversity studies with molecular tools in order to accelerate the process of species discovery in megadiverse groups of hymenopterans.

ABSTRACTS OF POSTERS

(* = in attendance)

Population dynamics of alfalfa weevil parasitoids in West Azarbaijan (Iran)

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Hypera postica Gyll. (Coleoptera, Curculionidae) is one of the most important pests in West Azarbaijan province of Iran. During 2007-2008 a survey on the population dynamics of natural enemies (parasitoids) of *H. postica* was carried out in two regions, Saadad (Chaldoran) and Shoot (Makoo). *Hypera postica* and other insects were swept weekly in both locations. Hundred sweepnet hits/location/sample were done in early morning, taking into account the pest behaviour. Collected insects were separated and counted and the density of *H. postica* larvae/sample was evaluated. An aspirator was used to collect adults of *H. postica* from the soil surface. Results showed, that *H. postica* was observed for the first time, from both, Makoo and Chaldoran, by mid-April and by mid-May, respectively. The population peaks of *H. postica* were recorded in Makoo and Chaldoran by mid-May and mid-June, respectively. The population density of *H. postica* in sampled two regions was different and also showed that the environmental conditions were better in 2008 than 2007.

A survey of three important parasitoids, *Bathyplectes curculionis* Thomson, *Bathyplectes anurus* Thomson and *Oomyzus* (= *Tetrastichus*) *incertus* Ratzeburg, showed nearly the same population density for all 3 species. The highest and lowest population densities were observed for *B. anurus* and *O. incertus*, respectively. Population peaks for *B. curculionis* and *B. anurus* were recorded in Makoo for May 20th and June 7th, respectively. In Chaldoran, population peaks of *B. curculionis* and *B. anurus* were observed on June 20th and June 7th. The correlation coefficient was calculated between *H. postica* and *B. anurus* ($R^2=0.841$). Population densities of predators in 2007 and 2008 were similar to those of parasitoids. The population density of *Coccinella septempunctata* was higher than of *Chrysoperla carnea*, both, in each of two years and each of two sampled regions.

Comparing wing shapes of the subspecies *Bombus* (*Thoracobombus*) *sylvarum citrinofasciatus* and *Bombus* (*Thoracobombus*) *sylvarum daghestanicus* (Hymenoptera: Apidae: *Bombus* Latreille) using landmark based geometric morphometrics

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Color patterns of bumble bees (*Bombus* (s.l.)) can be either similar or rather variable within species. The fact that different individuals within some species may show resemblance with a series of other species makes it hard to identify bumble bees according to their coat colors. This situation is regarded as a problem in bumble bees as it may lead individuals which look almost the same in color to be identified as the same species by mistake. Geometric morphometrics techniques are quite useful in analyzing shape differences. It is considered as a powerful tool in taxonomical studies in bumble bees by being advantageous compared with

other methods. *Thoracobombus* (s.str.) is a subgenus studied under the genus *Bombus* and it is one of the most diverse subgenus which is characterized by 14 species in Turkey. *Bombus* (*Thoracobombus*) *sylvarum* traditionally has two subspecies which are ssp. *citrinofasciatus* and ssp. *daghestanicus*. While ssp. *citrinofasciatus* shows distribution in western Turkey, ssp. *daghestanicus* appears both in eastern Turkey and in the southern part of Central Anatolia. The fact that these two subspecies are quite isolated from each other in distribution and that they show different coat color patterns makes it certain that they are clear subspecies. In this study, it was aimed to show if geometric morphometrics could be successful enough to distinguish them from each other. Wing shapes of these two subspecies were examined together with the other 11 species from the same subgenus using 20 landmarks. Analyses were carried out on 133 females and 42 males collected from various localities in Turkey. Cartesian coordinates were obtained from the fore wings of the specimens. Procrustes analysis was conducted to remove non-shape variation. Then PCA and CVA were conducted to examine the distribution of all species. Differences in wing shapes were shown on deformation grids. Mean values of all the specimens were calculated and SAHN clustering was performed to obtain dissimilarity trees. According to the results, these two subspecies were found to be significantly different from each other. Their deformation grids showed almost no deformation indicating that these two subspecies are similar according to their wing shapes.

Aligning insect anatomy ontologies: identifying congruence between Hymenoptera and Diptera

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Ontologies represent the formalized terminology (lexicon) of a domain of interest, and the logical relationships between terms (e.g., wing *is_a* appendage; ocellus *part_of* head). While there exist many types of ontologies, anatomy ontologies are becoming an important resource for studying phenotypic variation and genetic influences on morphology within a group of organisms. Thus far, insect anatomy ontologies have only been developed for Diptera, specifically the model organism genus *Drosophila* and the family Culicidae (mosquitoes). The Hymenoptera Anatomy Ontology (HAO) is a burgeoning insect ontology aimed at describing/relating the morphology of the hyper-diverse order Hymenoptera. Here we describe and discuss the ontological similarities (exact and inferred) between the HAO, FBbt (*Drosophila* gross anatomy ontology) and MA (mosquito adult gross anatomy ontology). We calculate these matches using existing ontology alignment software and novel matching tools, both of which are examined for their utility. Our results are persisted in the HAO database as a set of cross references which will inform future comparisons between taxa. We also compare major areas of incongruence between current insect anatomy ontologies and possible explanations for these disparities.

A new mechanical modification of an insect manipulator

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An improved design of stereomicroscope manipulator for observation of pinned or mounted insects is presented. The device allows movement of the observed object around three perpendicular axes in the field of vision at all magnifications of the stereomicroscope. The main improvement of this new modification is positioning of the guiding knobs for rotating around two axes next to each other, allowing faster and easier manipulation of the studied object. The device enables easily reaching a precession deviation in the intersection point of axes up to 0.5 mm in the process of assembling.

Bizzare wasps on the island New Caledonia – a revision of the genus *Arpactophilus* (Hymenoptera: Apoidea)

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The genus *Arpactophilus* belongs in the Pemphredonini within the digger wasps (Hymenoptera: Apoidea) and occurs exclusively in the Australasian region. It contains 43 described species and is morphologically highly diverse, which prompted Arnold Menke to speak of an ‘evolutionary explosion’ of *Arpactophilus* in that area. In the present project, I revised *Arpactophilus* from New Caledonia, where 17 species were currently known. I discovered 24 undescribed species, which brings the total number of *Arpactophilus* on New Caledonia to 41. Each species is diagnosed and described in detail. A remarkable new character is that in contrast to the majority of digger wasps, apparently including Australian species of *Arpactophilus*, the males of the New Caledonian *Arpactophilus* have 12 instead of 13 antennomeres.

Body weight change during the development of solitary wasp *Symmorphus allobrogus* (Hymenoptera: Vespidae: Eumeninae)

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We studied the change of body weight of eumenine wasp *Symmorphus allobrogus* during the development from egg to imago.

The brood cells for study were obtained using reed trap-nests in three localities of Lithuania in 2000-2006. Newly built nests were taken from the trap-nests every 7-14 days and dissected. We weighed the provision in fresh brood cells and measured weight and head width of wasp larva in older ones. A part of the developing wasp larvae was weighed and measured repeatedly every second day until the start of cocoon formation or defecation. Prepupae were reactivated in refrigerator at +4°C. We weighed the prepupae before and after reactivation, as well as pupae and freshly emerged imagos.

Larval development of *S. allobrogus* included 5 instars; the growth of body weight was exponential. The larvae of the 3rd, 4th and 5th instars could be reliably distinguished by their head width. Male larvae of all instars had significantly smaller average head width than female larvae.

On average, the female cells were provisioned with 27% larger amount of prey than male cells. However, the mean weight of fullgrown female larva was 37% larger than that of male larva. The relationship between larval body weight and weight increment per day was significantly different (Chow test), as well: female larvae of a certain weight had larger weight increment per day than male larvae. Thus, female larvae of *S. allobrogus* were growing faster and gaining more body weight per weight unit of consumed provision than male larvae.

Relative loss of body weight of larva during spinning the cocoon and defecation was significantly higher in male than in female. In contrast, the relative loss of body weight during reactivation was significantly higher in prepupae of females than in males.

Dependence of brood cell length on nesting cavity width in xylicolous solitary wasps of genera *Ancistrocerus* and *Symmorphus* (Hymenoptera: Vespidae: Eumeninae)

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The application of trap-nests for the studies of cavity-nesting Hymenoptera eventually implies a need for immediate nest identification using its structure. Possible nest characters that may be potentially useful for the separation of closely related species are body size-dependent metrical parameters of their brood cells.

We studied the dependence of brood cell length on nesting cavity width in ten cavity-nesting predatory wasp species. Five alternative hypotheses were erected and tested: a wasp adjusts the length of a brood cell depending on the width of the nesting cavity, (1) maintaining the volume of the cell more or less constant, or (2) maintaining the internal surface of the cell more or less constant, or (3) maintaining the area of the longitudinal section of the cell (product of its length and diameter) more or less constant, or (4) maintaining the perimeter of the longitudinal section of the cell (or the sum of its width and length) more or less constant; or (5) length of a brood cell is defined by the body length of wasp, and it does not depend on diameter of nesting cavity. We calculated the derived parameters of brood cells needed for testing the hypotheses and, applying correlation and linear regression, assessed the degree of fit of the actual data to the hypothesized dependences.

The results demonstrate that most (but not all) cavity-nesting wasp species have an adaptable nesting behavior: they build shorter brood cells in wider cavities. Out of ten studied species, only two wasps (*Symmorphus crassicornis* and *S. gracilis*) seem to build brood cells of random length for their brood of both sexes in nesting cavities of any suitable diameter. In the other eight species, the degree of such adaptability (quantified as a cell length – cavity width regression coefficient *b*) was statistically significant at least for the brood of one of sexes. The studied wasps seem to estimate and keep constant the sum or the product of length and width of a brood cell rather than its volume. This statement is supported by 13 out of 20 analyzed datasets, or by 8 out of 10 studied wasp species whose nest building behavior supports the hypotheses (3) or (4). In 3 studied wasp species, the datasets of cells with brood of different sex demonstrated dependences of cell length on nesting cavity width supporting different hypotheses. We conclude that metrical differences among brood cells of related cavity-nesting species, if present, are more likely to be found in the relation between their length and width than in their volume.

Assessment of anthropogenic impact at landscape scale using trap-nesting wasp and bee community in Europe

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The method of trap-nests for solitary Hymenoptera is more and more often used for assessment of state and changes in semi-natural and agricultural habitats. The authors of this project applied trap-nests for cavity-nesting bees and wasps placed on tree trunks and old buildings in 13 countries of Europe using possibilities of field site network of the EU FP6 project ALARM. The goal of the study was comparison of species composition of the trap-nesting Hymenoptera communities in semi-natural and agricultural landscapes and preliminary assessment of tolerance of these wasp and bee species to the anthropogenic impact at landscape level.

Results of the study demonstrate that there are no significant differences between the semi-natural and agricultural landscape in the abundance and species diversity of the communities of synanthropic cavity-nesting Hymenoptera occupying trap-nests placed on buildings. In contrast, the communities of the cavity-nesting Hymenoptera occupying trap-nests placed on tree trunks demonstrated significant differences between semi-natural and agricultural landscape. For instance, abundance of cavity-nesting Pompilidae and Crabronidae was significantly higher in semi-natural landscape than in agricultural one. Share of the nest cells with inquilines and parasitoids and the number of natural enemy species per host species in a trap-nest were significantly higher in semi-natural landscape, that is, the higher trophic ranks of the trap-nesting community were more abundant and diverse in the semi-natural landscape, in comparison to the agricultural landscape.

Comparing abundance of trap-nesting wasp and bee species in two landscape types, we found that some species (e.g. *Dipogon subintermedius*, *Trypoxylon figulus*, *Rhopalum clavipes* etc.) are significantly more often found in semi-natural landscape. On the other hand, a set of species was significantly more abundant in the agricultural landscape with dominating early succession stage habitats (e.g. *Ancistrocerus gazella*, *Symmorphus gracilis*, *Megachile centuncularis* etc.). We propose a preliminary “landscape naturalness index”, based on the ratio of the number of trap-nesting species related to semi-natural landscape to the number of those related to agricultural landscape, for further testing and elaboration.

Hymenoptera parasitoids of immature stages of Geometridae (Lepidoptera), associated with plants of a sub-native forest in the state of São Paulo, Brazil

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Larvae of Geometridae (Lepidoptera) were obtained from native understorey forest, interspersed with pine, on the campus of the Federal University of São Carlos, São Paulo, Brazil. Larvae were collected weekly by beating the vegetation on entomological umbrella, from March/2007 to May/2008 and April/2009 to April/2010. In the laboratory the larvae were kept in translucent plastic containers of 250 or 500 ml and fed with leaves of their respective host plants. The pupal stage and the emergence of adult moths or parasitoids

occurred in the same container where the larvae were kept. Head capsules of larvae of Geometridae, parasitized larvae and cocoons of parasitoids were properly preserved, allowing later identification of the hosts and their parasitoids. We collected so far 668 Geometridae specimens (21 species), of which 105 (8 species) were parasitized. The Braconidae, Microgastrinae and Ichneumonidae, Campopleginae were the most common parasitoids. *Macaria rigidata* (Geometridae) the most commonly species found, presented the largest number of Ichneumonidae parasitoid. *Diradops* sp. (Banchinae), *Neotheronia* sp. (Pimplinae) and *Jomini* sp. (Campopleginae) were first recorded as parasitoids respectively on the Geometridae *Macaria rigidata*, *Oxydia* sp. and *Prochoerodes* sp. Other information about the bionomy of the species are presented and illustrated. The material studied is deposited in collection of the Departamento de Ecologia e Biologia Evolutiva da Universidade Federal de São Carlos, São Carlos, SP, Brazil.

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Parasitic wasps of the Proctotrupeoidea, Platygastroidea and Ceraphronoidea in New Zealand: review and analysis

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We present an overview of the current state of knowledge of these three superfamilies of Apocrita in New Zealand based on published records and our accumulated unpublished experience from field work and examination of material in collections. Field collections made by sweeping and pan trapping in the cool, moist, temperate forests (the dominant habitat before human colonization) abound with individuals, particularly of the families Diapriidae and Platygastriidae. There are 101 named species across the three superfamilies but we estimate that there are ca 750 species awaiting description. The fauna is characterized by two distinct extremes, viz. a marked absence in NZ of large world genera on one side and a stunning speciation in several mega genera on the other. The bulk of species diversity lies in the Spilomicrini (Diapriidae: Diapriinae) and the Platygastriinae (Platygastriidae). Endemism at the species level is high (>90%) but tramp species are found in all families apart from the endemic Maamingidae. Strong Gondwanan relationships are found within the Proctotrupidae, Diapriidae (Ambositrinae, Belytinae), Scelionidae (*Archaeoteleia*) and Platygastriidae (Sceliotrachelinae) which has arisen from New Zealand's cataclysmic geological history.

Exotic fig pollinators and associates (Chalcidoidea: Agaonidae) of *Ficus* trees in Europe

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The family Agaonidae, represented by 6 subfamilies and about 757 species worldwide (Bouček 1988), contains chalcidoids associated with *Ficus* trees. Agaoninae are strictly pollinator wasps of figs (they are a coevolution model of the mutualistic interaction between pollinator insects and plants); other subfamilies includes inquilines / gall formers of figs or gall formers of other plant parts and also parasitoids of all previous groups. The family shows a distribution specially centred in the Afrotropical, Indo-Australian and Neotropical regions.

Three subfamilies and five species are known from Europe (Fauna Europea 2009): *Blastophaga psenes* and *Eupristina verticillata* (Agaoninae - pollinators of *Ficus carica* and *Ficus microcarpa*), *Josephiella microcarpae* and *Odontofroggata galili* (Epichrysomallinae - leaf gall former and fig gall former in *Ficus microcarpa*) and *Philotrypesis caricae* (Sycoryctinae - parasitoid of *B. psenes*).

A sampling work has been carried out on eleven species of ornamental *Ficus* trees in several cities of Eastern Spain and Balearic islands. Methodology combines both sweeping on the trees as collection of fig fruits. Results of this work are the record of seven species of Agaonidae, three of them (*Pleistodontes imperialis*, *Walkerella microcarpae* and *Philotrypesis emeryi*) are new for Europe; and the establishment of ten Agaonidae-*Ficus* relationships, seven are new cases for Europe and two of them (*Eupristina verticillata* - *Ficus benjamina* and *Pleistodontes imperialis* - *Ficus elastica*) are new additional cases. Other bibliographic information has been revised.

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Diversity of Heloridae (Proctotrupeoidea) in a protected natural area from Spain

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Heloridae (Hymenoptera: Proctotrupeoidea) contains twelve species worldwide, all of them included in the only one genus *Helorus*. The genus is represented by four species in the West Palaearctic region. Members of this family are parasitoids of larvae of *Chrysopa* species (Neuroptera: Chrysopidae).

The four European species (*H. anomalipes*, *H. nigripes*, *H. ruficornis* and *H. striolatus*) have been collected in a sampling work with a Malaise trap carried out in the Natural Park of "Tinença de Benifassa" (Valencian Community, Eastern Spain) during the three-year period 2005-2007. Specific identification characters are pointed out, phenology of each species is studied, and potential chrysopid hosts for the group are suggested.

This work has been supported by the Spanish Ministry of Education and Science and by European Regional Development Fund (ERDF) (Project CGL2004-02711).

Tracing the geographical origin of *Eupelmus vesicularis* and a molecular taxonomic analysis of the *Eupelmus vesicularis* species-complex

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Epelmus vesicularis (Retzius, 1783) is one of the most widespread and common Eupelmidae species in Europe. It is also present in North America, but here probably was accidentally introduced prior to the 19th century (Gibson 1990). It is also the only species of *Eupelmus* (*Macroneura*) in New Zealand (Bouček 1988), which suggests another introduction. A vast number of hosts from many insect orders are recorded in the literature for *E. vesicularis*. Among its more economically important hosts are the Hessian fly, *Mayetiola destructor* (Say) (Diptera: Cecidomyiidae) and jointworms (the larvae of *Tetramesa* spp., Hymenoptera: Eurytomidae), destructive pests of wheat. Another intriguing biological aspect of the species is that it reproduces by thelytokous parthenogenesis in North America but both sexes occur in Europe (Gibson 1990, Graham 1969). Because of the biological and morphological variability I suspected that more than one species might be included under what historically has been interpreted as *E. vesicularis* and initiated an integrated taxonomy approach to investigate this possibility. Cytogenetic (Fusu 2008) morphometric and allozyme data (Fusu 2010) showed that there are two species included under the name *E. vesicularis*. During these studies, further evidence gathered showing that it is possible that none of the two cryptic species detected so far is the true *E. vesicularis*. Current work, using one nuclear (ITS2) and one mitochondrial marker (COX) aims at building a molecular phylogeny of *Eupelmus vesicularis* species-group in order to detect cryptic lineages and is investigating the hypothesis that New Zealand and North American populations of the *E. vesicularis* species complex are in fact of Palearctic origin and represent naturalized species introduced to these areas in historic times.

The importance of morphological characters in the taxonomy of egg-parasitoids of the family Trichogrammatidae (Hymenoptera, Chalcidoidea)

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The family Trichogrammatidae includes over 830 species from 83 genera which are exclusively small-sized (less 1,0 mm) egg-parasitoids of insects from 11 orders (Coleoptera, Lepidoptera, Diptera, Heteroptera, Hymenoptera, Orthoptera, Thysanoptera, Psocoptera, Neuroptera, Megaloptera, Odonata). The family Trichogrammatidae is divided into two subfamilies and four tribes: Trichogrammatinae (Trichogrammatini) and Oligositinae (Chaetostichini, Oligositini, Paracentrobiini).

The fauna of Palearctic region consists of such genera: eleven of Trichogrammini: *Asynacta* Foerst., *Mirufens* Gir., *Neocentrobia* Gir., *Neocentrobiella* Gir., *Neolathromera* Ishii, *Ophioneurus* Ratz., *Poropoea* Foerst., *Pterandrophysalis* Now., *Soikiella* Now., *Trichogramma* Westw., *Trichogrammatoidea* Gir.; one of Paracentrobiini: *Paracentrobia* How., six of Oligositini: *Doirania* Waterst., *Epoligosita* Gir., *Megaphragma* Timb., *Oligosita* Walk., *Prestwichia* Lubb., *Pseudoligosita* Gir., fourteen of Chaetostichini: *Aphelinoidea* Gir., *Bloodiella* Now., *Chaetosticha* Walk., *Chaetostrichella* Gir., *Lathromeris* Foerst., *Lathromeroidea* Gir., *Lathromeromyia* Gir., *Monorthochaeta* Blood, *Tumidiclava* Gir., *Ufens* Gir., *Ufensia* Gir., *Uscana* Gir., *Xiphogramma* Now., *Zagella* Gir.

The combination of various morphological characters are used for genera and species identification of Trichogrammatidae: presence and distribution of setae on fore wings; fore wings venation; ratio of width to length of fore wings; number of setae on marginal vein; presence of large sensillae between marginal and submarginal vein; setae between linearly arranged setal tracks; presence of RS1 vein; funicular and clava segmentation; ratio and size

of funicular segments; presence of placoid sensillae on funicle and clava; segmentation of maxillary palps; shape and form of hind tibial spur; setae, sculpture and shape of mesoscutum and scutellum; shape and length of ovipositor; shape of metasomal tergites; and structures of male genitalia.

Large number of morphological structures of male genitalia are used for the identification of *Trichogramma* species: ratio of width to length of genital capsule; constriction of genital capsule and intervorsellar process; shape of parameres; form and position of apex of parameres; position of base of vorsellae and parameres; shape of vorsellae; width of vorsellae; presence and shape of apical process of vorsellae; level of extension of vorsellae beyond parameres; sclerotization and separation of vorsellae; presence and shape of intervorsellar process; shape of ventral ridge; presence of dorsal ridge and dorsal lamina; shape of posterior extension of dorsal lamina; shape of shoulders at base of dorsal lamina; shape and subdivision of aedeagus; ratio of aedeagus length to genital capsule length and apodemes length. The analysis of morphological characters together with a new molecular data and discovery of new biological information can greatly improve and justify current taxonomical position for many species of Trichogrammatidae.

Life-cycle of a fig wasp *Blastophaga psenes* L. (Hymenoptera, Agaonidae) as obligate pollinator and gall-former in *Ficus carica* L. (Magnoliopsida) in Crimea, Ukraine

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The study of biology of agaonid wasps (Agaonidae) reveals a great evolutionary success of the fig and fig wasps pollination mutualism. Figs and fig wasps represent one of the best examples of species-specific mutualism and coevolution. The community of "figs-fig wasps" can be considered as a model system for coevolution and phylogenetic study. Life cycle of fig wasp *Blastophaga psenes* (L.) (Chalcidoidea, Agaonidae) as example of coevolution of obligate symbionts-pollinators and parasitic agaonid wasps with fig trees (*Ficus carica* L.).

Material of *B. psenes* was collected in the fig tree plantations of the State Nikita Botanical Garden (Crimea, Yalta, Ukraine) during 2006-2009. New original data on life cycle, larval development, adult behaviour and phenology of three generations of *B. psenes* as an obligate pollinator of edible fig trees (*Ficus carica* L.) in the Crimea (Ukraine) were received by the author. Females and males of *B. psenes* induce a gall and develop from eggs into adults inside syconia on male fig trees (caprifigs). It was observed that in the Crimea the larvae of *B. psenes* overwinter in the galls inside caprifigs and pupate in the second or third weeks of April. The copulation of males and females occurs inside the caprifigs. The males emerge before the females and gnaw an exit hole from inside the caprifig through the scales of the stigma. The females escape through this hole later. In the spring (April-May) the females of 1st generation *B. psenes* lay eggs in short-style pistils inside the inflorescence of caprifigs. In June-July 2nd generation *B. psenes* females emerge from the caprifigs and migrate to pollinate long-style pistils inside the inflorescence of female fig trees. Near the end of this period of pollination (July-August) some 2nd generation females of *B. psenes* oviposit in the short-style pistils. In September-October females of the final 3rd generation of *B. psenes* lay eggs inside the caprifigs and the larvae of this generation hibernate until the following spring.

The emergence of 1st generation *B. psenes* was observed from the end of April up to the end of May (21.IV.-26.V.2007 and 28.IV.-30.V.2008). The 2nd generation *B. psenes* was

observed from the end of June to the end of July (25.VI.-26.VII.2007 and 02.VII.-25.VII.2008). The 3rd generation of *B. psenes* was observed from the end of September to the beginning of October (30.IX.-10.X.2007 and 03.X.-14.X.2008). The earliest dates of oviposition of *B. psenes* were recorded as: 1st generation – 21-28.IV., 2nd – 30.VII.-02.VIII, and 3rd – 30.IX.-03.X. Oviposition was observed to continue for: 1st generation 32-35 days, 2nd – 9-16 days, and 3rd – 11-12 days. The earliest dates of pollination of female fig trees by 2nd generation of *B. psenes* was noted as 25.VI.-02.VII. and continued for 23-31 days. The total period of development of each of the three generations of *B. psenes* were: 1st generation – 192-236 days, 2nd – 31-67 days, and 3rd – 65-77 days. One species of agaonid wasp, *Philotrypesis caricae* (L.) (Agaonidae), being the parasitoid of *B. psenes* was recorded in the Crimea on *F. carica*. It was observed that females of *Ph. caricae* do not participate in the pollination of *F. carica* trees. The larvae of *Ph. caricae* develop as parasitoids of *B. psenes* in the galled inflorescence of caprifigs of *F. carica*. The females of *Ph. caricae* have a very long ovipositor that exceeds the length of the female's body. Females of *Ph. caricae* penetrate the rounded galls inside young caprifigs and lay eggs inside the larvae of *B. psenes*.

Flower visiting by Sand Wasps in southern Africa

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The synthesis of the knowledge of the natural history and behaviour of the Sand Wasps by Howard Evans and Kevin O'Neill (2007) indicates that little has been published on flower visiting by Sand Wasps. This being so it seems of interest to examine the flower visiting records associated with the Albany Museum collection of Sand Wasps (Crabronidae: Bembicinae, as recognized by Pulawski 2010). The majority are derived from the purposeful collecting by Friedrich and Sarah Gess during the course of their study of aculeate wasps and bees in the semi-arid to arid areas of southern Africa.

The genera represented are *Bembix* (13 spp., 394 records), *Hopliosoides* (1 sp., 19 records), *Handlirschia* (1 sp., 10 records), *Kohlia* (1 sp., 117 records), *Bembecinus* (18 spp., 344 records), *Stizus* (6 spp., 184 records) and *Stizoides* (3 spp., 7 records).

In the semi-arid to arid areas of southern Africa these genera most commonly visit small flowered readily accessible flowers of one or more of the families, Asteraceae, Fabaceae (*Acacia*), Amaranthaceae, Molluginaceae, Aizoaceae (non-Mesembryanthema), Apiaceae, Nyctaginaceae, Zygophyllaceae, Celastraceae and Scrophulariaceae (in particular *Selago*), all generalist flowers. Some *Bembix* species are in addition not uncommon visitors to Aizoaceae (Mesembryanthema) and Apocynaceae (*Asclepias*).

No species of Bembicinae are broadly polyphagous as are some bees, most notably in the family Apidae. None are specialists. As regards pollination services, all transport pollen and can be considered to be amongst the potential pollinators of the generalist flowers. *Bembix* and *Stizus*, visiting flowers of Apocynaceae, like spider hunting wasps (Pompilidae) visiting these flowers, transport pollinia giving them the potential to be pollinators. Most 'mesems' are most frequently and dependably pollinated by pollen wasps (Masarinae) and bees, however, *Bembix* do have the potential to be additional pollinators of the 'mesem' flowers that they visit.



Chromosomes of *Xyela julii* (Xyelidae) and karyotype evolution in the order Hymenoptera

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The order Hymenoptera is the largest group of haplodiploid insects with the predominantly arrhenotokous mode of reproduction. Chromosomes of approximately 1800 species of the Hymenoptera are studied up to now. These species belong to all traditional major subdivisions of the order, namely: the suborder Symphyta (about 400 studied species) as well as Parasitica (more than 400 studied species) and Aculeata (about 1000 studied species); two latter groups are usually merged into the suborder Apocrita. Although a few attempts of phylogenetic analysis of chromosomal diversity in the order were made since the 1970s, karyotype structure of the most ancient hymenopteran family Xyelidae which was detected in the fossil record since the middle of the Triassic, was previously unknown. I have managed for the first time to study chromosomes of the common European species of this family, *Xyela julii* (Brébisson). This species has $2n = 50$; most chromosomes are relatively small subtelocentrics and acrocentrics. These data confirm an assumption that a number of moderate reductions in the chromosome number (to $n = 18-20$ and less) through chromosomal fusions occurred within different groups of the Symphyta. These reductions, however, were more substantial (to $n = 7-10$ and less) in the superfamily Tenthredinoidea where large biarmed chromosomes predominate in many species. On the other hand, the superfamily Pamphilioidea is likely to have higher ancestral n values (20 to 26). A chromosome set with $n = 14-19$ is considered ancestral for the suborder Apocrita. A number of independent decreases in chromosome number (to $n = 10-11$ and then to $n = 4-6$ and less) were also detected in various groups of the Parasitica. The phenomenon of parallel reductions in the chromosome number within different groups of the order, especially within the Symphyta and Parasitica, represents an excellent example of the so-called karyotypic orthoselection. Although Aculeata are usually considered the best karyotypically studied group of the order, many aspects of the existing pattern of karyotype evolution within this group are still poorly known. For example, the highest chromosome number in the Hymenoptera, $2n = 120$ found in South American *Dinoponera lucida* Emery (Formicidae), was published just about two years ago. Moreover, according to the results of the preliminary phylogenetic analysis, the trend towards an increase in the chromosome number through centric fissions that is traditionally ascribed to the superfamilies Vespoidea and Formicoidea, is likely to have operated only at the level of certain genera and species.

Foodweb structure and diversity of parasitoid communities (Hym., Chalcidoidea) of herb gallwasps (Hymenoptera, Cynipidae) inducing galls on Lamiaceae

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We compiled literature data and unpublished qualitative and quantitative information on the parasitoid community (Hymenoptera Chalcidoidea) of herb gall wasps (Hymenoptera,

Cynipidae, "Aylacini") inducing galls on different species of plants of the family Lamiaceae. The host gall community is composed of 4 cynipid species inducing galls on stems, leaves and fruits of different species of *Glechoma*, *Nepeta* and *Salvia*. *Liposthenes glechomae* (Linnaeus, 1758) galling stems and leaves of *Glechoma hederacea* L.; *L. kernerii* (Wachtl, 1891) on fruits of *Nepeta ssp.*; *Neaylax salviae* (Giraud, 1859) on fruits of *Salvia lavandulifolia* Vahl. and *N. verbenacus* (Nieves-Aldrey, 1988) also on fruits of *Salvia verbenaca* L. The studied associated parasitoid community accounted 16 identified species belonging to six chalcidoid families as follows: Eulophidae (2), Eupelmidae (3), Eurytomidae (3), Ormyridae (2), Pteromalidae (2) and Torymidae (4) (Hym., Chalcidoidea). The two cynipid species galling fruits of *Salvia* share related parasitoid components although *Neaylax salviae* accounted more species. The parasitoid community associated to *Liposthenes glechomae* is more diverse than the one observed in *L. kernerii*. Semiquantitative food webs and quantitative data for the studied communities are presented.

Larval morphology of Pteromalidae (Hymenoptera, Chalcidoidea) parasitoids of gallwasps (Hymenoptera: Cynipidae) in Europe

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The large chalcidoid family Pteromalidae is one of the main components of the parasitoid community inhabiting cynipid galls (Hymenoptera: Cynipidae). About 50 pteromalid species taking part of that community have been recorded in the Palearctic. However knowledge of larval morphology and biology for most species is still poor. Here is presented a comprehensive and comparative study of larval morphology and biology of seven species of Pteromalidae parasitoids of gall wasps in Europe. The studied species were: *Rivasia fumariae* Askew & Nieves-Aldrey, *Stinoplus lapsanae* Graham, *Pteromalus bedeguaris* (Thomson), *Pteromalus hieracii* (Thomson), *Pteromalus isarchus* Walker, *Arthrolytus glandium* Boucek and *Cecidostiba fungosa* Geoffroy in Fourcroy. The studied species are representatives of the specific parasitoid components associated to different gall wasp food guilds: galls on herbs, shrubs, and galls on oaks. In the larval descriptive study special reference was made upon body shape, head capsule, mouthparts and mandibles and also on chaetotaxy of head. The terminal-instar larvae of all studied species is for the first time thoroughly described and illustrated with SEM pictures as well as diagnostic characters for the studied genera are provided. A key for the identification of terminal instar larvae of the seven species reared from cynipids galls is also given. Information, including new rearing records, is given on the larval biology of each species. Most studied pteromalid larvae are solitary ectoparasitoids of the host cynipid larvae with different trophic ranges from monophagous to polyphagous.

Diversity and distribution of the *Formica* species in Georgia (Hymenoptera: Formicidae)

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144 species of ants belonging to 4 subfamilies and 35 genera are recorded from Georgia. The most widely distributed and species-rich genus is *Formica* making up 18 species. The subgenus *Serviformica* is represented by 11 species, the subgenus *Formica* s.str. by 3 species, the subgenus *Coptoformica* - by 3 species, while the subgenus *Raptiformica* is represented by only 1 species. One species of the subgenus *Coptoformica* from the Great Caucasus is new for science. Queens of *Formica georgica* Seifert, 2002 are recorded for the first time. Maps of Georgia are presented showing the collecting sites for each subgenus. Faunistic similarity coefficients between the ants living in the different administrative regions and vegetation belts are estimated and the corresponding cluster diagrams are presented.

First record of *Wolbachia* in *Trissolcus* species (Hymenoptera: Scelionidae)

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The sunn pest *Eurygaster integriceps* Puton (Hemiptera: Scutelleridae) is a major pest of wheat and barley in wide areas of the near and middle east, west and central Asia, north Africa, and eastern and south Europe (Brown 1965; Critchley 1998; Praker *et al.* 2002). The pest feeds on both vegetative stages of the plant and maturing grain. Sunn pest infestations in some areas can lead to 100% crop loss in the absence of control measures. The current management strategy for this pest mainly relies on chemical control. In addition to the high cost, insecticides pose a risk to the balance of nature and resistance has developed to various types of insecticides. Thus new control methods are needed to diminish reliance on insecticides for control of this serious crop pest. Among natural controls the most promising of them are the egg parasitoids. The most important egg parasitoids belong to the genus *Trissolcus* Ashmead and *Telenomus* Haliday (Hymenoptera, Scelionidae). Especially frequently observed parasitoid species play a potential role in suppressing sunn pest populations below the economic threshold however, the success of the parasitoid varies among the regions and varies from year to year. Several studies have been conducted in order to improve the efficiency of the parasitoid. Since the success of a biological control is dependent on many factors, including mass rearing of the beneficial in the laboratory and release of the beneficial which can be a great concern. We hypothesized *Wolbachia* infection might affect the establishment of *Trissolcus* species. *Wolbachia* is an intracellular symbiont which causes reproductive alterations including cytoplasmic incompatibility, feminization, parthenogenesis and male-killing in many host insects (O'Neill *et al.* 1992; Bourtzis & O'Neill 1998; Werren 1997; Hurst *et al.* 2000). In this study we detected *Wolbachia* as an endosymbiont of *Trissolcus* species, for the first time, by using polymerase chain reaction (PCR) analysis. We used universal primers of *wsp* gene encoding a surface protein of *Wolbachia* in PCR amplifications. After cloning PCR products we designed new primers which are specific to *Wolbachia* harbored in *Trissolcus* species. Using species specific primers we scanned *Trissolcus* species including *T. festiva*, *T. grandis*, *T. simoni*, *T. semistriatus*, *T. vassillievi*, *T. rufiventris* and *T. flavipes* in terms of *Wolbachia* infection. *Wsp* gene sequences of different parasitoids have been reported. With this study *Wolbachia* infection status of various *Trissolcus* species was recognized. Further cross mating



experiments should be done in order to learn more about the role of *Wolbachia* in cytoplasmic incompatibility.

**Some biological aspects of a seed pest wasp, *Bruchophagus astragali*
(Hym.: Eurytomidae), in rangelands of Chaharmahal & Bakhtiary province of Iran**

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The most important forage plants in rangelands of Chaharmahal & Bakhtiary province of Iran belong to the family Papilionaceae. The knowledge of the main factors that affect these valuable plant species is important for their management and maximum decreasing of the damage level. A survey carried out during 2002-07, showed that the eurytomid wasp, *Bruchophagus astragali*, is one of the most important seed pests of plants in the Papilionaceae family. This insect was reported for the first time by the authors from Chaharmahal & Bakhtiary province in 2004. The wasp lays eggs into seed pods, the hatched larvae feed in seeds and by the end of their developing entirely consume the seed. The infected seed pods were collected from rangelands and adults were reared under the laboratory conditions. Different species of Papilionaceae were proposed to the reared adults and the results indicate that *B. astragali* were active on plants from all genera of Papilionaceae, therefore, *B. astragali* is an oligophagous pest. The most important natural enemy of this pest appeared to be a parasitoid chalcid wasp from the genus *Tetrastichus* sp (Chalcidoidea: Eulophidae), an ectoparasitoid of larvae. The parasitism rate of *B. astragali* by this parasitoid was 9- 13%.

**New data on the occurrence of stephanids (Hymenoptera, Stephanidae)
in Turkey and Greece**

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Stephanidae is a small cosmopolitan family occurring mostly in tropical and subtropical forest ecosystems, where these idiobiont parasitoids are associated with wood boring beetles. In the Palaearctic the family is predominantly known from the southern part of the region. Stephanids are rare in collections and only *Stephanus serrator* Panzer is recorded from many countries (Fauna Europaea). From Turkey, where the diversity of potential hosts of stephanids is as high as or higher than in Europe, stephanids have been recorded only recently (Yildirim & Kolarov 2006). Similarly in Greece only the most common *S. serrator* has been listed so far. In the present work some results of collecting and rearing stephanids are presented. Three species are new for Turkey: *Megischus anomalipes* Foerster, *S. serrator*, and *Afromegischus gigas* (Schletterer) as well as a new record of *Foenatopus turcomanorum* Semenov. *M. anomalipes* is recorded as new for Greece. Data on host and habitat are presented for some species.



Research of the family Ichneumonidae in the Czech Republic

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The family Ichneumonidae is one of insufficiently explored insect families in the Czech Republic (CZ). The total number of species has been estimated as 3,000; however, the checklist, which is currently under preparation, lists only approximately 2,000 species. A regularly updated checklist version is available online at <http://hymenopteracz.sweb.cz/>. Many individuals found within the CZ territory are dispersed in foreign museums and private collections. Should you have any information about species not included in the checklist, please let me know.

The family Ichneumonidae has been studied intensively in the Czech Republic only by Frantisek Gregor sen. during the first half of the last century and Josef Sedivy in the second half of 20th century and at the beginning of the 21st century. In the forties and fifties of the last century the Ichneumonologist Radoslav Obrtel was very active, as well as Serhij Kolubajiv in the middle of the century who studied the importance of ichneumonids as parasitoids of forest insect pests. Currently, 2 – 3 researchers are extensively engaged in the research of this family in the CZ.

Predominant majority of historical collections of the family Ichneumonidae are located in the National Museum, Prague (collection of J. Sedivy and F. Gregor) and Moravian Museum, Brno. Smaller collections are found in the Silesian Museum, Opava; Crop Research Institute, Prague; Forestry and Game Management Research Institute, Strnady; and Museum of Eastern Bohemia, Hradec Kralove.

A systematically arranged collection can be found only in the National Museum, Prague, and in the Museum of Eastern Bohemia, Hradec Kralove. The other collections are gradually being classified in subfamilies. Only the individuals of the subfamily Rhyssinae have been determined in their entirety and entered in a database from all museum collections, and the subfamilies Acaenitinae, Agriotypinae and Collyriinae are about to be completed.

The occurrence and ecological demands of selected species will be presented at the conference.

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The resources of Trichogrammatidae and Mymaridae and their utilization in biological control in Xinjiang, China

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Based upon the extensive investigation of Trichogrammatidae and Mymaridae fauna in Xinjiang, China during 2001-2008, mainly collected by sweeping and further examination of mounted specimens in thousands of slides, 19 genera with 48 species of Trichogrammatidae and 16 genera with 54 species of Mymaridae were found and described, including new distribution records for China and new species for science.

Additionally, *Trichogramma pinto* Voegelé was found in much arid region (Fukang desert), and *Ufensia xinjiangensis* Hu et Lin is widely distributed in Xinjiang, which provide a scientific reference for the use of the native natural enemy to control pests in Xinjiang. The

biological characters of these two species were studied. The richest trichogrammatid and mymarid fauna is in Jungar basin where the fauna component is very complex. The Tarim basin species richness is lower, the fauna component is simpler. Species richness in Eastern basins is higher than in Tarim basin. The species richness in Tianshan Mountains is lower than in Jungar and Tarim basins mainly due to the inadequate collecting.

Xinjiang is the largest province in China, encouning 1/6 of total area. There are two large basins, many of them are oasis, with wide and flat land, it is beneficial to control the pest by natural enemy, especially for using *Trichogramma* for controlling *Helicoverpa armigera* and *Ostrinia furnalis*. For thirty years, the plant protection experts in Xinjiang (Yang Haifeng, Guo Wenchao, Ma Qi etc.) introduced *T. chilonis*, *T. pintoi* and *T. ostrinae* from Central Asia and inner land of China into Xinjiang, to control the dominant pest, *Helicoverpa armigera* and *Ostrinia furnalis*, but it was difficult for these species to adapt to the extremely dry and hot environment, so looking for the native species is the key to biocontrol the pest.

EOS, Revista ibérica de Entomología, soon available online

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Eos, the earliest Spanish magazine devoted to Entomology, had to be closed in 1994, after a life of sixty-nine year, due to budget adjustments of the CSIC, the Spanish Scientific Research Council. Now, thanks to a project funded by the institution itself, we are working on digitizing the contents of the 69 volumes of the journal in order to upload them to Internet.

In this communication we report the current status of our project and the website where the journal could be localized in a near future. We also offer details about the contents of the magazine as subjects, authors, geographic areas covered, descriptions of new taxa, and so on.

Contribution of *EOS, Revista Española de Entomología*, (1925-1994) to the knowledge of the Hymenoptera

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This communication presents an analysis of the articles about the Order Hymenoptera that were published in EOS during his 69 years of life. These papers constitute a significant volume in the magazine since they represent nearly the 20% of the total of 1201 articles published in it.

It provides data on the authors, types of research and contents of these works, the faunas and geographical areas considered, as well as the new taxa described and most relevant revisions.



Updates to the evolution of torymids (Hymenoptera: Torymidae)

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Torymidae is one of the middiverse group of chalcids (together about 650 described species worldwide classified into ca 70 genera). Up to now, phylogeny was reconstructed by Grissell (1995) based on morphological characters. He estimated two subfamilies (Megastigminae and Toryminae) and 7 tribes within Toryminae. Phylogenetic position of 7 genera is still unresolved and they are classified as incertae sedis. Most of the torymids are primarily ectoparasitoids of various gall makers (mainly of Cynipidae and Cecidomyiidae), mantids eggs or larvae of bees, phytophagous species are quite rare within subfamily Toryminae. On the other hand, the number of known species of Megastigminae are phytophagous species, mostly they belong to the genus *Megastigmus*. But there are also some genera of Megastigminae which are ectoparasitoids of various gall makers. It is generally supposed that Megastigminae is the more primitive than Torymidae and the phytophagous strategy is ancestral for whole family.

Based on sequencing of 28S rDNA of about half of known genera of torymids I have got evidence to support all estimated tribes. The subfamily Megastigminae seems to be really more basal to the rest of the family. All of tribes are also well supported but their position to each other is still unclear. The most basal tribe of Toryminae seems to be tribe Chalcimerini. Position of nearly all taxa published by Grissell (1995) as incertae sedis are classified based on 28S rDNA into known tribes. The phytophagy as ancestral strategy can not be refused, but there is new theory that phytophagy can be secondarily developed and the ancestor of torymids could be rather zoophagous.

Morphometrics and host information for the support of phylogenetic relations in genera *Microterys* Thomson and *Aschitus* Mercet (Hymenoptera: Encyrtidae)

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The systematic relationship between the encyrtid genera *Microterys* and *Aschitus* was investigated using a phylogenetic analysis based on 35 morphometric character traits scored from 26 species housed in the Museo Nacional de Ciencias Naturales, Madrid. The results of the analysis were combined with host information which was obtained from the Universal Chalcidoidea Database and ScaleNet. In all, 78 species of hosts have been recorded for 18 of the studied parasitoid species. Preliminary results show that *M. zarina* and *M. aeneiventris* should be transferred back to *Microterys* from *Aschitus*. A separate morphometric study indicates that *Aschitus incertus* should be regarded a new, subjective synonym of *Aschitus madyes*.



Preliminary investigation of Chalcidoidea in Hainan Island, China

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Hainan province is the southernmost and smallest province of China, located in the South of China Sea. There are many islands in Hainan province, of which the largest island is Hainan Island. Hainan Island is located in tropical areas south of the Tropic of Cancer, separated from Guangdong's Leizhou Peninsula to the north by a shallow and narrow strait. Investigation of Biodiversity of Hainan Island is a Basic research supported by the Ministry of Sciences and Technology of the China. This project is began four years ago and initiated in November 2006. The project planned as a five-year project, and the goal was to investigate and discover species including plant, Vertebrate, Invertebrates and Fungi in the Island. We collected 3 times once a year at different season and till now we had collected 5500 specimens of Chalcidoidea.

We found there are 16 families of Chalcidoidea distributed in Hainan Island. They are Agaonidae, Aphelinidae, Chalcididae, Encyrtidae, Eucharitidae, Eulophidae, Eupelmidae, Eurytomidae, Mymaridae, Ormyridae, Pteromalidae, Signiphoridae, Tanaostigmatidae, Tetracampidae, Torymidae, Trichogrammatidae. Among these, four families, Ormyridae, Signiphoridae, Tanaostigmatidae and Tetracampidae are newly recorded in Hainan Island.

There are 106 genus recorded (no include genus of Encyrtidae, Eulophidae and Agaonidae): 7 genus of Aphelinidae, 5 genus of Chalcididae, 3 genuse of Eucharitidae, 6 genus of Eupelmidae, 7 genus of Eurytomidae, 9 genus of Mymaridae, 1 genus of Ormyridae, 52 genus of Pteromalidae, 1 genus of Signiphoridae, 1 genus of Tanaostigmatidae, 2 genus of Tetracampidae, 9 genus of Torymidae, 3 genus of Trichogrammatidae. Among these, four families, Ormyridae, Signiphoridae, Tanaostigmatidae and Tetracampidae 85 genus of them are new records in Hainan Island, including 13 genus newly recorded in China (*Schizaspidia* Westwood, *Orasema* Cameron, *Plutarchia* Girault, *Ramdasoma* Narendran, *Epiclerus* Haliday, *Tetracampe* Förster, *Australoodera* Girault, *Rhynchotocida* Bouček, *Signiphora* Ashmead, *Apocynetrone* Bouček, *Aggelma* Delucchi, *Pseudocatolaccus* Masi, *Caenacis* Förster).

Till now, there are 142 species which had been identified. 92 species of them are new records in Hainan Island; including 39 species are newly recorded in China.

The project is still ongoing. There are probably 7-16 new species which will be described. Based on all the material which we collected, 10 percent of all the specimens is Pteromalidae, 70 percent is Eulophidae. The other 20 percent is material of all the other families. It shows that Pteromalidae, Eulophidae, Encyrtidae and Agaonidae are very richness in Hainan Island. The further taxonomic work will be focus on these families.

The Swedish Malaise Trap Project One step further!

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The Swedish Malaise Trap Project (SMTP) was launched in 2003 with the aim of making fresh material available for morphological and molecular research on insects, particularly poorly known groups such as the Hymenoptera and Diptera. The field part was concluded in 2006 and resulted in 1,900 samples (190 trap-years) containing an estimated 40 million specimens. Since then, the focus has been on sorting and sending out the material for identification and taxonomic research, and about 40 % of the material are sorted hitherto. The out-sorted insects have shown to be a real gold mine for entomologists and a network of professional systematists and amateur taxonomists are now working on the material.

The main goals for the SMTP is to (1) sort and distribute all the collected insects; (2) compile and make available species lists for the identified material; (3) build, adequately document and preserve our reference collection for future barcoding of the Swedish insect fauna; (4) analyze the efficiency of the SMTP in collecting the Swedish insect fauna to better estimate the size and composition of the fauna and to optimize future collecting efforts in Sweden as well as world wide; and (5) engage in outreach activities inspired by the results obtained in the project.

We estimate that at least half the Swedish insect species, probably more, are represented in the material. Species lists and reference material for DNA barcoding are already continuously returned and the results so far indicate that the material may contain up to 5,000 new Swedish species, more than 1,000 of which may be new to science. These results appear to support our initial guess that the SMTP would increase the known Swedish insect fauna from 25,000 to more than 30,000.

Only a few results reported so far by the SMTP specialists can be mentioned here. The richest single source of new additions to the Swedish insect fauna are the Phoridae (Diptera). The most recent tally of the megadiverse phorid genus *Megaselia* resulted in 800 morphospecies in the SMTP material, 523 of which are new to science. Highlights from the Hymenoptera include the reports of the ichneumonids *Cladeutes discedens* (Tryphoninae; genus new to Sweden), *Diacritus aciculatus* (Diacritinae; subfamily new to Sweden), and *Micromonodon tener* (Cryptinae; genus new to Sweden). Seventeen new species of the Meteorinae (Hym.: Braconidae), sixteen of which were undescribed, are discovered. In the Diplazontinae (Hym.: Ichneumonidae), 19 new species have been recorded from Sweden so far, four or five of which are new to science. In the Ichneumoninae, 28 new Swedish species have been recorded with 10 – 20 more expected. Five new Cheloninae (Braconidae) from Sweden and seven new Platygastriidae for science are also reported.

But even if these reports are impressive, they are based just upon a fraction of the collected insects. About 300 people have hitherto contributed in one way or the other to the project. Our guess is that when the project is done in the future, there will be maybe 300 more. Are you one of them?

Field observations on the defense and hunting behaviour of Pompilidae species (Hymenoptera: Insecta)

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This study was conducted at 8 sites determined in the south-west of Kars rural area between 2005 and 2008. During the study which was conducted between 9 am and 6 pm in a day,

female members of *Anoplius viaticus* (Linnaeus 1758) of Pompilidae family, which were caught at the sites marked with GPS, were marked and its hunting success, refinding the prey that was lost, and the number of nests dug on a daily basis were examined. The study has found out that, female members of pompilids Asilidae (Diptera: Insecta) family attacked directly, whereas the members of *Formica rufa* Linnaeus, 1761 attacked indirectly to pompilids. Obtained information is new about pompilids.

A review of the wasp genus *Lyroda* from Thailand (Hymenoptera: Apoidea)

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The apoid wasp genus *Lyroda* belongs in the Miscophini and comprises 25 described species from all regions yet. Typical *Lyroda* are inconspicuous, mostly black wasps. Previously only one species was known to occur in Thailand. A large number of *Lyroda* from Thailand recently collected by the Thailand Inventory Group for Entomological Research (TIGER) gives us the possibility to re-examine the diversity of *Lyroda* in Thailand and neighbouring countries. At least ten undescribed species were found among the TIGER specimens. On the basis of external morphological characters, the new species were compared with already described species and with the relevant literature.

The evolution of antennal courtship in parasitoid wasps of the subfamily Diplazontinae (Hymenoptera, Ichneumonidae)

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Because of their potential to cause reproductive isolation, characters associated with courtship behaviour are believed to play an important role in the diversification of life. In the species-rich insect order Hymenoptera, the use of the antennae during courtship is very widespread, but the reconstruction of its evolutionary history is obstructed by the lack of courtship data for most species.

Recently, we reported a new mode of antennal courtship in the parasitoid wasp *Syrphoctonus tarsatorius* where the male curls its antennae in double-coils around the antennae of the female. We developed a method to reproduce this movement in amputated antennae which allows retrieving information about antennal courtship from museum specimens. Applying this method to the parasitoid subfamily Diplazontinae, we obtain courtship data for 40 species. To reconstruct the evolution of antennal courtship in diplazontines, we compiled a molecular phylogeny based on two mitochondrial and two nuclear genes. With one exception, the resulting phylogeny confirms the current genus-level classification. Mapping the mode of antennal courtship on the phylogeny, we found that the mode of antennal coiling is tightly linked to the position of antennal structures connected to internal glands. Moreover, a single origin is most probable for both single- and double-coiling, and coiling has been lost on three separate occasions. These results suggest a low speed of evolution of this character and



contradict the hypothesis that antennal coiling had a major impact on the diversification of this subfamily.

Trophical links of Bumblebees (Hymenoptera: Apidae, *Bombus*) in Vologda Region of Russia

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There is a great species variety of vascular plants in Vologda Region: 1706 species of vascular plants are reckoned among 137 families. About 36% of them are entomophilous plants. The study of trophical links was carried out in 2001–2009. 4487 visits of 121 species of entomophilous plants reckoned among 36 families made by bumblebees were registered. The most numerous family in Vologda Region – *Asteraceae* – is the most frequently visited one, it was registered that its 26 species were visited by 28 species of bumblebees. We registered that 25 species of bumblebees visited 13 species of *Fabaceae*, 25 – 2 *Dipsacaceae*, 19 – 2 *Onagraceae*, 18 – 13 *Rosaceae*, 18 – 5 *Scrophulariaceae*, 16 – 12 *Lamiaceae*, respectively. *Centaurea pseudophrygia* (*Asteraceae*) and *Knautia arvensis* (*Dipsacaceae*) are the most frequently visited species of plants visited by 25 species of bumblebees each. 22 species of bumblebees were registered on *Vicia cracca* (*Fabaceae*), 20 – *Trifolium pratense* (*Fabaceae*), 19 – *Chamaenerion angustifolium* (*Onagraceae*), 16 – *Cirsium arvense* (*Asteraceae*), 15 – *Carduus crispus* (*Asteraceae*), 15 – *Rhinanthus minor* (*Scrophulariaceae*), respectively. The attractiveness index shows these plants are the most attractive for all species of bumblebees including rare ones.

The analysis of the spectrum of plants which are visited by bumblebees proved that the widest spectrum (31–52 species) is typical for 7 most numerous species of the region (out of 23 species of the regional species of bumblebees): *B. hypnorum*, *B. hortorum*, *B. lapidarius*, *B. lucorum*, *B. pascuorum*, *B. ruderarius* and *B. terrestris*.

The analysis of the preference of the certain bumblebees to the prevailing species of plants shows that *B. pratorum* and *B. hypnorum* prefer *Chamaenerion angustifolium*, *B. hortorum* – *Trifolium pratense*, *B. ruderarius* – *Vicia cracca*, *B. pascuorum* and *B. veteranus* – *Trifolium pratense* and *Vicia cracca*, *B. lucorum* – *Vicia cracca*, respectively.

Among 30 most frequently visited species of plants 23 species (77%) have a corolla of pink-violet range of colour, 6 species (20%) – yellow and 1 species – white. It is connected with the trichromatic system of colour vision of bumblebees.

Taxonomy of the genus *Eurypterna* with biological notes on *E. cremieri* (Ichneumonidae, Hybrizontinae)

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The genus *Eurypterna* is known from three species, *cremieri* (de Romand, 1838) from Europe and Japan, *rufiventris* Tobias, 1988 and *angustifacialis* Tobias, 1988 from Primorskiy Terr., Russia. They are relatively large in body size (more than 1 cm) and rarely collected. For distinguishing these three species, the following characters have been used: Ratio of width

and height of face; ratio of lengths of hind basitarsus and remainder of hind tarsus; body color; color of hind leg.

In October, 2008, many individuals of *E. cremieri* were found flying around an old tree, *Juglans mandshurica* var. *sieboldiana*, in Sapporo, Hokkaido, Japan. A colony of *Lasius nipponensis* Forel, 1912 was exist in the trunk of the tree and an ant runway was formed from a hole on the trunk to the ground about 1.4 m long. The females of *cremieri* were hovering over the ant runway and the males were flying around the tree. Copulation and newly emerged adults escaping from the colony through the hole on trunk were observed. In October 2009, oviposition was also observed at the same site.

In total, 17 females and 42 males of *E. cremieri* were collected there in 2008 and 2009. Examined these specimens, it was revealed that the characters which have been used to distinguish species, such as the ratio of width and length of the face and the ratio of length of hind basitarsus and remainder of hind tarsus, are only the differences between female and male. Moreover, the male holotype of *rufiventris*, the female holotype of *angustifacialis* and some additional specimens of *cremieri* were examined. As the result, it was concluded that *angustifacialis* should be synonymized with *cremieri*.

The biology of *E. cremieri* was revealed as follows by the observation from October 2008 to October 2009. In October, the host ant workers carry their larvae from the colony in tree trunk to the colony under ground. The female of *cremieri* hovers above the ant runway and when she finds a worker carrying a larva, she attacks it and lays one egg into the larva. In May, the ant workers carry their larvae from the ground to the tree trunk colony. And, newly emerged adults of *cremieri* escape from the colony in tree trunk from late September to October. Thus, the parasitoid is considered to grow in the colony in tree trunk. It is a mystery how this parasitoid grows up to such a big size, because the parasitoid is more than twice as long as its host in body length.

The separation of cereal aphid parasitoids, *Aphidius rhopalosiphi*, *A. uzbekistanicus* and *A. avenaphis* (Hymenoptera: Aphidiinae), using mt-DNA (COI) sequences

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Aphidius rhopalosiphi De Stefani and *Aphidius uzbekistanicus* Luzhetskii are a key solitary endoparasitoid species parasitizing cereal aphids in the West Palearctic. Owing to similarity of morphological characters and a similar host range pattern where cereal aphids are concerned, the identification of these two species has shown to be very difficult. In the present study, we analyzed phylogenetic relationships of two close related *Aphidius* species, *A. rhopalosiphi* and *A. uzbekistanicus* on the basis of sequence information of a fragment of the mitochondrial cytochrome oxidase subunit I (COI) gene. Individuals were obtained from 12 countries (Slovenia, Slovakia, Hungary, Serbia, Germany, Sweden, Poland, Czech Republic, Montenegro, Iran, Pakistan, and USA) with known hosts and host plants. The purpose of our research was to confirm the presence distinct species on the basis of preliminary morphological determined characters, followed by molecular analysis. The value of molecular techniques in the identification of closely-related parasitoid species is discussed.

Rare giants – A review of Leptofoeninae (Chalcidoidea: Pteromalidae) and discovery of the first *Doddifoenus* from Indomalaya

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Leptofoeninae is one of the smallest and least known of the 31 subfamilies of Pteromalidae (Chalcidoidea) recognized by Noyes (2010). Members of this subfamily are very rarely collected but morphologically are of special interest because of their very large body size and a number of character states that are uncommon in Chalcidoidea. Leptofoeninae comprises only two genera, *Doddifoenus* Bouček and *Leptofoenus* Smith (Noyes 2010). *Leptofoenus* Smith contains five extant species and is restricted to the New World. The first fossil species of *Leptofoenus* was recently described from Dominican amber dating back the age of the genus at least to the early Miocene. The genus *Doddifoenus* Bouček previously included two species restricted to Australasia (Papua New Guinea and Northeastern Australia). Here we present a remarkable new species of *Doddifoenus*, which was just recently described from Thailand and Laos (Krogmann & Burks 2009). *Doddifoenus wallacei* is the first species of the genus occurring west of Wallace's Line, and one of the longest known chalcidoid wasps. All specimens of *D. wallacei* were collected from naturally fallen trees in primary tropical rainforests. No host records are known for *Doddifoenus* or any other Leptofoeninae, but they are presumed to be parasitoids of wood-boring insects. Results from a detailed anatomical study of the mesosomal skeleton of *Doddifoenus* are presented and compared with characters analyzed previously (Krogmann & Vilhelmsen 2006) for Pteromalinae, Cleonyminae and other Chalcidoidea. The metafurcal arms in *Doddifoenus* are basally fused, like in some Cleonyminae, but are always separated in Pteromalinae. This may indicate a plesiomorphic condition in *Doddifoenus* and some Cleonyminae relative to the condition in Pteromalinae. Other metafurcal characters of *Doddifoenus* are highly derived, like the complete fusion between metafurcal arms and metapleural apodemes, which has not been found in any other chalcidoid species. The phylogenetic relationships between Leptofoeninae and the other pteromalid subfamilies remains an open question that needs to be addressed by a broad phylogenetic analysis.

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Contributions to knowledge of Pimplinae wasps (Hymenoptera, Ichneumonidae) from Brazil

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Pimplinae is the most biologically diverse group of Ichneumonidae associated with a wide range of hosts, comprising about 1,500 species, most of them ecto- or endoparasitoids of holometabolous insects. *Hymenoepimecis*, *Ticapimpla* and *Schizopyga* pertaining to polysphincta genus-group, formed by 21 genera composed exclusively by koinobiont ectoparasitoids of spiders. The material was collected from their hosts, using Malaise traps, sweeping the vegetation and comes in São Paulo, and Bahia, States of Brazil. We described recently five new species of *Hymenoepimecis* from State of São Paulo: *Hymenoepimecis silvanae*, *Hymenoepimecis jordanensis*, *Hymenoepimecis veranii*, *Hymenoepimecis japi*, *Hymenoepimecis sooretama*. *Hymenoepimecis veranii*, was observed attacking and laying eggs on spiders *Araneus omnicolor* (Araneidae). After the attack, these parasitoids allow the hosts to continue their normal activities and the larvae do not kill or consume the hosts until they have pupate. *Hymenoepimecis japi* specimens were collected parasitizing females of spider *Leucauge roseosignata* (Tetragnathidae), *Hymenoepimecis sooretama* attached to the webs of spider *Manogeta porracea* (Araneidae); the cocoon webs of host species are distinct from their normal webs. One female of *Ticapimpla vilmae* was obtained from Malaise trap, from Mata da Esperança in Ilhéus, State of Bahia, Brazil, 0-200 m of altitude. The specimen studied, presented some variation in coloration: the hind tibia more extensive blackish, as well the last two tergites of metasoma. Two females of *Schizopyga moreirae* were obtained from São Paulo State, Brazil, at 600 and 1200 m, using Malaise traps. This is the first record of *Schizopyga* from Brazil and a new species was described. All the material is deposited in the collection (DCBU) of Universidade Federal de São Carlos, Departamento de Ecologia e Biologia Evolutiva, São Carlos, São Paulo, Brazil.

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TIGER wasps – a preliminary review of the apoid wasp diversity in Thailand

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Thailand is one of the countries in Southeast Asia with a remarkably rich but fragmentarily known insect diversity. Since its beginning in 2006, the Thailand biodiversity inventory, known as TIGER project, has resulted in about 5000 specimens of apoid wasps. Here we compare the preliminary results of our taxonomic analysis of this large sample with the published species diversity in Thailand. Until now, 155 species have been explicitly recorded

from Thailand, representing 42 genera, but more than 500 species in 55 genera from Thailand including neighboring countries. The species diversity is rather unevenly divided between the genera. Numerous genera are represented by a single species each, whereas a few markedly diverse genera comprise the majority of species. Highly diverse genera like *Trypoxylon* (about 100 species known from the area) and *Psenulus* (about 50 species known) are not only diverse in terms of species numbers, but are also markedly abundant in the TIGER material. As an example, about 30% (more than 1500 specimens) of the TIGER specimens studied so far belong in *Trypoxylon*, representing a still unknown number of species. Not surprisingly, the portion of stem-nesting species among the TIGER material is markedly large, as is well known from other tropical habitats. This bias towards stem-nesting is also reflected in the small average body size, although this might partially be the result of the collecting method, since smaller species are more likely collected by Malaise traps than large species. We also found a large number of hitherto undescribed species. Such newly found species are more common in genera with smaller species, which are more likely to be overlooked without Malaise traps and other mass collecting methods. However, even among the largest sphecids from Thailand, which are members of the genus *Sphex*, we found undescribed species. As far as we can tell now, the total number of species and genera among the TIGER material will approach the total number of apoid wasp species and genera already recorded from Thailand, although we predict significant differences in the specific species composition. Of the 55 genera reported from Thailand and its neighbouring countries, only 41 genera have been found in the TIGER samples so far. However, additional 14+ genera found by us have not been reported from this geographical region before. This increases the total number of known genera from Thailand by 30%. Although there are still many taxonomic problems to be solved, particularly in the highly diverse genera like *Trypoxylon*, it already became clear that the TIGER project significantly contributes to the knowledge of the wasp diversity in Thailand, with many implications for Southeast Asia.

Hymenopterous parasitoids of safflower fruit flies (Diptera: Tephritidae) in Iran

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The fruit flies (Diptera: Tephritidae) are the serious pests of safflower fields in Iran. Associated hymenopterous parasitoids (Hymenoptera) of them including nine species were listed and related data presented. They belong to the families Braconidae, Eulophidae, Ormyridae, Pteromalidae and Torymidae. *Pronotalia carlinarum* (Szelényi & Erdős) (Eulophidae) and *Pteromalus albipennis* Walker (Pteromalidae) were recorded for first time from Iran. Some descriptive and biological remarks are given on parasitoids. An illustrated identification key was provided for these species.

The first braconid species record of subfamily Charmontinae from Iran:

***Charmon extensor* (L.) (Hym., Braconidae: Charmontinae)**

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During the study of natural enemies in apple orchards of Iran, one braconid species of the subfamily Charmontinae was collected and identified. This is the first record of this subfamily in Iran. Charmontinae with two genera *Charmon* and *Charmontia* is a worldwide subfamily and the species of these genera known as parasitoids of lepidopterous larvae. The apple orchard which in this braconid species was collected, was heavily infected by *Grapholita molesta* (Busck) (Lep., Tortricidae). It is *Charmon extensor* (Linnaeus, 1758), a new record for Iran. Distribution: Eastern Palaearctic, Europe, Nearctic, Neotropical, Oriental and Ethiopian Regions, and Western Palaearctic. Material examined: West Azarbaijan, Orumiyeh, 23.7.2009. Leg. A. Masnadi-Yazdinejad.

The ichneumonid parasitoids (Hym., Ichneumonidae) of *Yponomeuta malinellus* Zeller (Lepidoptera: Yponomeutidae) in Iran

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The apple ermine moth, *Yponomeuta malinellus* Zeller, 1838 (Lep.: Yponomeutidae), is one of the most serious pest of the apple orchards and widely distributed throughout the temperate regions of the Palaearctic region. This univoltine defoliator of apple trees has some hymenopterous parasitoids, most important of which belong to the family Ichneumonidae. During the study of natural enemies of apple ermine moth in apple orchards of Iran, 9 ichneumonid species from five subfamilies (Campopleginae, Pimplinae, Ichneumoninae, Cryptinae and Anomaloninae) were collected and identified, 2 species of which (marked with two asterisks) are newly recorded for Iran, and 3 species (marked with an asterisk) are recorded for the first time as ichneumonid parasitoids of *Y. malinellus* in Iran. The next parasitoid species were reared from *Y. malinellus* in Iran:

Campopleginae. *Campoletis ensator* (Gravenhorst, 1829). Earlier recorded from Iran (Davachi & Shojaei 1968). Material examined: Ardabil, 31.4.2009, Leg. A. Masnadi-Yazdinejad. **Diadegma armillata* (Gravenhorst, 1829). Earlier recorded from Iran (Masnadi-Yazdinejad *et al.* in press). Material examined: West Azarbaijan, Orumiyeh, 24.7.2009. Leg. A. Masnadi-Yazdinejad.

Pimplinae. *Itopectis tunetana* (Schmiedeknecht, 1914). Earlier recorded from Iran (Aubert 1969). Material examined: Tehran, Karaj, 11.6.2009. Leg. A. Masnadi-Yazdinejad. *Pimpla turionellae* (Linnaeus, 1758). Earlier recorded from Iran (Kasparyan 1974). Material examined: Azarbayejan-e sharghi, Tabriz, 12.9.2009, Leg. A. Masnadi-Yazdinejad. **Pimpla contemplator* (Muller, 1776). Earlier recorded from Iran (Kolarove & Ghahari 2006). Material examined: Tehran, Varamin, 14.7 2009. Leg. A. Masnadi-Yazdinejad. **Gregopimpla inquisitor* (Scopoli, 1763). Earlier recorded from Iran (Masnadi-Yazdinejad & Jussila 2008). Material examined: Fars, Samirom, 11.8.2009. Leg. A. Masnadi-Yazdinejad.

Ichneumoninae. **Herpestomus brunnicornis* (Gravenhorst, 1829). Earlier recorded from Iran (Masnadi-Yazdinejad & Jussila 2008). Material examined: Fars, Goyom, 27.2.2010. Leg. M. Hooshmand.

Cryptinae. ***Gelis agilis* (Fabricius, 1775). New record for Iran. Material examined: Fars, Ghasrodashat, 6.8.2009. Leg. K. Abootorabi.

Anomaloninae. ***Agrypon flavelatum* (Gravenhorst, 1829). New record for Iran. Material examined: Mashhad, 11.6.2009. Leg. A. Abbasi.

Two newly recorded ichneumonid species as parasitoid wasp of Codling Moth (*Cydia pomonella* L. (Lepidoptera: Tortricidae) from Iran

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Codling moth (*Cydia pomonella* Linnaeus, 1758) is a serious pest of pear and apple orchards. Two ichneumonid parasitoid species from Cremastinae and Pimplinae were reared and identified from the material collected in Iran. This is the first record of these two species for the Iranian fauna as well as a new record of the parasitoid of *Cydia pomonella* L in Iran.

Cremastinae. *Pristomerus armatus* (Lucas, 1849). New record for Iran. Material examined: Fars, Eghlid, 10.6.2009. Leg. A. Abdollahi.

Pimplinae. *Dolichomitus messor* (Gravenhorst, 1829). New record for Iran. Material examined: Fars, Shiraz, 11.9.2009. Leg. A.Masnadi-Yazdinejad.

Comparison of parasitoid communities between insular and mainland populations of *Pseudasphondylia neolitseae* (Diptera: Cecidomyiidae) in the Izu district, Japan

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The Izu Islands consist of volcanic islands located south of the Izu Peninsula, Honshu, Japan, extending for about 230 km from north to south, and have unique biota of insects, terrestrial reptiles and plants. In 2009 and 2010, we surveyed gall midge populations and associated parasitoids in these areas. Parasitoid communities were compared among different islands and the Izu Peninsula for *Pseudasphondylia neolitseae* that induces leaf galls on *Neolitsea sericea* (Lauraceae) and some other gall midges of Asphondyliini (Diptera: Cecidomyiidae). In 2009, two hymenopteran ectoparasitoids, *Bracon tamabae* (Braconidae) and *Sigmophora* sp. (Eulophidae), and one endoparasitoid, *Gastrancistrus* sp. (Pteromalidae), were observed to attack *P. neolitseae* in the Izu Peninsula and on northern islands. On southern islands such as Miyake and Hachijo Islands, only *B. tamabae* was found. *B. tamabae* is polyphagous and has a very long adult life span (up to three months). In contrast, the *Gastrancistrus* sp. is monophagous and has a relatively short adult life span. Because of such differences, *B. tamabae* might be able to colonize these islands easier than *Gastrancistrus* sp. At the moment, reasons why *Sigmophora* sp. is not distributed on southern islands are not known. Molecular analysis in 2009 revealed that *B. tamabae* has a mitochondrial DNA haplotype that is common among populations through out localities surveyed except the most southern and distant island, Hachijo, where another haplotype exists. In contrast, *P. neolitseae* has a common mitochondrial DNA haplotype in all localities surveyed including Hachijo Island. This suggests that the Hachijo population of *B. tamabae* has derived from a place that is different from distribution range of *P. neolitseae* in the Izu Peninsula and northern Izu Islands. In addition to *P. neolitseae*, parasitoid communities of the following gall midge



species were surveyed: *Asteralobia sasakii* inducing axillary bud galls on *Ilex crenata* (Aquifoliaceae) and *Illiciomyia yukawai* inducing leaf galls on *Illicium anisatum* (Illiciaceae).

Systematics and diversity of oak gallwasps (Hymenoptera: Cynipidae: Cynipini) of Panama

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The great part of the representatives of the family Cynipidae are grouped within the tribe Cynipini or oak gallwasps. There are about 1000 described species distributed mainly across the Holarctic Region. From the Neotropical region only 13 Cynipini species have been recorded, although actual evidence is how that the group could also be species rich and phylogenetically diverse in the neotropics. The aim of this work was to perform a taxonomical and biological study of the gall-inducing Cynipini on *Quercus* of Panama, where only one species was previously recorded. Field data were taken from samplings made between December 2007 and May 2009 in nineteen sites of the western of Panama. Eight of the nine *Quercus* species recorded in this country were surveyed monthly: *Q. salicifolia*, *Q. benthamii*, *Q. cortesii*, *Q. gulielmi-treleasei*, *Q. humboldtii*, *Q. bumelioides*, *Q. lancifolia* and *Q. insignis*. The preliminary identification found 10 genera of the tribe Cynipini. Sixty three morphotypes of galls induced by cynipids associated with six species of *Quercus* were collected, 53% of the galls were found on leaves, 37% on stems, 4% on acorns, 4% on buds and 1% on catkins. Adult gall-inducers were reared from 43 gall morphotypes (68% of total) of whom 25% corresponded to a sexual generation. One new genus of oak gall wasp has been detected and it is being studied. The identified genera and its species-richness were: *Amphibolips* Reinhard (3 species), *Andricus* Hartig (12 species), *Bassettia* Ashmead (1), *Callirhytis* Frster (1), *Cynips* Linnaeus (4), *Disholcaspis* Dalla Torre & Kieffer (2), *Loxaulus* Mayr (1 specie), *Neuroterus* Hartig (8), *Odontocynips* Kieffer (2) and *Trigonaspis* Hartig (8). Only two species previously recorded from the Neotropical region were identified (*Andricus championi* Cameron and *Odontocynips hansonii* Pujade-Villar). The other 95% of the studied species represent new undescribed species. The *Quercus* species with the greatest diversity of galls was *Quercus bumelioides* (Sect. *Quercus*), with 33 different galls associated. On the distribution of Cynipidae in Panama, the preliminary results showed a high Cynipini species richness (but in low densities), concentrated in several species of *Quercus* relatively extended in areas of the western of Panama, while that presence of cynipids in others *Quercus* species, more scarcely or locally distributed, was almost null.

A preliminary study on the gallwasp fauna of Kemaliye (Turkey), with a new record for Turkey (Hymenoptera: Cynipidae)

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The members of the Cynipidae (Hymenoptera) family, also known as the gallwasps, induce some of the most structurally complex plant galls. In this study, we have examined the gallwasps and their galls collected from Kemaliye (Turkey) and its surrounding. Kemaliye is located on the Anatolian Diagonal which separates the Eastern and Western parts of Turkey by a certain division, and therefore has a very interesting topography and plant composition which combines various faunistic and floristic components of Anatolia (such as Mediterranean, Pontic, Eucsin, Turano-Eremial, Alpine and even African). In this study which was carried out in Kemaliye and its surrounding, it was aimed to contribute to the further studies concerning this subject. Field trips were made on September and November of 2007 and May, June, July, September and October of 2008. During the field trips, gall specimens which belong to the family Cynipidae which develop on host plants were collected from the genus *Quercus* (Fagaceae) and the species *Rosa canina* (Rosaceae). At the end of the study, 24 species which belong to 5 genera were determined. Moreover, *Andricus moreae* was found to be a new record for Turkey.

A second European species of *Netomocera* Bouček (Hymenoptera: Pteromalidae: Diparinae), with notes on other diparines

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The genus *Netomocera* was described by Bouček in 1954, having as type species *N. setifera* Bouček (orig. design. and monotypy), which is known to occur mainly in south-eastern Europe. Since then other six species have been described, three Afrotropical, one Nearctic, one Oriental, and one Australian. Thus, the newly described species is the second one recorded in Europe; it was collected in southern Romania and it most closely resembles *N. setifera*. The submacropterous female can be separated from that of *setifera* mainly by its longer gaster, the first tergite occupying only half of the gaster length, while the macropterous male in having larger eyes and thinner antennae. Both sexes significantly differ from *setifera* in body coloration, especially the males which are partly reddish-yellow and not completely black. An illustrated key to separate the two species is given, as well as distributional notes on other diparines.

Calesinae: morphological examination and molecular phylogenetics of an enigmatic chalcidoid taxon

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Although the monophyly of some groups of Chalcidoidea is strongly supported by morphological and/or molecular synapomorphies, higher-level relationships within the superfamily remain uncertain. Several families are regarded as either paraphyletic or even polyphyletic. This uncertainty regarding sister-group relationships, combined with hyperdiversity of form and function, has left some chalcid groups unplaced into higher taxonomic categories. Establishing relationships within Chalcidoidea is further hindered by a dearth of comprehensive morphological studies, either across character systems or across taxa. Calesinae (Howard) is a small group of Australian and Neotropical parasitoids of

whiteflies, comprising a single genus, *Cales*. Historically, the Calesinae have been included within the Trichogrammatidae and Mymaridae, though they are most often associated with the Aphelinidae. In addition, they share some features with the Eulophidae. The subfamily is currently unplaced within the superfamily Chalcidoidea. Here we present a detailed morphological examination and a molecular phylogenetic analysis of the three described species in addition to a newly discovered species from New Zealand. The apparently apomorphic characteristics of the head, mouthparts, antennae, wings, mesosoma and genitalia, are weighed against characteristics suggesting affinities with established chalcidoid families. In addition, we provide a species-level molecular phylogeny of the group, suggesting a possible cryptic species complex within the new world species, *Cales noacki*.

Molecular Phylogeny of Eucharitidae

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Within Hymenoptera, eucharitids comprise the most numerous and diverse group of eusocial insect parasitoids. Fifty-three genera of Eucharitidae are distributed worldwide in nearly every zoogeographical region. Phylogenetic relationships have previously been analyzed within a cladistic framework using morphological character coding, genetic markers, and a concatenated 'total evidence' data matrix. Morphology, molecules, and shared life history traits unite the Eucharitidae as a demonstrably monophyletic group, with three subfamilies: Gollumiellinae, Oraseminae, and Eucharitinae. However, many lower-level relationships are unclear and vary according to dataset and analytical method. We present a molecular phylogeny based on an expanded matrix of over 375 taxa from both the Eucharitidae and Perilampidae. Molecular evidence from a combined-gene dataset (28S-D2-D3, 18S, COI and COII) is used to assess relationships.

We present an updated hypothesis of congruence between host and parasitoid using the most recent ant phylogenetic relationships. Eucharitidae are known to attack six subfamilies of ants, but we focus on the host poneromorph ant subfamilies. Though the host ant patterns are predictive among the eucharitid groups, there have been a number of instances of hypothesized host-switching. Evolution of ant host associations will be considered in light of the new eucharitid phylogeny.

The effects of prey abundance on nesting behavior of solitary wasp *Symmorphus allobrogus* (Hymenoptera: Vespidae: Eumeninae)

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It has been demonstrated that species richness and diversity of trap-nesting Hymenoptera community are sensitive to a wide range of human-caused environmental changes, therefore this community may be considered a potential bioindicator of anthropogenous impacts at habitat or landscape scale. We may expect that, in addition to presence and abundance, some other parameters like body size, sex ratio and nest size can reflect the effects of environmental changes on the state of species populations. The current experimental study aimed to ascertain

whether progeny size, sex ratio and number of cells per nest depend on prey abundance in the environment and may be used in estimation of wasp population state.

We conducted a laboratory experiment with inseminated females of *Symmorphus allobrogus* – abundant solitary wasp species in Lithuania. Each female were kept in a transparent plastic 5 litre container with food (honey solution), water, nesting places (reed stem internodes) and material for building cell partitions (clay) available. Wasps were provided with different amount of prey: 5, 10 or 20 specimens of leaf-beetle *Gonioctena quinquepunctata* or *Linaeidea aenea* larvae per day. A total of 37 wasps were used in the experiment. The content of 154 nests produced during the experiment was examined.

Wasp females responded to a higher amount of available prey by building nests with a higher number of brood cells. The wasps that received 20 prey items per day produced approximately twice as many cells per nest (3.9 ± 0.4) as the wasps receiving 5 prey items per day (2.1 ± 0.1). The amount of available prey did not affect the progeny size: both male and female progeny had the same average body mass irrespective of the number of prey specimens given to the mother wasp. Results of our experiment did not confirm the hypothesis that a higher availability of provision would lead to a higher proportion of the larger (female) sex in the progeny produced by the mother wasp: the proportion of female progeny per nest was approximately equal in the nests produced by wasps receiving 5 and 20 prey items per day. However, the wasps that were provided with 10 prey items per day produced nests with a significantly lower share of female progeny. The reasons of such U-shaped dependence of the proportion of female progeny in a nest on the amount of prey remain unclear.

Parasitization of *Tetrastichus brontispae*, a potential biological control agent of the coconut hispine beetle *Brontispa longissima*

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The gregarious endoparasitoid *Tetrastichus brontispae* (Hymenoptera: Eulophidae) is one of important natural enemies of the serious pest, the coconut hispine beetle *Brontispa longissima* (Coleoptera: Chrysomelidae) which recently invaded and causes serious damages on coconut palm plants in Southeast Asia. To understand the ability of the parasitoid as the control agent in the region, development time at different temperatures, oviposition, superparasitism and influence of host age on parasitization of this parasitoid were investigated in the laboratory using last instar larvae and pupae of *B. longissima* as the host. Total development time from oviposition to adult emergence decreased as temperature increased from 22°C to 30°C. No parasitoid completed development at 31°C. Temperatures had no effect on the sex ratio of parasitoid offspring. Host age affected parasitization which was high on prepupa and day 0-1 pupae. Findings of this study provide the valuable information for optimizing rearing procedures of the parasitoid and we discuss probabilities to use this species as a biological control agent of the beetle.



An inordinate fondness of beetles? Even more fond of microhymenoptera!

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Asked what could be inferred about the work of the Creator from a study of His works, the British scientist J.B.S. Haldane is reported to have replied, that He has "*an inordinate fondness for beetles*." It is true that more species of beetles have been catalogued than any other group with estimates of up to 400000 species (about 20% of all living organisms) having been described to date and on the face of it Haldane's statement would seem to be correct. The second largest group currently being the Hymenoptera with about 130000 described species. Yet, an extrapolation of the British fauna, the best known in the world, suggests that beetles may represent only the *third* largest group (*ca* 5000 British species) well behind Diptera (*ca* 6950 species) and Hymenoptera (*ca* 7100 species). Recent surveys using sweep net sampling in the forests of Costa Rica supports this view. For instance, one six hour sample provided an incredible 1286 species of microhymenoptera compared with only 504 species of beetles. Similar differences were found at 8 other sites at various altitudes from 75 m to 1400 m across Costa Rica. At all sites the Chalcidoidea alone represented more species than the Coleoptera and was by far the largest group both in terms of numbers of species and numbers of individuals, surpassing even ants. This poster presents the detailed breakdown of all families collected in the survey using a screen sweep-net fitted with a 4 mm screen which allowed only smaller individuals (<6 mm long) to pass through.

Rare in collections, common in the forest – the occurrence of the pimpline spider parasitoid *Reclinervellus nielsenii* in Finland

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Rearing parasitoids from their hosts is a well-known way of obtaining rarely collected species. It also offers valuable information on the biology of the parasitoids. The *Polysphincta* group of genera (Ichneumonidae: Pimplinae), are all koinobiont ectoparasitoids on spiders. A project aimed at collecting and rearing parasitised spiders in Finland has been going on since 2003, rendering more than 800 reared specimens. *Reclinervellus nielsenii* (Roman), a species recently discovered in Finland through this project, is a parasitoid of the araneid spider genus *Cyclosa*. Of the two *Cyclosa* species widely distributed in northern and central Europe, *C. conica* (Pallas) and *C. oculata* (Walckenaer), only *C. conica* occurs in Finland. Thus, in this region, *R. nielsenii* can be considered to have a very narrow realised host range consisting of a single species. *R. nielsenii* has not been reared from any other spider species in Europe.

Since the discovery of *R. nielsenii* in Finland in 2004, the species has turned out to be common throughout the range of the boreal spruce (*Picea abies*) forests in Finland. A total of 80 specimens have been reared, whilst only two specimens, from 1914 and 1975 respectively, have been found in entomological collections, both misidentified as *Polysphincta boops*.

This clearly demonstrates that the number of specimens of certain species in entomological collections does not indicate the true abundance of the species, and highlights bias introduced

by the methods used on our knowledge of biodiversity. The few old specimens and the lack of more recent representation in collections clearly indicate that *R. nielsen* is not a real novelty to the country. Rather, it had passed unnoticed due to difficulties with collecting adults with traditional methods and due to specimens being confused with another similarly coloured species. A new version of the Red List of threatened species in Finland according to IUCN criteria will be published by the end of 2010. Here, the species of the *Polysphincta* group of genera will be evaluated for the first time. The methods used in the concerned rearing project have provided invaluable data for the evaluation of *R. nielsen* and several other species of this group. Our work shows that the choice of collection method can significantly affect the results.

The chalcidoid parasitoids of Coccoidea in southeastern Anatolia Region of Turkey

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Southeastern Anatolia Region in terms of diversity of cultivated plants is an important area in Turkey. Depending on the diversity of cultivated plants, significant yield losses are due to the most harmful organisms. In between pests, species in the superfamily Coccoidea play an important role. The undamaged nature of the region, free from chemical pesticides, supporting several natural enemies of Coccoidea that were recognized in our studies, especially chalcidoid parasitoids which play an important role in the population dynamics of scale insects. Since 2000 we investigated the chalcidoid parasitoid fauna of Coccoidea of the Southeastern Anatolia region. Parasitoids might be important biological agents in controlling scale insects.

New systematics of Australian Thrasorinae (Hymenoptera: Cynipoidea: Figitidae) with a description of two new genera and a new subfamily

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The Thrasorinae are a stem group of Figitidae (Hymenoptera: Cynipoidea) that are associated with galls of other wasps (Cynipoidea and Chalcidoidea) on various trees and bushes, being not inquilines but rather parasitoids of the gall inducers or some other hymenopteran inhabitants in the galls with which they are associated. This makes this group a very important focus of study in order to elucidate the evolutionary history of the Figitidae in particular and the Cynipoidea as a whole, with its different life strategies: entomophagy and phytophagy. The systematics of the Thrasorinae has always been problematic: two new figitid subfamilies, the Plectocynipinae (2007) and Euceroptrinae (2008), have been erected recently to include some genera previously included in the Thrasorinae. A new systematics of Australian Thrasorinae is proposed herein. The genus *Mikeius* Buffington is transferred from Thrasorinae to Mikeiinae Paretas-Martínez & Pujade-Villar n. subf and a new species of *Mikeius* is described. Two new genera of Thrasorinae are erected to include species previously included



in *Mikeius* (*M. schauffi* Buffington and *M. neumanni* Buffington) and *Amblynotus* (*A. pilosiscutum* Girault). A new species of *Thrasorus* Weld is described. A phylogenetic analysis including all these new taxa and all genera previously included in the Thrasorinae is given.

New records of Braconidae (Hymenoptera) genera from Brazil in the state of São Paulo

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The knowledge of the family Braconidae in Brazil is largely incomplete due to lack of regional studies and the taxonomic complexity of this group. The diversity of the Braconidae in Brazil is estimated at a much higher than is currently known. From the thirty-four subfamilies of Braconidae recognized in the New World, twenty-eight of them have been reported from Brazil. In an effort to understand the richness and distribution of the Braconidae family in Brazil and specifically in the State of São Paulo, many collections have been made using Malaise traps and sweeping the vegetation. At least 191 from the 341 genera recorded from the Neotropical region are recorded from Brazil. This is a high number given that the number of genera recorded for Canada and United States is approximately 240. First records are reported for some rare genera of Braconidae in Brazil and in the State of São Paulo based on material deposited in Universidade Federal de São Carlos, São Carlos, SP, Brazil. Those genera are: *Andesipolis* (Rhysipolinae), *Topaldios* (Helconinae), *Paphanus* (Sigalphinae) and *Syntretus* (Euphorinae). New species to those genera are presented and figured. *Andesipolis* occurs exclusively in South America with distribution restricted to the Andes. This is the first record for the genus outside of this mountain range.

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What is “the news” about the institute of studies on parasitoid Hymenoptera from southeastern Brazil – HYMPAR-SUDESTE ?

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The **HYMPAR-SUDESTE** is an initiative of a group of researchers working in the Brazilian Southeastern region, in order to integrate the conservation and sustainable development efforts. The acquired scientific knowledge of biodiversity will be applied to education and economic activities as agriculture and ecotourism and to the development of mechanisms for providing environmental services. The specific objectives are to estimate the number of species of Hymenoptera parasitoids at each selected site of the Southeastern region of Brazil, contributing to the knowledge of the geographical distribution of the taxonomic group studied; implement taxonomic collections of parasitoid Hymenoptera; identify areas of high incidence of endemic species for wildlife study; identify biotic interactions, involving different trophic levels; classify the studied reserve fragments in relation to their fragility in relation to biodiversity loss, contribute to the establishment of priority areas for conservation.

Structure and integrate projects, especially those concerned with the sustainability of the ecosystems studied, in order to reduce the fragmentation of existing forests indicating conservation priorities and promoting reforestation in rural properties; strength partnerships with public governmental agencies and non-governmental and private agribusiness institutes in the context of the integrated ecological knowledge; maintain a constant flow of information subsidizing the establishment of projects for work optimization; promote the interaction between research institutions, private companies, schools and the community; establish pilot procedures in environmental education and continuing education in areas adjacent to reserves in order to spread the knowledge and experiences that promote the protection of biodiversity and a decrease in anthropic pressure on the conservation units; define environmental indicators allowing the assessment and implementation of possible payment for environmental services with the maintenance of biodiversity; provide knowledge for implementation of environmental laws; establish human resources trained in the major issues on biodiversity, involving cooperation in national and international levels. Since last May, 2009, using 150 Malaise traps during 12 months in 32 localities we have collected several thousands of insects; the Ichneumonoidea and Chalcidoidea are mounted on pins to be identified. The most common are the Microgastrinae (Braconidae), the Campopleginae (Ichneumonidae) and the Eulophidae (Chalcidoidea). Several rare genera have been collected. We have found new trophic interactions between Hymenoptera parasitoids and Lepidoptera, in special to Geometridae species. Several training courses to study the Hymenoptera parasitoids were given, involving under graduated and graduated students. Several papers, Master dissertations and PhD thesis are been prepared and published.

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Diversity of Alysiniinae (Hymenoptera: Braconidae) in protected areas from the Comunidad Valenciana, Spain

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The study of Hymenoptera parasitoids has a great interest from the point of view of biodiversity and conservation because the interactions with their hosts allow the maintenance of insect populations in balance in the ecosystem.

A sampling work with Malaise traps from April 2004 to December 2007 was done in three protected natural areas of the Comunidad Valenciana (Spain): Natural Park of Las Lagunas of La Mata-Torre Vieja, Natural Park of Font Roja and Natural Park of La Tinença Benifassà. Each of these areas shows particular climatic conditions.

In this communication we analyze the richness of the genera belonging to Alysiniinae subfamily and we compare the similarity of the sampled areas.

This work was supported by the research project CGL-2004-02711, cofinanced by the Ministry of Science and Technology and the European Union (European Funds for Regional Development).

Habitat distribution patterns of Alysiiinae community (Hymenoptera: Braconidae) in a forest reserve in Spain

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Alysiiinae braconids are a wide subfamily composed of 1500 species world-wide described. Two tribes are recognized: Alysiiini and Dacnusiini. The members of Alysiiini parasite a wide range of cyclorrhapha hosts while the members of Dacnusiini are almost exclusively confined to leaf-miners hosts, such as Agromyzidae, Ephydriidae and Chloropidae.

The capture of these Hymenoptera was done during a period of two years using Malaise traps in the Reserve of Artikutza placed in the Natural Park of Peñas de Aia (Navarra). This natural area contains two habitats: mixed forest and beech forest.

The collected specimens are analyzed to know if Alysiiinae community has a preference selection in the habitat distribution. When analyzing the samples, it is possible to see that the diversity is higher in the mixed forest than in the beech forest. And, it is possible to distinguish a significant difference between habitats in relation with the particular community of Alysiiinae.

Little known facts about a well known hymenopteran: on the field life history of *Nasonia vitripennis* (Walker, 1836) (Chalcidoidea: Pteromalidae)

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The gregarious parasitoid *Nasonia vitripennis* is easy to rear on puparia of various flies and has become a well established laboratory model organism over the last few decades. Its use has found its temporary pinnacle in the recent publication of the complete genome of this species and its sibling taxa *N. giraulti* and *N. longicornis*.

However, data are missing on its natural field life history in terms of e.g. host finding, host range, habitat choice and phenology. We investigated on some of these aspects over the last years and present in this poster a preliminary synopsis of our work.

N. vitripennis lives in nests of some bird species. Those nests are its primary habitat and the species can be found there in high quantities. We show its position in a birds' nest food web along with its main field hosts and few other much less specialised parasitoid species. The field hosts are mainly bloodsucking *Protocalliphora* spp. and necrophagous *Calliphora vicina* (Calliphoridae) and to a lesser proportion saprophagous *Potamia littoralis* (Muscidae). Earlier results from experimental placing of sentinel hosts corroborate the assumption that to a far extent *N. vitripennis* specialises on birds' nests: It only parasitizes hosts in greater heights and does not parasitize hosts in empty nest boxes. Also, the synchronisation of the birds breeding season and the phenology of *N. vitripennis* is well known. In olfactometer tests we were able to show that *N. vitripennis* females largely use olfactory cues of the birds nest material in their host finding process.

We also present results on the actual and the potential host range of the species as well as fecundity and sex ratio data from field hosts of different size.



With these and future studies we hope to contribute to a more complete understanding of the model *Nasonia* merging genetics, genomics, experimental studies and field life history traits.

**Confirmation of the species rank of *Torymus macrurus* (Föerster, 1859)
(Hymenoptera: Chalcidoidea: Torymidae)**

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Förster (1859) described just the female of this species, as *Syntomaspis macrurus*, from a single specimen obtained from galls on *Quercus pedunculata* in Hungary. The holotype of this species is apparently lost and the status of this species was “species inquirendae” for long time. Erdős (1960) mentioned that there no material in museum from Budapest. Grissell (1995) enumerate this species as *Torymus macrura* in his world catalogue of Toryminae. Graham & Gijswijt (1998) mentioned that they could not find any material in Naturhistorisches Museum from Vienna in 1993 and they mentioned that this species was reared in Poland but don’t offer any other information (the paper, the author). They don’t include the species in the key of the European species of the genus *Torymus* but they discuss this species in a special chapter of “species inquirendae”. Zavada (2003) placed this species in the *cyaneus* species group and mentioned at the materials examined 1♀ 1♂ obtained from galls of *Cynips quercusfolii* (Hymenoptera: Cynipidae) in Moldavia (collected by Plugaru in 1963), 1♀ from the same host obtained in Ukraine (collected by Rayevsky in 1973) and other 6 ♀♀ from the same country (collected by Diakonchuk in 1974), all this materials belongs to the collection of the Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine (Kiev, Ukraine). Popescu (2003) mentioned *T. macrurus* also from *Cynips quercusfolii* in Romania. Zerova & Seryogina (2003) placed this species in the *Syntomaspis* subgenus of the *Torymus* genus and mentioned it from *Biorhiza pallida*. Zerova *et al.* (2003) mentioned specimens of *T. macrurus* obtained from *C. quercusfolii* being in the collection of Schmalhausen Institute of Zoology, collected in 1963, 1973 and 1974 years.

I obtained 3♀ from galls of *Cynips quercusfolii* (L.) (agamic generation) on leaves of *Quercus* sp. collected on 04.2000 at Repedea, Iași county, Romania and 1♀ from the same host and locality, galls collected on 29.03.2006. The species is closely related to *Torymus cyaneus* and differ mainly by longer ovipositor. I describe the species using drawings, SEM and photonic microscopy, giving a modern description of this apparently rare species with questionable status through time.

**The maxillo-labial complex in scelionid wasps
(Hymenoptera: Platygastroidea)**

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The parasitoid wasp superfamily Platygastroidea, traditionally divided into two families, the Platygastriidae and the Scelionidae (e.g., Masner 1993, 1995; Austin *et al.* 2005), is the third largest of the parasitic superfamilies after the Ichneumonoidea and Chalcidoidea and

represents some 4460 described species worldwide (Austin et al. 2005), but the world fauna is estimated to be about 10000 species (Masner 1993).

Characters of MLC, like any morphological and anatomical characters are an important source of data in systematic and taxonomic research. Quicke (1993, in Winson 1999) defines a taxonomic character as “any physical structure (macroscopic, microscopic or molecular) or behavioral system that can have more than one form (character state), the variation in which potentially provides phylogenetic information.” The mouthparts throughout the orders of Insecta are composed of a set of homologous components rich in variation, so, from this reason, they should provide excellent data for phylogenetic studies (Krenn 2007).

The aim of this study is to present a clear description of the MLC in scelionids, proper recognition of homologous characters with other hymenopterans and of synonymies between terms used by different authors. The second goal is to emphasize the peculiarity of MLC in scelionids and establish the ground plan character states for scelionids and relate them to structures observed in other hymenoptera. Finally, we seek to provide a precise nomenclature for MLC in scelionids for use in systematics, and thus to contribute to further advances in our understanding of the taxonomy and interrelationships of its constituent groups.

To emphasize the peculiarity of MLC in scelionids, we made a comparison between MLC in *Sparasion* (Scelionidae: Platygastroidea) and MLC in *Helorus* (Heloridae: Proctotrupeoidea), *Proctotrupes* (Proctotrupidae: Proctotrupeoidea) and *Belyta* (Diapriidae: Proctotrupeoidea).

These three genera were chosen for comparison for 2 reasons: (1) superfamily Proctotrupeoidea is, at least apparently, very old (Masner, 1993) so, we have the chance to identify for each character the plesiomorphic state; (2) until relatively recently (Masner 1956; Masner 1993), Proctotrupeoidea and Platygastroidea were regarded as a single superfamily and we can see if characters of MLC are valuable in the high level classification of microhymenoptera, or eventually, if at the level of MLC there are characters what could show a link between these two superfamilies.

Characters of MLC like: degree of sclerotization, shape of cardo, shape of stipes, position of maxillary palpus and position of galea and lacinia, relationships between galea and lacinia, shape of prementum seems to confirm the idea of Masner (1993) that Proctotrupeoidea consists of two natural units, one comprises Peleciniidae, Vanhorniidae, Proctotrupidae, Heloridae, Peradeniidae and Roproniidae and the second comprises Monomachidae, Austroniidae and Diapriidae. At level of MLC there are more similarities between *Helorus* and *Proctotrupes* than between any of these genera and *Belyta*. Furthermore, characters of MLC in *Belyta* look intermediary between (*Helorus* + *Proctotrupes*) and *Sparasion*. It seems that the detailed study of MLC could provide important characters for the higher-level taxonomy of Proctotrupeoidea s. l.

First record of *Dicopus minutissimus* Enock (Hymenoptera: Mymaridae) from the European mainland

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The genus *Dicopus* Enock 1909, belongs to the family Mymaridae and it is considered one of the most rarely collected fairy flies. The species belonging to this genus are tiny parasitoids

(0.2 -0.4 mm). From Europe, three species have been described: *Dicopus minutissimus* Enock, 1909, *Dicopus citri* Mercet, 1912 and ?*Dicopus cervus* Morley, 1930. The species described in 1930 by C. Morley as *D. cervus* obviously does not belong to the family Mymaridae (Ogloblin 1956).

It is the first time when *Dicopus minutissimus* is found on the European mainland; the species is known until now only from England; the genus *Dicopus* Enock is also mentioned for the first time from Romania. We illustrate the species distribution, the morphology of: wings, antennas in male and female - head, thorax and abdomen. Also we describe the male genitalia and give the biometry for some females and males. The taxonomic status of the specimen belonging to *Dicopus* found by Baquero & Jordana (2002) in Spain should be confirmed in relation to *Dicopus minutissimus* Enock, as the clava and the last funicle articles are longer and thinner than in Enock's original description. Enock (1909) in his original description reveals a very important feature that the antennal club is equal in length to the 6th, 7th, 8th, and 9th antennal segments combined, a feature that is found in our specimens. Mercet (1912) noted that the species *D. citri* has wider wings, compared with *D. minutissimus*, a species with narrow wings and also the last three articles of the female antenna have different proportions between the two species. Beside some important - genus features: scape with 2 or 3 setaceous teeth, mandibles projecting downward and away from the head (bladelike), we also mention some new features for this genus and species: antennal clava in females has a gap (gouge-like) to the distal end, with a modified trichoid sensilla; hind tibia with an apical tooth, and also a propodeal carina as an overturned "Y" is also present (probably different in each species). Male genitalia is almost cylindrical, (phallobase united to aedeagus), long, narrowed proximal and distal, not strongly sclerotized, with long parameres and with long and strongly sclerotized volsellar digiti, apparently each with three hooklets. Our material was collected during 2008-2009 from different locations found in the North-Eastern part of Romania – Bistritei Mountains, and it is preserved in a personal collection belonging to Emilian Pricop.

Parasitoids wasps reported on willow aphids in Iran

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Willows are considered as the most important elements for park design; willow extract is widely used in various medicinal industries in Iran. Thus, studies on willow pests and the biotic factors influence the pest populations are essential for the integrated pest management.

Several aphid species reported as pests of willow trees in Iran, which cause direct damage to the plants and also serve as vectors for different pathogens. Next aphid species on willows are reported from Iran: *Aphis farinosa* Gmel, *Cavariella aquatica* (Gill. & Bragg), *C. aegopodii* (Scop.), *C. cicutae* (Koch), *C. archangelicae* (Scop.), *Chaitophorus truncates* Hausmann, *Ch. pakistanicus* HRL, *Ch. salicti* (Schrank), *Ch. vitellinae* (Schrank), *Ch. remaudierei* Pintera, *Ch. salijaponicus* ssp. *niger* Mordv, *Ch. nigritus* HRL, *Plocamaphis flocculosa* Weed ssp. *goernitzii* Boerner, *Pterocomma pilosum* Buckt, *Phylloxera salicis* Lichtenstein, *Tuberolachnus salignus* (Gmelin). The Willow giant aphid (*Tuberolachnus salignus*) is the most important aphid pest on willows, reported from 16 *Salix* species in Iran. The honeydew



of *T. salignus* is considered as a by-product of willow in Iran and widely used in pharmacology under name Bidkhesht.

Five species of Aphidiinae (Braconidae) were reported on willow aphids from Iran: *Adialytus salicaphis* (Fitch, 1855) on *Chaitophorus remaudierei* (Pintera) and *Ch. salijaponicus* (Mordvilko), *Aphidius cingulatus* (Ruthe, 1859) on *Pterocoma pilosum* Buckt., *Aphidius salicis* (Haliday, 1834) on *Cavariella aegopodii* (Scopoli), *Binodoxys brevicornis* (Haliday, 1833) on *C. aegopodii*, and *Ephedrus helleni* (Mackauer, 1968) on *C. aquatica* (Gillette & Bragg).

New species of the genus *Lathrolestes* (Hymenoptera, Ichneumonidae) from the World

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The genus *Lathrolestes* Förster, 1869 (Hymenoptera, Ichneumonidae) is a large, mainly Holarctic genus with 61 described species (Yu *et al.* 2005). Of these, 32 species occur in the Nearctic region (Barron 1994), 26 species in the Palearctic region, predominantly Europe (Yu *et al.* 2005), one species in the Afrotropical region, Congo (Benoit 1955), four species in the Neotropics, Costa Rica (Gauld *et al.* 1997), and two species in the Oriental region (Uchida 1932, 1940). This genus belongs to the subfamily Ctenopelmatinae (Hymenoptera, Ichneumonidae) and the tribe Perilissini which is distributed worldwide except Australia and Oceania with 23 genera and over 250 species.

The larvae of members of this genus feed as koinobont endoparasitoids of sawflies mainly. The world distribution of Symphyta allows to assume a high biodiversity of the genus *Lathrolestes*. Last finds confirm this. Several new species of *Lathrolestes* were described or determined by author recently from different zoogeographical regions.

Two new Oriental species have been discovered in Taiwan and Japan (Reshchikov, in press). One new species was collected in Sichuan, China by American naturalist D.C. Graham in 1930. The fauna of Ichneumonidae (Hymenoptera) of Nepal is not known satisfactorily. Mainly members of the subfamilies Ichneumoninae and Campopleginae, and no until now members of the subfamily Ctenopelmatinae, are known from this country. While examining Ichneumonidae collected during the Canadian Expedition to Nepal in 1967 author came across one new species of the genus *Lathrolestes* [unpublished data].

Members of *Lathrolestes* were not registered in Mexico but according to the neighbour faunas (Barron 1994, Gauld *et al.* 1997), roughly 9 known species could be found there. Description of four new species from Mexico is prepared [unpublished data]. One new species of *Lathrolestes* was described in collaboration with Finnish colleagues from Ecuador (Reshchikov *et al.*, in press). These are additions to Neotropical fauna which includes four species of *Lathrolestes* (Gauld *et al.* 1997).

Five species were described as new from the USA in support of the biological control of invasive European tenthrinid leafminers in North America. Two of them were reared from *Profenusa thomsoni*, pest of birch which was introduced in North America (Reshchikov *et al.* 2010).

The biggest biodiversity of the genus was detected in Eastern Palearctic where 17 new species were determined. In Western Palearctic, fauna of which is well known, 3 new species were



determined [unpublished data]. The revision of the Palearctic species of *Lathrolestes* is coming.

Thus, 34 species of *Lathrolestes* are going to be described as new, further to 61 previously described species. Further studies of the genus *Lathrolestes* is required to provide the work on phylogeny of the tribe Perilissini, since it could bring some new characters of some new species.

Oak gallwasp fauna of Iran (Hymenoptera, Cynipidae, Cynipini)

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36 species of oak gallwasps were known earlier from Iran (Chodjai 1980) which from near 1/3 of species were erroneously listed or misidentified and only 24 species were correctly listed (marked with asterisk below). This study was carried out during 2001-2007. Six main species of *Quercus* were sampled: *Q. infectoria*, *Q. macranthera*, *Q. petraea*, (in *Quercus* s.s. section of oaks), and *Q. brantii*, *Q. libani*, *Q. castaneifolia* (in *Cerris* section oaks) in Zagross, Arasbaran, Fandoghlo, Andabil, Tarom Olya & Sofla, and Caspian forests of Iran. Eighty two (82) oak gallwasp species were found on different oak species in Iran, which from 20 species are new records for the Iranian fauna and 25 species were described as new for science. The next 57 species, known also from other regions, were found in Iran: *Andricus aries*, *A. askewi*, *A. caliciformis*, *A. caputmedusae**, *A. cecconii**, *A. conglomeratus**, *A. coriarius**, *A. corruptrix*, *A. crispator*, *A. curtisii**, *A. curator*, *A. cydoniae*, *A. dentimitratus*, *A. foecundatrix**, *A. galeatus*, *A. glandulae*, *A. gemmeus*, *A. grossulariae**, *A. hystrix*, *A. infectorius**, *A. inflator*, *A. insana**, *A. kollari**, *A. lucidus**, *A. malpighii*, *A. moreae*, *A. multiplicatus*, *A. pictus*, *A. polycerus*, *A. sternlichti*, *A. theophrastea**, *A. tomentosus**, *Aphelonyx cerricola*, *Biorhiza pallida**, *Callirhytis glandium*, *C. reticulatus*, *C. rufescens*, *Cerroneuroterus gyulaigaraiae*, *C. lanuginosus**, *Cynips cornifex*, *C. divisa*, *C. korsakovi*, *C. loricatus*, *C. quercus**, *C. quercusfolii**, *Chilaspis israeli*, *Neuroterus albipes*, *N. anthracinus*, *N. numismalis**, *N. quercusbaccarum**, *N. tricolor**, *Pseudoneuroterus macropterus**, *P. saliens**, *Synophrus olivieri*, *S. politus**, *Trigonaspis megaptera*, *T. synaspis**.

25 new species were described during this project from Iran: *Andricus assarehi*, *A. atkinsonae*, *A. chodjii*, *A. coriariformis*, *A. csokai*, *A. istvani*, *A. libani*, *A. megalucidus*, *A. megatruncicolus*, *A. pseudoaries*, *A. pujadevillari*, *A. sadeghii*, *A. schoenroggei*, *A. stellatus*, *A. stonei*, *Aphelonyx persica*, *A. kordestanica*, *Dryocosmus caspiensis*, *D. jungalii*, *D. mikoi*, *D. tavakolii*, *Pseudoneuroterus mazandarani*, *P. nichollsi*, *Synophrus libani*, *S. syriacus*.

Study on the biology and efficiency determination testes of *Habrobracon hebetor* Say (Hymenoptera: Braconidae) on larvae of *Plodia interpunctella* Hübner (Lepidoptera: Pyralidae)

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The results of laboratory studies on the biology *H. hebetor* at 30 ± 2 °C, $60 \pm 5\%$ RH and ultimate larvae of *Plodia interpunctella* indicated that developmental duration of this parasitoid takes place in 10.765 days (egg 1.575 ± 0.30 days, larvae 2.592 ± 0.11 days and pupa 6.598 ± 0.15 days). Newly emerged female parasitoid responded well to host larvae. The adult lived longest when provided with both honey and water, without food they survived less than 4 days. Results showed that female parasitoid deposited eggs throughout the 24 hours, period. There were no significant difference, in reproduction and longevity between virgin and mated females. Development and survival periods of *H. hebetor* on *P. interpunctella* were studied at five temperatures ranging from 17 to 35°C. The lower developmental thresholds for eggs, larvae and pupa were extrapolated from the linear relationship between temperature and growth rate lower developmental thresholds were estimated to be 5.907 (egg), 14.749 (larvae), 15.7156 (pupa). Degree-day (DD) accumulations of 41.88, 45.05 and 89.14 were required for completion of the egg, larvae and pupa stages. Variation of trend of progeny sex ratio and sex ratio in relation to host density and effect of age parasitoid and host size on it showed that *H. hebetor* has a male biased sex ratio. The total number of eggs per female per day (mean) increased from 13.8 to with the host density increasing from 1 to 16. study coordinative effect of age parasitoid and host size on progeny sex ratio showed that age parasitoid increased sex ratio (female/ total) significantly, but host size had no effect on sex ratio and interaction between age parasitoid and size host on sex ratio of progeny have not significant effect.

Structural colours in Hymenoptera wings

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The patterns of bright structural colours on transparent wings of small Hymenoptera (body length ≤ 3 mm, e.g. most species in superfamily Chalcidoidea) have been totally overlooked by biologists. The wing morphology regarding colour patterns in such groups has been described in terms of “black and brown” with complete disregard for the colourful reflections of the wing surface. With the discovery of WIP (see below) real colour patterns can now be observed, and investigated to get a more complete evolutionary picture, and the usual concept that wings in the Hymenoptera can not match the incredible diversity of butterfly wing patterns seems now an oversimplification.

Transparent wings of tiny Hymenoptera are extremely thin (between 100 and 1000 nanometers thick) and display vivid colour patterns due to thin film interference. We call these patterns WIP – Wing Interference Patterns, and they reflect uneven physical thickness of the wing membrane and are non-iridescent and taxon-specific. The physics of this optical phenomenon is pretty simple – two beam interference, but morphological features of the wings play their role to dioptrically stabilize and reinforce WIP by membrane corrugations, setae arrangements, venation and pigmentation.

WIPs appear strong both in live and dry museum specimens and they are relatively easy to document digitally which makes this new morphological character a user-friendly tool in biodiversity investigations. WIP have a large potential in the studies of diversity and evolution in insects, integrating biophysics, taxonomy, genetics and behavioral biology.

The ant genus *Monomorium* in Australia: morphological plasticity or cryptic diversity?

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Monomorium Mayr (Formicidae) is a highly abundant, widespread and diverse genus of ants. Several Australian “species” show considerable morphological and chemical variation, while evidence from ecological and preliminary molecular research suggests significant cryptic diversity. However, rigorous morphological criteria that support separate species have proved difficult. In this study we are using sequence data from multiple loci to generate a phylogeny for the Australian species in order to test the current species group relationships and to generate hypotheses for species boundaries in the seed harvesting *M. “rothsteini”* complex. Preliminary results indicate that species groups, as currently understood, are not reflected in the molecular phylogeny and that several groups may be paraphyletic or polyphyletic. Our results also provide preliminary evidence that *M. “rothsteini”* represents a large complex of species distributed across the continent.

The effect of grassland restoration on bee communities – a preliminary study in Hortobágy National Park, Hungary

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The decline of ecosystem services in response to agricultural intensification has become a worldwide phenomenon, and pollinators are extremely threatened. We studied bee assemblages in the Egyek-Pusztakócs marsh and grassland system in Hortobágy National Park in the summer of 2009. Grassland restoration was carried out on 760 ha former croplands (alfalfa, wheat and sunflower fields) between 2005 and 2008. Year 1 following restoration was characterized by dense cover of weeds. The cover of grasses exceeded that of weeds by Year 2, and the first non-sown grasses and dicotyledonous species occurred from Year 3. The aim of our preliminary study was to compare bee communities on one-, two-, three- and four-year-old grassland restorations and native grasslands and to compare capture success of traps with different placement and killing liquid. The four age treatments plus the native grassland were replicated at two sampling sites (10 sites total). At each site, twelve yellow plate-traps (25cm diameter x 3cm high) were set, with two placement methods (on the ground, on a 1.2-m stick) and two killing liquids (ethylene-glycol with detergent, water with detergent) each replicated by three traps. The distance between traps was 10 m in every direction. We analyzed data by one-way analyses of variance (ANOVA) using species richness and abundance as response variables. We found a significant positive correlation between bee species richness and abundance and the age of grasslands. Both species richness and abundance decreased from Year 1 to 2, and increased afterwards. Year 4 grassland restorations had significantly more species and higher abundances than Year 2 restorations.



Although several traps were destroyed by grazing livestock, mowing or fire management, most bee specimens were collected by traps placed on sticks and filled with ethylene-glycol plus detergent. Our results suggest that grassland restoration effectively increases the species richness and abundance of bee communities and can be useful in protecting pollinators and maintaining ecosystem services.

Turkish Eurytomidae and Torymidae (Hymenoptera, Chalcidoidea): published data and new records

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In the present paper all available published data concerning Turkish Eurytomidae and Torymidae (Hymenoptera, Chalcidoidea) is summarized. Seventy-three species from Eurytomidae and 40 species from Torymidae were recorded in entomological papers till now. As a result of our study, new records to the Turkish fauna are herein presented: 7 species from Eurytomidae (*Bruchophagus platypterus* (Walker, 1834); *Eurytoma augasmae* Zerova, 1977; *Eurytoma herbaria* Zerova, 1994; *Eurytoma koeleriae* Erdős, 1969; *Eurytoma strigifrons* Thomson, 1875; *Rileya asiatica* Zerova, 1976 and *Systole conspicua* Erdős, 1951) and 10 species from Torymidae (*Eridontomerus fulviventrus* Erdős, 1954; *Megastigmus stigmatizans* (Fabricius, 1798); *Megastigmus synophri* Mayr, 1874; *Pseudotorymus arvernensis* (Walker, 1833); *Pseudotorymus papaveris* (Thomson, 1875); *Pseudotorymus rosarum* (Zerova et Seregina, 1992); *Torymus cyaneus* Walker, 1847; *Torymus flavipes* (Walker, 1833), *Torymus longicalcar* (Graham, 1994) and *Torymus pygmaeus* (Mayr, 1874).

Montage Ultra: High Resolution Imaging of Parasitic Hymenoptera

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The small size of parasitic wasps hinders an appreciation of their existence by much of society. Here, a simple method for producing very large, high resolution images is presented, with the intention of increasing awareness via the aesthetic forms of microhymenoptera. The results have myriad uses, including public museum display, morphological diagrams, and home decoration.

Parasitoid communities (Chalcidoidea) of oak gallwasps of Iran (Hymenoptera: Cynipidae)

Majid Tavakoli^{1*}, George Melika, S. Ebrahim Sadeghi, Richard R. Askew, Graham N. Stone, Hassan Barimani, Davood Aligholizadeh, Ali asghar Dordaii, Hamid Yarmand, Mohammad Reza Zargaran & Seadat Mozafarian

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This study was carried out during 2001-2008. Six main species of *Quercus* were sampled: *Q. infectoria*, *Q. macranthera*, *Q. petraea*, (in *Quercus s.s.* section of oaks), and *Q. brantii*, *Q. libani*, *Q. castaneifolia* (in *Cerris* section oaks) in Zagross, Arasbaran, Fandoghlo, Andabil, Tarom Olya & Sofla, and Caspian forests of Iran. Eighty two (82) oak gallwasp species were found on different oak species in Iran. Under laboratory conditions 42 species of chalcidoid parasitoids were reared and identified from 52 species of oak gallwasps (from 46 asexual and 6 sexual gall forms): Eurytomidae – 8 species (*Sycophila biguttata*, *S. flavicollis*, *S. iracemae*, *S. variegata*, *Eurytoma brunniventris*, *E. pistacina*, *E. sp. nr infracta*, *Eurytoma ?strigifrons*); Torymidae – 6 (*Megastigmus dorsalis*, *M. stigmatizans*, *Torymus auratus*, *T. cyaneus*, *T. flavipes*, *T. geranii*), Ormyridae – 2 (*Ormyrus nitidulus* and *O. pomaceus*), Pteromalidae – 9 (*Cyrtotypx robustus*, *Cecidostiba fungosa*, *C. semifascia*, *Hobbya stenonota*, *Mesopolobus albitarsus*, *M. amaeus*, *M. fasciiventris*, *M. sericeus*, *M. tibialis*), Eupelmidae – 6 (*Eupelmus annulatus*, *E. cerri*, *E. matranus*, *E. rostratus*, *E. urozonus*, *E. vesicularis*), Eulophidae – 11 (*Aulogygnus arsames*, *A. gallarum*, *A. testaceoviridis*, *A. trilineatus*, *Cirrospilus viticola*, *Closterocerus trifasciatus*, *Pediobius rotundatus*, *P. lysis*, *Aprostocetus sp.*, *Aprostocetus sp. nr domenichinii*, *Baryscapus berhidanus*). Around 106 species of chalcids and ichneumonids are recorded from oak cynipid galls in the Western Palaearctic, mainly in Europe which from near 50% of known species occur in Iran also.

Oak cynipid gall inquiline of Iran (Hymenoptera: Cynipidae: Synergini)

Majid Tavakoli¹*, George Melika, S. Ebrahim Sadeghi, Juli Pujade-Villar, Graham N. Stone, Hassan Barimani, Davood Aligholizadeh, Ali asghar Dordaii, Hamid Yarmand, Mohammad Reza Zargaran & Seadat Mozafarian

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This study was carried out during 2001-2008. Six main species of *Quercus* were sampled: *Q. infectoria*, *Q. macranthera*, *Q. petraea*, (in *Quercus s.s.* section of oaks), and *Q. brantii*, *Q. libani*, *Q. castaneifolia* (in *Cerris* section oaks) in Zagross, Arasbaran, Fandoghlo, Andabil, Tarom Olya & Sofla, and Caspian forests of Iran. Eighty two (82) oak gallwasp species were found on different oak species in Iran. Fifteen known cynipid inquiline species associated with oak cynipid galls (Hymenoptera, Cynipidae: Synergini and Cynipini), were recorded for the Iranian cynipid fauna: *Ceroptres cerri* Mayr, *C. clavicornis* Hartig, *Saphonecrus haimi* (Mayr), *Synergus gallaepomiformis* (B. de Fonsc.), *S. pallidipennis* Mayr, *S. pallipes* Hartig, *S. reinhardi* Mayr, *S. thaumacerus* (Dalman), *S. umbraculus* (Olivier) and *S. variabilis* Mayr. Five new species of cynipid inquilines were recently described (Sadeghi *et al.* 2006), *Saphonecrus irani* Melika & Pujade-Villar, *Synergus acsi* Melika & Pujade-Villar, *Synergus bechtoldae* Melika & Pujade-Villar, *Synergus palmirae* Melika & Pujade-Villar and *Synergus mikoi* Melika & Pujade-Villar. Recently morphological and molecular data was used to revise the inquiline genus *Synophrus* Hartig, 1843 members of which are notable for extensively modifying the structure of galls induced by oak gallwasp hosts on oaks in the section *Cerris* of *Quercus* subgenus *Quercus* in the Western Palaearctic (Pénzes *et al.* 2009). Previous taxonomic treatments have recognized three Western Palaearctic species of *Synophrus*: *S. pilulae*, *S. politus* and *S. olivieri* which from the two last species were known from Iran also. As the result of the revision, other two new species were described from Iran: *S. libani* Melika et Pujade-Villar and *S. syriacus* Melika et Pujade-Villar, thus the total number of *Synophrus* species known from Iran is four while 19 inquiline species were recorded all together.

Mitochondrial COI gene sequence in European Eumeninae wasps (Hymenoptera: Vespidae): intra-specific diversity and applicability for DNA barcoding

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The aim of the study was to estimate the intra- and interspecific genetic variability within selected European Eumeninae wasps and to examine the utility of partial sequence of the mitochondrial cytochrome oxidase subunit I gene (COI) for species barcoding and for assessment of intra-specific population structure at different geographic scales.

Wasps of six cavity-nesting Eumeninae genera were reared from trap-nests exposed in semi-natural and agricultural landscapes of 13 European countries, including Austria, Estonia, France, Germany, Greece, Hungary, Italy, Lithuania, Poland, Serbia, Spain, Sweden, and United Kingdom. The specimens represented 19 species: *Ancistrocerus antilope*, *A. claripennis*, *A. gazella*, *A. nigricornis*, *A. parietinus*, *A. trifasciatus*, *Discoelius dufourii*, *D. zonalis*, *Euodynerus notatus*, *E. posticus*, *E. quadrifasciatus*, *Leptochilus regulus*, *Symmorphus allobrogus*, *S. bifasciatus*, *S. crassicornis*, *S. debilitatus*, *S. gracilis*, *S. murarius*, and *Tachyancistrocerus rhodensis*.

DNA was extracted from wasp thoracic muscles according standard protocols. We amplified partial sequences of the COI gene (672bp). For 17 species, these sequences were established for the first time. They were compared using neighbour-joining (NJ) analysis, implemented in MEGA2.1. The haplotype networks for polymorphic species were constructed using the software TCS 1.13.

Most of the studied European species demonstrated a very limited intraspecific variation and formed discrete clusters in the NJ tree. Out of them, the highest haplotype diversity was found in *Discoelius zonalis* and *Symmorphus bifasciatus*. Haplotypes of some species, like *Ancistrocerus trifasciatus*, displayed geographic variations, however, in *Discoelius zonalis* and *Symmorphus bifasciatus*, the intra-specific variability did not demonstrate a geographic pattern.

Previously published partial sequences of the COI gene of other (mostly Nearctic) eumenine species were retrieved from the GenBank database and included into NJ analysis. Overall NJ analysis of distances among all representatives of the subfamily with known COI gene sequence resulted in a well resolved tree, with only two clades including more than one species. Our results demonstrate that the mtDNA COI gene sequence of Eumeninae wasps is useful for species barcoding and, for some species, may be applied for the intra-specific diversity studies.

Systematic and phylogeny of the endemic south-eastern Asiatic *Pristaulacus comptipennis* species group (Hymenoptera Evanioidea: Aulacidae)

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Aulacidae comprise some 221 extant species belonging to two genera: *Aulacus* Jurine, 1807, with 75 species and *Pristaulacus* Kieffer, 1900 (including the former *Panaulix* Benoit, 1984), with 146 species. Both genera are represented in all zoogeographic regions, except Antarctica (Smith, 2001, *Contributions on Entomology, International* 4(3): 261-319). Aulacidae are koinobiont endoparasitoids of wood-boring larvae of Hymenoptera and Coleoptera. Hosts are larval Xiphydriidae (Hymenoptera) and, most frequently, Buprestidae and Cerambycidae (Coleoptera). In south-eastern Asia, Aulacidae are essentially unexplored, and there is no comprehensive treatment, most all work being individual species descriptions or treatments of a smaller geographic areas. Here we present the results of the first comprehensive research on the distinctive *Pristaulacus comptipennis* species-group, which is endemic to south-eastern Asia and occurs from Japan to China, Thailand, and Viet Nam. The group was shown to be monophyletic in the phylogenetic study by Turrisi et al. (2009, *Invertebrate Systematics* 23: 27-59) and is mainly characterized by one autapomorphy, the more or less deep occipital median emargination of the head, which is most obvious in dorsal view. Based on our study, sixteen valid species are recognized, of which only 5 were previously described (type material examined), and 11 are newly described (from China, Laos, Thailand and Viet Nam). Phylogenetic analyses are based on a previous set of 79 morphological characters provided by Turrisi et al. (2009) plus 3 additional ones. Of this data set, 23 informative characters are selected and scored for analyses under different conditions (unordered, ordered, equal and implied weighting), using TNT for Parsimony Analysis. Two main large subgroups were retrieved, the first one (containing 5 species) having two tooth-like processes on the lateroventral margin of pronotum, anterior part of mesoscutum protruding and acutely shaped and six tooth-like processes on the claws; the other large clade (with 11 species) is characterized by the long pronotum (height/length < 1.0) and the long petiole (length/width: > 3.0). Other minor clades are identified and discussed. For all treated species a comprehensive illustrated key is proposed.

The gallwasp venom apparatus

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Comparisons of the female venom apparatus in Cynipoid insect parasitoids and gall inducers show that the venom reservoir is most often relatively larger in the gall inducing females. The function of the venom in gall wasps is unknown and the present study aims at describing the ultrastructure of the venom apparatus as well as exploring possible functions of the venom. Light and transmission electron microscopy indicate that there are no muscles in the venom reservoir walls, and thus ejection of venom is probably controlled by the muscles of the ovipositor apparatus surrounding the venom apparatus unlike many other Hymenoptera which have independent muscle control of the venom apparatus. Thus the cynipoid venom is probably transferred to a host together with the eggs which may indicate that the venom is involved in host manipulation. Change in the physical appearance between the venom in the gland canal and the venom in the reservoir is observed and the glandular activity is apparently not restricted to the venom gland, but probably also occur in the reservoir wall.



**Taxonomic notes on the oak gallwasp *Callirhytis hakonensis* Ashmead
(Hymenoptera: Cynipidae), with description of the sexual generation**

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Callirhytis Foerster, 1869 (Hymenoptera: Cynipidae: Cynipini) is a Holarctic genus of oak gallwasps, most of which have the alternation of generations (a life cycle involving the sexual and asexual generations over the course of one year). This genus has 150 species, four of which occur in the Eastern Palearctic Region. One of them, *C. hakonensis* Ashmead, 1904, is distributed in Japan. The original description of this species is very simple and is based on a single adult female with no mention of the presence of the transversely rugose mesoscutum, which is the main diagnostic feature of the genus *Callirhytis*. Some taxonomists have suggested that this species is most probably an asexual female of *Andricus*.

The late Mr. Masuda previously demonstrated the alternation of generations in this gall wasp by rearing experiments. Comparisons of the external morphology of the holotype (female adult) of *C. hakonensis* and the female adults reared and identified as the asexual generation of this species by him corroborated the accuracy of his identification. The holotype (the asexual generation) of this cynipid is re-described, and female and male adults of the sexual generation are described on the basis of specimens reared by him.

Since the adults of the asexual and sexual generations had the diagnostic features of the genus *Andricus* and not *Callirhytis*, this gall wasp should be transferred to the genus *Andricus*. Judging from the descriptions of the wasps and galls, *A. symbioticus* Kovalev and *A. attractus* Kovalev, which were described from Russia, may be synonymized with this species.

Seed affecting wasps of none-legume forage plants in Iran

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Biotic agents have been blamed for significant loss to forage plant seeds. Generally insects are the principal seed predators in Iran. None-legume forage plants are facing a serious problems in this regard due to various insects especially many species of wasps. Insects eat seeds within pods, causes abortion of developing seeds. The present study started in 2009 provides insight into the complex of insects, as well as information on the wasps' affecting major none legume range plants across the country. We monitored fields with sweep net beginning pre-bloom to harvest time. The insects were collected by search-out method. Seeds were dissected and examined to determine infestation at harvest. Larvae feeding on developing seeds were collected and placed in rearing jars for further development. Data collection was made at 15 days interval during the entire study period. Data was recorded on the wasps associated with the seeds, their periodicity, population density and damage. The obtaining data base will be used for designing appropriate strategies to protect viable seeds. This will be useful for our future work since it provide deep insight into the complex of biotic agents which play an important role in maintaining and supplying healthy seeds for range development plans across the country.



Record on Indian species of *Trichogramma* Westwood, along with two new species, their host range and application against forest insect pests

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Genus *Trichogramma* Westwood, 1833, with the type species *Trichogramma evanescens* is belonging to the order Hymenoptera, with size ranging from 0.4-0.6 mm. Species of *Trichogramma* have been utilized in biological control of insect pests all over the world. Major contributions on the release of *Trichogramma* spp. for biological control of lepidopterous pests have been made in last three decades. *Trichogramma* spp. have been utilized against the insect pests of agricultural crops, commercial cash crops, orchards and forest insect pests as well. They control the population of harmful insects at egg stage. Hence, the release of *Trichogramma* spp., have been made extensively all over the world for biological control of lepidopterous pests.

Systematic survey for screening the indigenous species of *Trichogramma* was carried out (2005-2008) from central India, covering Madhya Pradesh, Chhattisgarh, Maharashtra and Orissa. Three species: *T. breviciliata* Yousuf & Hassan, *T. latipennis* Yousuf & Hassan and *T. kankerensis* Yousuf & Hassan have already been reported. Two more new species of *Trichogramma*: *T. breviflagellata* sp.n. and *T. paraplasseyensis* sp.n., are being reported. The new species have been illustrated and described in detail. As a whole till date, twenty six species of *Trichogramma* (*T. achaeae* Nagaraja & Nagarkatti, *T. agriae* Nagaraja, *T. breviciliata* Yousuf & Hassan, *T. brevifringiata* Yousuf & Shafee, *T. chilonis* Ishii, *T. chilotraeae* Nagaraja & Nagarkatti, *T. convolvuli* Nagaraja, *T. cuttackensis* Nagaraja, *T. danausicida* Nagaraja, *T. flandersi* Nagaraja & Nagarkatti, *T. hebbalensis* Nagaraja, *T. hesperidis* Nagaraja, *T. japonicum* (Ashmead), *T. kankerensis* Yousuf & Hassan, *T. kashmirica* Nagaraja et. al., *T. latipennis* Yousuf & Hassan, *T. manii* Nagaraja & Gupta, *T. pallidiventrtris* Nagaraja, *T. plasseyensis* Nagaraja, *T. poliae* Nagaraja, *T. raoi* Nagaraja, *T. sankarani* Nagaraja, *T. semblidis* (Aurivillius) and *T. thalense* Pinto & Oatman including two new species, *T. breviflagellata* sp. n. and *T. paraplasseyensis* sp.n.) have been recorded from India. Host-range of all *Trichogramma* species, recorded from India has been up-dated.

Laboratory culture of *Trichogramma raoi*, *T. plasseyensis* and *T. breviciliata* has been maintained on the eggs of *Corcyra cephalonica* and these have been tested against forest insect pests. Laboratory rearing of forest insect pests was also carried out. Eggs of forest insect pests (*Hyblaea puera*, *Eutectona machaeralis* and *Hasora alexis*) were pasted on paper stripes (100 eggs on each 2X 7 cm stripe with ten replications) and introduced *Trichogramma* species in each case having a set of one and five pairs of *Trichogramma* wasps. All three species of *Trichogramma* accepted the eggs of insect pests, introduced for testing. Results on the laboratory efficacy of *Trichogramma raoi*, *T. plasseyensis* and *T. breviciliata* against teak defoliator (*Hyblaea puera*) and teak skeletonizer (*Eutectona machaeralis*), and *Trichogramma breviciliata* against defoliator of *Holoptelia integrifolia* (*Hasora alexis*) have been discussed in detail.

Field efficacy of five *Trichogramma* was carried out in teak forest against teak skeletonizer (*E. machaeralis*) by releasing these wasps in 1.5 lakhs/ha, with four replications, having plot size of one ha each with buffer of two ha; for three years. Skeletonization of teak leaves in the released teak forest area was reduced about 50 % and details on results obtained on field efficacy of *Trichogramma raoi* along with *T. chilonis*, *T. brasiliensis*, *T. japonicum* and *T.*

pretiosum, commonly utilized species in biological control programmes, against teak skeletonizer has also been discussed.

Hymenopterans on tree barks along climatic and altitudinal gradients in Ecuador

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In the present study Hymenopterans collected in the course of the MACAG-Project (“Monitoring of Arthropods along Climate and Altitude Gradients”) are studied. The MACAG-Project aims at monitoring and evaluating climate change and altitudinal gradient driven impacts on the arthropod faunas on undamaged tree barks in primeval and near-to-nature forests.

In this context we analysed the composition of the Hymenoptera collected in 2007 in six plots (10 x 10 m, 10-12 trees each) in Podocarpus NP in SE-Ecuador at three different altitudes (rainforest 1000 m, mountain rain forest 2000 m and Páramo 3000 m). On 71 trees 131 specimens out of 97 species and 16 families were found, displaying a substantial singleton proportion. This pattern indicates a high level of trophic position of the recorded – almost solely parasitoid – Hymenoptera in the bark fauna-foodweb, where mites (mostly grazers and predators) and beetles (mostly fungi feeders and mite-predators) are the dominant groups worldwide (unpubl. data Schmidl).

In contrast to the low specimen-species-ratio of 1.15 in Hymenoptera, the beetle fauna of the same 71 sampled tree barks has a specimen-species-ratio of 3.0. This corroborates the assumption that the low abundance is a foodweb matter – thus a functional rarity – and not only the typical rarity of tropical rainforest insects (“singleton problem”). Total abundance (Coleoptera: 940 specimens, Hymenoptera: 131 specimens) gives additional evidence and highlights the different biology of these two mega-diverse insects orders.

The diversity pattern of Hymenoptera along the altitudinal gradient shows the highest species number at mid elevation (very similar to the beetle results), with (on average) 12.5 species per plot at 1000 m (rainforest), 27 sp. at 2000 m (mountain rain forest), and 12 sp. at 3000 m (Páramo), reflecting the structural properties of the forest and richness of the tree bark vegetation as trophic basis. Nevertheless, the specimen-species-ratio (between 1.04 and 1.33) does differ more between plots of the same altitudinal level than between altitudes, supporting the “functional rarity” stated above. A Soerensen-Index calculation reveals that there is almost no similarity between the Hymenoptera species sets of the three altitudinal levels, and also extremely low between plots of the same levels, a logical consequence of the low specimen-species-ratios.

A similar diversity pattern is reflected on family-level: The highest diversity was also found at 2000 m with 12 of 16 families, followed by 1000 m with 11 and 3000 m with 8 families.

Further sample analyses with more than 250 additional samples from 2008 and 2009 will allow deeper insights into diversity patterns and total species richness, using rarefaction and multivariate methods on a broader data basis.



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