

September 27 – 29, 2013

Japanisches Palais Dresden

Palaisplatz 11 · 01097 Dresden

6th Dresden Meeting on **Insect Phylogeny**

On Friday, September 27, at 18:00,

there will be a talk on early dinosaurs in the same building
(Japanisches Palais; in German):

„Auf den Spuren früher Saurier zwischen Thüringer Wald und
Rocky Mountains“

Sebastian Voigt
(GEOSKOP Urweltmuseum Burg Lichtenberg)

Organisation staff

Main organiser

Klaus-Dieter Klass

Co-organiser

Niklas Wahlberg

Logistic support

Birgit Walker

Sigrid Beutner

Technical support/IT

Andreas Weck-Heimann

Matthias Nuß

Conference Logo and Layout

Markward Herbert Fischer

Oral Presentations — Friday, September 27



Chair of *morning* session:
Chair of *afternoon* session:

Klaus-Dieter Klass
Niels Peder Kristensen

09:00 — 09:05 **Opening**

KLAUS-DIETER KLASS (Senckenberg Natural History Collections Dresden, Germany)

09:05 — 09:50 **Molecular phylogenetics of Arthropoda: capturing phylogenetic signal from serine with 21-amino-acid models**

ANDREAS ZWICK (Department of Entomology, State Museum of Natural History Stuttgart, Germany) — **JEROME REGIER** (Institute for Bioscience and Biotechnology Research & Department of Entomology, University of Maryland, USA) — **DERRICK ZWICKL** (Department of Ecology and Evolutionary Biology, University of Arizona, USA)

09:50 — 10:05 **Introduction to 1KITE and the first steps in the project's workflow: aims, people, subprojects, taxon sampling and collecting**

KAREN MEUSEMANN (CSIRO Ecosystem Sciences, Australian National Insect Collection, Acton, Australia; Zoologisches Forschungsmuseum Alexander Koenig, Zentrum für Molekulare Biodiversitätsforschung, 53113 Bonn, Germany) — **RALPH S. PETERS** (Zoologisches Forschungsmuseum Alexander Koenig, Abteilung Arthropoda, 53113 Bonn, Germany) — on behalf of the 1KITE Consortium

10:05 — 10:35 **Towards a hexapod tree of life: pitfalls and challenges of the phylogenomic approach**

BERNHARD MISOF (Zoologisches Forschungsmuseum Alexander Koenig, Zentrum für Molekulare Biodiversitätsforschung, 53113 Bonn, Germany) — on behalf of the 1KITE Consortium

10:35 — 10:50 **Potential and limits of the 1KITE transcript data for facilitating the application of DNA enrichment protocols in insect phylogenetics**

OLIVER NIEHUIS (Zoologisches Forschungsmuseum Alexander Koenig, Zentrum für Molekulare Biodiversitätsforschung, 53113 Bonn, Germany) — **MANUELA SANN** (Museum für Naturkunde, 10115 Berlin, Germany) — **CHRISTOPH MAYER** (Zoologisches Forschungsmuseum Alexander Koenig, Zentrum für Molekulare Biodiversitätsforschung, 53113 Bonn, Germany) — **KAREN MEUSEMANN** (CSIRO Ecosystem Sciences, Australian National Insect Collection, Acton, Australia) — **ALEXANDER DONATH** (Zoologisches Forschungsmuseum Alexander Koenig, Zentrum für Molekulare Biodiversitätsforschung, 53113 Bonn, Germany) — **RALPH PETERS** (Zoologisches Forschungsmuseum Alexander Koenig, Abteilung Arthropoda, 53113 Bonn, Germany) — **CHRISTOPH BLEIDORN** (Universität Leipzig, Molekulare Evolution und Systematik der Tiere, 04103 Leipzig, Germany) — **MICHAEL OHL** (Museum für Naturkunde, 10115 Berlin, Germany)

10:50 — 11:20 **Coffee Break**

Oral Presentations — Friday, September 27



Chair of *morning* session: Klaus-Dieter Klass
Chair of *afternoon* session: Niels Peder Kristensen

11:20 — 12:00

Insect morphology in the age of phylogenomics

ROLF G. BEUTEL (Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany) —
HANS POHL (Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany) —
BENJAMIN WIPFLER (Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany) —
FRANK FRIEDRICH (Biozentrum Grindel und Zoologisches Museum, Universität Hamburg, Germany)

12:00 — 12:30

A super matrix approach to the phylogeny of Odonata

FRANK L. CARLE (Rutgers University, Department of Entomology, 93 Lipman Dr., New Brunswick, NJ 08901, USA) — **MICHAEL L. MAY** (Rutgers University, Department of Entomology, 93 Lipman Dr., New Brunswick, NJ 08901, USA) — **KARL M. KJER** (Rutgers University, Department of Ecology, Evolution and Natural Resources, 14 College Farm Rd., New Brunswick, NJ 08901, USA)

12:30 — 12:50

First insights in the embryonic development of the damselfly *Ischnura elegans*

SABRINA SIMON (Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024, USA) — **MERCER R BRUGLER** (Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024, USA) — **ROB DESALLE** (Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024, USA) —
HEIKE HADRYS (ITZ, Ecology & Evolution, Stiftung Tierärztliche Hochschule Hannover, 30559 Hannover, Germany)

12:50 — 14:00

Lunch Break

14:00 — 14:35

Lower neopteran relationships — new insights into an old problem

BENJAMIN WIPFLER (Friedrich Schiller Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Vor dem Neutor 1, 07743 Jena, Germany)

14:35 — 15:05

Global biogeography of the family Grylloblattidae (Grylloblattodea) and their underappreciated species richness

SEAN D. SCHOVILLE (University of Wisconsin, Madison, Department of Entomology, Room 237 Russell Labs Building, 1630 Linden Drive, Madison, WI 53706, USA)

15:05 — 15:25

Coffee Break

15:25 — 16:25

Poster Session I

Presenters of all posters are kindly asked to stay with their posters

Oral Presentations — Friday, September 27



Chair of *morning* session: Klaus-Dieter Klass
Chair of *afternoon* session: Niels Peder Kristensen

16:25 — 16:55

Finding the sistergroup of Cryptocercidae + Isoptera: a dark horse wins

MARIE DJERNÆS (Natural History Museum, London, United Kingdom) — **KLAUS-DIETER KLASS** (Senckenberg Natural History Collections Dresden, Germany) — **PAUL EGGLETON** (Natural History Museum, London, United Kingdom)

16:55 — 17:15

Praying mantis revisionary systematics and the origins of plant mimicry in the Hymenopodidae (Mantodea)

GAVIN SVENSON (Cleveland Museum of Natural History, Cleveland, Ohio, USA) — **FRANK WIELAND** (Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, Hamburg, Germany)

Oral Presentations — Saturday, September 28

Chair of *morning* session: Brian Wiegmann
Chair of *afternoon* session: Niklas Wahlberg



09:00 — 09:30 The Palaeozoic and Early Mesozoic stems of palaeopterans and polyneopterans

OLIVIER BÉTHOUX (CR2P UMR 7207, MNHN, UPMC, CNRS, 8 rue Buffon, CP38, 75005 Paris, France)

09:30 — 10:00 Nomenclatural dissidence applied to pterygotans

OLIVIER BÉTHOUX (CR2P UMR 7207, MNHN, UPMC, CNRS, 8 rue Buffon, CP38, 75005 Paris, France)

10:00 — 10:25 The Fossil Calibration Database

JESSICA L. WARE (Rutgers University, 195 University Avenue, room 206, Newark, NJ, 07102, USA) — **DANIEL KSEPKA** (National Evolutionary Synthesis Center, North Carolina Research Triangle, USA) — **JAMES PARHAM** (California State University, Fullerton, Department of Geological Sciences, California State University, Fullerton, CA 92834-6850, USA)

10:25 — 10:55 Coffee Break

10:55 — 11:20 Wing base structure of Paraneoptera and its phylogenetic significance

KAZUNORI YOSHIZAWA (Systematic Entomology, Hokkaido University, Japan)

11:20 — 11:50 The thrips in their paraneopteran context

BRUCE S. HEMING (University of Alberta, Department of Biological Sciences, Edmonton, Alberta, CW 405, Biological Sciences Bldg., Canada, T6G 2E9) — **GERALD B. MORITZ** (Martin-Luther-University Halle-Wittenberg, Department of Biological Sciences, Institute for Biology, Domplatz 4, 06108 Halle / Saale, Germany)

11:50 — 12:10 Relative rates of genomic divergence between humans, chimps, and their lice

KEVIN P. JOHNSON (Illinois Natural History Survey, Univ. of Illinois, Champaign, IL, USA) — **JULIE M. ALLEN** (Illinois Natural History Survey, Univ. of Illinois, Champaign, IL, USA) — **BRETT P. OLDS** (Department of Animal Biology, Univ. of Illinois, Urbana, IL, USA) — **LAWRENCE MUGISHA** (College of Veterinary Med., Makerere Univ., Kampala, Uganda) — **DAVID L. REED** (Florida Museum of Natural History, Univ. Florida, Gainesville, FL, USA) — **KEN N. PAIGE** (Department of Animal Biology, Univ. of Illinois, Urbana, IL, USA) — **BARRY R. PITTENDRIGH** (Department of Entomology, Univ. of Illinois, Urbana, IL, USA)

12:10 — 12:25 We make a Photo!

All speakers and visitors of the meeting are invited to group for a photo in the central yard of the building (Japanisches Palais); please go there immediately after the end of the last morning talk!

Oral Presentations — Saturday, September 28

Chair of *morning* session: Brian Wiegmann

Chair of *afternoon* session: Niklas Wahlberg



12:25 — 13:30

Lunch Break

13:30 — 14:05

Molecular phylogenetics of beetles

ALFRIED P. VOGLER (Department of Life Sciences, NHM, London, United Kingdom; Department of Life Sciences, Imperial College London, Ascot, Berkshire, United Kingdom) — **CARMELO ANDUJAR** (Department of Life Sciences, NHM, London, United Kingdom) — **CHRIS BARTON** (Department of Life Sciences, NHM, London, United Kingdom; Department of Life Sciences, Imperial College London, Ascot, Berkshire, United Kingdom) — **ANDRES BASELGA** (Departamento de Zoología, Facultad de Biología, Universidad de Santiago de Compostela, c 15782 Santiago de Compostela, Spain) — **LADISLAV BOCAK** (Department of Life Sciences, NHM, London, United Kingdom; Dept. Zoology, Faculty of Science UP, Olomouc, Czech Republic) — **DOUGLAS CHESTERS** (Department of Life Sciences, NHM, London, United Kingdom; Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Beijing, 100101, China) — **ALEX CRAMPTON-PLATT** (Department of Life Sciences, NHM, London, United Kingdom; University College London, Gower Street, London, United Kingdom) — **CONRAD GILLETT** (Department of Life Sciences, NHM, London, United Kingdom; University of East Anglia, School of Biological Sciences, Norwich, United Kingdom) — **BENJAMIN LINARD** (Department of Life Sciences, NHM, London, United Kingdom) — **MARTIJN J. T. N. TIMMERMANS** (Department of Life Sciences, NHM, London, United Kingdom; Department of Life Sciences, Imperial College London, Ascot, Berkshire, United Kingdom)

14:05 — 14:30

Phylogeny and evolutionary history of the Hydrophilidae (Coleoptera: Hydrophiloidea) inferred from a multi-gene dataset

ANDREW E.Z. SHORT (Division of Entomology, Biodiversity Institute and Department of Ecology and Evolutionary Biology, University of Kansas, Lawrence, KS, USA) — **MARTIN FIKÁČEK** (Department of Entomology, National Museum in Prague & Department of Zoology, Faculty of Science, Charles University in Prague, Prague, Czech Republic)

14:30 — 14:50

Phylogeny of the herbivorous ladybird beetles (Coccinellidae) from the genus *Epilachna*

KAROL SZAWARYN (Museum & Institute of Zoology, Polish Academy of Sciences, Poland) — **WIOLETTA TOMASZEWSKA** (Museum & Institute of Zoology, Polish Academy of Sciences, Poland)

14:50 — 15:10

Coffee Break

15:10 — 15:40

Poster Session II

Presenters of all posters are kindly asked to stay with their posters

Oral Presentations — Saturday, September 28

Chair of *morning* session: Brian Wiegmann
Chair of *afternoon* session: Niklas Wahlberg



15:40 — 16:20

Genes and genomes reveal new insights into the evolution of weevil (Coleoptera: Curculionoidea) megadiversity

DUANE D. MCKENNA (University of Memphis, Department of Biological Sciences, USA)

16:20 — 16:40

Molecular phylogenetic analysis of the longhorned beetle subfamilies Prioninae and Parandrinae (Coleoptera: Cerambycidae)

EUGENIO H. NEARNS (Systematic Entomology Lab, National Museum of Natural History, Washington, DC, USA) — **SEÁN BRADY** (National Museum of Natural History, Smithsonian Institution, Washington, DC, USA) — **IAN P. SWIFT** (California State Collection of Arthropods, Sacramento, CA, USA) — **TRACI L. GRZYMALA** (Department of Environmental Science, University of California, Berkeley, CA, USA) — **APRIL J. JEAN** (Department of Biology, Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM, USA) — **KELLY B. MILLER** (Department of Biology, Museum of Southwestern Biology, University of New Mexico, Albuquerque, NM, USA)

16:40 — 17:00

Geometric morphometrics and phylogeny: insight from beetles, ice crawlers and mammals

MING BAI (Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Box 92, No. 1, Beichen West Road, Chaoyang District, Beijing, 100101, China) — **XINGKE YANG** (Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Box 92, No. 1, Beichen West Road, Chaoyang District, Beijing, 100101, China) — **ROLF G. BEUTEL** (Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany)

18:00 — 22:00

Dinner
also in the „Japanisches Palais“

Oral Presentations — Sunday, September 29



Chair of *morning* session:

Karl Kjer

Chair of *afternoon* session:

Ulrike Aspöck

09:00 — 09:30

New genomic evidence to resolve phylogenetic radiations in true flies

BRIAN M WIEGMANN (North Carolina State University, Department of Entomology, Raleigh, NC 27695, USA) — **MICHELLE D. TRAUTWEIN** (North Carolina Museum of Natural Sciences, Raleigh NC, USA) — **DAVID K. YEATES** (Australian National Insect Collection, CSIRO Ecosystem Sciences, Black Mountain Laboratories, PO Box 1700, Canberra, ACT, Australia)

09:30 — 10:00

From Sanger to NGS: resolving the phylogenetic relationships of an insect family (Sepsidae)

RUDOLF MEIER (Department of Biological Sciences, and University Scholars Programme, National University of Singapore, 14 Science Dr 4, Singapore 117543) — **KATHY F SU** (Department of Biological Sciences, National University of Singapore, 14 Science Dr 4, Singapore 117543) — **ZHAO LEI** (Department of Biological Sciences, National University of Singapore, 14 Science Dr 4, Singapore 117543) — **MINDY TUAN** (Department of Biological Sciences, National University of Singapore, 14 Science Dr 4, Singapore 117543) — **DIEGO PITTA DE ARAUJO** (Department of Biological Sciences, National University of Singapore, 14 Science Dr 4, Singapore 117543) — **JAYANTHI PUNIAMOORTHY** (Department of Biological Sciences, National University of Singapore, 14 Science Dr 4, Singapore 117543)

10:00 — 10:35

Phylogeny of the Hymenoptera: new pieces into the old jigsaw(fly) puzzle

TOBIAS MALM (University of Eastern Finland, Joensuu, Finland; University of Turku, Finland) — **TOMMI NYMAN** (University of Eastern Finland, Joensuu, Finland; University of Zurich, Switzerland)

10:35 — 11:00

Coffee Break

11:00 — 11:30

New dates for old wasps: total-evidence dating the early hymenopteran lineages

LARS VILHELMSSEN (Natural History Museum of Denmark, Universitetsparken 15, DK-2100 Denmark) — **SERAINA KLOPFSTEIN** (Swedish Museum of Natural History, Box 5007, SE-104 05 Stockholm, Sweden) — **ALEXANDR RASNITSYN** (Russian Academy of Sciences, Profsoyuznaya Ulitsa 123, Moscow 117647, Russia) — **SUSANNE SCHULMEISTER** (Faculty of Biology, Ludwig-Maximilians-University, D-82152 Martinsried, Germany) — **DEBRA MURRAY** (Department of Biology, Duke University, Box 90338, Durham, NC 27708, USA) — **FREDRIK RONQUIST** (Swedish Museum of Natural History, Box 5007, SE-104 05 Stockholm, Sweden)

11:30 — 11:55

Extant Chalcidoidea (Hymenoptera) — developing a phylogenetic hypothesis for a hyperdiverse group of insect parasitoids

JOHN HERATY (Department of Entomology, University of California, Riverside, CA 92521, USA)

Oral Presentations — Sunday, September 29

Chair of *morning* session: Karl Kjer
Chair of *afternoon* session: Ulrike Aspöck



11:55 — 12:20 Fossil Chalcidoidea — a neglected source of phylogenetic data

LARS KROGMANN (State Museum of Natural History, Entomology, Rosenstein 1, 70191 Stuttgart, Germany)

12:20 — 13:30 Lunch Break

13:30 — 14:05 Amphiesmenopteran origins in time based on molecular evidence

NIKLAS WAHLBERG (Department of Biology, University of Turku, 20014 Turku, Finland)

14:05 — 14:40 New insights on the phylogeny of Trichoptera: transcriptomes and new techniques

PAUL B. FRANSEN (Rutgers University, Department of Entomology, 93 Lipman Dr., New Brunswick, NJ 08901, USA) — **JESSICA THOMAS** (Hofreiter Ancient Biomolecules Lab, Department of Biology, University of York, York, YO10 5DD, United Kingdom) — **KARL M. KJER** (Rutgers University, Department of Ecology, Evolution and Natural Resources, 14 College Farm Rd., New Brunswick, NJ 08901, USA)

14:40 — 15:15 The newly discovered 'Kangaroo Island Moth': unexpected complexity in early Lepidoptera evolution

NIELS P. KRISTENSEN (Natural History Museum of Denmark, University of Copenhagen)

15:15 — 15:40 Coffee Break

15:40 — 16:10 Phylotranscriptomics with 1000 genes: how many loci are needed for a robust phylogeny of the silk moth superfamily Bombycoidea?

AKITO Y. KAWAHARA (Florida Museum of Natural History, University of Florida, Gainesville, FL 32611, USA) — **JESSE W. BREINHOLT** (Florida Museum of Natural History, University of Florida, Gainesville, FL 32611, USA)

16:10 — 16:30 A semantic model for morphological description

ISTVÁN MIKÓ (Frost Entomological Museum, Pennsylvania State University, University Park, PA, USA) — **JAMES P. BALHOFF** (National Evolutionary Synthesis Center, Durham, NC, USA) — **MATTHEW J. YODER** (Species File, Prairie Research Institute, University of Illinois, Champaign, IL, USA) — **ANDREW R. DEANS** (Frost Entomological Museum, Pennsylvania State University, University Park, PA, USA)

16:30 — 16:40 Closure

KLAUS-DIETER KLASS (Senckenberg Natural History Collections Dresden, Germany)



Position Presentation

01 Comparative morphology of male genitalia in Archaeognatha

NATALIA A. MATUSHKINA (Dept. of Zoology, Faculty of Biology, Kiev National University, Volodymirska str. 64, 01033 Kiev, Ukraine) — **KLAUS-DIETER KLASS** (Senckenberg Natural History Collections Dresden, Königsbrücker Landstrasse 159, 01109 Dresden, Germany)

02 Dating the origin of major mayfly (Ephemeroptera) lineages

SEREINA RUTSCHMANN (Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Müggelseedamm 301, D-12587 Berlin, Germany) — **PING CHEN** (The Key Laboratory of Jiangsu Biodiversity and Biotechnology, College of Life Sciences, Nanjing Normal University, Nanjing 210046, China) — **CHANGFA ZHOU** (The Key Laboratory of Jiangsu Biodiversity and Biotechnology, College of Life Sciences, Nanjing Normal University, Nanjing 210046, China) — **MICHAEL T. MONAGHAN** (Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Müggelseedamm 301, D-12587 Berlin, Germany)

03 The thorax musculature of Zygoptera nymphs (Odonata)

SASKIA HECKMANN (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany) — **THOMAS HÖRNSCHEMEYER** (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany) — **SEBASTIAN BÜSSE** (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany)

04 The thorax musculature of *Epiophlebia* nymphs (Odonata)

BENJAMIN HELMKER (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany) — **THOMAS HÖRNSCHEMEYER** (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany) — **SEBASTIAN BÜSSE** (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany)

05 The thorax musculature of Anisoptera nymphs (Odonata)

SEBASTIAN BÜSSE (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany) — **THOMAS HÖRNSCHEMEYER** (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany)



Position **Presentation**

06 **Generalized Odonata thorax**

SEBASTIAN BÜSSE (Abteilung Morphologie, Systematik & Evolutionsbiologie, JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany)

07 **Clarification of the Paoliida (Insecta) problem: sister group of Neoptera or Dictyoptera?**

JAKUB PROKOP (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — **WIESLAW KRZEMIŃSKI** (Institute of Systematics and Evolution of Animals, PAS, Kraków, Poland) — **EWA KRZEMIŃSKA** (Institute of Systematics and Evolution of Animals, PAS, Kraków, Poland) — **THOMAS HÖRNSCHEMEYER** (Georg-August-Universität Göttingen, Göttingen, Germany) — **JAN-MICHAEL ILGER** (Clausthal University of Technology, Clausthal-Zellerfeld, Germany) — **CARSTEN BRAUCKMANN** (Clausthal University of Technology, Clausthal-Zellerfeld, Germany) — **PHILIPPE GRANDCOLAS** (Muséum National d'Histoire Naturelle, Paris, France) — **ANDRÉ NEL** (Muséum National d'Histoire Naturelle, Paris, France)

08 **Thoracic morphology of ensiferans and its phylogenetic implications**

FANNY LEUBNER (Abteilung Morphologie, Systematik und Evolutionsbiologie; JFB-Institut für Zoologie & Anthropologie der Georg-August-Universität Göttingen, Germany)

09 **The phylogeny and evolution of praying mantids (Dictyoptera: Mantodea)**

PHIL ERKELING (Zoologisches Forschungsmuseum Alexander Koenig, Abteilung Arthropoda, 53113 Bonn, Germany) — **FRANK WIELAND** (Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, 20146 Hamburg, Germany) — **KAI SCHÜTTE** (Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, 20146 Hamburg, Germany) — **GAVIN SVENSON** (Department of Invertebrate Zoology Cleveland Museum of Natural History, Cleveland, OH 44106, USA) — **RALPH S. PETERS** (Zoologisches Forschungsmuseum Alexander Koenig, Abteilung Arthropoda, 53113 Bonn, Germany)

10 **Phylogenetic reconstruction of wing states in cockroaches (Blattaria)**

MICHAEL KOTYK (Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7, 12844 Prague 2, Czech Republic) — **DANIEL FRYNTA** (Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7, 12844 Prague 2, Czech Republic) — **ZUZANA VARADÍNOVÁ** (Department of Zoology, Faculty of Science, Charles University in Prague, Viničná 7, 12844 Prague 2, Czech Republic)

11 **The phylogeny of *Arenivaga* (Rehn) (Blattodea: Corydiidae: Polyphaginae)**

HEIDI HOPKINS (University of New Mexico, Museum of Southwestern Biology, Albuquerque, NM, USA)



Position Presentation

12 Neotropical Nasutitermitinae (Isoptera: Termitidae): a preliminary morphology-based phylogenetic analysis supports three new nasute genera

TIAGO F. CARRIJO (Museu de Zoologia da Universidade de São Paulo, 04218-970, São Paulo, SP, Brazil) — **CAROLINA CUEZZO** (CONICET - Instituto Superior de Entomología "Dr. A. Willink", Facultad de Ciencias Naturales e Instituto Miguel Lillo, UNT, Miguel Lillo 205, T4000JFE San Miguel de Tucumán, Tucumán, Argentina) — **ELIANA M. CANCELO** (Museu de Zoologia da Universidade de São Paulo, 04218-970 São Paulo, SP, Brazil)

13 Dwarfish sexuales of Thelaxinae (Hemiptera, Aphidoidea) — review of species and life cycles

ŁUKASZ JUNKIERT (University of Silesia, Faculty of Biology and Environmental Protection, Department of Zoology, Bankowa 9, 40-007 Katowice, Poland) — **MARIUSZ KANTURSKI** (University of Silesia, Faculty of Biology and Environmental Protection, Department of Zoology, Bankowa 9, 40-007 Katowice, Poland) — **KARINA WIECZOREK** (University of Silesia, Faculty of Biology and Environmental Protection, Department of Zoology, Bankowa 9, 40-007 Katowice, Poland)

14 The identity of *Eulachnus alticola* Börner, 1940 (Hemiptera: Aphidoidea: Lachninae) in light of morphological research

MARIUSZ KANTURSKI (Department of Zoology, Faculty for Biology and Environmental Protection, University of Silesia, Bankowa 9, 40-007 Katowice, Poland) — **KARINA WIECZOREK** (Department of Zoology, Faculty for Biology and Environmental Protection, University of Silesia, Bankowa 9, 40-007 Katowice, Poland)

15 Potential geographic distribution of true bugs of the subfamily Diaspidiinae Miller, 1959 (Heteroptera: Reduviidae)

DOMINIK CHŁOND (University of Silesia, Faculty of Biology and Environmental Protection, Department of Zoology, ul. Bankowa 9, 40-007 Katowice, Poland) — **AGNIESZKA BUGAJ-NAWROCKA** (University of Silesia, Faculty of Biology and Environmental Protection, Department of Zoology, ul. Bankowa 9, 40-007 Katowice, Poland)

16 Phylogeny of the water boatmen Corixoidea (Heteroptera)

JAKOB DAMGAARD (Laboratory of Molecular Systematics, Botanical Garden and Museum, Natural History Museum of Denmark, Sølvgade 83 Opg. S., 1307 Copenhagen K, Denmark) — **CHRISTIAN W. HÄDICKE** (Zoological Institute and Museum, Cytologie & Evolutionary Biology, Ernst-Moritz-Arndt-Universität, Soldmannstraße 23, D-17487 Greifswald, Germany)



Position Presentation

17 Unique protection of the eggs within the insects — a case of the family Plataspidae (Heteroptera: Pentatomoidea)

JITKA VILÍMOVÁ (Charles University, Faculty of Science, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic) — **PETR JANŠTA** (Charles University, Faculty of Science, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic)

18 Tiny eggs and minute larvae — the embryonic development of *Stylops ovinae* (Strepsiptera)

HANS POHL (Entomology Group, Friedrich-Schiller-Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstr. 1, 07743 Jena, Germany) — **MAXIMILIAN FRAULOB** (Entomology Group, Friedrich-Schiller-Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstr. 1, 07743 Jena, Germany)

19 Molecular phylogeny of the leaf beetle subfamily Criocerinae (Coleoptera: Chrysomelidae) and co-evolution of male and female reproductive organs

YOKO MATSUMURA (Entomology Group, Friedrich-Schiller-Universität Jena, Germany) — **IZUMI YAO** (Laboratory of Systematic Entomology, Hokkaido University, Japan) — **ROLF G. BEUTEL** (Entomology Group, Friedrich-Schiller-Universität Jena, Germany) — **KAZUNORI YOSHIZAWA** (Laboratory of Systematic Entomology, Hokkaido University, Japan)

20 Dispersal is linked to habitat preference in 59 species of tropical water beetles (Coleoptera: Adepnaga)

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21 O Sister, Where Art Thou? Conflicting hypotheses on basal branchings in Neuroptera

SUSANNE RANDOLF (Natural History Museum Vienna, Austria) — **DOMINIQUE ZIMMERMANN** (Natural History Museum Vienna, Austria) — **ULRIKE ASPÖCK** (Natural History Museum Vienna, Austria)

22 High throughput mitogenomics for lepidopteran phylogenetics

MARTIJN J.T.N. TIMMERMANS (Natural History Museum, London, United Kingdom; Imperial College, London, United Kingdom) — **THOMAS J. SIMONSEN** (Natural History Museum, London, United Kingdom) — **D.C. LEES** (Cambridge University, Cambridge, United Kingdom) — **ALFRIED P. VOGLER** (Natural History Museum, London, United Kingdom; Imperial College, London, United Kingdom)



Position Presentation

23 Head morphology of adult caddisflies (Trichoptera) and its phylogenetic implications

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24 Phylogeography of *Rhyacophila tristis* (Trichoptera: Rhyacophilidae)

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25 Morphological and phylogenetic characterization of caddisfly larvae of genus *Himalopsyche*

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26 The larval abdomen of the enigmatic Nannochoristidae (Mecoptera)

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Position Presentation

27 The evolution of the adult head in Diptera

KATHARINA SCHNEEBERG (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, FSU Jena, Germany)

28 Fly on the wall — attachment devices in lower Diptera

KATRIN FRIEDEMANN (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, FSU Jena, Germany) — **KATHARINA SCHNEEBERG** (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, FSU Jena, Germany)

29 Raptorial Phantom Midges — the larval head of Chaoboridae (Diptera)

MARIA FÖRSTER (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, FSU Jena, Germany) — **KATHARINA SCHNEEBERG** (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, FSU Jena, Germany)

30 Phylogeny of the Diaphorinae (Diptera: Dolichopodidae)

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31 Molecular phylogeny of Platypezidae (Diptera)

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32 *Baltorussus* total makeover: rejuvenation and sex change in an ancient parasitoid wasp lineage (Hymenoptera: Orussidae)

DOMINIQUE ZIMMERMANN (Natural History Museum of Vienna, Austria) — **LARS VILHELMSSEN** (Natural History Museum of Denmark)



Position **P**resentation

33 **Phylogeny of the family Torymidae (Hymenoptera: Chalcidoidea)**

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Molecular phylogenetics of Arthropoda: capturing phylogenetic signal from serine with 21-amino-acid models

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The evolutionary relationships of arthropods have been studied extensively during the past century, but consensus on the higher relationships has remained elusive. Among the many debated hypotheses, the origin of Hexapoda is of particular interest. Advances in sequencing technology have spurred the study of arthropod relationships with very large molecular data sets for the last decade, yet, the number of truly independent data sets is more limited than it might seem. One of these data sets is based on 62 nuclear, protein-coding genes from representatives of all pancrustacean classes, including Hexapoda (Regier et al. 2010). It provides a robustly supported topology for most Arthropoda, placing Hexapoda as sister to Xenocarida (Remipedia + Cephalocarida). This and five other higher pancrustacean clades are of particular interest and were newly named by Regier et al. (2010): Xenocarida, Miracrustacea, Communostraca, Multicrustacea, Vericrustacea, and Altocrustacea.

However, for five of these six clades support values of nucleotide and codon model analyses are significantly higher than for amino acid models, and this discrepancy casts doubt on the validity of these taxa. In-depth analyses reveal that the strong support in nucleotide and codon model analyses is largely contributed by serine, while support is reduced in standard 20-amino-acid analyses due to a lack of distinction between two disjunct clusters of serine codons (TCN / ATY). This is directly evidenced by novel 21-amino-acid models that do distinguish between these two clusters, yielding high support values for the nodes of interest (Zwick et al. 2012).

The average substitution rate between the two clusters of serine is intermediate between non-synonymous and synonymous substitution rates of other amino acids. In phylogenetic analyses, this unique characteristic of serine might be particularly informative for clades of a certain age, while it might be uninformative or even misleading through codon usage bias for very old clades. In the case of Pancrustacea, we demonstrate that the strong signal of serine is A) not linked to a serine codon usage bias that could drive the analyses, and B) congruent with the signal of other amino acids.

With the discrepancy in support being explainable by the nature of the genetic code, and with congruence between the signals from serine and other amino acids, we argue that this large data set strongly supports the postulated higher pancrustacean taxa.

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Introduction to 1KITE and the first steps in the project's workflow: aims, people, subprojects, taxon sampling and collecting

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The 1KITE project (1K Insect Transcriptome Evolution) is an international research initiative started in 2011. It aims at studying the evolutionary history of insects in all of its aspects. To achieve this aim, scientists in the 1KITE project are sequencing and analyzing the transcriptomes of more than 1,000 insect species encompassing all recognized extant insect orders.

The project focuses on inferring robust phylogenetic trees for all major lineages of hexapods, but also fosters the development of new and advanced methods and software tools for data quality assessment, phylogenetic reconstruction, and molecular dating, and paves the way for numerous additional projects that will be feasible with the generated transcriptome data.

Scientists involved include experts in insect morphology, taxonomy, systematics, paleontology, embryology, molecular biology, bioinformatics, and scientific computing. Overall, more than 120 scientists from sixteen nations are collaborating in 1KITE.

The project consists of a first project that aims at inferring a phylogenetic backbone tree for the entire hexapod clade, and several taxonomic subprojects that address the phylogeny and evolution of subordinated taxa, namely basal hexapods, Odonata, Polyneoptera, Dictyoptera, Paraneoptera, Hymenoptera, Coleoptera, Neuropterida, Lepidoptera, Trichoptera, and Antliophora (www.1kite.org). First major challenge in the 1KITE project workflow was to select 1,000 species from the unprecedented diversity of insects, and to newly collect and specifically preserve specimens of each selected species. Preserved samples were sent to the BGI, Shenzhen, China, for transcriptome sequencing and assembly. Taxon sampling and collecting, which are coordinated at the Zoologisches Forschungsmuseum Koenig in Bonn (Germany), are almost completed. Status as of 13 Sept 2013, the transcriptomes of 825 species have been successfully sequenced; 308 additional species are still in progress.

Towards a hexapod tree of life: pitfalls and challenges of the phylogenomic approach

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[No abstract available]

Potential and limits of the 1KITE transcript data for facilitating the application of DNA enrichment protocols in insect phylogenetics

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The 1KITE project will soon provide entomologists around the globe access to nucleotide sequence data of sequenced transcriptome libraries from more than 1,000 species of hexapods. While the primary aim of generating these data has been to infer the phylogenetic relationships of all extant major insect lineages, the obtained data bear the



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potential to significantly foster also future molecular phylogenetic studies with a more narrow taxonomic scope. For example, the 1KITE nucleotide sequence data will allow designing degenerated oligonucleotide PCR primers that bind to the DNA of a wide array of taxa. However, we see even a greater potential of the 1KITE data for designing custom baits for capturing target DNA. This approach has already been applied successfully in the recent past to enrich DNA of interest in various species of vertebrates — a group that differs significantly in its substitution rates from that of insects. In a project that aims at inferring the phylogeny of digger wasps (Hymenoptera: Ampulicidae, Sphecidae, Heterogynaidae, Crabronidae), we decided to evaluate the potential of the DNA enrichment approach by exploiting the 1KITE transcriptome libraries of 24 digger wasp species and the sequenced genomes of various ants, the honeybee, and the parasitoid wasp *Nasonia*. Here, we present our bioinformatic procedure for custom bait design. Specifically, we show (1) our strategy and software for reliably assigning transcript to clusters of single-copy genes, (2) point to steps that have to be considered when dealing with transcripts rather than genomic nucleotide sequences, and present (3) a new method that makes use of artificial bait sequences instead of centroid sequences to minimize the amount of baits required to capture the target DNA in a wide array of species. Given that we intend to apply these baits also on species of distantly related lineages, for which transcriptomic data were not available to us, we accepted a maximum difference of less than 6 % between bait nucleotide sequences and the target DNA of our sequenced reference species. Applying these criteria, we were able to design baits for capturing 376 exons from 286 genes: 150k bp of coding DNA in total.

Insect morphology in the age of phylogenomics

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The state of the art in hexapod systematics is outlined with special emphasis on the role of morphology. Interactions between molecular and morphological investigations are addressed. An important result of molecular studies was the placement of Hexapoda as a subordinate group of Pancrustacea (e.g., Meusemann et al. 2010). This profoundly changed the view of the early evolution of the group and revealed new morphological apomorphies of hexapods. The basal splitting events are still ambiguous (Entognatha/Cercophora, Ellipura/Nonoculata), whereas the monophyly of Insecta, Dicondylia, and Zygentoma is confirmed. Palaeoptera (Odonata + Ephemeroptera) gained new support in morphological studies (e.g., Blanke et al. 2012a,b), but the alternatives cannot be ruled out at present. Morphological and molecular evidence supports a placement of Zoraptera among the polyneopteran orders. Several clades within this large lineage are well supported by morphology and molecular data, but the backbone is still unstable, and the monophyly of the entire group not fully confirmed. In Acercaria, the position of Thysanoptera and the interrelationships within Hemiptera are still uncertain. The monophyly of Holometabola is largely resolved including the position of Strepsiptera as sistergroup of Coleoptera (Niehuis et al. 2012). Evolutionary morphology will continue to play a vital role in insect systematics. It provides an independent data set for critically evaluating molecular phylogenies and it is the only source of information for placing fossil taxa. A complex and well-founded evolutionary scenario for the megadiverse Hexapoda will be based on a combination of a robust molecular phylogeny, morphology, developmental biology and palaeontological data.

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A super matrix approach to the phylogeny of Odonata

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Over the past decade, a number of research teams have explored the phylogeny of Odonata with molecular data. Each has targetted their own set of genes, and their own taxa, and little effort has been made to coordinate efforts, or consolidate data from multiple sources. Here we construct a supermatrix from 4 independent genes (28S, 18S; 12S, 16S, COI, COII; EF1a and H3) and over 500 species, representing all families of Odonata. Our phylogenetic results are largely congruent with those we reported in Carle et al. 2008, with monophyletic suborders (Anisoptera and Zygoptera). We find coenagrionoids and calopterygoids together with lestoids relatively basal. We find *Epiophlebia* as sister to Anisoptera, with aeshnoids at the base of the Anisoptera. We discuss our strategies for alignment, data exclusion, combining taxa, discovering contaminants and reducing missing data.

References: Carle F.L., Kjer K.M., May M.L. 2008: Evolution of Odonata, with special reference to Zygoptera. *Arthropod Systematics & Phylogeny* 66: 37–44.

First insights in the embryonic development of the damselfly *Ischnura elegans*

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The new sequencing technologies have massively increased the amount of data available for comparative transcriptomics which can be used to infer insect relationships but also to study the transcriptional signatures and dynamics of developmental processes. In addition, for *Drosophila* species it has been shown that expression divergence correlate with sequence divergence among putative orthologous genes, making comparative gene expression analyses to a useful tool in molecular phylogenetics (Zhang et al. 2007; Kalinka et al. 2010). However, transcriptomic data across developmental stages are mainly available for derived holometabolous insects, especially drosophilid dipteran species.

Here, we fill in an important gap for future comparative gene expression analyses by analyzing and comparing transcriptomic data across the embryonic development of the damselfly *Ischnura elegans*. Roche 454-multiplexed transcriptomic data was generated for four time-periods (day 1–3, 4–5, 6–7, 8–9) spanning the entire embryonic



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lifespan. The assembled 454 reads and comparative analyses between the different embryonic stages will provide the first insights in the temporal gene expression changes during early damselfly development. In addition, high-quality ds cDNA libraries for each embryonic developmental stage (day) were generated for further in-depth gene expression analyses using quantitative RT-PCR.

The long-term goal of this ongoing research project is to systematically search for expression divergence between distantly related insect species, their correlation to sequence divergence (known phylogenetic relationships) and to study their role in morphological changes.

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Lower neopteran relationships — new insights into an old problem

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The lower neopterous insects or Polyneoptera traditionally include eleven orders: Plecoptera (stoneflies), Embioptera (web-spinners), Phasmatodea (stick insects), Orthoptera (crickets, katydids, and grasshoppers), Dermaptera (earwigs), Mantophasmatodea (heel walkers), Grylloblattodea or Notoptera (ice crawlers), Mantodea (mantids) and Blattodea including Isoptera (roaches and termites). Additionally some authors consider Zoraptera (angel insects) to be part of the group. The monophyly and relationships among these groups are almost completely unresolved and remain one of the major riddles of insect systematics.

Here we present the biggest morphological data set to date, with 292 characters from all parts of the body, as well as the first transcriptomic study which contained all relevant groups both support the monophyly of Polyneoptera. However, the group is characterized by extremely short, ancient internodes, and critical analysis reveal a high degree of homoplasy in the data, thus the question of the common ancestry of the lower neopterous insects remains debatable. Within the group, Dictyoptera (mantids, roaches and termites) has long been supported, and recent research clearly supports a sistergroup relationship between Mantophasmatodea and Grylloblattodea and the fact that Zoraptera is a group of lower neopterous insects. Additionally there is some evidence for clades comprising Phasmatodea and Embioptera as well as Dermaptera and Plecoptera.

Global biogeography of the family Grylloblattidae (Grylloblattodea) and their underappreciated species richness

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The family Grylloblattidae Walker (1914) consists of a small number of species (32 currently described), but despite this limited taxonomic diversity, grylloblattids represent an important link in the classification of neopterous insects. In part, this is due to their blend of morphological features, which has led to uncertain phylogenetic placement in several alternative classifications. Here I focus on the diversity and relationships within Grylloblattidae, using



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genetic approaches to identify several limitations in the current taxonomy. Phylogenetic analyses suggest generic revision is warranted for the taxa *Namkungia* Storozhenko & Park (2002) and *Galloisiana* Caudell & King (1924), with the possible recognition of new genera. These analyses also reveal a remarkable level of cryptic species diversity in both Asia and North America. Using genetic approaches in conjunction with comprehensive surveys throughout northeast Asia and North America, I discuss how the evolutionary biology of Grylloblattidae is illuminated by biogeographic analyses. Notably, diversity patterns in North American *Grylloblatta* and southern Siberian *Grylloblattella* were driven largely by glacial climate fluctuations, with the North American species providing an elegant example of cyclical divergence at both the population and species level. In contrast, Japanese *Galloisiana* lineages were shaped by geological events, with most species forming during mountain-building events in the Miocene. Finally, I discuss the importance of climate in shaping morphological innovation, ecological variation, and the physiological ecology of Grylloblattidae.

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Finding the sistergroup of Cryptocercidae + Isoptera: a dark horse wins

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Recent phylogenetic studies have established that termites belong within the cockroaches as sister to Cryptocercidae. *Cryptocercus* shares several important behavioural and life history traits with termites, thus we need to understand the phylogenetic position of Cryptocercidae + Isoptera to determine how these traits evolved. However, placement of Isoptera + Cryptocercidae has remained uncertain. Suggested sister groups include Polyphagidae + Lamproblattidae, Polyphagidae + Nocticolidae, Blattidae, Tryonicidae, Blattidae + Tryonicidae, and all other Dictyoptera. None of the possible sister groups are known to share more similarities in lifestyle with Cryptocercidae + Isoptera than the others; e.g. a few representatives of all have been found in rotting wood.

We present a combined molecular (12S, 16S, 18S, 28S, COII and H3) and morphological phylogenetic study of Dictyoptera which includes all previously suggested sister groups of Isoptera + Cryptocercidae as well as other potentially important taxa. We also produced a fossil-calibrated estimate of divergence times for the major splits within Dictyoptera using three calibration points.

We found the sistergroup of Isoptera + Cryptocercidae to be *Anaplecta*, a completely unexpected group which was previously placed basalmost in Blaberoidea. We included six morphologically diverse *Anaplecta* species; these consistently formed a monophyletic clade as sister to Isoptera + Cryptocercidae. The branch below *Anaplecta* consisted of Lamproblattidae + Tryonicidae, a less surprising result. The basal branch within Blattodea consisted of Eucorydiidae (formerly Polyphagidae) and Nocticolidae, with morphological data firmly associating Nocticolidae with Eucorydiidae. Divergence time analysis places the origin of major lineages in Blattodea in the Triassic, much older than the generally presumed Cretaceous origin, with the Blattodea-Mantodea dichotomy placed in middle Permian. Wood/fungus feeding may have been driving the evolution of sociality in the ancestor of Isoptera + Cryptocercidae.



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Praying mantis revisionary systematics and the origins of plant mimicry in the Hymenopodidae (Mantodea)

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With new phylogenetic data sourced from genes and morphology, an effort to revise higher-level groups and genera is well underway. Current projects include the revision of Neotropical Earless Mantises, the Hymenopoidea superfamily, and genera such as *Liturgusa*, *Pyrgomantis*, and others. With paraphyly confusing most high-level relationships, the next great push within mantodean systematics is the expansion of taxon sampling and completion of robust analyses aimed at determining deep level relationships. In the effort to gather new morphological data, we investigated the origins of plant mimicry in the praying mantis family Hymenopodidae, which includes some of the most well-known and ornate species. By coding characters related to mimicry of plants we established a threshold of character state presence to classify a plant mimicking mantis. We built an expanded phylogeny incorporating new genera not previously included and used Diversitree and BISSE and Time dependent BISSE models to investigate one, two, and three epoch models specifically focused on the best fit for three parameters (extinction, transition, and speciation rates). We found that the two epoch model fit our data best and transition rates between mimic and non-mimic character states was faster during the first epoch with a slowdown in the second. We overlay this timing with the origins and diversification of higher level angiosperm lineages and suggest an association between the evolution of flowering plants and the increased transition rates of plant mimicry.

The Palaeozoic and Early Mesozoic stems of palaeopterans and polyneopterans

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All major lineages of palaeopteran and polyneopteran insects have been documented from the Late Palaeozoic to the Early Mesozoic. However this early record comes with several pitfalls. First, as early as documented (viz. in the early Late Carboniferous), several groups are composed of phylogenetically distant relatives, which are successive (extinct) stem-relatives of extant lineages. This is the case for at least stem-Odonatoptera and stem-Orthoptera. This situation makes the use of these lineages hazardous for node dating, because the actual divergence date of these lineages likely is much more ancient. Therefore recourse to representatives of more inclusive groups, appearing in more recent outcrops, such as genuine stem-Ensifera in the Late Permian, is probably more insightful. The second issue concerns the identification of particular fossil species as stem-representatives of particular extant groups. Although some of these identifications are undisputed, many proved problematic. For example, 'cockroachoids' are well-documented in Late Carboniferous localities. Whether they are stem-Dictyoptera, or stem-Blattodea, can be considered an unresolved question. The position of the Late Carboniferous *Triplosoba pulchella*, is another vivid example of this type of issue. Until Early Carboniferous localities providing sufficient samples are discovered, the very early record of palaeopteran and polyneopteran insects will remain problematic to use for node dating.



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Nomenclatural dissidence applied to pterygotans

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The nomenclatural procedure most commonly used is the ICZN-governed one, and is primarily characterized by binominal species names, and the application of ranks, some with standardized endings. Actual cases, selected among fossil and extant polyneopterans, and demonstrating the inadequacy of this procedure, will be presented. In order to address the corresponding issues, an alternative procedure, namely the cladotypic one, was developed in the last years. Under this procedure, taxon names are associated with a definition involving a hypothesis of character (state) homology. To achieve this, the definition includes a formulation of a character state (ideally together with its antonym), and the designation of two type species (in the facts, two type specimens, named 'cladotypes'). Lanham's species names, composed of the species epithet and full authorship data, ie. without reference to a genus, are favoured. To date, this approach has mainly been applied to fossil and extant orthopterans. Actual cases selected among these applications will be presented (e.g. the *ligata*, *Miamia*, *Titanoptera*, and *Grylloptera* cases), demonstrating the higher optimality of the procedure, in its current state. Future applications will allow further testing of the procedure.

The Fossil Calibration Database

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The Fossil Calibration Database has developed new protocols and resources to improve divergence-dating studies using fossil calibrations. "Molecular dating", combining temporal data from the fossil record with branch length data from molecular phylogenetic trees, represents a rapidly expanding approach to understanding biodiversity. Major disparities have been recognized between molecular divergence dating estimates and ages provided by the fossil record for critical nodes in the Tree of Life, but broad scale patterns and underlying drivers remain elusive. Unfortunately, many fossils used to calibrate divergence dating analyses are not phylogenetically constrained and/or have incorrect ages assigned to them. Molecular systematists have largely led divergence dating studies, and the development of rigorous methods for using paleontological data has lagged behind the development of statistical methods for analyzing genetic sequences. This online database of vetted fossil calibrations, the "Fossil Calibration Database" is a dynamic resource for all systematists.

Wing base structure of Paraneoptera and its phylogenetic significance

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The wing base structure of insects is composed of many sclerites located between the notum and wing. Very sophisticated wing movements (flapping and folding) are achieved by these sclerites, and slight modification of these sclerites can make insects flightless. Because of these constraints, this structure is known to evolve very slowly. Thus, the wing base structure should contain useful phylogenetic information for uncovering deep insect



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divergence. Characters selected from the wing base have been applied to estimating the higher level phylogeny of Paraneoptera. These studies have provided support for Paraneoptera + Holometabola (Yoshizawa 2011), monophyly of Paraneoptera, Thysanoptera + Hemiptera (= Condylognatha), Fulgoromorpha + Cicadomorpha (= Auchenorrhyncha) (Yoshizawa & Saigusa 2001), monophyly of Cicadomorpha, and Cicadoidea + Cercopoidea (Yoshizawa & Wagatsuma 2013). Most of these relationships have also received support from molecular phylogenies, but monophyly of Paraneoptera has not been recovered using molecular evidence. Support values for non-monophyly of Paraneoptera from the molecular data are typically weak, whereas the wing base characters provided a total of 9 non-homoplasious autapomorphies of Paraneoptera. Therefore, monophyly of Paraneoptera can be regarded as highly plausible and deserves further examination using additional molecular data.

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The thrips in their paraneopteran context

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The order Thysanoptera (thrips) includes some 6,000 described species worldwide of minute, slender insects with narrow, strap like wings fringed with long setae. Because of their many synapomorphies thrips have long been recognized as holophyletic and are presently classified into 2 suborders: a paraphyletic Terebrantia with 8 extant families and a monophyletic Tubulifera with 1 extant family (Phlaeothripidae). Thrips are classified within the higher taxon Paraneoptera along with bark, book, and parasitic lice (Psocodea) and true bugs (Hemiptera). Regardless of diet, thrips use unique, asymmetric, 'punch and suck' mouthparts to feed housed within a mouth cone below the head. Larvae and adults walk on protrusible, pretarsal bladders (arolia) at the tips of their legs, and their metamorphosis is convergently holometabolous.

The known fossil record suggests that stem group Paraneoptera originated in the Upper Carboniferous from a polyneopterous ancestor. The earliest known fossils of stem group Psocodea, Sternorrhyncha, Fulgoromorpha, Cicadomorpha, and Prosorrhyncha are from the Lower Permian to Upper Jurassic while the oldest known fossil thrips occur in Upper Triassic rocks of Virginia and Kazakhstan; thus most stem group hemipterans probably originated before the first thysanopterans. Zherikhin (2002) and Grimaldi et al. (2004), following earlier Russian paleoentomologists derived thrips from the extinct, paraphyletic, psocopteroid lineage †Lophioneurida, probably diverging from them in the Upper Permian to Lower Triassic. Lophioneurids were small to relatively large, had a pronounced, symmetric, prognathous beak and some females, upturned valvular ovipositors, but were plesiotypic to extant thrips in body and wing shape, parking, surface and venation (that of fossil and of extant basal thrips can be derived convincingly from that of Permian lophioneurids), in their lack of long wing cilia, and in their legs, antennae and presumed lack of asymmetric mouthparts and protrusible arolia, in the lack of long wing cilia, and in their legs, antennae and presumed lack of asymmetric mouthparts and protrusible arolia. Consideration of these fossils and limited structural and molecular evidence suggest that thrips are more closely related to psocids than to bugs, their numerous similarities to the latter having arisen through convergence. Because of these similarities,



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thrips are usually placed as sister to Hemiptera in the taxon Condylognatha, though Kristensen (1991) had them originating in a trichotomy with Psocodea and Hemiptera while recent fossil evidence suggests that thrips originated within Psocodea despite there being few synapomorphies between extant psocids and thrips. Recent molecular phylogenetic analyses using various loci yielded very different relationships within the Thysanoptera at the family and subfamily level than had earlier analyses based on structural characters suggesting a need for further investigation and better understanding of the thrips genome.

We define 141 collective, ancestral (ground plan) character states for extant paraneopterans and for basal members of each of its principal taxa. Unlike the classical sister group relationship between Hemiptera and Thysanoptera, these new data support a closer relationship between Thysanoptera and Psocodea. Here we assemble structural, developmental and chromosomal/ molecular evidence from ground plan characteristics of extant Psocodea, Thysanoptera, and Hemiptera as a contribution to solving the problem of thysanopteran origins and relationships. Unfortunately, some character states addressed have been examined in few representatives and may not be universal in the higher taxa to which they are assigned; only further comparative study will show if they are.

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Relative rates of genomic divergence between humans, chimps, and their lice

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The rate of DNA mutation and divergence is highly variable across the tree of life. However, the reasons underlying this variation are not well understood. Comparing the rates of genetic changes between hosts and parasite lineages that diverged at the same time is one way to begin to understand differences in genetic mutation and substitution rates. Such studies have indicated that the rate of genetic divergence in parasites is often faster than that of their hosts when comparing single genes. However, the variation in this relative rate of molecular evolution across different genes in the genome is unknown. We compared the rate of DNA sequence divergence between humans, chimpanzees, and their ectoparasitic lice for 1534 protein coding genes across their genomes. The rate of DNA substitution in these orthologous genes was on average 14 times faster for lice than for humans and chimpanzees. In addition, these rates were positively correlated across genes. Because this correlation only occurred for substitutions that changed the amino acid, this pattern is likely produced by similar functional constraints across the same genes in humans, chimpanzees, and their ectoparasites.



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Molecular phylogenetics of beetles

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We are taking a two-pronged approach to study the diversity of Coleoptera, with the long-term aim of providing a phylogenetic tree at the species level. First, an aligned matrix of publicly available DNA data is constantly updated and currently includes approximately 13,000 species. Numerous problems remain with data extraction because of population level variation and uneven gene coverage. New algorithms are used to minimise these difficulties. At higher hierarchical levels (families and subfamilies) the taxon coverage of the tree of Coleoptera is nearly complete. Our second approach is the use of full mitochondrial genomes to consolidate basal relationships. We will report on a methodology for generating numerous mitochondrial genomes by metagenomic sequencing. Applications of this method will be demonstrated for taxonomic and ecological studies. The technique is particularly useful for the analysis of poorly characterised, complex environmental samples, as those from soil ecosystems and tropical forest canopies.

Phylogeny and evolutionary history of the Hydrophilidae (Coleoptera: Hydrophiloidea) inferred from a multi-gene dataset

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We inferred the phylogeny and evolutionary history of the water scavenger beetles (Coleoptera: Hydrophilidae) based on comprehensive Bayesian and maximum parsimony analyses of DNA sequence data from six genes (COI, COII, 16S, 18S, 28S and arginine kinase) of 151 taxa representing all subfamilies, tribes and subtribes that have ever been proposed in the family. Our results strongly disagree with prior classifications of the Hydrophilidae, and instead suggest that all three smaller subfamilies (Horelophinae, Horelophopsinae and Sphaeridiinae) are derived from within the Hydrophilinae; existing tribal classification is more compatible with our results, but many significant differences are evident. We propose a new classification of the Hydrophilidae comprising 6 subfamilies and 12 tribes, most of which are also supported by morphological characters. Our results confirm that aquatic habits are ancestral for the family and repeated transitions to terrestrial ways of life took place during the evolution of the group. We also bring the first insight into the biogeography of particular clades (e.g., revealing the monophyly of the endemic southern hemisphere Rygmodinae and the *Oosternum*-group of the Megasternini) and provide new



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hypotheses on the evolution of many morphological characters (e.g., antennal morphology, stridulatory file and the mesofurca). Complete results were published recently by Short & Fikáček (2013).

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Phylogeny of the herbivorous ladybird beetles (Coccinellidae) from the genus *Epilachna*

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Epilachna Chevrolat, 1837 is the largest genus within the ladybird beetle subfamily Epilachninae. At present there are known about 600 species distributed mostly in tropical and subtropical regions. Epilachninae are untypical among the mostly carnivorous ladybird beetles because they are phytophagous. As they feed on many plants from families like Solanaceae (potatoes, tomatoes), Cucurbitaceae (cucumbers, pumpkins) or Poaceae (sorgo, rice) they are regarded as serious pests. All Epilachninae species are quite uniform in external morphology and they caused many problems with classification. Earlier researchers revised just regional faunas like Dieke (1947) and Bielawski (1963) — Asia and Oceania, Fürsch (1963, 1991) — Africa and Gordon (1975) — America. But *Epilachna* has never been revised as a whole. These investigators found that in each region it is possible to distinguish several morphological groups but they did not find enough characters that could support division of the genus *Epilachna* into several smaller genera.

The main aim of the study is to reveal internal relationships in the genus *Epilachna*, and investigate its monophyly. 68 species of *Epilachna* from Asia, Africa and both Americas were analyzed that represent most of the species groups described by earlier researchers. As outgroup taxa representatives of 11 other Epilachninae genera (out of 23 currently recognized) and 5 other subfamilies of Coccinellidae were used. Both morphological and molecular approaches were used for the same set of species. The morphology of each species was studied in detail using classical methods and scanning electron microscopy. A matrix of morphological characters was prepared. In molecular part four gene regions were amplified: whole 18S rDNA and partial sequences of 28S rDNA, 16S rDNA and COX1. Totally about 4000 bp were sequenced for each species. To compute phylogenetic trees maximum parsimony and bayesian inference were used. Genes were treated as separate partitions as well as each codon position of the protein-coding gene. For each partition the model of sequence evolution was calculated separately. Based on the final phylogenetic tree morphological character transformations were reconstructed and evolutionary tendencies are discussed.

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Genes and genomes reveal new insights into the evolution of weevil (Coleoptera: Curculionoidea) megadiversity

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Weevils (superfamily Curculionoidea) are an extremely successful lineage of phytophagous beetles, comprising > 62,000 described species in ~5,800 genera. They exhibit a remarkable diversity of body sizes, shapes and structures, reflecting an equally remarkable range of habits. On account of their intimate and often highly specialized interactions with plants and fungi, they are among the most significant pests of agriculture and forestry. The phylogeny of weevils has received much recent attention using traditional molecular phylogenetic and morphological data and methods. Nonetheless, many aspects of weevil phylogeny and evolution, particularly the phylogeny of the unusually diverse weevil family Curculionidae (> 51,000 described species), remain controversial. To quote Crowson (1955; reiterated in Oberprieler et al. 2007) "Classification of Curculionidae into natural subfamilies and tribes probably remains the largest outstanding problem in the higher classification of Coleoptera [(beetles)]." The lack of a robust phylogeny for Curculionidae has prevented comprehensive studies of weevil evolution and has significantly impeded taxonomic, systematic and applied research on weevils. In this talk I will present reconstructions of the phylogeny of weevils, including the family Curculionidae, based on analyses of traditional molecular phylogenetic data (6 genes; McKenna et al. 2009; McKenna 2011) and emerging phylogenomic data (hundreds of genes). The resulting phylogenies resolve the most challenging of weevil relationships, and provide a robust foundation for testing long-standing hypotheses about weevil evolution (particularly in relation to the diversification and rise of flowering plants (angiosperms) to floristic dominance) and for ongoing further/deeper study of the uniquely diverse weevil family Curculionidae.

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Molecular phylogenetic analysis of the longhorned beetle subfamilies Prioninae and Parandrinae (Coleoptera: Cerambycidae)

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The phylogenetic relationships among the tribes and genera of longhorned beetle subfamilies Prioninae Latreille and Parandrinae Blanchard were inferred from DNA sequence data. Four genes (12S rRNA, 28S rRNA, cytochrome oxidase I, and histone III) were sequenced for 60 species representing the ingroup subfamilies Cerambycinae Latreille, Lamiinae Latreille, Lepturinae Latreille, and Spondyliidinae Audinet-Serville; and outgroup family Disteniid Thomson. Parsimony, maximum likelihood, and Bayesian analyses were conducted. Prioninae including Paran-



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drinae and the cerambycine genus *Plectogaster* was recovered as a monophyletic group in both the maximum likelihood and Bayesian analyses. In the parsimony analysis, Prioninae including Parandrinae but excluding two prionine genera as well as *Plectogaster* was recovered as a monophyletic group. All analyses recovered Parandrinae as a derived lineage within Prioninae. In addition, all analyses recovered the subfamilies Lamiinae, Lepturinae, and Spondyliidinae as monophyletic groups, as well as the Parandrinae + Prioninae clade as sister to Cerambycinae. *Plectogaster* and two prionine species were recovered within a basal clade sister to the rest of Prioninae in the maximum likelihood and Bayesian analyses. In the parsimony analysis, *Plectogaster* was recovered within the cerambycine tribe Holopleurini LeConte. Relationships among prionine-parandrine tribes had low support values in all analyses. Five fossils were included to estimate the date of divergence for various lineages within the subfamilies Cerambycinae, Lepturinae, and Spondyliidinae.

Geometric morphometrics and phylogeny: insight from beetles, ice crawlers and mammals

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Geometric morphometrics is a collection of approaches for the multivariate statistical analysis of Cartesian coordinate data, usually limited to landmark point locations. Shape is the geometrical information that remains when location, scale and rotational effects are filtered out from an object (Kendall 1977). The analysis of shape is a fundamental element of biological research. The traditional comparative morphological approach has a very long history in taxonomy and systematics. As statistics developed, the transition of biology from a descriptive discipline to a quantitative science began. In the 1980s, the nature of the data gathered and analyzed changed fundamentally, with a focus on the coordinates of landmarks and the geometric information about their relative positions. The developing novel approach was referred to as geometric morphometrics (Adams et al. 2004). Geometric morphometrics data can be applied to many research fields, such as for instance phylogeny, development, and ecology. This often requires a sophisticated quantitative representation of the phenotype that captures the functional, genetic or developmental attributes that are biologically important for the hypothesis to be tested, by linking the data. We will present several examples illustrating this approach, including analyses of hind wings of extant and extinct scarab beetles (Bai et al. 2011, 2012a,b), elytra of *Coraeus hastanus* (Buprestidae) (Xu et al. 2013), thoraces of ice crawlers (Bai et al. 2010), wings of an encyrtid parasitoid species complex (Chesters et al. 2012), and mandibles of *Parascaptor leucura* (Mammalia, Talpidae) (He et al. 2013). Geometric morphometrics is combined with cladistics analyses in these cases. The phylogenetic potential of this approach is discussed.

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New genomic evidence to resolve phylogenetic radiations in true flies

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Recent efforts to recover the fly tree of life have greatly advanced our knowledge of fly phylogeny. Fly evolution has taken place in episodic bursts, including 3 ancient rapid radiations corresponding to: lower Diptera (mosquitoes; 220 Ma), lower Brachycera (horse flies; 180 Ma), and Schizophora (*Drosophila*, house flies; 65 Ma). Ancient lineages that underwent rapid radiations, such as these, are often left unresolved by standard phylogenetic methods. Insect systematics is in transition toward large-scale gene harvests to obtain increasingly large data sets for previously intractable phylogenetic radiations. We are applying transcriptomic data to construct datasets of over 1000 orthologous genes to investigate fly phylogeny above the family level. A major goal is resolving the placement and diversification history of key fly families. Combining new transcriptomes, sequenced and analyzed in our laboratory, with previously published ESTs and genomes across the Diptera, and with data from large collaborative projects such as 1Kite.org, we are finding new support for controversial relationships — including: Apystomyidae as sister group of the Cyclorhapha and relationships among major schizophoran groups, such as Ephydroidea and Calyptratae. These new data provide new phylogenetic evidence for previously uncertain relationships, but also reveal patterns and process in genes and genomes associated with specialized life histories, morphology, and behavior in diverse fly clades.

From Sanger to NGS: resolving the phylogenetic relationships of an insect family (Sepsidae)

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Many phylogenetic trees based on morphological or molecular data suffer from “backbone” problems: Higher-level relationships are poorly supported and there is topological conflict between MP and ML trees. Sepsidae are no exception. Here we use taxon and gene sampling (transcriptomics) to address these issues. We find that the



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addition of 50 species to an existing dataset with 70 species does not solve the backbone problems. However, the addition of gene data from transcriptomes for 13 species resolves the issues and generates high branch support and congruent results. I then use the well-resolved and supported tree to explore several rarely used character systems. I start by discussing the evolution of genome size and chromosome number. The latter remains constant in Sepsidae while genome size varies by a factor of three and distinct increases of genome size have evolved thrice. I will then demonstrate that the evolution of the osmeterium, a gland on the hind tibia of male sepsids, can only be reconstructed by combining morphological and chemical information that is obtained through Ultraviolet Laser Desorption/Ionization (UV-LDI). Lastly, I discuss the evolution of copulation duration and separation behavior in Sepsidae.

Phylogeny of the Hymenoptera: new pieces into the old jigsaw(fly) puzzle

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The Hymenoptera constitutes one of the largest, and ecologically and economically most important insect orders. During the last decade, a number of hypotheses on the phylogenetic relationships among hymenopteran families and superfamilies have been presented, based on analyses of molecular and/or morphological data. Nevertheless, many questions still remain open, particularly when it comes to the evolutionary history of the ancestrally herbivorous 'sawfly' lineages, which form the basal, paraphyletic suborder Symphyta. Because a large part of the uncertainty appears to stem from limited molecular and taxonomic sampling, we set out to investigate the phylogeny of Hymenoptera using nine protein-coding genes, of which five are new to analyses of the order. In addition, we more than tripled the taxon coverage across the symphytan grade, introducing representatives for many previously-unsampled lineages. We recover a well-supported phylogenetic structure for these early herbivorous hymenopteran clades, with new information regarding the monophyly of Xyelidae, the placement of the superfamily Pamphilioidea, as well as the interrelationships among the 'higher' tenthredinoid families Tenthredinidae, Cimbicidae, and Diprionidae. In particular, our results give new insights into subfamilial relationships within the Tenthredinidae and other species-rich sawfly families. Among other new classificational suggestions, we propose the elevation of one tenthredinid tribe to family level, and another to subfamily level within the family. The expanded gene set, which is evaluated gene-by-gene as for information content and explanatory power in hymenopteran phylogenetics, provides a useful toolbox for future detailed analyses of symphytan subgroups, especially within the diverse superfamily Tenthredinoidea.

New dates for old wasps: total-evidence dating the early hymenopteran lineages

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Ronquist et al. (2012) introduced total-evidence dating (TED) for simultaneously estimating phylogeny and divergence time in a Bayesian framework. In TED, the fossils are scored for morphology and can influence tree



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topology as well as dating. This is in contrast with the previously widely applied node dating (NOD) approach, where fossils are assigned to nodes a priori and cannot influence topology. The placement of the fossils in the phylogeny is hence not evaluated in NOD, and morphological divergence between fossils and extant taxa has little influence on divergence time estimates. As a test case for TED, a character set comprising 343 morphological characters was assembled for 45 fossil and 68 extant taxa of basal Hymenoptera. In addition, seven molecular markers with a total of approx. 5 kb sites were included for the extant taxa. Most of the fossils included were poorly preserved (4–20% of the morphological characters could be scored) and hence there was considerable uncertainty in the placement of them. Nevertheless, they contributed significantly to the estimation of divergence times and on average, the estimates were less sensitive to prior assumptions and more precise than those obtained by node dating. Divergence time estimates often predate first appearance of a given lineage in the fossil record by several tens of millions of years. For instance, Hymenoptera is estimated to have arisen 300+ million years ago, whereas the earliest known fossil hymenopteran has an age of approx. 235 million years. In the future, perhaps improvements in analytical methods and increased knowledge of the fossil record will make it possible to reduce such gaps.

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Extant Chalcidoidea (Hymenoptera) — developing a phylogenetic hypothesis for a hyperdiverse group of insect parasitoids

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Using morphological and molecular methods, we are beginning to get a much better understanding of the evolution of the order Hymenoptera, which includes the ants, bees and wasps. The evolution of a parasitic lifestyle occurred only once in the suborder Apocrita, followed by subsequent changes to other important lifestyles such as nest provisioning, pollination and phytophagy. Within Apocrita, the Chalcidoidea are an extremely diverse group of parasitic wasps. With over 500,000 estimated species, this superfamily represents one of the greatest post-Cretaceous radiations among the insects.

Ranging in size from the smallest insect at 0.13 mm to veritable giants at over 20 mm, most species average 2–4 mm in size. Their morphological diversity is staggering. Convergent morphology is rampant, and many features are independently derived in very divergent taxonomic groups. The morphological diversity of Chalcidoidea is matched by their biological diversity. Although mostly parasitoids, phytophagous species are known from six families. Their animal host range includes 13 insect orders, spiders, ticks, mites and even gall-forming Nematoda. Species attack all life stages from eggs to adults, and as internal parasitoids, often multiple life stages. Species can be primary, secondary or even tertiary parasitoids, with some taxa required to parasitize their own species to complete development (heteronomous autoparasitism).

We have been able to address the phylogenetic relationships of Hymenoptera and Chalcidoidea through a series of projects focused on molecular methods, morphological character coding, and a worldwide collaboration of researchers using novel methods of on-line character coding. This resulted in the first comprehensive phylogenetic analysis of the Chalcidoidea based on 300 taxa coded for three gene regions and 233 morphological characters. The results allow us to study various processes including the evolution of heteronomy, phytophagy, and parasitism of various groups. These are also our first insights into the explosive radiation of the Chalcidoidea during the Cretaceous and Eocene periods.



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Fossil Chalcidoidea — a neglected source of phylogenetic data

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Chalcidoidea are a diverse and biologically important group of predominantly parasitoid wasps. The evolutionary history of the superfamily is largely unknown mainly because their rich fossil record has never been comprehensively studied. Here, the first overview of the fossil history of Chalcidoidea is presented based on a study of more than 1,000 fossils from Cretaceous, Eocene and Miocene ambers. Previously unrecognized fossils from Lebanese amber significantly increase the minimum age of the superfamily to about 135 million years. Chalcidoidea already exhibited a broad diversity in the Lower Cretaceous. Recently discovered fossils from Burmese amber (~99 mya) help dating the crucial transitions from endo- to ectoparasitoidism and from egg to larval/pupal parasitoidism. The minimum ages of further biological transitions are presented based on new fossil records of various chalcidoid families and subfamilies. The new fossils provide important calibration points for ongoing molecular phylogenetic studies and constitute a rich source of phylogenetic data. A brief discussion on the importance of the principles of phylogenetic systematics for the analysis of fossils is presented along with potential pitfalls in the interpretation of fossil data.

Amphiesmenopteran origins in time based on molecular evidence

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The two orders belonging to Amphiesmenoptera, Trichoptera and Lepidoptera, have very different fossil records, with the aquatic Trichoptera having a better record than the terrestrial Lepidoptera. The fossil record suggests that Amphiesmenoptera is at least Early Jurassic in age, but the majority of existing fossils are from the Cenozoic, leaving much of the evolutionary history of the lineages in the Jurassic and Cretaceous unknown. Recent work based on DNA sequences in both Trichoptera and Lepidoptera is bringing new light on the early diversification of the two orders. Independent studies suggest that the common ancestor of Trichoptera and Lepidoptera began diverging in the Late Triassic — Early Jurassic and that most of the early divergences in both lineages happened during the Jurassic. The rise of angiospermous plants had a huge impact on Lepidoptera diversifications in the Cretaceous, while Trichoptera diversified more evenly over time.

New insights on the phylogeny of Trichoptera: transcriptomes and new techniques

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Conflicting hypotheses have been generated for the relationships among suborders and families within the insect order Trichoptera. It has been particularly difficult to generate a phylogeny with high support for the relationships among the three suborders, Integripalpia (“tube case-makers”), Anulipalpia (“retreat-makers”), and “Spicipalpia” (5 families with diverse larval behaviors). Relationships among the families within the suborder Integripalpia are also difficult to resolve. Since these relationships inform interesting behavioral and morphological evolutionary histories, their resolution is of special interest to Trichopterists. Our most recent PCR based multi-gene dataset has finally



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produced high support values for the relationships among the suborders. However, trees estimated with data taken from 15 transcriptomes sampled throughout Trichoptera deliver conflicting answers from the PCR based analysis. We explore the differences between our PCR-based results and transcriptomic results. We find that with huge transcriptomic datasets, differences in partitioning schemes, data exclusion criteria, and whether nucleotides or amino acids are analyzed result in strongly supported, contradictory phylogenies.

The newly discovered 'Kangaroo Island Moth': unexpected complexity in early Lepidoptera evolution

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It has long been known that the 'Hennigian comb' pattern of the base of the lepidopteran family tree entails more complexities (parallelisms/character reversals) than appeared to be the case when it was first recognized in the mid-20th century. This has been due both to availability of more information about long-known taxa and to the discovery of previously unknown taxa which have proved to be additional 'teeth' in the comb. Still, a morphology-based phylogeny which can be formalized as Micropterigidae + (Agathiphagidae + (Heterobathmiidae + (Eriocraniidae + (Acanthopteroctetidae + (Lophocoronidae + (Neopseustidae + (Exoporia + Heteroneura)))))) has for some time been considered reasonably well substantiated, and recent molecular evidence for alternative arrangements has so far not had sufficient support to be considered compelling.

An unexpected challenge to the systematization of the basalmost Lepidoptera comes from a new homoneurous moth taxon discovered in 2009 on Kangaroo Island off continental South Australia, and with ample material only available since October 2012. It is conifer-associated, the larva being an apodous twig miner in *Callitris*, and the adults have the mouthparts so reduced that it is not immediately obvious whether the tiny galeae represent an original condition or are a reduced proboscis. An account will be given of the moth's principal structural traits, which give highly conflicting evidence on its phylogenetic position. According to the latest (and still inconclusive) molecular analysis it does belong within the Glossata; this is also suggested by a suite of anatomical characters, while others indicate that it arose in an earlier splitting event. Indeed no placement of the new taxon can be proposed, which will not necessitate disturbing assumptions of homoplasy in characters so far considered truly informative.

Phylotranscriptomics with 1000 genes: how many loci are needed for a robust phylogeny of the silk moth superfamily Bombycoidea?

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It has been presumed that the inclusion of next-gen sequence data into phylogenetic studies will lead to a drastic increase in resolution and node support. While support values tend to increase with the addition of loci, nodes can remain weakly supported. We used bombycoid moths, a traditionally difficult group to resolve some key inter-familial relationships, as a model to test how codon position and saturation might influence resolution and node support on a next-gen dataset that included 19 taxa and 938 genes (1,210,419 bp). Maximum likelihood, parsimony, and species tree analysis using gene-tree parsimony resulted in topological congruence as well as high support.



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The third codon position was saturated and phylogenetic analysis of this position alone supported a completely different, misleading sister group relationship. We conducted a RADICAL analysis to assess the number of genes needed to fix difficult nodes. One such node needed a total of 850 genes, but only needed 250 when synonymous changes were removed. While transcriptomics can provide the power needed to resolve many difficult phylogenetic relationships, the importance of assessing the effect of synonymous substitutions and third codon positions in next-gen datasets still remains.

A semantic model for morphological description

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Recent advances in Web technology and information sciences, especially the development of knowledge representation systems — ontology languages (Web Ontology Language) and syntaxes (Manchester syntax) — are now infiltrating the world of insect biodiversity research (Balhoff et al. in press; Vogt et al. in press; Deans et al. 2012a,b; Mullins et al. 2012). Data generated from taxonomic revisions, comparative morphology studies, and other enterprises now have the potential to be shared broadly and to be computed across — i.e., they are rendered semantic — in order to address questions relevant to multiple domains in the life sciences. In this presentation we will provide an insight of the philosophy behind these new tools and the mechanisms by which they operate. While formalizing morphological descriptions using ontology-based, semantic representation increases the accessibility of morphological descriptions for other disciplines, zoomorphology itself also benefits from the establishment of taxon specific ontologies. Not only do these ontologies facilitate the standardization of morphological terminology (Mikó et al. 2012), but they also serve as referencable collections of ontogenetic and positional or topographical similarities that are the operational contexts in which homology assessments are made (Seltmann et al. 2012). We provide examples using real data and describe some limitations of the ontology-based semantic reasoning.

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1 Comparative morphology of male genitalia in Archaeognatha

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The ventral exoskeleton of abdominal segments 7–9, which includes the male genitalic region, is described in detail for the five archaeognathans *Machilis hrabei* and *Lepismachilis notata* (Machilidae-Machilinae), *Pedetontus unimaculatus* (Machilidae-Petrobiinae), *Petrobiellus takunagae* (Machilidae-Petrobiellinae), and *Machillinus* sp. (Meinertellidae). Descriptions are based on stereomicroscopy and scanning electron microscopy. Focal topics are the sclerite patterns of the segments and fine structures on the cuticular surface of all parts. The results are compared with earlier descriptions of the male genitalic region in archaeognathans and with conditions in some other basal lineages of Insecta. Insect-level homology hypotheses and terminologies for elements of the insect genitalia that were developed in recent years are applied to the male of Archaeognatha for the first time. This allows to use genitalic characters as a source of information for subsequent reconstruction of phylogenetic relationships among insect lineages. Particularly noteworthy results are: (1) Compared to the pregenital segments, the male genital (9th) segment possesses distinctly larger mesal sclerotizations (derivatives of (eu)sternites). (2) Male genitalia and female genitalia in the most basal Archaeognatha are structurally similar and consist of the same sclerotizations — except for the penis, which is peculiar to males. (3) In the most derived family, Meinertellidae, insemination without carrier thread is accompanied by partial reduction of the penis and gonapophyses and by restriction of its movement caused by inclusion of the basal sclerites into the 9th venter. (4) Hypertrophy of the penis in *Petrobiellus takunagae* is also followed by fusion of some of the basal sclerites but without loss of penis movability.

2 Dating the origin of major mayfly (Ephemeroptera) lineages

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Our understanding of the phylogenetic relationships among major arthropod lineages has greatly benefited from the development of new sequencing technologies. Nonetheless, relationships among the oldest winged insects, the Ephemeroptera (mayflies) and Odonata (dragonflies and damselflies), remain unclear. Our aim was to resolve the phylogenetic origin of the mayflies in relation to the more derived insect lineages and the phylogenetic relationships among the major mayfly lineages. Therefore, we sequenced whole mitochondrial genomes of four representative mayfly species, applying Sanger sequencing and next-generation sequencing technologies. Mitochondrial genomes were extracted, annotated and incorporated with available protein-coding genes of other insect taxa. Preliminary results suggest that the mayflies are the most ancient winged insects and indicate superiority of shotgun libraries over Sanger sequencing in terms of feasibility and time investment.



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3 The thorax musculature of *Zygoptera* nymphs (Odonata)

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Odonata are arguably the insect group with the most impressive flight skills (e.g. Corbet 1999). Each wing pair can be controlled independently and some species are even able to fly backwards (Hatch 1966). The muscles responsible for the wing movement are connected directly to the wings (Tannert 1958). This exclusively direct mechanism of wing movement distinctly sets Odonata apart from all other winged insects; where the wing beat is done mainly through a system of indirect muscles, many of which are highly reduced or missing in the Odonata (e.g. Snodgrass 1935).

Here we present a comparative morphological investigation of the thoracic flight musculature of damselflies (*Zygoptera*). The results for *Nehalennia speciosa* (Charpentier, 1840) and *Ischnura elegans* (Vander Linden 1820) allow first insights into our comprehensive study.

Nymphs are aquatic predators, which feed on other Arthropods, whereas adults are arial predators (e.g. Corbet 1999). The amount and kind of muscles therefore significantly differ between nymphal and adult Odonata, which are adapted to their respective habitat (e.g. Asahina 1954; Maloeuf 1935).

We used synchrotron radiation micro computed tomography (SRμCT), aided by 3-D reconstruction to study the thorax of *Zygoptera*. The muscles were identified following the nomenclature introduced by Friedrich and Beutel (2008) as well as the homology hypothesis of Büsse et al. (2013) and Büsse & Hörnschemeyer (subm.).

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4 The thorax musculature of *Epiophlebia* nymphs (Odonata)

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Epiophlebia is the single taxon inside the recent Odonata, which combines characters of the Anisoptera and the *Zygoptera*. The four known species of *Epiophlebia* differ in only a few morphological features (e.g. Asahina 1961;



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Li et al.2011; Carle 2012). Recent publications (Büsse et al. 2012) show that the genetics of three of these species varies very little.

This study investigates the thoracic musculature of different nymphal instars of *Epiophlebia laidlawi* and *Epiophlebia superstes* in order to further reveal the relationship of the two species. Based on Maloeuf's (1935) nomenclature for the thoracic musculature of the Odonata and Asahina's (1954) studies on *E. superstes*, the nymphs were examined via Synchrotron radiation micro computer tomography (SruCT). Furthermore the identified muscles were homologized with the ones found in the Zygoptera (Büsse et al. 2013) and Anisoptera (Büsse & Hörnschemeyer subm.), based on the nomenclature established by Friedrich & Beutel (2008). The thoracic musculature of *E. laidlawi* and *E. superstes* is highly similar. Every muscle described by Maloeuf (1935) and Asahina (1954) could be confirmed in both species. Five muscles differ from the description of both authors. In addition, thirteen new muscles could be identified, of which one might be unique to the Epiprocta.

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5 The thorax musculature of Anisoptera nymphs (Odonata)

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Among the winged insects (Pterygota) the Odonata (dragon- and damselflies) are special for several reasons. Their thorax morphology differs significantly from that of other Pterygota by a reduced number of muscles (e.g. Asahina 1954; Maloeuf 1935). Even within one individual, between the nymph and adult stage, the musculature is significantly different (e.g. Maloeuf 1935).

Here we present a comparative morphological investigation of the thoracic musculature of dragonfly (Anisoptera) nymphs. For representatives of the Libellulidae, Aeshnidae and Cordulegasteridae we describe 71 muscles, 19 muscles of the prothorax, 26 muscles of the mesothorax and 27 muscles of the metathorax. This includes nine muscles that were so far unknown in Odonata, as well as seven muscles for which no homologous muscles could be identified in the neopteran thorax. Our results support and extend the homology hypotheses for the thoracic musculature of Odonata and Neoptera (Büsse et al. 2013) thus supplementing our understanding of the evolution of Pterygota and providing additional characters for phylogenetic analyses comprising all subgroups of Pterygota.



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6 Generalized Odonata thorax

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The odonatan thorax is a highly specialized and therefore a highly derived character system (e.g. Asahina 1954; Büsse et al. 2013). The generalized odonatan thorax shows all the muscles that have been found in Odonata to date. It compiles all the results of Büsse et al. (2013) and Büsse & Hörnschemeyer (subm.) and is completed by four muscles located independently by both Asahina (1954) and Maloeuf (1935), only.

For simplicity's sake, for comparison to Neoptera in particular, the generalized odonatan thorax is shaped like a nymphal thorax, which resembles the neopteran thorax. In order to present an overview, all structures, attachment points and directions have been simplified. It includes all muscles found homologous to Neoptera (Büsse et al. 2013; Büsse & Hörnschemeyer subm.) and the newly described Odonata muscles with no homologies to neopteran thorax (Büsse & Hörnschemeyer subm.).

The aim of the generalized odonatan thorax is to gain clear understanding of Odonata's muscle setup. It also represents an initial attempt to develop a hypothetical odonatan ground pattern of a stem-group representative.

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7 Clarification of the Paoliida (Insecta) problem: sister group of Neoptera or Dictyoptera?

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Late Palaeozoic Paoliida Handlirsch, 1906 (= Protoptera Sharov, 1966) is an insect group of highly controversial composition and equally controversial affinities. Herein we consider the Paoliida as an undisputed neopteran clade. Based on our comprehensive study we propose a new delimitation of the insect order Paoliida sensu nov. on the basis of the specific wing venation characters. Paoliida is considered as a potential sister group of the Dictyoptera on the basis of the presence of well-defined anterior branches of CuA, with the same convexity as the median vein and more concave than the posterior branches of the same vein (synapomorphy). The polarities of the other characters



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shared by these clades are discussed. New diagnoses of the order Paoliida and the family Paoliidae are provided. In addition we consider the families Herbstiidae, Idelliidae, and Protoblattinidae as junior synonyms of Paoliidae. Paoliids display relatively high abundance in early Pennsylvanian ecosystems with surprisingly low morphological diversity in comparison to the other groups of neopteran insects well diversified from the Duckmantian/Bolsovia boundary.

8 Thoracic morphology of ensiferans and its phylogenetic implications

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Ensiferans (katydids and crickets) form one of the most species-rich taxa among the “Lower Neoptera” or Polyneoptera. Morphology-based attempts to unravel the phylogenetic interrelationships of this taxon are sparse and led to largely inconsistent results. Therefore, new character complexes should be investigated and tested for their phylogenetic significance. Firstly, a comparative morphological study of the thoracic skeletomuscular system is presented including three representatives of the Ensifera: a schizodactylid (*Comicus calcaris*), a cave cricket (*Troglophilus* sp.), and a true cricket (*Gryllus bimaculatus*). Computer-based 3D reconstructions were applied to document the examined structures and to visualize the different character states. Secondly, the compiled dataset was analyzed in order to find potentially informative characters for the reconstruction of ensiferan phylogeny.

9 The phylogeny and evolution of praying mantids (Dictyoptera: Mantodea)

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Although the praying mantids are an extraordinarily charismatic group of insects, several questions concerning their phylogeny and evolution are still unanswered. The complete and robust resolution of the mantodean phylogeny is essential to the understanding of the evolutionary and the biogeographical history of the group. Studying the phylogeny of Mantodea based on morphology is hampered by multiple homoplasies. On the other hand, molecular phylogenetic analysis of this order had been lacking some of the key lineages of Mantodea until Svenson & Whiting (2009) published the most extensive dataset to date, using nine genes of 288 mantodean species. However, a robust hypothesis of the phylogenetic relationships of some crucial mantodean taxa is still needed. To address these problems, we are currently studying the transcriptomes of 51 selected Mantodea species in the framework of the 1KITE project (www.1kite.org), using a state-of-the-art workflow to phylogenetically analyze the data. These analyses of a large phylogenomic dataset will potentially yield a robust backbone tree of Mantodea and answer still open questions like (i) the position of the three presumably early diverging families Chaeteessidae, Mantoididae, and Metallitidae, (ii) the monophyly of the “earless mantises” of the neotropics, (iii) the position of the genera *Gonatista*, *Liturgusa*, and *Humbertiella*, with regard to the remaining individual genera of the polyphyletic “Liturgusidae” and (iv) the relationships between Hymenopodidae and Empusidae, between *Orthodera* and



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Choeradodis, and between *Pseudempusa* and *Deroplatus*. Phylogenetic results will allow us to trace the evolutionary history of phenotypic characters, for example, of the spination patterns on the raptorial fore legs, the cyclopan ear, the wing venation, and the color patterns and eye spots on the tegmina. Furthermore, they will allow us to give a new estimation of the time frame of Mantodea evolution; however, while we will have the largest molecular sequence dataset so far, the number of fossils reliably assigned to extant families is still very scarce.

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10 Phylogenetic reconstruction of wing states in cockroaches (Blattaria)

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Although the wings are one of the most important evolutionary innovations of insects, across almost all insect orders arise forms with partial (brachyptery) or complete (aptery) wing reduction. Order Blattaria is one of the most variable, yet poorly explored group in this regard, despite the fact that they are, with 50–60% of their species manifesting some degree of wing reduction, the order with the third highest occurrence of apterous and brachypterous species (Roff 1990). This makes them a suitable group for exploring wing reduction and regain processes.

Therefore our research aims to map the wing states and evolutionary trends both within the whole order and inside the main monophyletic groups. We applied a dataset of 82 species that are distributed equally throughout the order and whose phylogenetic relationships were analyzed in a recent study (Inward et al. 2007). Information on the wing state of both sexes were obtained from the literature, by visiting collections and from internet sources. Data were analyzed and ancestral states reconstructed using the software Mesquite.

Some groups exhibit a relatively low proportion of wing reductions, like Polyphagidae (87.5% males macropterous) and two groups of paraphyletic Blattellidae (100% and 80% respectively). Although Cryptocercidae are apterous, they exhibit no variability in wing changes and thus are not very interesting. In Blaberidae we noticed wing reduction in 57% of observed species, but mostly centred in apterous Oxyhaloinae group. The most interesting group seems to be Blattidae where 79% males of observed species exhibit wing reduction. Moreover 36% blattid species are sexually dimorphic in their wing state.

Reconstruction of ancestral states supports a macropterous cockroach ancestor and the wing reduction occurring many times independently. We did not find any support for regain of wings once lost. More interestingly, we could not support step-by-step wing reduction from macroptery through brachyptery to aptery. We could only support change from macroptery to brachyptery and directly from macroptery to aptery. For a more accurate interpretation of evolutionary processes we aim to use a denser sample of cockroach species from a subordinate taxonomic unit.

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11 The phylogeny of *Arenivaga* (Rehn) (Blattodea: Corydiidae: Polyphaginae)

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My doctoral research comprises a phylogenetic revision of the genus *Arenivaga* (Rehn), a genus of cockroach adapted to life in the deserts of the American southwest, Florida, and Mexico. Also known as sand cockroaches, the females and nymphs “swim” through sand and feed on detritus and mycorrhizal fungi on the roots of desert shrubs. The two sexes are dimorphic; the females are robust and apterous, whereas mature males are gracile and winged. Prior to this study, nine species were known. After lengthy examination of over 5000 male specimens, I have identified, (re)described and mapped the geographic boundaries of the original nine and 39 new species. This poster presents the first phylogeny of this genus and uses it to discuss the disjunct populations of *A. tonkawa*, the possibility of incomplete speciation between populations in the Mohave Desert, and the rate of speciation in the genus. It will also review a basal divergent clade and the characters that unite it.

12 Neotropical Nasutitermitinae (Isoptera: Termitidae): a preliminary morphology-based phylogenetic analysis supports three new nasute genera

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Nasutitermitinae (Isoptera, Termitidae) is a well corroborated monophyletic group with a worldwide distribution, having a high richness of both genera and species, and the widest diversity of feeding and nesting habits. The subfamily is represented by 28 genera and 161 species in the Neotropical region, and it is always one of the most dominant groups in South American termite surveys. The genus *Nasutitermes* was never revised, and its taxonomy is quite confuse, so the identification of the Neotropical species is not always easy. During the study of type material of Neotropical *Nasutitermes* species deposited in different Isoptera collections, some morphological inconsistencies in relation to the general “*Nasutitermes* pattern”, mainly in the worker digestive tube was found; thus, suggesting that these species should be removed from *Nasutitermes*. In order to reconstruct the phylogenetic relationships among Neotropical Nasutitermitinae genera and test the monophyly of *Nasutitermes*, a preliminary cladistic analysis involving the type species of all Neotropical Nasutitermitinae genera was conducted. According to the previous evidence of Nasutitermitinae relationships, two species of Syntermitinae (*Cornitermes cumulans* and *Procornitermes striatus*) and two of Termitinae (*Amitermes amifer*, *Microcerotermes strunckii*), were chosen as outgroup taxa, with *A. amifer* rooting the trees. A matrix with 83 characters was analyzed under parsimony criteria with TNT 1.1, using the ‘new technology search’ under default settings. Analyzes were performed with equal weights, as well as with implied weights with concavity factor ranging from $k = 6$ to 15. Some multistate characters were treated as additive. For the cladogram branch support, the relative Bremer support was calculated and a symmetric resampling was performed. The analysis under equal weights produced six most-parsimonious trees (642 steps), while the one with implied weights produced three different topologies for the range of values of k . In all the topologies the species *N. gagei*, *N. robustus* and *N. hubbardi* let the genus *Nasutitermes* paraphyletic. These species are differentiated mainly by the worker characters, particularly those of the digestive tube in situ (dorsal torsion, isthmus and U-turn) and the mandibles. In this way, our preliminary results support the designation of three new genera which includes species previously described as *Nasutitermes*.



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13 Dwarfish sexuales of Thelaxinae (Hemiptera, Aphidoidea) — review of species and life cycles

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Thelaxinae is a small subfamily consisting of 18 species in 4 genera: *Glyphina* Koch, *Kurisakia* Takahashi, *Neothelaxes* Chakrabarti & Quednau and *Thelexes* Westwood. Aphids belonging to this subfamily are characterized by wingless, dwarfish sexuales and unusual life cycles. The immature sexuales of *Thelexes* aestivate in summer and adult oviparae and males occur in autumn. *Glyphina*, on the other hand, have an abbreviated life cycle with sexuales appearing at the beginning of the summer. Moreover, the external genitalia of males of the studied species are strongly modified, with parameres fused into one structure and a reduced basal part of the phallus. Because of peculiarities of the life cycle and the small sizes, sexuales of some species of Thelaxinae have never been described (e.g. *T. suberi* (del Guercio), *G. jacutensis* Mordvilko), or need a re-description (e.g. *G. betulae* (L.)). The life cycle and sexuales of *Kurisakia* and *Neothelaxes* have remained unknown. In the evolution of aphids dwarfish sexuales appeared independently in Mindarinae, Hormaphidinae, Anoeciinae, Thelaxinae and Eriosomatinae. Thelaxinae represents the monoecious type of the life cycle (similarly like Mindarinae), whereas Hormaphidinae, Anoeciinae and Eriosomatinae are characterized by the dioecious one (pemphigid host alternation) where sexuparae return to the primary host.

14 The identity of *Eulachnus alticola* Börner, 1940 (Hemiptera: Aphidoidea: Lachninae) in light of morphological research

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The genus *Eulachnus* Del Guercio, 1909 (Aphidoidea: Lachninae) comprises about 15 species of small and spindle shaped aphids, trophically associated with pine (*Pinus* spp.). Aphids from this genus are known to be remarkably cryptic, they do not form colonies, are hidden when feeding and very active when disturbed. They feed on needles of several year branches and if they are present, they are very rarely visited by ants (Blackman & Eastop 2013). Due to their biology some morphs of many species are unknown or were characterised very briefly in descriptions concentrated exclusively on basic features. Many species of this genus are very closely related, especially those belonging to the "agilis" group, some of which are treated as synonyms of *E. agilis* (Kaltenbach, 1843). A clear example of this problem is the identity of *E. alticola*, which lives on *Pinus mugo* Turra. This species is known from few localities, and prefers submontane and montane areas in central and eastern Europe. Due to its close similarity to *E. agilis*, which is oligophagous on many *Pinus* species, some authors (e.g. Blackman & Eastop 2013) consider *E. alticola* as a synonym of *E. agilis*. On the other hand many authors (i.e. Pintera 1968; Szelegiewicz 1978) distinguish *E. alticola* as a separate species as it lives on another *Pinus* species, *P. mugo*, and has a different geographical range. The aim of the research, based on morphological analysis was to conclusion about the identity of *E. alticola*.



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15 Potential geographic distribution of true bugs of the subfamily Diaspidiinae Miller, 1959 (Heteroptera: Reduviidae)

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Assassin bugs (Reduviidae) belonging to the subfamily Diaspidiinae are represented by three genera: *Cleontes* Stål, 1874, *Diaspidius* Westwood, 1857 and *Rodhainiella* Schouteden, 1913. All known species belonging to the mentioned genera are distributed exclusively in the Afrotropical Region, but there is only one paper concerning a revision of the genus *Diaspidius* Westwood, 1857. Very little attention has also been paid to distributional pattern of genera and species of Diaspidiinae.

The potentially suitable habitats for representatives of Diaspidiinae in Africa and Madagascar are presented. All species distribution models were developed using the Maxent software, based on a maximum entropy algorithm. Those species of the subfamily that were reported for mainland of Africa, during the climate analysis of potentially suitable habitats were recognized mainly in the tropical type of climate like tropical monsoon climate, tropical wet and dry or savanna climate and tropical rainforest climate. Those climates are characterized by a constant high temperature with an average of 18°C (64°F) or higher all over the year. For those species that inhabit Madagascar, potentially suitable habitats also have been indicated in the tropical climates, but in the central part of the island additionally shown areas in the type of mesothermal climates.

The jackknife test showed that annual precipitation (Bio12) followed by temperature annual range (Bio07) and precipitation of warmest quarter (Bio18) are the environmental parameters that bear the most useful information by themselves. On the other hand, also annual precipitation (Bio12) and the percentage of tree cover are variables that have a significant portion of information that is not contained in the other variables.

16 Phylogeny of the water boatmen Corixoidea (Heteroptera)

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We investigated phylogenetic relationships among water boatmen (Insecta: Heteroptera: Nepomorpha: Corixoidea) in a combined parsimony analysis. Our analysis is based on 432–444 bp of 16S rRNA, 502–533 bp of 24S rRNA, 1300 bp of mitochondrial COI+II and morphological data. Apart from a dense selection of outgroup taxa (Gerromorpha: Mesoveliidae; Nepomorpha: Nepidae, Notonectidae), our analysis included representatives of all known corixoidean taxa. We included representatives of all families of Corixoidea (Diaprepocoridae, Micronectidae and Corixidae) and from Corixidae we included representatives of the subfamilies Cymatiinae, Heterocorixinae and Corixinae.



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A strict consensus of four equally parsimonious trees resolved Diaprepecoridae as sistergroup of Micronectidae + Corixidae ('Anocellia'). In Corixidae the found Cymatiinae to be the sistergroup of Heterocorixinae + Corixinae ('Odontopalae'). The Corixinae split into Agraptocorixini and an assemblage of Glaenocorisini, Graptocorixini and Corixini. The tribes Glaenocorisini and Graptocorixini cluster within Corixini. Among genera of Corixini, *Trichocorixa*, *Callicorixa*, *Corixa*, *Ectemnostega* and *Arctocorixa* are revealed monophyletic, while *Hesperocorixa* and *Sigara*, incl. many subgenera, are paraphyletic. Based on optimization of morphological characters onto the strict consensus tree arising from the phylogenetic analysis we present and evaluate diagnostic character combinations for various clades at higher taxonomic levels, such as families, subfamilies, tribes and informally named clades such as 'Odontopalae' (Corixinae + Heterocorixinae); 'Embolipennae' ('Odontopalae' + Cymatiinae), and 'Anocellia' (Micronectidae + Corixidae). Finally, we point out directions for future research on the phylogeny of this group of insects, especially high-level taxa yet to be included, such as Micronectidae-Synaptogobinae and Corixidae-Stenocorixinae.

17 Unique protection of the eggs within the insects — a case of the family Plataspidae (Heteroptera: Pentatomoidea)

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Insects developed various strategies to effectively increase the fitness of offspring, including a defence of the eggs, from parental care to oviposition inside tissues of organisms to covering the eggs with substance forming a structure called ootheca. Apart from the best known examples of the ootheca, e.g. in the Blattoptera, Mantodea and Orthoptera-Acrididae (summary e.g. Nichols & Schuh 1989), this pattern of egg defence is distributed in more insect taxa. An ootheca occurs also in heteropteran families Reduviidae, Urostylidae and Plataspidae (Southwood 1956). In all insects mentioned above, except the Plataspidae, the substance of the ootheca originates from colleterial and pseudocolleterial glands connected with the genital tract. The ootheca formed by the plataspid *Libyaspis flavosparsa* (Montandon, 1894) is a unique structure by its origin. The substance is secreted from a distinctly modified epithelium of the posterior part of the midgut. The arrangement of eggs in a batch of *L. flavosparsa* is similar to a batch freely deposited, however, the eggs in the ootheca have a slightly different shape. In particular, the micropylar processes are long and the chorion is partly smooth. Above each egg, the elongated, wale-shaped secretion is deposited, tightly depressed each to other. The total shape of the ootheca copies roughly the shape of the egg batch, which results in a roof-shaped structure laterally separated from a substratum. The ability to form an ootheca occurs not only in other Heteroptera but also in Auchenorrhyncha: Fulgoridae (e.g. Han et al. 2008) and Membracidae (e.g. Wood 1980). Thus we can suppose that such disposition can develop and exist already in an ancestor of the entire taxon Hemipteroidea. However, the question why the oothecal substance of the quite unique origin within all insects did develop just in the Plataspidae remains to be answered.

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18 Tiny eggs and minute larvae — the embryonic development of *Stylops ovinae* (Strepsiptera)

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Strepsiptera are a small endoparasitic group of Holometabola. The available information on this “enigmatic” group has tremendously increased in recent years. However, the embryology is only covered by few older studies (Hoffmann 1913, 1914; Noskiewicz & Poluszynski 1928, 1935) and is still insufficiently understood. Consequently the primary aim of our study was to document the embryonic stages using modern techniques.

The monophyly of Coleopterida (Strepsiptera + Coleoptera) is well established (e.g. Niehuis et al. 2012) and the embryology of the beetle genus *Tribolium* is well investigated. This and information on outgroup taxa (Neuroptera) makes it possible to investigate possible changes which may have occurred in the embryogenesis of Strepsiptera and which may have made possible unusual specialisations including vivipary, miniaturisation, hypermetamorphosis and endoparasitism within this group. The eggs and embryonic stages of *Stylops ovinae* were investigated using SEM and DAPI-staining and are described briefly in the following.

The minute eggs (ca. 50 µm in size) are roughly spheroidal. The embryonic development is asynchronous: females two weeks after fertilisation contain eggs and embryos of almost all stages. The early embryos are strongly bent dorsally. The distinct anlagen of the mouthparts lie directly behind the large cephalic lobes. Antennal anlagen are missing. The anlagen of appendages are distinct in the thoracic area, but completely missing on the abdomen (except for cerci), which is straightened in its middle region.

In the next stages the differentiation of the legs and mouthparts continues. The latter are retracted into a preoral cavity (secondary entognathy). Thin appendages form on the caudal portion of the abdomen. The abdomen bends from the dorsal to the ventral side.

In the last stages the differentiation of segments and appendages is completed. The typical cuticular spines have formed. The last stage resembles the primary larva.

The new data allowed to address the homology of the highly unusual cephalic ventral plate of the larvae. During the earlier stages the prospective plate is represented by paired anlagen of the mandibles and maxillae and an unpaired anlage of the labium. In later stages, the paired prospective mandibles and maxillae approach each other, respectively and are then located near the mouth opening. The labium is greatly reduced and not recognisable as a prominent structure.

In later stages the mandibles and the mouth opening lie within the expanding preoral cavity. The maxillae are connected medially, thus forming an unpaired maxillary bridge. Expanding paired cephalic duplicatures enclose the vestigial labium laterally.

Finally, in obviously last stages the mandibles are completely enclosed in the preoral cavity and form long blade-like structures. The maxillary bridge is widened and the labium is fully enclosed by the cephalic duplicature. This shows that the ventral plate is a product of fusion of parts of the head capsule, the maxillae and the labium as suggested by Pohl (2000).

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19 Molecular phylogeny of the leaf beetle subfamily Criocerinae (Coleoptera: Chrysomelidae) and co-evolution of male and female reproductive organs

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The leaf beetle subfamily Criocerinae is considered an early branch of Chrysomelidae (e.g. Gómez-Zurita et al. 2008). The food plants (e.g. Schmitt 1988), the interspecific variability of reproductive (e.g. Matsumura & Yoshizawa 2012) and stridulatory organs (Schmitt 1990), and the chemical ecology of larval fecal shields (e.g. Aiello & Vencel 2006) are well investigated. In contrast, despite its potential for investigations in evolutionary biology, the phylogeny is only poorly understood (e.g. Schmitt 1985, Vencel et al. 2004). This is due to insufficient taxon and/or data sampling. We estimated phylogenetic relationships among criocerine species selected from major genera using molecular data (mitochondrial cytochrome oxidase I, 12S rDNA, and nuclear histone 3) and reconstructed the evolutionary pattern of divergent reproductive organs. The ingroup comprises 38 species. Six additional chrysomelids and one cerambycid species were used as outgroup.

All analyses supported a clade Criocerinae. The *Lema* group was recovered as monophyletic and as sister group of *Lilioceris*. Both were placed as sister group of *Crioceris*. *Oulema* and *Neolema*, already previously treated as a synonym of *Lema*, were indeed embedded within this genus.

Ancestral states of the reproductive organs were reconstructed based on parsimony. Elongation of a part of the intromittent organ occurred several times independently as already suggested by morphological comparisons (Matsumura & Yoshizawa 2012). To verify a correlated evolutionary pattern of the length of male and female reproductive organs, we used Felsenstein's independent contrast. The length of the male and female reproductive ducts, which have physical contact during copulation, showed a tight positive correlation, which strongly suggests co-evolution. We also found that the shape of the spermatheca diversified in the subfamily, and that a complicated coiled spermatheca probably evolved several times independently. The potential sister group, i.e. Donaciinae, has only a simple type of spermatheca and a very short flagellum (e.g. Hayashi 2004). Based on our data, we will investigate why a diversification of the reproductive organs only occurred in Criocerinae.

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20 Dispersal is linked to habitat preference in 59 species of tropical water beetles (Coleoptera: Adephtaga)

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Lentic habitats (standing water, such as ponds and lakes) differ from lotic habitats (running water; streams and rivers) in their spatiotemporal persistence, with lentic habitats being more ephemeral in evolutionary time. This habitat instability is thought to select for dispersal, and several phylogenetic and macroecological studies have suggested that lentic species are more dispersive than lotic ones. We tested the generality of this hypothesis using a comparative population genetic and phylogeographic approach. We analyzed mitochondrial DNA of 59 aquatic beetle species, sampled across Madagascar, using at least 10 individuals per species. Species were classified as lotic ($n = 25$), lentic ($n = 25$), or lotolentic (associated with both running and standing water; $n = 9$). Hierarchical population genetic structure (AMOVA), nucleotide diversity (π), and phylogeographic structure were compared among habitat types. Population genetic parameters were compared by phylogenetic generalized least squares (PGLS) ANOVA in order to correct for phylogeny. Lotic species had significantly greater population structure ($\Phi_{ST} = 0.83$, hierarchical AMOVA) than lentic ($\Phi_{ST} = 0.04$) and lotolentic ($\Phi_{ST} = 0.13$) species. Body size was independent of habitat preference, and did not explain any of the intraspecific variation. A greater proportion of lotic species were endemic to Madagascar and lotic species had more pronounced geographic structure in their haplotype networks. The results indicate that dispersal is consistently lower among lotic species, independent of phylogenetic relatedness, and that this has macroevolutionary consequences. Insights in dispersal patterns are relevant for conservation in this tropical biodiversity hotspot.

21 O Sister, Where Art Thou? Conflicting hypotheses on basal branchings in Neuroptera

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In most recent analyses either the Nevrothidae or the Sisyridae compete for the first bifurcation in Neuroptera. Characters and character complexes supporting either one or the other hypothesis are discussed. Concretely, larval characters, characters of the head of adults and of the genital sclerites are combined in different ways and analysed. An analysis of larval characters alone yields Nevrothidae as the basalmost neuropteran lineage and Sisyridae within the Hemerobiiformia. The addition of characters of the adult head or the genital sclerites provokes a sistergroup-relationship of the Sisyridae and all other Neuroptera. Finally, the likeliness of common origin or independent evolution is discussed for the conflicting characters.



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22 High throughput mitogenomics for lepidopteran phylogenetics

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The field of molecular systematics is being revolutionised by Next Generation Sequence technologies that capture DNA sequences 'en masse'. Popular targets within this context are mitochondrial genomes. The divergent nature of these phylogenetic markers allows their correct assembly from pooled DNA samples. This implies that large numbers can be analysed in parallel, hence aiding the optimal and cost effective usage of the offered sequencing capacity. To investigate the strength of mitogenomics for lepidopteran phylogenetics we PCR amplified mitochondrial genomes from representatives of 22 superfamilies. Fragments were pooled and sequenced on an Illumina Miseq using ~1% of the machines capacity. A total of 25 full and three partial genomes were obtained. Gene annotation revealed a tRNA translocation that supports Tischerioidea, Adeloidea and 'Australian palaephatids' as being closer related to Ditrysia than other non-ditrysiian Heteroneura. Genomes were combined with all publicly available mitogenome sequences, for a total of 105 taxa for phylogenetic analyses under a Bayesian framework using four different coding schemes (i.e. 1: full dataset, 2: all synonymous changes excluded, 3: 1st codon site RY recoded-third base removed, 4: translated to amino acids) and software was applied to obtain the most appropriate partition schemes. Some interesting, well-supported relationships were revealed: Tineoidea are the sister of the remaining Ditrysia, with Gracillarioidea + Yponomeutoidea the next lineage within Ditrysia; as other studies have reported, Papilionoidea (butterflies) are not macro Lepidoptera, with Pyraloidea being the sister of 'classical macro moths'. Relationships among lower apoditrysians, however, remain largely unresolved. We assume this in part to be due to poor taxon sampling and that denser sampling will help us gain better understanding of these relationships. Obtaining information on these under-sampled lineages should not be an issue now that high throughput sequencing methods are in place for mitogenomics and molecular systematics.

23 Head morphology of adult caddisflies (Trichoptera) and its phylogenetic implications

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Caddisflies are a medium sized group of holometabolous insects (app. 14,500 species) with primarily aquatic larvae and terrestrial adults. Traditionally, the group is divided into three major lineages (Annulipalpia, Integripalpia and Spicpalpia). Over the last decades the phylogeny of the group was discussed controversially but remains mainly unsolved. Furthermore, comprehensive data on internal and external adult structures are extremely scarce and fragmentary. This impedes the understanding of the evolution of major morphological and behavioral traits in Trichoptera.

Goals of this study are the acquisition of detailed morphological data covering the major trichopteran lineages and the reconstruction of the groundplan conditions of the order focusing on adult head structures. Ten representatives covering all suborders were investigated using a combination of micro-computed-tomography, histology and scanning electron microscopy. Computer-based 3D-reconstructions were carried out to analyze and visualize the raw data.



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The presented data give insights into morphological modifications of skeleton and musculature during the evolution of the trichopteran head. Potential groundplan features of Trichoptera are: (1) moderately sized and well sclerotized mandibles, (2) a small, granulose haustellum, (3) five-segmented maxillary palps in both sexes, (4) apically pointed and flexible terminal segment of maxillary palp, and (5) well-developed mandibular adductor and abductor muscles. Some of these features undergo remarkable modifications within Integripalpia: The haustellum is broadly enlarged, whereas the mandibles are strongly reduced forming small membranous lobes. Also the size of maxillary palps differs remarkably. In contrast representatives of Annulipalpia and most of the spicipalpian groups (e.g., Rhyacophilidae) retained these groundplan features almost unchanged. It remains unclear whether the reduction of the dorsal tentorial arms, as present in non-integripalpian caddisflies, has to be considered as a groundplan feature of Trichoptera. Alternatively, the strongly sclerotized tentorium of Integripalpia could represent the plesiomorphic condition. Similar conditions known from several groups of Lepidoptera, but basal representatives of this group (e.g., Micropterigidae) do not possess distinct dorsal arms. This rather supports convergent reinforcement of the cephalic endoskeleton within Trichoptera and Lepidoptera. It seems to be reasonable that the increased size of extrinsic antennal muscles, which usually originate from the tentorium, caused these drastic modifications in Integripalpia.

24 Phylogeography of *Rhyacophila tristis* (Trichoptera: Rhyacophilidae)

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During the last decade phylogeographic studies of European aquatic insects have revealed numerous different patterns from those observed in terrestrial species. Here we analyzed the genetic population structure and phylogeography of the wide-spread highland caddisfly *Rhyacophila tristis* Pictet, 1834 based on a range-wide sampling of mitochondrial sequence data (mtCOI) from 520 specimens. Previous studies illustrate that the closely related sister species of the *R. tristis* are micro-endemics with multiple refugia in Europe. Therefore, we hypothesize that the wide-spread *R. tristis* may also present a complex of evolutionary lineages that persisted in independent glacial refugia. We used median-joining networks, analysis of molecular variance (AMOVA) and Mantel test of isolation by distance to examine population structure. We found 81 haplotypes and differentiation among mountain ranges and three regional clades (southern, eastern and central). The high level of genetic differentiation between mountain ranges provides evidence for the existence of multiple glacial refugia in Europe. Shared haplotypes between clades suggest retention of ancestral polymorphism or inter-regional dispersal. We employed SIMCOAL to explore different migration-models that could explain the observed haplotype distribution. Considering the potential threat to montane species under land use and climate change we used SDMs to investigate the future distribution of climatically suitable areas and assessed the potential associated loss of haplotype diversity and evolutionary lineages in *R. tristis*.



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25 Morphological and phylogenetic characterization of caddisfly larvae of genus *Himalopsyche*

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Despite several unusual adaptations and the interesting biogeography of genus *Himalopsyche* (Trichoptera: Rhyacophilidae) little is known of species-level relationships within the genus. The genus comprises 52 species, but larvae and pupae of only three species have been morphologically characterized: *H. japonica*, *H. phryganea*, and *H. tibetana* from Japan, North America and the Himalaya, respectively. In this study, we examine the morphology of 184 larvae of *Himalopsyche* from China and Nepal to characterize further species of *Himalopsyche* in the larval stage. Larvae were collected from 25 mountain streams in 7 regions of the Qinghai Tibetan Plateau and the Himalayas, and cover an altitudinal range from 1500 to 4100 masl. We used molecular sequence data from two genes (mtCOI, D2-region of 28S) to validate the distinction of morphotypes as independent evolutionary lineages based on GMYC models and to associate the larvae with known adults. Diagnostic features of the various morphotypes are illustrated using photographs. Ecological preferences of individual lineages are based on surveys of habitat parameters at the sampling sites including water temperature, O₂-concentration, pH, mean current velocity and substrate composition. Ecological preferences will be linked to relevant morphological characteristics, e.g. gill shape and structure. Our study thus provides an important background for future studies on traits and species evolution in *Himalopsyche* and the family Rhyacophilidae.

Caddisfly larvae are vital participants in aquatic food webs and good indicators of stream health. They are thus frequently used for biological assessment. Our study will help improve the basis for biomonitoring in Himalayan countries by providing identification tools for an important predator of Alpine streams in Asia.

26 The larval abdomen of the enigmatic Nannochoristidae (Mecoptera)

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Nannochoristidae is a controversial taxon of holometabolan insects, usually assigned to Mecoptera, but also treated as a separate order by some authors. It is a relict group with only eight described species in one genus and restricted to the southern hemisphere. The knowledge of the morphology has dramatically increased in recent years. However, this does not apply to the postcephalic anatomy of the aquatic larvae, which differ dramatically



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from all other known mecopteran immatures in the life habits and morphology and is only partly treated by one paper (Pilgrim 1972). This induced us to investigate the abdominal segments, with emphasis on the posterior region with its complex internal structures.

Like the entire postcephalic body, the larval abdomen of *Nannochorista* sp. is extremely slender and nearly cylindrical. The anterior segments are largely unmodified. The surface is smooth and lacks any protuberances or prolegs in contrast to other mecopteran larvae.

The muscles of segment X are highly modified. They move the membranous pouch, the anal papillae, and the terminal lobes. The presence of these structures is likely an adaptation to the specific aquatic life style of nannochoristid larvae. The anal papillae are possibly homologous to the 4-lobed terminal attachment apparatus of larvae of *Caurinus* (Boreidae) and *Pistillifera* (Panorpidae, Bittacidae, Choristidae) but this is uncertain. The specific conditions in both groups, i.e. two retractile papillae with tracheae and Malpighian tubules in Nannochoristidae, and a 4-lobed exposed attachment device in *Pistillifera* and Boreidae (groundplan) are very likely autapomorphic for both groups, respectively. A slender abdomen with smooth surface is very likely plesiomorphic within Antliophora and Mecoptera. This condition is found in Trichoptera (partim), Nannochoristidae, Siphonaptera, and many basal groups of Diptera. An eruciform or scarabaeiform body shape with a soft and largely unsclerotized cuticle is probably a synapomorphy of Boreidae and *Pistillifera*. The presence of ventral protuberances resembling prolegs on the anterior segments is an autapomorphy of the latter group. The homology of paired or unpaired terminal appendages of segment X is uncertain. However, the specific condition of paired and 3-segmented appendages with hooks in Nannochoristidae is almost certainly autapomorphic for this family. The protracted opening of the hind gut on the membranous pouch is another potential autapomorphy of Nannochoristidae. Aquatic habits of larvae, also very likely an apomorphic condition, have likely evolved several times independently in Mecoptera and Antliophora.

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27 The evolution of the adult head in Diptera

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Diptera is one of the species richest orders of holometabolous insects. They are highly diverse in their ecology. The head is an essential feature of adult insects, bearing a number of important sensory organs as well as containing the brain. I investigate 36 taxa and the taxon sampling includes at least one specimen from almost all families of lower Diptera, but also some brachyceran and outgroup taxa. The head of adult Diptera is characterized by many reductions. Mandibles and their associated musculature are present in the groundplan of the order, but missing in most groups. The presence of mandibles is directly correlated with the feeding habit. They are present in blood-sucking species, like members of Culicidae, Ceratopogonidae or Tabanidae. In most dipteran groups the tentorium is a straight hollow tube, connecting anterior and posterior tentorial pits. In some specimens the tentorium is completely reduced (Nymphomyiidae or Tipulidae). However, in the dipteran groundplan anterior, posterior and dorsal arms are well developed (present in Simuliidae and Tabanidae), but a typical corpotentorium is missing in all groups. The tendency to shift the origin of the antennal muscles from the tentorium to the head capsule is correlated with the far reduction of the tentorium, but without a recognizable phylogenetic pattern. The potentially basal families of Diptera, Deuterophlebiidae and Nymphomyiidae, are extremely specialized in their morphology and life cycle. Thereby the interpretation of the features appears difficult.



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28 Fly on the wall — attachment devices in lower Diptera

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Diptera display a broad array of adhesive devices occurring on different parts of the legs. Characters of the distal leg region of 32 species and 10 outgroups were mapped onto the phylogeny of Wiegmann et al. (2011) to evaluate the evolution of attachment structures in Diptera.

Smooth and hairy attachment structures are present in Diptera. A smooth arolium is present in Tipulomorpha but missing in the remaining dipterans. It has very likely evolved independently from the arolia of the outgroups, though a possible re-evolution is discussed as well. Hairy empodia are a groundplan feature of Diptera, but missing in several genera. Hairy pulvilli can be found in most subgroups. However, two species evolved smooth pulvilli. Very often both pulvilli and empodia are present. The size and shape of these two structures is very variable. The shape of the tips of tenent hairs differs considerably between the different groups. The potential to modify pretarsal attachment devices in their structural details has probably contributed to the very successful diversification of Diptera.

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29 Raptorial Phantom Midges — the larval head of Chaoboridae (Diptera)

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The predaceous larvae of phantom midges (Chaoboridae) are almost completely unpigmented and weakly sclerotized. They live exclusively in standing water and feed on copepods and water fleas. They capture the prey with raptorial antennae, a unique mechanism within Diptera. This unusual feature and the unclear homology of different larval head structures induced us to investigate the mouthparts and the internal cephalic structures of the larvae of *Chaoborus crystallinus* De Geer 1776. The head is strongly compressed laterally. The closely adjacent antennae have a similar function as the mantid raptorial forelegs. They are 1-segmented, elongated and strongly sclerotized. Their location in front of the compound eyes ensures a good coordination in the prey-catching process. The abduction is caused indirectly: the hemolymph pressure is increased by the contraction of the *M. transversus* rostralis. The two pairs of labral retractors also contribute by stabilizing the membranous mouth region. The mouthparts are located on the ventral side. The labrum is a very narrow, strongly elongated and largely sclerotized on the ventral side of the head. It is inserted on a small trapezoid ventral clypeus. Its unsclerotized parts are equipped with brushes. The elongated dorsal sclerite previously addressed as clypeofrons is in fact only the frons. The labium and the maxillae are largely reduced. The function of the mandibles (abducted by *M. abductor mandibulae*) and the labrum (depressed by *M. adductor epipharyngis*) is to hold down the prey. During the capturing process, *M. retractor* antennae accomplishes the adduction of the antennae. The labrum is elevated by *M. abductor epipharyngis* and the mandibles adducted by *M. adductor mandibulae*. The laciniae mobilis form a rake confining the prey in the space between them.

A close relationship of Chaoboridae with Culicidae and Dixidae is confirmed. A sistergroup relationship with the former family is more likely.



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30 Phylogeny of the Diaphorinae (Diptera: Dolichopodidae)

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Dolichopodidae is the fourth family of Diptera in number of described species (7600+), usually recognized by individuals with slender legs, metallic thoracic color and reduced wing venation. Male dolichopodids often display striking sexual secondary characters, assumed to play a role during male-female courtship recognition. The subfamily Diaphorinae comprises around 12% of the known diversity of Dolichopodidae, although being an ill-defined taxon, with no phylogenetic hypothesis of relationships for the group. This study performed the first comprehensive cladistic analysis of Diaphorinae, based on adult morphology and including all genera of the subfamily. A data matrix with 67 ingroup and 16 outgroup terminals, and 77 characters (70 binary and 7 three-state) was analysed under parsimony criterium, using implied weighting ($100 \geq k \geq 1$). The boundaries of the subfamily could be reassessed, and two uniquely derived features were recovered as synapomorphies for the group: the lateral groove on the female tergite 10 (= acanthophorite) and the loss of the distal part of the male sternite 9 (= hypandrium). Based on the results of the cladistics analysis, the following genera were excluded from the Diaphorinae: *Keirosoma* Van Duzee, *Phasmaphleps* Bickel and *Terpsimyia* Dyte (left *incertae sedis* within Dolichopodidae), *Nurteria* Dyte & Smith (nested within the Sympycninae), and *Argyra* Macquart, *Dactylonotus* Parent, *Somillus* Brèthes (including *Pseudargyra* Van Duzee) and *Symbolia* Becker (composing the Argyrini Negrobov along with *Anepsiomyia* Bezzi, and left *incertae sedis* within Dolichopodidae). The inner taxonomic arrangement of the Diaphorinae was recovered as a polytomy of three supra-generic taxa: (1) *Aphasmaphleps* Grichanov, *Asyndetus* Loew, *Cryptophleps* Lichtwardt and *Shamshevia* Grichanov; (2) *Achradocera* Becker, *Chrysotus* Meigen, *Dubius* Wei, *Falbouria* Dyte and *Lyroneurus* Loew; (3) *Diaphorus* Meigen, *Melanostolus* Kowarz, *Ostenia* Hutton and *Trigonocera* Becker. No reliable evidence was found to keep full generic status for *Dubius* (separated from *Chrysotus*) and *Melanostolus* (separated from *Diaphorus*), and maintenance of generic rank for *Cryptophleps* probably implies a paraphyletic *Asyndetus*. Further studies should focus on the relationships within the subfamily (genera and supra-generic taxa), as well as the discovery of the sister-group of the Diaphorinae.

31 Molecular phylogeny of Platypezidae (Diptera)

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Platypezidae is a family of brachycerous flies, with more than 250 species in 19 genera worldwide, with a unique phylogenetic position in the cyclorhaphan Diptera. The known larvae are mycophagous or trophically related to fungal mycelia. Studies of phylogenetic relationships of Platypezidae were based almost exclusively on morphological characters of adults or larvae, and no comprehensive molecular systematic study across the family has been published. The first morphology-based survey of phylogenetic relations was presented by Chandler (2001). Characters of larval morphology were used in the phylogenetic study of Rotheray et al. (2004). The most complete morphological study of the group was performed by Tkoč (2011) in his unpublished MSc. thesis. Here, we present results of Vaňhara et al. (submitted), the most complete molecular phylogenetic study.



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Although the tree topologies are generally consistent with the previous morphological studies, there are still several dissimilarities, which are pointing to the problematic parts of the previous studies and are stating new questions about the flat-footed flies phylogeny and systematics. The resulting tree was generated based on analysis of molecular data for 47 species of Platypezidae of 18 genera, using representative species of the cyclorrhaphan families Opetiidae, Atelestidae, Hybotidae, Phoridae, Lonchopteridae (one species each) as outgroup taxa. The reconstruction performed by Bayesian analysis is based on nucleotide sequences for genes from the mitochondrial (12S, 16S, COI) and nuclear (28S) genome (for complete methods see Vaňhara et al. submitted). The results were highly congruent with recent morphological analyses except for the position of Microsaniinae and show that Platypezidae consists of three well-supported monophyletic clades: the subfamilies Platypezinae, Callomyiinae and Melanderomyiinae. Microsaniinae form a lineage distant from Platypezidae, in sister relationship with Opetiidae, Hybotidae and Lonchopteridae. At the generic level, the genus *Agathomyia* was not resolved as a monophyletic lineage and seems to be paraphyletic. Family Platypezidae (*Microsania* excluded) is monophyletic. The monophyly of Melanderomyiinae, Callomyiinae and Platypezinae is documented with high support (PP = 1.0). The position of Microsaniinae is comparable with three recently recognized families of Opetiidae, Hybotidae and Lonchopteridae. Thus, Microsaniinae should be excluded from Platypezidae and its new systematic position should be defined. Without *Microsania*, the Platypezidae will be much better morphologically defined. If *Microsania* forms unique clade of cyclorrhaphan evolution or is part of some other bigger group (e.g. Phoridae) is still a question and will be tested in the following studies. All the resulting relationships among genera (excl. *Agathomyia*) are in agreement with the previous morphological analyses. Therefore, the genus *Agathomyia*, *Bertamyia* and *Chydaeopeza* need to be revised and new taxonomy of this paraphyletic cluster should be stated.

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32 *Baltorussus* total makeover: rejuvenation and sex change in an ancient parasitoid wasp lineage (Hymenoptera: Orussidae)

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The Orussidae is an obscure group of parasitoid wasps that emerge as sister group to the Apocrita in most recent comprehensive treatments of hymenopteran phylogeny (e.g., Sharkey et al. 2012; Klopstein et al. 2013). Their fossil record is correspondingly poor, a total of four fossil taxa being unequivocally assigned to the family, all described from amber inclusions. *Baltorussus velteni*, the first known orussid from Baltic amber, was recently described by Schedl (2011) from a single, allegedly female specimen. By applying micro-CT scanning to the specimen we have been able to reveal a number of details not reported in the original description. Evidence suggests that the specimen is in fact a male; a second specimen, also a male, has been discovered this year. By combining observations from these two specimens, approx. 60% of the characters for the data set assembled by Vilhelmsen (2003) for extant Orussidae could be scored, enough to confidently place *Baltorussus* within the phylogeny of the



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family. The position of *Baltorussus* as sister to a large clade comprising all the extant genera except *Orussonia* and *Orussella* indicates that the age of the basal splitting events based on the distributional history was hitherto overestimated. The radiation of crown group Orussidae is now inferred to have occurred from the mid Cretaceous (100 Mya) onwards rather than in the Early Jurassic (180 Mya) as suggested by Vilhelmsen (2004). The geographic provenance of *Baltorussus* disproves that the earliest splitting events among extant Orussidae were restricted to southern hemisphere continents.

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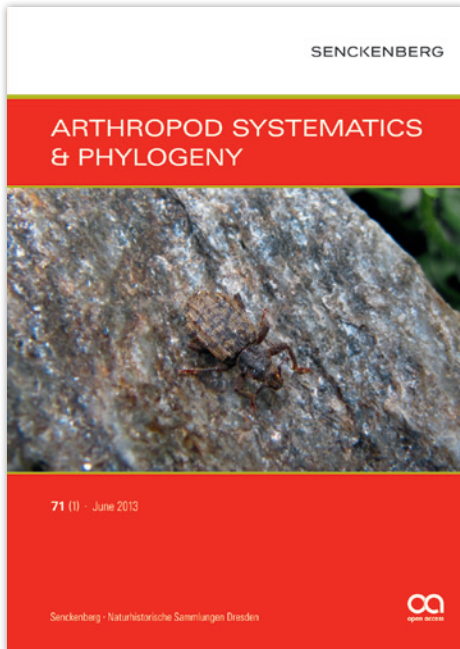
33 Phylogeny of the family Torymidae (Hymenoptera: Chalcidoidea)

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A phylogeny of the Torymidae (Hymenoptera: Chalcidoidea) is reconstructed using 4809 nucleotides from 5 genes (18S rDNA, 28S rDNA, EF1 α , COI and Wg). Altogether, 10 outgroup and 227 ingroup taxa were used, representing 45 of the 67 recognized genera from two known subfamilies (Megastigminae and Toryminae) of Torymidae. Phylogenetic trees were estimated using maximum likelihood (ML) and Bayesian methods. All analyses produced similar topologies and demonstrate that based only on molecular data Torymidae is probably not a monophyletic group and Megastigminae is the sister taxon of Ormyridae: (Ormyridae + Megastigminae) + Toryminae. Most of the tribes within subfamily Toryminae recognized by morphological characters (Grissell 1995) were supported (i.e. Chalcimerini, Microdontomerini, Monodontomerini, Torymini, Torymoidini, and Palachiini + Podagrionini) and two tribes are classified for the first time (i.e. Boucekini and Glyphomerini). Genus *Glyphomerus* is paraphyletic and 7 other genera classified as incertae sedis based on morphology were assigned to specific tribes (i.e. *Cryptopristus*, *Echthrodape*, *Exopristoides*, *Exopristus* and part of *Glyphomerus* to Microdontomerini; *Thaumatorymus* to Chalcimerini; *Zaglyptonotus* to Monodontomerini). Finally, we discuss biogeographical history and host association of the subfamilies Toryminae and Megastigminae.

References: Grissell E.E. 1995: Toryminae (Hymenoptera: Chalcidoidea: Torymidae): a redefinition, generic classification and annotated world catalogue of species. Memoirs on Entomology International 2: 1–474.

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