

7<sup>th</sup> Dresden Meeting on **Insect Phylogeny**

September 25 – 27, 2015

**Japanisches Palais Dresden**

Palaisplatz 11 · 01097 Dresden



This meeting is supported by the German Research Foundation



## Organisation staff

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## Financial support



Deutsche Forschungsgemeinschaft  
German Research Foundation

GZ KL 1162/10-1

# Oral Presentations — Friday, September 25



Chair of *morning* session:

Niklas Wahlberg

Chair of *afternoon* session:

Ulrike Aspöck

<b>09:00 – 09:15</b>	<b>Opening</b> <b>KLAUS-DIETER KLASS</b> (Senckenberg Natural History Collections Dresden, Germany)
<b>09:15 – 09:40</b>	<b>Willi Hennig's time in Dresden</b> <b>MICHAEL SCHMITT</b> (Ernst-Moritz-Arndt-Universität, Allgemeine & Systematische Zoologie, Anklamer Str. 20, Greifswald, Germany; michael.schmitt@uni-greifswald.de)
<b>09:40 – 09:55</b>	<b>1KITE: Challenges with big data: pipeline overview</b> <b>BERNHARD MISOF</b> (Zoologisches Forschungsmuseum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany; b.misof@zfmk.de) — On behalf of the <b>1KITE CONSORTIUM</b>
<b>09:55 – 10:10</b>	<b>1KITE: Alignment and error detection</b> <b>CHRISTOPH MAYER</b> (Forschungsmuseum Alexander Koenig, Bonn, Germany; c.mayer.zfmk@uni-bonn.de) — On behalf of the <b>1KITE CONSORTIUM</b>
<b>10:10 – 10:25</b>	<b>1KITE: Data pruning in phylogenomic datasets: Alignment masking and design of meaningful datasets</b> <b>KAREN MEUSEMANN</b> (Australian National Insects Collection, CSIRO National Research Collections Australia, Canberra, Australia; mail@karen-meusemann.de) — <b>BERNHARD MISOF</b> (Centre for Molecular Biodiversity Research, Zoological Research Museum A. Koenig, Bonn, Germany; bmisof@uni-bonn.de) — <b>KARL M. KJER</b> (Department of Entomology and Nematology, Davis University of California, Davis, CA, USA; karl.kjer@gmail.com) — On the behalf of <b>1KITE</b>
<b>10:25 – 10:50</b>	<b>Coffee Break</b>
<b>10:50 – 11:05</b>	<b>1KITE: Model selection in phylogenomics</b> <b>PAUL B. FRANSEN</b> (Smithsonian Institution, Washington, D.C., USA; frandsenp@si.edu) — <b>BERNHARD MISOF</b> (Zoologisches Forschungsmuseum Alexander Koenig (ZMFk) / Zentrum für Molekulare Biodiversitätsforschung (ZMB), Bonn, Germany; b.misof.zfmk@uni-bonn.de) — <b>CHRISTOPH MAYER</b> (Zoologisches Forschungsmuseum Alexander Koenig (ZMFk) / Zentrum für Molekulare Biodiversitätsforschung (ZMB), Bonn, Germany; c.mayer.zfmk@uni-bonn.de) — <b>KARL KJER</b> (Department of Entomology and Nematology, University of California-Davis, Davis, CA, USA; karl.kjer@gmail.com)
<b>11:05 – 11:20</b>	<b>1KITE: Fossil calibration and dating</b> <b>JESSICA L. WARE</b> (Rutgers University, 195 University Ave, Newark, NJ, 07102, USA; jware42@andromeda.rutgers.edu; jware@amnh.org) — <b>TOMAS FLOURI</b> (Heidelberg Institute for Theoretical Studies, Heidelberg, Germany; flouris@gmail.com) — <b>TORSTEN WAPPLER</b> (University of Bonn, Germany; twappler@uni-bonn.de) — <b>JES RUST</b> (University of Bonn, Germany) — <b>PASHALI KAPLI</b> (Greece; k.pashalia@gmail.com) — <b>1KITE CONSORTIUM</b>

# Oral Presentations — Friday, September 25



Chair of *morning* session: Niklas Wahlberg  
Chair of *afternoon* session: Ulrike Aspöck

<b>11:20 – 11:35</b>	<b>1KITE: Alternatives to bootstrapping; quartet mapping, robustness to model variation</b>  <b>BERNHARD MISOF</b> (Zoologisches Forschungsmuseum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany; b.misof@zfmk.de) — <b>KARL M. KJER</b> (University of California, Dept. of Entomology and Nematology, UC Davis Briggs Hall, Room 367, Davis, CA 95616-5270, United States; karl.kjer@gmail.com) — On behalf of the <b>1KITE CONSORTIUM</b>
<b>11:35 – 12:10</b>	<b>1KITE: Current insect phylogeny and next directions</b>  <b>KARL M. KJER</b> (University of California, Dept. of Entomology and Nematology, UC Davis Briggs Hall, Room 367, Davis, CA 95616-5270, United States; karl.kjer@gmail.com) — <b>BERNHARD MISOF</b> (Museum Koenig, Adenauerallee 160, 53113 Bonn, Germany; bmisof@uni-bonn.de) — <b>XIN ZHOU</b> (BGI-Shenzhen, Beishan industry zone, Yantian dist. Shenzhen, Guangdong 518083, China; xinzhoubgj@foxmail.com)
<b>12:10 – 13:20</b>	<b>Lunch Break</b>
<b>13:20 – 13:50</b>	<b>Arthropod coeloms: Structure, function, and evolution</b>  <b>MARKUS KOCH</b> (Institute of Evolutionary Biology and Ecology, University of Bonn, Germany; mkoch@evolution.uni-bonn.de) — <b>BJÖRN QUAST</b> (Institute of Evolutionary Biology and Ecology, University of Bonn, Germany; bquast@evolution.uni-bonn.de) — <b>THOMAS BARTOLOMAEUS</b> (Institute of Evolutionary Biology and Ecology, University of Bonn, Germany; tbartolomaeus@evolution.uni-bonn.de)
<b>13:50 – 14:15</b>	<b>Unraveling the seedling phase of the giant sequoia in animal phylogeny: Early splits of hexapods using transcriptomics and advanced morphological analyses</b>  <b>DANIELA BARTEL</b> (Institute of Integrative Zoology, University of Vienna, Austria; daniela.bartel@univie.ac.at) — <b>ALEXANDER BLANKE</b> (School of Engineering, University of Hull, UK; blanke@uni-bonn.de) — <b>KAREN MEUSEMANN</b> (Australian National Insect Collection, CSIRO NRCA, Canberra, Australia and Zoologisches Forschungsmuseum Alexander Koenig (ZMFK) / Zentrum für Molekulare Biodiversitätsforschung (ZMB), Bonn, Germany; karen.meusemann@csiro.au)
<b>14:15 – 14:45</b>	<b>The phylogeny of Palaeoptera – recent progress in molecular and morphological phylogenetics</b>  <b>JESSICA WARE</b> (Rutgers University, Newark, NJ, USA; jware@amnh.org; jware42@andromeda.rutgers.edu) — <b>ALEXANDER BLANKE</b> (Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany; blanke@uni-bonn.de) — <b>CAROLA GREVE</b> (Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany) — <b>OLIVER NIEHUIS</b> (Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany) — <b>RYUICHIRO MACHIDA</b> (University of Tsukuba, Japan) — <b>KARL KJER</b> (University of California, Davis, CA, USA) — <b>BERNHARD MISOF</b> (Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany)
<b>14:45 – 15:10</b>	<b>Coffee Break</b>

# Oral Presentations — Friday, September 25



Chair of *morning* session: Niklas Wahlberg  
Chair of *afternoon* session: Ulrike Aspöck

15:10 – 15:25	<p><b>A dated phylogeny of over 500 dragonfly species reveals differential diversification in Anisoptera (Odonata), potentially triggered by different habitat use</b></p> <p><b>HARALD LETSCH</b> (Department für Botanik und Biodiversitätsforschung, Universität Wien, Austria; harald.letsch@univie.ac.at) — <b>BRIGITTE GOTTSBERGER</b> (Department für Botanik und Biodiversitätsforschung, Universität Wien, Austria) — <b>JESSICA WARE</b> (Department of Biological Sciences, Rutgers University, Newark, USA)</p>
15:25 – 15:50	<p><b>Polyneoptera? A transcriptomic-morphological perspective</b></p> <p><b>SABRINA SIMON</b> (Biosystematics, Wageningen University, The Netherlands; sabrina.simon@wur.nl) — <b>BENJAMIN WIPFLER</b> (Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität Jena, Germany; benjamin.wipfler@uni-jena.de) — <b>POLYNEOPTERA-GROUP</b></p>
15:50 – 16:20	<p><b>Early splitting of Hexapoda reviewed from the comparative embryology: a revised synthesis</b></p> <p><b>SHIGEKAZU TOMIZUKA</b> (Echigo-Matsunoyama Museum of Natural Science 'Kyororo'; tomizuka@matsunoyama.com) — <b>MAKIKO FUKUI</b> (Graduate School of Science and Engineering, Ehime University; fukui.makiko.me@ehime-u.ac.jp) — <b>KAORU SEKIYA</b> (Research Administration Office, University of Tsukuba; kaorus1203@gmail.com) — <b>RYUICHIRO MACHIDA</b> (Sugadaira Montane Research Center, University of Tsukuba; machida@sugadaira.tsukuba.ac.jp)</p>
16:20 – 16:45	<p><b>Coffee Break</b></p>
16:45 – 17:05	<p><b>Cephalic endoskeleton of <i>Baculentulus densus</i> (Imadaté) (Hexapoda: Protura: Acerentomidae): a preliminary embryological study</b></p> <p><b>MAKIKO FUKUI</b> (Graduate School of Science and Engineering, Ehime University, 2-5 Bunkyo-cho, Matsuyama, Ehime 790-0826, Japan; fukui.makiko.me@ehime-u.ac.jp) — <b>RYUICHIRO MACHIDA</b> (Sugadaira Montane Research Center, University of Tsukuba, 1278-294 Sugadaira Kogen, Ueda, Nagano 386-2204, Japan; machida@sugadaira.tsukuba.ac.jp)</p>
17:05 – 17:25	<p><b>Embryonic development of <i>Eucorydia yasumatsui</i> Asahina (Insecta: Blattodea: Corydiidae)</b></p> <p><b>MARI FUJITA</b> (Sugadaira Montane Research Center, University of Tsukuba; fujita@sugadaira.tsukuba.ac.jp) — <b>RYUICHIRO MACHIDA</b> (Sugadaira Montane Research Center, University of Tsukuba; machida@sugadaira.tsukuba.ac.jp)</p>

# Oral Presentations — Saturday, September 26

Chair of *morning* session: Rudolf Meier  
Chair of *afternoon* session: Karl Kjer



09:00 – 09:30	<b>Resolving an ancient rapid radiation: Biodiversity of the stick and leaf insects (Phasmatodea)</b>  <b>SVEN BRADLER</b> (Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Str. 28, 37073 Göttingen, Germany; sbradle@gwdg.de) — <b>JULIA GOLDBERG</b> (Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Georg-August-Universität Göttingen, Berliner Str. 28, 37073 Göttingen, Germany; jule.goldberg@gmail.com) — <b>THOMAS R. BUCKLEY</b> (Landcare Research, Private Bag 92170, New Zealand; buckleyt@landcareresearch.co.nz)
09:30 – 10:00	<b>The Orthoptera Tree of Life: Elucidating patterns and processes of orthopteran evolution</b>  <b>HOJUN SONG</b> (Department of Entomology, Texas A&M University, USA; hsong@tamu.edu)
10:00 – 10:25	<b>Phylogeny and origins of diversity in Dictyoptera</b>  <b>DOMINIC A. EVANGELISTA</b> (Rutgers, The State University of New Jersey; dominicev@gmail.com) — <b>1KITE CORE GROUP</b> and <b>1KITE DICTYOPTERA GROUP</b>
10:25 – 10:50	<b>Coffee Break</b>
10:50 – 11:15	<b>Phylogeny of Blaberoidea (Blattodea): taxonomy and life history</b>  <b>MARIE DJERNÆS</b> (Natural History Museum, London; UK; marie_djernaes@hotmail.com) — <b>ZUZANA VARADINOVÁ</b> (Charles University, Prague, Czech Republic) — <b>MICHAEL KOTYK</b> (Charles University, Prague, Czech Republic) — <b>UTE EULITZ</b> (Senckenberg Naturhistorische Sammlungen Dresden, Germany) — <b>KLAUS-DIETER KLASS</b> (Senckenberg Naturhistorische Sammlungen Dresden, Germany)
11:15 – 11:45	<b>Revision in Neotropical praying mantises (Acanthoidea and Vatinæ)</b>  <b>GAVIN J. SVENSON</b> (Department of Invertebrate Zoology, Cleveland Museum of Natural History, 1 Wade Oval Drive, Cleveland, Ohio, USA; gavin.svenson@gmail.com) — <b>JULIO RIVERA</b> (Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, ON, Canada; jrivera@lamolina.edu.pe)
11:45 – 12:15	<b>Zoraptera – a phantom in insect evolution</b>  <b>ROLF BEUTEL</b> (Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität Jena, Jena, Germany; rolf.beutel@uni-jena.de) — <b>YOKO MATSUMURA</b> (Department of Biology, Keio University, Yokohama, Japan; yoko.matsumura.hamupeni@gmail.com) — <b>YUTA MASHIMO</b> (Sugadaira Montane Research Center, University of Tsukuba, Sugadaira, Japan; mashimo@sugadaira.tsukuba.ac.jp)
12:15 – 12:25	<b>We make a Photo!</b> 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!
12:25 – 13:35	<b>Lunch Break</b>

# Oral Presentations — Saturday, September 26

Chair of *morning* session:

Rudolf Meier

Chair of *afternoon* session:

Karl Kjer



<b>13:35–13:50</b>	<b>Phylogenomics and morphology of the hemipteroid insect orders</b>  <b>JULIE M. ALLEN</b> (Illinois Natural History Survey, University of Illinois; juliema@illinois.edu) — <b>CHRISTOPHER H. DIETRICH</b> (Illinois Natural History Survey, University of Illinois) — <b>CHIP AUSTIN</b> (Illinois Natural History Survey, University of Illinois) — <b>BRET M. BOYD</b> (Illinois Natural History Survey, University of Illinois) — <b>STEPHEN L. CAMERON</b> (Earth and Biological Sciences Department, Queensland University of Technology) — <b>KIMBERLY K. O. WALDEN</b> (Department of Entomology, University of Illinois) — <b>HUGH M. ROBERTSON</b> (Department of Entomology, University of Illinois) — <b>KEVIN P. JOHNSON</b> (Illinois Natural History Survey, University of Illinois)
<b>13:50–14:10</b>	<b>Phylogeny and morphology of Dipsocoromorpha (Hemiptera: Heteroptera)</b>  <b>ALEXANDER KNYSHOV</b> (University of California, Riverside, USA; aknys001@ucr.edu) — <b>CHRISTIANE WEIRAUCH</b> (University of California, Riverside, USA; christiane.weirauch@ucr.edu)
<b>14:10–14:30</b>	<b>From termite assassin to transcriptome: exposing the phylogeny of assassin bugs (Hemiptera: Reduviidae)</b>  <b>CHRISTIANE WEIRAUCH</b> (University of California, Riverside, 900 University Avenue, 92521 Riverside, California, USA; christiane.weirauch@ucr.edu)
<b>14:30–14:40</b>	<b>Coffee Break</b>
<b>14:40–15:40</b>	<b>Poster Session</b> Presenters of posters are kindly asked to stay with their posters.
<b>15:40–16:10</b>	<b>Hopper Hype: an Auchenorrhyncha phylogeny update</b>  <b>JASON R. CRYAN</b> (North Carolina Museum of Natural Sciences, 11 West Jones Street, Raleigh, NC 27601, USA; jason.cryan@naturalsciences.org)
<b>16:10–16:30</b>	<b>BIG4 network: training insect systematists of the future</b>  <b>ALEXEY SOLODOVNIKOV</b> (Natural History Museum of Denmark, Zoological Museum; asolodovnikov@snm.ku.dk)
<b>16:30–16:45</b>	<b>Extinct diversity and integrated phylogeny of a relictual beetle lineage using data from <math>\mu</math>CT reconstruction of amber fossils</b>  <b>ADAM BRUNKE</b> (Naturhistorisches Museum Wien, Burgring 7, Vienna, 1010, Austria; adam.j.brunke@gmail.com) — <b>ALEXEY SOLODOVNIKOV</b> (BioSystematics, University of Copenhagen, Universitetsparken 15, Copenhagen, 2100, Denmark) — <b>BRIAN METSCHER</b> (Dept. of Theoretical Biology, University of Vienna, Althanstrasse 14, Vienna, A-1090, Austria) — <b>NEZRINE AKKARI</b> (Naturhistorisches Museum Wien, Burgring 7, Vienna, 1010, Austria)
<b>19:30–01:00</b>	<b>Social Evening at Institute in Dresden-Klotzsche</b> (see page 53) [Please pay <b>10 €</b> when you enter. Take care: different from foregoing meetings, there won't be complete dinner. Snacks, beer and wine will be offered at a cheap price; non-alcoholic beverages are free].

# Oral Presentations — Sunday, September 27

Chair of *morning* session: Brian Wiegmann  
Chair of *afternoon* session: Christiane Weirauch



<b>09:00–09:30</b>	<b>The phylogeny and evolution of beetles (Coleoptera) as revealed by new molecular phylogenetic and comparative genomic data</b>  <b>DUANE D. MCKENNA</b> (University of Memphis, 3700 Walker Avenue, Memphis, TN, USA; dmckenna@memphis.edu) — The <b>BEETLE TREE OF LIFE PROJECT CONSORTIUM</b> , the <b>1KITE BEETLES PROJECT CONSORTIUM</b> , the <b>1K WEEVILS PROJECT CONSORTIUM</b>
<b>09:30–10:00</b>	<b>Molecular phylogeny of ant nest beetles (Coleoptera: Carabidae: Paussinae)</b>  <b>WENDY MOORE</b> (University of Arizona, Department of Entomology, Tucson, Arizona, USA; wmoore@email.arizona.edu) — <b>JAMES A. ROBERTSON</b> (University of Arizona, Department of Entomology, Tucson, Arizona, USA)
<b>10:00–10:30</b>	<b>2015's state of knowledge on the phylogeny of Hymenoptera</b>  <b>RALPH S. PETERS</b> (Zoologisches Forschungsmuseum Alexander Koenig, Abteilung Arthropoda, Adenauerallee 160, 53113 Bonn, Germany; r.peters@zfmk.de) — <b>LARS KROGMANN</b> (Staatliches Museum für Naturkunde Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany; lars.krogmann@smns-bw.de) — <b>OLIVER NIEHUIS</b> (Zoologisches Forschungsmuseum Alexander Koenig, Zentrum für Molekulare Biodiversitätsforschung, Adenauerallee 160, 53113 Bonn, Germany; o.niehuis.zfmk@uni-bonn.de)
<b>10:30–10:55</b>	<b>Coffee Break</b>
<b>10:55–11:25</b>	<b>The impact of Niels Peder Kristensen on insect phylogenetics</b>  <b>LARS VILHELMOSEN</b> (Natural History Museum of Denmark, Universitetsparken 15, DK-2100, Denmark, lbvilhelmsen@snm.ku.dk)
<b>11:25–11:40</b>	<b>The contributions of N. P. Kristensen to the understanding of Lepidoptera phylogeny</b>  <b>NIKLAS WAHLBERG</b> (Department of Biology, University of Turku, Finland and Department of Biology, Lund University, Sweden; niklas.wahlberg@utu.fi)
<b>11:40–12:10</b>	<b>Phylogeny of Lepidoptera utilizing transcriptomes and hybrid enrichment data</b>  <b>AKITO KAWAHARA</b> (Florida Museum of Natural History, University of Florida, Gainesville, FL, USA; kawahara@fimnh.ufl.edu) — <b>JESSE BREINHOLT</b> (Florida Museum of Natural History, University of Florida, Gainesville, FL, USA; jessebreinholt@gmail.com) — <b>KAREN MEUSEMANN</b> (Australian National Insect Collection, Acton, ACT, Australia; karen.meusemann@csiro.au) — <b>ANDREAS ZWICK</b> (Australian National Insect Collection, Acton, ACT, Australia; andreas.zwick@csiro.au) — <b>CHARLES MITTER</b> (University of Maryland, MD, USA) — <b>RALPH PETERS</b> (Zoologisches Forschungsmuseum Alexander Koenig, Germany; r.peters@zfmk.de) — <b>KARL KJER</b> (Rutgers University, NJ, USA; kjer@aesop.rutgers.edu) — <b>BERNHARD MISOF</b> (Zoologisches Forschungsmuseum Alexander Koenig, Germany; bmisof@uni-bonn.de)



# Oral Presentations — Sunday, September 27



Chair of *morning* session:

Brian Wiegmann

Chair of *afternoon* session:

Christiane Weirauch

<b>12:10–12:25</b>	<b>A target capture approach to butterfly phylogeny (Lepidoptera)</b>  <b>MARIANNE ESPELAND</b> (McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida; marianne.espeland@gmail.com) — <b>JESSE BREINHOLT</b> (McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida) — <b>NAOMI PIERCE</b> (Museum of Comparative Zoology, Harvard University) — <b>KEITH WILLMOTT</b> (McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida) — <b>AKITO Y. KAWAHARA</b> (McGuire Center for Lepidoptera and Biodiversity, Florida Museum of Natural History, University of Florida)
<b>12:25–13:35</b>	<b>Lunch Break</b>
<b>13:35–13:55</b>	<b>1KITE: New insights on the phylogeny of Trichoptera from transcriptomes and targeted enrichment</b>  <b>KARL M. KJER</b> (University of California, Dept. of Entomology and Nematology, UC Davis Briggs Hall, Room 367, Davis, CA 95616-5270, United States; karl.kjer@gmail.com) — <b>PAUL FRANSDEN</b> (Smithsonian Institution, Washington D.C., United States; paulfransden@gmail.com) — <b>XIN ZHOU</b> (BGI-Shenzhen, Beishan industry zone, Yantian dist. Shenzhen, GuangDong 518083, China; xinzhoubg@foxmail.com)
<b>13:55–14:10</b>	<b>Molecular phylogenetics offers insight on the ecological diversification of aquatic insects</b>  <b>STEFFEN U. PAULS</b> (Senckenberg Biodiversity and Climate Research Centre, Frankfurt am Main, Germany; Steffen.Pauls@senckenberg.de) — <b>WOLFRAM GRAF</b> (University of Natural Resources and Life Sciences, Vienna, Austria) — <b>KARL KJER</b> (Rutgers University, New Brunswick, New Jersey, USA) — <b>PAUL B. FRANSDEN</b> (Smithsonian Institution, Washington, D.C., USA) — <b>ALAN R. LEMMON</b> (Florida State University, Tallahassee, Florida, USA) — <b>SIMON VITECEK</b> (University of Vienna, Vienna, Austria) — <b>JOHANN WARINGER</b> (University of Vienna, Vienna, Austria)
<b>14:10–14:25</b>	<b>The adult and pupal head of Trichoptera – ground plan pattern and the evolution of major morphological traits</b>  <b>MARTIN KUBIAK</b> (Centrum für Naturkunde (CeNaK) – Zoologisches Museum, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg; martin.kubiak@uni-hamburg.de) — <b>RALPH S. PETERS</b> (Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Adenauerallee 160, 53113 Bonn) — <b>FRANK FRIEDRICH</b> (Biozentrum Grindel, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg)
<b>14:25–14:50</b>	<b>Fleas, Flies, Scorpionflies: phylogenetic relationships of Antliophora based on transcriptomics</b>  <b>KAREN MEUSEMANN</b> (Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, Australia; mail@karen-meusemann.de) — <b>DAVID YEATES</b> (Australian National Insect Collection, CSIRO National Research Collections Australia, Canberra, Australia; david.yeates@csiro.au) — <b>ALEXANDROS VASILIKOPOULOS</b> (Centre for Molecular Biodiversity Research, Zoological Research Museum A. Koenig, Bonn, Germany) — <b>BERNHARD MISOF</b> (Centre for Molecular Biodiversity Research, Zoological Research Museum A. Koenig, Bonn, Germany; bmisof@uni-bonn.de) — <b>ROLF G. BEUTEL</b> (FSU Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum Jena, Germany) — On the behalf of the <b>1KITE ANTLIOPHORA GROUP</b> ( <a href="http://www.1kite.org/subprojects.html">www.1kite.org/subprojects.html</a> )

# Oral Presentations — Sunday, September 27

Chair of *morning* session:

Brian Wiegmann

Chair of *afternoon* session:

Christiane Weirauch



14:50–15:15

## Coffee Break

15:15–15:45

### Phylogenomics to resolve radiations in diverse fly lineages

**BRIAN M. WIEGMANN** (William Neal Reynolds Professor of Entomology, North Carolina State University, Raleigh, NC, 27695, USA; [bwiegman@ncsu.edu](mailto:bwiegman@ncsu.edu))

15:45–16:15

### Malaise trap phylogenetics: affordable and fast assessment of species and phylogenetic diversity with NGS

**RUDOLF MEIER** (Lee Kong Chian Natural History Museum and Department of Biological Sciences, National University of Singapore, Singapore; [meier@nus.edu.sg](mailto:meier@nus.edu.sg)) — **DARREN YEO** (Department of Biological Sciences, National University of Singapore, Singapore; [darrn.yeo@gmail.com](mailto:darrn.yeo@gmail.com)) — **WENDY WANG** (Department of Biological Sciences, National University of Singapore, Singapore; [wywang24@gmail.com](mailto:wywang24@gmail.com)) — **AMRITA SRIVATHSAN** (Department of Biological Sciences, National University of Singapore, Singapore; [asrivathsan@gmail.com](mailto:asrivathsan@gmail.com)) — **MAOSHENG FOO** (Lee Kong Chian Natural History Museum, National University of Singapore, Singapore; [nhmfoom@nus.edu.sg](mailto:nhmfoom@nus.edu.sg))

16:15–16:35

### *Stilbopteryx* meets *Pseudimares* – a challenging hypothesis (Neuropterida: Neuroptera: Myrmeleontidae)

**ULRIKE ASPÖCK** (Natural History Museum Vienna, 2nd Zoological Department, Burgring 7, 1010 Vienna, Austria; [ulrike.aspoeck@nhm-wien.ac.at](mailto:ulrike.aspoeck@nhm-wien.ac.at)) — **HORST ASPÖCK** (Institute of Specific Prophylaxis and Tropical Medicine, Medical Parasitology, Medical University of Vienna, Kinderspitalgasse 15, 1090 Vienna, Austria; [horst.aspoeck@meduniwien.ac.at](mailto:horst.aspoeck@meduniwien.ac.at)) — **ELISABETH HARING** (Natural History Museum Vienna, Central Research Laboratories, Austria, Burgring 7, 1010 Vienna, Austria; [elisabeth.haring@nhm-wien.ac.at](mailto:elisabeth.haring@nhm-wien.ac.at))

16:35–16:45

## Closure

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

# Poster Presentations



Position	Presentation
01	<p><b>Comparative embryology of arctoperlarian Plecoptera</b></p> <p><b>SHODO MTOW</b> (Sugadaira Montane Research Center, University of Tsukuba, Japan) — <b>RYUICHIRO MACHIDA</b> (Sugadaira Montane Research Center, University of Tsukuba, Japan)</p>
02	<p><b>Diversity of egg structures and reproductive systems in Zoraptera</b></p> <p><b>YUTA MASHIMO</b> (Sugadaira Montane Research Center, University of Tsukuba, Japan) — <b>ROMANO DALLAI</b> (Department of Life Sciences, University of Siena, Italy) — <b>ROLF BEUTEL</b> (Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität Jena, Germany) — <b>CHOW-YANG LEE</b> (School of Biological Sciences, Universiti Sains Malaysia) — <b>RYUICHIRO MACHIDA</b> (Sugadaira Montane Research Center, University of Tsukuba, Japan)</p>
03	<p><b>The “other” earwig: <i>Hemimerus</i> sp. and its cephalic adaptations towards commensalism</b></p> <p><b>DAVID NEUBERT</b> (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany) — <b>ROLF BEUTEL</b> (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany) — <b>BENJAMIN WIPFLER</b> (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany)</p>
04	<p><b>First chromosomal study of Mantophasmatodea: Karyotype of <i>Karoophasma biedouwense</i> (Austrophasmatidae)</b></p> <p><b>DOROTA LACHOWSKA-CIERLIK</b> (Institute of Zoology, Jagiellonian University, Cracow, Poland) — <b>ANNA MARYAŃSKA-NADACHOWSKA</b> (Institute of Systematic and Evolution of Animals, PAS, Cracow, Poland) — <b>VALENTINA KUZNETSOVA</b> (Zoological Institute Russian Academy of Sciences, St. Petersburg, Russia) — <b>MIKE PICKER</b> (Department of Biological Sciences, University of Cape Town, Rondebosch, Cape Town, South Africa)</p>
05	<p><b>Chromosome numbers &amp; nuclear DNA content comparison in <i>Cimex</i> bed bugs</b></p> <p><b>DAVID SADÍLEK</b> (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — <b>JITKA VILÍMOVÁ</b> (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — <b>TOMÁŠ URFUS</b> (Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic)</p>
06	<p><b>Cuticular structures of nymphal dorsoabdominal scent glands in the Pentatomomorpha</b></p> <p><b>JITKA VILÍMOVÁ</b> (Charles University in Prague, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic) — <b>MARKÉTA ROHANOVÁ</b> (Buková 4, 130 00 Praha 3, Czech Republic) — <b>PETRA KŘÍŽKOVÁ</b> (Charles University in Prague, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic)</p>
07	<p><b>Features determining functional dorsoabdominal scent glands in Heteroptera adults – use in phylogeny of Pentatomomorpha</b></p> <p><b>PETRA KRIZKOVA</b> (Charles University in Prague, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic) — <b>JITKA VILÍMOVÁ</b> (Charles University in Prague, Department of Zoology, Viničná 7, 128 44 Praha 2, Czech Republic)</p>



Position	Presentation
08	<p><b>Morphological changes correlated with decreasing size in skeleton and musculature of the male genitalia in the higher Tephritoidea (Diptera: Tephritidae, Otitidae, Ulidiidae, and Platystomatidae)</b></p> <p><b>TATIANA V. GALINSKAYA</b> (Department of Entomology, Faculty of Biology, Lomonosov Moscow State University; Leninskie Gory 1–12, Moscow, 119991, Russia) — <b>O.G. OVTSHINNIKOVA</b> (Zoological Institute, Russian Academy of Sciences, St. Petersburg, Russia)</p>
09	<p><b>Evolution of hunting behaviour and morphology in the genus <i>Leptogenys</i> (Hymenoptera: Formicidae) from the Oriental region</b></p> <p><b>KOICHI ARIMOTO</b> (Entomological Laboratory, Kyushu University, Japan) — <b>MUNETOSHI MARUYAMA</b> (Kyushu University Museum, Japan) — <b>FUMINORI ITO</b> (Kagawa University, Japan) — <b>SEIKI YAMANE</b> (Kagoshima University, Japan)</p>
10	<p><b>Speciation and molecular divergence in a group of ant parasitoids</b></p> <p><b>JOHN M. HERATY</b> (Department of Entomology, University of California, Riverside, CA, USA; john.heraty@ucr.edu) — <b>J.M. MOTTERN</b> (USDA-ARS Systematic Entomology Laboratory, Washington, DC, USA) — <b>R.A. BURKS</b> (Department of Entomology, University of California, Riverside, CA, USA) — <b>R. PETERS</b> (Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany) — <b>A. LEMMON</b> (University of Florida, Tallahassee, FL, USA) — <b>E. LEMMON</b> (University of Florida, Tallahassee, FL, USA)</p>
11	<p><b>Crossing the borders of orders: head anatomy of <i>Coniopteryx pygmaea</i> (Insecta: Neuroptera: Coniopterygidae) and convergent miniaturization effects in insects</b></p> <p><b>SUSANNE RANDOLF</b> (Natural History Museum Vienna, Burgring 7, 1010 Vienna, Austria) — <b>DOMINIQUE ZIMMERMANN</b> (Natural History Museum Vienna, Burgring 7, 1010 Vienna, Austria)</p>
12	<p><b>Aenigmatineidae – a new family of microlepidoptera from Kangaroo Island, Australia, and its phylogenetic placement in Lepidoptera</b></p> <p><b>NIELS P. KRISTENSEN</b> (Natural History Museum of Denmark, University of Copenhagen, Denmark; deceased 6 December, 2014) — <b>DOUGLAS J. HILTON</b> (University of Melbourne, Department of Zoology, Victoria, Australia) — <b>AXEL KALLIES</b> (University of Melbourne, Department of Zoology, Victoria, Australia) — <b>LIZ MILLA</b> (University of Melbourne, Department of Zoology, Victoria, Australia) — <b>JADRANKA ROTA</b> (Laboratory of Genetics, Department of Biology, University of Turku, Finland) — <b>NIKLAS WAHLBERG</b> (Laboratory of Genetics, Department of Biology, University of Turku, Finland) — <b>STEPHEN A. WILCOX</b> (The Australian Genome Research Facility, Victoria, Australia) — <b>RICHARD V. GLATZ</b> (D'Estrees Entomology &amp; Science Services; The University of Adelaide, School of Agriculture, Food and Wine; South Australian Museum, Terrestrial Invertebrates, South Australia, Australia) — <b>DAVID A. YOUNG</b> (D'Estrees Entomology &amp; Science Services, South Australia, Australia) — <b>GLENN COCKING</b> (Australian National Insect Collection, CSIRO, Australian Capital Territory, Australia) — <b>TED EDWARDS</b> (Australian National Insect Collection, CSIRO, Australian Capital Territory, Australia) — <b>GEORGE W. GIBBS</b> (School of Biological Sciences, Victoria University, Wellington, New Zealand) — <b>MIKE HALSEY</b> (Murray-Darling Freshwater Research Centre, Victoria, Australia)</p>



Position	Presentation
13	<p><b>Molecular phylogenetic analysis helps to reveal homoploid hybrid speciation events: a case study in <i>Agrodiaetus</i> blue butterflies (Lepidoptera, Lycaenidae)</b></p> <p><b>NAZAR SHAPOVAL</b> (Zoological Institute of the Russian Academy of Sciences; Saint-Petersburg State University, Russia) — <b>VLADIMIR LUKHTANOV</b> (Zoological Institute of the Russian Academy of Sciences; Saint-Petersburg State University, Russia)</p>
14	<p><b>Inner maturity – the cephalothorax of <i>Stylops ovinae</i> (Strepsiptera)</b></p> <p><b>STEPHAN LÖWE</b> (Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstrasse 1, 07743 Jena, Germany) — <b>ROLF G. BEUTEL</b> (Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstrasse 1, 07743 Jena, Germany) — <b>HANS POHL</b> (Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstrasse 1, 07743 Jena, Germany)</p>
15	<p><b>The contribution of fossils to the phylogeny of Steninae (Coleoptera, Staphylinidae)</b></p> <p><b>DAGMARA ŻYLA</b> (Biosystematics, Natural History Museum of Denmark, University of Copenhagen, Universitetsparken 15, Copenhagen 2100, Denmark, zyladagmara@gmail.com)</p>
16	<p><b>Evolution of habitat shifts in “terrestrial” clades of hydrophilid beetles (Hydrophilidae: Rygmodinae and Sphaeridiinae)</b></p> <p><b>VÍT SÝKORA</b> (Department of Zoology, Faculty of Sciences, Charles University in Prague, Viničná 7, CZ-128 43 Praha 2, Czech Republic; e-mail: sykoravi@natur.cuni.cz) — <b>MARTIN FIKÁČEK</b> (Department of Zoology, Faculty of Sciences, Charles University in Prague, Viničná 7, CZ-128 43 Praha 2, Czech Republic and Department of Entomology, National Museum, Cirkusová 1740, CZ-19300 Praha 9, Czech Republic; mfikacek@gmail.cz)</p>
17	<p><b>Leptodirines (Staphylinioidea: Leiodidae: Cholevinae) possess pore plates on the terminal tarsomeres</b></p> <p><b>CAIO ANTUNES-CARVALHO</b> (Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil and Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie, Friedrich-Schiller-Universität Jena, Germany) — <b>ROLF BEUTEL</b> (Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Germany) — <b>PEDRO GNASPINI</b> (Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, SP, Brazil)</p>
18	<p><b>The use of sex pheromones as a tool for integrative taxonomy and phylogeny – An example from the cryptic click beetle complex <i>Idolus</i> (Coleoptera: Elateridae)</b></p> <p><b>CHRISTIAN KÖNIG</b> (University of Hohenheim, Germany) — <b>TILL TOLASCH</b> (University of Hohenheim, Germany) — <b>JOHANNES L.M. STEIDLE</b> (University of Hohenheim, Germany)</p>
19	<p><b>Phylogenetic relationships and evolution of host plant use in the Palearctic Apioninae (Curculionoidea, Coleoptera)</b></p> <p><b>SVEN WINTER</b> (Department für Botanik und Biodiversitätsforschung, Universität Wien, Austria) — <b>JONAS J. ASTRIN</b> (Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany) — <b>ARIEL L.L. FRIEDMAN</b> (Department of Zoology, Tel Aviv University, Tel Aviv, Israel) — <b>HARALD LETSCH</b> (Department für Botanik und Biodiversitätsforschung, Universität Wien, Austria; harald.letsch@univie.ac.at)</p>



Position	Presentation
20	<p><b>Phylogeny and phylogeography of <i>Liophloeodes</i> (Coleoptera: Curculionidae) populations</b></p> <p><b>BENIAMIN WACLAWIK</b> (Department of Entomology, Institute of Zoology, Faculty of Biology and Earth Sciences, Jagiellonian University, Poland)</p>
21	<p><b>Phylogenetic analyses reveal complex evolutionary patterns in the flower chafer genus <i>Eudicella</i> (Scarabaeidae: Cetoniinae)</b></p> <p><b>MATTHIAS SEIDEL</b> (Zoology, Faculty of Science, Charles University in Prague, Viničná 7, CZ-12844 Praha 2, Czech Republic) — <b>MARTIN HUSEMANN</b> (General Zoology, Institute of Biology, Martin-Luther-University Halle-Wittenberg, Hoher Weg 8, D-06120 Halle, Germany)</p>
22	<p><b>Countless forms of cockroach wings – the beauty of reduction</b></p> <p><b>ZUZANA VARADÍNOVÁ</b> (Department of Zoology, Faculty of Science, Charles University in Prague; Department of Zoology, National Museum, Prague, Czech Republic; varadinovaz@gmail.com) — <b>MICHAEL KOTYK</b> (Department of Zoology, Faculty of Science, Charles University in Prague; National Museum, Prague, Czech Republic) — <b>DANIEL FRYNTA</b> (Department of Zoology, Faculty of Science, Charles University in Prague, Czech Republic) — <b>GEORGE BECCALONI</b> (Department of Entomology, Natural History Museum, London, United Kingdom)</p>
23	<p><b>The steps towards an inconspicuous vein fusion documented in Stenosmylinae forewings (Neuroptera: Osmylidae)</b></p> <p><b>GUILLAUME COUSIN</b> (Sorbonne Université - CR2P - MNHN, CNRS, UPMC-Paris6, 8 rue Buffon, Paris, France) — <b>OLIVIER BÉTHOUX</b> (Sorbonne Université - CR2P - MNHN, CNRS, UPMC-Paris6, 8 rue Buffon, Paris, France; obethoux@mnhn.fr)</p>
24	<p><b>Testing monophyly of megadiverse Spilomelinae (Lepidoptera: Pyraloidea)</b></p> <p><b>RICHARD MALLY</b> (University Museum of Bergen, Natural History Collections, Realfagbygget, Allégaten 41, 5007 Bergen, Norway; richard.mally@um.uib.no) — <b>CHRISTOPH NEINHUIS</b> (Technische Universität Dresden, Institut für Botanik, 01062 Dresden, Germany; christoph.neinhuis@tu-dresden.de) — <b>MATTHIAS NUSS</b> (Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde, Königsbrücker Landstraße 159, 01109 Dresden, Germany; matthias.nuss@senckenberg.de)</p>
25	<p><b>Transcriptomic and phenotypic data related to the geographic distribution of two spurge hawk moth lineages of the <i>Hyles euphorbiae</i> complex (Lepidoptera: Sphingidae)</b></p> <p><b>KATJA BUCHWALDER</b> (Senckenberg Natural History Collections Dresden, Germany) — <b>M. BENJAMIN BARTH</b> (Senckenberg Natural History Collections Dresden, Germany) — <b>ANNA K. HUNDSDOERFER</b> (Senckenberg Natural History Collections Dresden, Germany; Anna.Hundsdoerfer@senckenberg.de)</p>



## Abstracts — Oral Presentations

### Willi Hennig's time in Dresden

**MICHAEL SCHMITT** (Ernst-Moritz-Arndt-Universität, Allgemeine & Systematische Zoologie, Anklamer Str. 20, Germany; michael.schmitt@uni-greifswald.de)

Willi Hennig, born 20.04.1913 in Dürrhennersdorf, Lower Lusatia (Saxony), 60 km east of Dresden, came to this place at the age of 14. He was fortunate enough to get accepted to the "Landesschule Dresden". Here, he began his first investigations on insects – a report on the insects found in the area of the school over a period of three years. Moreover, he got into contact with scientists at the Dresden State Museum of Zoology: Fritz Isidor van Emden (03.10.1898 – 02.09.1958, keeper of the entomological collection), Wilhelm Meise (12.09.1901 – 24.08.2002, ornithologist), and Klaus Günther (07.10.1907 – 01.08.1975, successor of F. van Emden). From these scientists, he received a professional education in entomology, biogeography, and systematics. He continued a serious collaboration with the Dresden museum during his studies at the University of Leipzig, especially while he worked on his PhD thesis on the copulatory apparatus of the Diptera Cyclorrhapha.

Willi Hennig's time in Dresden does not just mark the starting point of the development of his phylogenetic method. Here, the basis was laid for the development of his scientific thinking. Moreover, here he met people who became more than anybody else influential models and important partners – and friends – far beyond the years he spent in this city.

### 1KITE: Challenges with big data: pipeline overview

**BERNHARD MISOF** (Zoologisches Forschungsmuseum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany; b.misof@zfmk.de) — On behalf of the **1KITE CONSORTIUM**

The generation and analyses of phylogenomic data is becoming more and more common place due to enormous technical advancements in sequencing and computing technologies. However, we are still far from fully exploiting the potential of phylogenomic data. In this presentation, I will present the approaches developed within the 1KITE consortium to achieve reliable and robust phylogenetic inferences based on extensive phylogenomic data. In particular I will quickly review sequencing strategies, measurements of quality control, strategies of orthology prediction and finally strategies concerning the computational efficiency of tree reconstructions. I will try to outline potential pitfalls and achievements within each step and will show directions which are in need of particular attention in future research.

### 1KITE: Alignment and error detection

**CHRISTOPH MAYER** (Forschungsmuseum Alexander Koenig, Bonn, Germany; c.mayer.zfmk@uni-bonn.de) — On behalf of the **1KITE CONSORTIUM**

In phylogenetic workflows, errors and systematic biases can be introduced at many stages, e.g. orthology prediction, alignment, model selection, and the final tree reconstruction, just to mention the most important steps. In the 1KITE project (Misof et al. 2014) we reconstructed a phylogenetic tree using about 500.000 amino acids from 1478 genes for a total of 144 sequences. For such a data set, not every single step in the analysis pipeline can be supervised manually. This signals the need for a stringent quality control in every step. If a problem is detected the first attempt



## Abstracts — Oral Presentations

has to be to refine the methods to deal with this problem. If this is not possible, data should be excluded from the analysis in a stringent but unbiased way.

In this talk I will show and discuss many of the problems we faced in the first paper of the 1KITE project and how we dealt with these problems.

**References:** Misof B., Liu S., Meusemann K., Peters R.S., Donath A., Mayer C., Frandsen P.B., Ware J., Flouri T., Beutel R.G., Niehuis O., Petersen M., Izquierdo-Carrasco F., Wappler T., Rust J., Aberer A.J., Aspöck U., Aspöck H., Bartel D., Blanke A., Berger S., Böhm A., Buckley T.R., Calcott B., Chen J., Friedrich F., Fukui M., Fujita M., Greve C., Grobe P., Gu S., Huang Y., Jermin L.S., Kawahara A.Y., Krogmann L., Kubiak M., Lanfear R., Letsch H., Li Y., Li Z., Li J., Lu H., Machida R., Mashimo Y., Kapli P., McKenna D.D., Meng G., Nakagaki Y., Navarrete-Heredia J.L., Ott M., Ou Y., Pass G., Podsiadlowski L., Pohl H., von Reumont B.M., Schütte K., Sekiya K., Shimizu S., Slipinski A., Stamatakis A., Song W., Su X., Szucsich N.U., Tan M., Tan X., Tang M., Tang J., Timelthaler G., Tomizuka S., Trautwein M., Tong X., Uchifune T., Walz M.G., Wiegmann B.M., Wilbrandt J., Wipfler B., Wong T.K., Wu Q., Wu G., Xie Y., Yang S., Yang Q., Yeates D.K., Yoshizawa K., Zhang Q., Zhang R., Zhang W., Zhang Y., Zhao J., Zhou C., Zhou L., Ziesmann T., Zou S., Li Y., Xu X., Zhang Y., Yang H., Wang J., Wang J., Kjer K.M., Zhou X. 2014. Phylogenomics resolves the timing and pattern of insect evolution. *Science* **346**(6210): 763–767.

### 1KITE: Data pruning in phylogenomic datasets: Alignment masking and design of meaningful datasets

**KAREN MEUSEMANN** (Australian National Insects Collection, CSIRO National Research Collections Australia, Canberra, Australia; mail@karenmeusemann.de) — **BERNHARD MISOF** (Centre for Molecular Biodiversity Research, Zoological Research Museum A. Koenig, Bonn, Germany; bmisof@uni-bonn.de) — **KARL M. KJER** (Department of Entomology and Nematology, Davis University of California, Davis, CA, USA; karl.kjer@gmail.com) — On behalf of **1KITE CONSORTIUM**

The massive amount of available RNASeq data for inferring phylogenetic relationships has challenged the analytical methods used to analyse these data. An aim of these methods should be to ensure that systematic bias is minimised even though it may gain significant support in large-scale datasets. We will discuss two issues out of many steps in phylogenetic analyses we developed and applied within the 1KITE project (1K transcriptome evolution, [www.1kite.org](http://www.1kite.org)) to address bias, (1): alignment masking and (2) assembling meaningful datasets that maximise information content by both including relevant taxonomic samples and excluding uninformative partitions.

### 1KITE: Model selection in phylogenomics

**PAUL B. FRANSEN** (Smithsonian Institution, Washington, D.C., USA; frandsenp@si.edu) — **BERNHARD MISOF** (Zoologisches Forschungsmuseum Alexander Koenig (ZMFK) / Zentrum für Molekulare Biodiversitätsforschung (ZMB), Bonn, Germany; b.misof.zfmk@uni-bonn.de) — **CHRISTOPH MAYER** (Zoologisches Forschungsmuseum Alexander Koenig (ZMFK) / Zentrum für Molekulare Biodiversitätsforschung (ZMB), Bonn, Germany; c.mayer.zfmk@uni-bonn.de) — **KARL KJER** (Department of Entomology and Nematology, University of California-Davis, Davis, CA, USA; karl.kjer@gmail.com)

When selecting any scientific model, there should be enough complexity to appropriately describe the processes of interest, but the model should also be simple enough to avoid estimating more than the data can accurately support (over-fitting). Data partitioning is often used in molecular phylogenetics, because it is reasonable to assume that different sites in a multiple sequence alignment are under heterogeneous selection pressures. Data partitioning allows for the selection of an independent model and model parameters for subsets of an alignment in order to better





## Abstracts — Oral Presentations

accommodate among site heterogeneity. Traditionally, alignments have been partitioned by locus, codon position, or some combination of the two. We find this approach for accounting for among site heterogeneity to be expedient, but overly simplistic. Here we describe two partitioning techniques used in the 1KITE project (Misof et al. 2014), the first, applied to nucleotide data, treats each site as separate and clusters similar sites together into subsets based on their estimated substitution rates. The second, applied to amino acid alignments, partitions the alignment into subsets based on protein domains *a priori*, then uses a heuristic algorithm to join similar subsets together. With both methods, we find a substantial improvement in the fit of the model to the data using information theoretic metrics like the Akaike information criterion (AIC).

**References:** Misof B., Liu S., Meusemann K., Peters R.S., Donath A., Mayer C., Frandsen P.B., Ware J., Flouri T., Beutel R.G., Niehuis O., Petersen M., Izquierdo-Carrasco F., Wappler T., Rust J., Aberer A.J., Aspöck U., Aspöck H., Bartel D., Blanke A., Berger S., Böhm A., Buckley T.R., Calcott B., Chen J., Friedrich F., Fukui M., Fujita M., Greve C., Grobe P., et al. 2014. Phylogenomics resolves the timing and pattern of insect evolution. *Science* **346**: 763–767.

### 1KITE: Fossil calibration and dating

**JESSICA L. WARE** (Rutgers University, 195 University Ave, Newark, NJ, 07102, USA; [Jware42@andromeda.rutgers.edu](mailto:Jware42@andromeda.rutgers.edu); [jware@amnh.org](mailto:jware@amnh.org)) — **TOMAS FLOURI** (Heidelberg Institute for Theoretical Studies, Heidelberg, Germany; [flouris@gmail.com](mailto:flouris@gmail.com)) — **TORSTEN WAPPLER** (University of Bonn, Germany; [twappler@uni-bonn.de](mailto:twappler@uni-bonn.de)) — **JES RUST** (University of Bonn, Germany) — **PASHALI KAPLI** (Greece; [k.pashalia@gmail.com](mailto:k.pashalia@gmail.com)) — **1KITE CONSORTIUM**

Insects have a strong fossil record, and their origin has been hotly debated in the literature. As part of the 1KITE initiative, we reconstructed a robust phylogeny of insects. We then undertook a comprehensive approach to date this insect tree, using transcriptomic data and well calibrated fossils. Here we report on the methodology of partitioning big datasets for divergence time estimation, and discuss the impact of missing data and fossil placement on estimation error. Lastly, we discuss the dates we recovered in light of the known fossil record, and suggest areas for future exploration Regarding the evolution of this diverse class of organisms.

### 1KITE: Alternatives to bootstrapping; quartet mapping, robustness to model variation

**BERNHARD MISOF** (Zoologisches Forschungsmuseum A. Koenig, Adenauerallee 160, 53113 Bonn, Germany; [b.misof@zfmk.de](mailto:b.misof@zfmk.de)) — **KARL M. KJER** (University of California, Dept. of Entomology and Nematology, UC Davis Briggs Hall, Room 367, Davis, CA 95616-5270, United States; [karl.kjer@gmail.com](mailto:karl.kjer@gmail.com)) — On behalf of the **1KITE CONSORTIUM**

The inference of a phylogenetic tree is a statistical enterprise based on the comparative analyses of data using models of character state changes. Since the distribution of character states among taxa is never fully congruent with the inferred tree topology, we need to invoke measurements of robustness to support results. In molecular analyses, bootstrapping is traditionally used to assess the influence of stochastic error on tree reconstructions. However, with very large data, stochastic effects vanish and bootstrapping might become uninformative. In order to discriminate between several different confounding factors in tree reconstruction we need to complement resampling techniques with new approaches. I will present an approach based on a quartet strategy and data permutations which does help to discriminate between signals coming from model misspecification, the distribution of missing data and phylogenetic signal.



## Abstracts — Oral Presentations

### 1KITE: Current insect phylogeny and next directions

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The 1KITE initiative is an international collaboration involving the collection of insect transcriptomes, analyzed and interpreted by molecular and organismal experts from at least xx countries. The first paper using the transcriptomes from 1KITE on insect phylogeny was published almost a year ago. This phylogeny largely corroborated previous morphological hypotheses, but the size of the dataset, with 1478 genes, showed full resolution, and strong support for almost every node. Nonocculata was rejected in favor of grouping Diplura with Insecta. Although Chiasmomyaria was favored with quartet mapping techniques, Palaeoptera was recovered in the combined analysis. The most unusual result was the recovery of Psocodea as the sister group to Holometabola, rendering Paraneoptera paraphyletic. Confidence in both of these problematic relationships will be discussed in the context of problems with interpreting branch support with large datasets with traditional measures, such as bootstrapping. One reason for some confidence in our results came from the virtually ideal results recovered from both amino acid, and second codon nucleotide analyses, despite the different models involved. Following the discussion of our current results, we preview our future plans. We have transcriptome data from over 1400 taxa. Analyses are underway for 10 independent taxonomic subprojects, including “basal hexapods”, Odonata, Polyneoptera, Dictyoptera, “Paraneoptera”, Hymenoptera, Coleoptera, Neuropterida, Diptera, Lepidoptera, and Trichoptera. Each of these subprojects include between 3,500 and 4,500 genes from 60 to 220 taxa. Following the publication of the subprojects, we will be combining all data into a single paper, as well as a large multi-chapter book project, to be published in the next two years. Besides the phylogenetic projects, we discuss a few of the many side projects that have been published, or are underway as the result of this cooperative consortium.

### Arthropod coeloms: Structure, function, and evolution

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Arthropod coeloms are traditionally considered as to provide the main source for mesodermal tissues during organogenesis. This assumption is revised based on combined histological, ultrastructural and immuno-histochemical studies used for 3-D reconstruction of the early mesoderm and its derivatives in selected representatives of velvet worms, chelicerates, and pancrustaceans. Insights obtained reveal a remarkable degree of misinterpretations and artefacts in previous considerations of coelomogenesis in arthropods, including the previous view that the musculature, the blood vascular system, and segmental nephridial organs are derived from transient coeloms. The interpretation of the coeloms as mesoblastic organs is rejected for arthropods but confirmed for velvet worms. A new model for the evolution of the coeloms in arthropods is proposed that considers variable steps towards a decoupling of the coeloms from organogenesis, yielding multiple, convergent instances of entire suppression of coeloms during mesoderm development. Current hypotheses on arthropod phylogeny reveal the occurrence of coeloms in insects as a reversal, potentially due to heterochronic shifts. Putative ancestral states of the mesoderm development question a homology of coeloms in arthropods and annelids in demonstrating marked differences in almost all details of coelomogenesis.



## Abstracts — Oral Presentations

### Unraveling the seedling phase of the giant sequoia in animal phylogeny: Early splits of hexapods using transcriptomics and advanced morphological analyses

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Starting more than 400 million years ago, two major transitions border the hexapod evolutionary success story: (i) the conquest of land, or terrestrialization, and (ii) the conquest of air, with the development of wings. Earliest splits presumably diverged from a hexapod stem group traditionally called “apterygotes” or “basal hexapods” comprising Collembola, Protura, Diplura, Archaeognatha, and Zygentoma. Despite their importance to understand the evolutionary success of hexapods, these lineages are highly underrepresented in phylogenomic and morphological studies. The subgroup “basal hexapods” of the 1KITE consortium, investigates early split events after terrestrialization using a massive amount of new transcriptomic data. Advanced analytical methods allow us to account for analytical bias. We present preliminary results based on molecular data for around 100 taxa and introduce recent morphological research. As an example of the latter we will introduce a feature which we propose to call structural mouthpart interaction (SMI). Formerly known as a characteristic of several “higher” insect groups, we will discuss evidence for a much earlier occurrence in hexapod evolution. Our studies even shed some light on how stem group representatives of Hexapoda may have looked like.

### The phylogeny of Palaeoptera – recent progress in molecular and morphological phylogenetics

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Dragonflies and damselflies (Odonata) are a charismatic insect order with a little more than 6000 species; their closest relatives are the mayflies, but the inter-ordinal relationships among these lineages has remained elusive. Within Odonata, the two suborders, Anisoptera and Zygoptera, are well supported. In contrast, the interrelationships among families within each suborder have remained unclear since datasets partly contradict each other. Here we present and discuss our efforts in the “TransOdonata” 1KITE subproject, which aims to use morphology and transcriptomics to infer the phylogeny of Odonata, Ephemeroptera, and the umbrella grouping of “Palaeoptera”. We will highlight our taxon selection, and discuss the results of our sequencing and morphological work to date, which resulted in a dataset with over 3000 genes for over 100 odonate and mayfly taxa.



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### **A dated phylogeny of over 500 dragonfly species reveals differential diversification in Anisoptera (Odonata), potentially triggered by different habitat use**

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Ecological diversification of aquatic insects has long been suspected as a result of differences in the occupied freshwater habitat systems. These be classified into two different groups: 1) flowing (lotic) waters, like springs, small streams and rivers, and 2) standing (lentic) water bodies, like swamps, pools or lakes. The contrasting spatial and temporal characteristics of lotic and lentic freshwater systems, imply different ecological constraints on their inhabitants. The ephemeral and discontinuous character of most lentic water bodies may make dispersal more necessary for lentic species, whereas species living in more stable lotic habitats are suggested to be less dispersive. High dispersal ability may reduce geographical isolation between populations leading to lower inter-population genetic variability. Thus, the probability for allopatric or peripatric speciation should be higher in lotic species, whose limited dispersal abilities might be seen as a kind of isolation mechanism. In the present study, we intend to apply a phylogenetic approach to assess the impact of habitat use on diversification patterns in the insect suborder of dragonflies (Anisoptera, Odonata). Based on a molecular dataset, consisting of eight ribosomal RNA and protein coding genes and representing all dragonfly subgroups, we inferred species diversification with a model-based evolutionary framework, to first account for rate variation through time and among lineages and to estimate the impact of lentic or lotic habitat choice on the potentially non-random diversification among anisopteran groups. Our phylogenetic reconstruction proposes Aeshnoidea as the first branch in Anisoptera and Gomphoidea as sister group to Cavilabiata, the latter being subdivided into Cordulegastroidea and Libelluloidea. Ancestral state reconstruction revealed lotic (flowing) fresh water systems as primary habitat, while lentic (still) fresh water bodies have been colonised independently in Aeshnidae, Corduliidae and Libellulidae. However, speciation rate analyses clearly contradict the proposed scenario of faster speciation in lotic groups. Speciation rates are uniform among all lotic groups, whereas they increased in lentic Aeshnidae and also in Libellulidae. The timing of increased speciation rates indicates that the capability of using relatively ephemeral lentic habitats might be a prerequisite for radiations in times of warmer climate with high humidity.

### **Polyneoptera? A transcriptomic-morphological perspective**

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Polyneoptera is a clade comprising the traditional orders Orthoptera, Blattodea, Mantodea, Phasmatodea, Embioptera, Grylloblattodea, Mantophasmatodea, Plecoptera, Dermaptera and Zoraptera. The relationship among these groups and their potential monophyly remains one of the biggest problems of systematic entomology. To address these questions we analyzed transcriptomes of in total 106 species (72 transcriptomes of Polyneoptera comprising all orders and 34 outgroup taxa). In an independent approach, we gathered a morphological data set comprising 287 characters of multiple character systems. Our results indicate strong support for the monophyly of Polyneoptera but no convincing morphological apomorphy. Within Polyneoptera, both morphological and molecular data support



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a sistergroup relationship between Mantophasmatodea and Grylloblattodea as well as the inclusion of Zoraptera in Polyneoptera. With respect to other clades such as Xenonomia (= Embioptera + Phasmatodea) or the polyneopteran backbone both analyses provide ambiguous results.

### Early splitting of Hexapoda reviewed from the comparative embryology: a revised synthesis

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Phylogenetic relationships of hexapod basal clades have been much argued from multiple sources, but are still not satisfactorily resolved. Doubt has been cast on the reality of the Entognatha-Ectognatha system, especially regarding the status of Entognatha. In the past few decades, much embryological knowledge concerning hexapod lineages has been accumulated. We have discussed the phylogenetic reconstruction of hexapod basal lineages, referring to recent advances of apterygote comparative embryology.

Careful comparisons of entognathy formations among three “entognathan” orders revealed that Protura and Collembola closely resemble each other but that of Diplura differs markedly from those of the former two orders, in terms of major points such as the origin of mouth folds and formation of posterior limit of entognathy. Thus, the monophyly of Entognatha is not always substantiated because the homology of entognathy between the Protura and Collembola and the Diplura is suspect, but the monophyly of Ellipura is well supported because its constituents possess the well-homologizable plan in their entognathy. The entognathy of Protura and Collembola can be designated as the “ellipuran type”, whereas that of Diplura as the “dipluran type”.

Comparative embryological analyses on the major lineages of Hexapoda clearly demonstrate an anagenetical transition of the functional specialization between embryonic membranes and embryo proper, leading to the acquisition of elaborate structures derived from the embryonic membranes, such as the amnioserosal fold – amniotic cavity system as shown in Pterygota. In this context, the most noticeable is that Diplura and Ectognatha share two significant embryological features. One is the “acquisition of a second embryonic membrane or the amnion”, and another is the “loss of ability in serosa for differentiating into the body element or the participation in the definitive dorsal closure”. These two can be regarded as being synapomorphic to Diplura and Ectognatha, to suggest the monophyly of their assemblage “Cercophora”. To this, integrating the information on the entognathy formations, the basal splitting of Hexapoda may be concluded as being formulated as: “Ellipura (= Protura + Collembola) + Cercophora (= Diplura + Ectognatha (= Archaeognatha + Dicondylia (= Zygentoma + Pterygota)))”, hereat Entognatha is dismissed.



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### Cephalic endoskeleton of *Baculentulus densus* (Imadaté) (Hexapoda: Protura: Acerentomidae): a preliminary embryological study

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The tentorium is a cephalic endoskeletal brace serving as muscle attachment and mechanical reinforcement of cranium, being composed of the anterior and posterior tentorial arms, which unite to form the central body or corpotentorium in pterygotes. Two pairs of tentorial invaginations can be one of the groundplan of Ectognatha, and the evolutionary transition of tentorium has been clearly illustrated (Snodgrass 1952; Matsuda 1965). Entognathous hexapods also have cephalic skeletal structures called the “(hypopharyngeal) fulcra”, “fulcro-tentorium” or simply “tentorium” (Folsom 1900; Hansen 1930; François 1959; Snodgrass 1960; Koch 2000; Klass and Kristensen 2001). However, the structures concerned in entognathous hexapods have not been well understood due to their minute size, and it remains unclear whether these structures are homologous with the tentoria of Ectognatha or which parts of these structures correspond to the tentoria of Ectognatha (Koch 2000; Klass 2009). In the present study, we examined the developmental process of the cephalic skeletal structure called the “fulcro-tentorium” in Protura which has been variously argued (Denis 1949; Tuxen 1959; Snodgrass 1960; François et al. 1992), using *Baculentulus densus* (Imadaté) as materials, to discuss its origin and structure.

In the fulcro-tentorium which shows an elongate X-shape, three areas are distinguished: i.e., a pair of anterior arms, a long central body and a pair of posterior arms. Major part of fulcro-tentorium is not a structure as is comparable to the ectognathan tentorial invaginations but an exoskeletal thickening of the gnathal pouch, although further analysis is needed especially concerning the posterior arms. In the posterodorsal region of the developing head capsule of the later stage embryos, paired ectodermal depressions are formed as found in the later stage embryos of Collembola (Tomizuka and Machida in press) and Diplura (Sekiya and Machida in prep.). These depressions are prominent in the embryonic stages, but after hatching externally disappear, only recognized as cuticular thickenings, which contact with both the posterior arms of fulcro-tentorium and cardo but never unite with them. They originate in the boundary of maxillary and labial segments or the postoccipital suture, and may be homologues of the posterior tentorial pits of Ectognatha. The structures comparable to the ectognathan anterior tentorial pits could not be found.

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### Embryonic development of *Eucorydia yasumatsui* Asahina (Insecta: Blattodea: Corydiidae)

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Dictyoptera, the assemblage of “Blattaria”, Isoptera and Mantodea, is well supported to be monophyletic, and the recent phylogenetic works give the subordinate position in “Blattaria” to Isoptera, the assemblage of “Blattaria” and Isoptera being called Blattodea. However, the relationships among principal lineages of Blattodea have been variously argued. For the reconstruction of their groundplan and phylogeny, much more information from various disciplines covering the blattodean major lineages are strongly desired. Comparative embryology is one of the most useful methods for reconstructing the groundplan and solving phylogenetic issues. Many embryological studies have been done on Blattodea, but most of them concern several species with economic importance of the derived families Blattidae and “Blattellidae” such as *Periplaneta* spp., *Blatta* spp. and *Blattella germanica*. As a first step of our comparative embryological study of Blattodea, we have tackled the Corydiidae, of which embryological information is totally lacking, using a Japanese corydiid, *Eucorydia yasumatsui* Asahina.

The egg of *E. yasumatsui* is with 10 to 15 micropyles on the ventral side of its posterior half. Grouped micropyles on the ventral side of the egg may be an apomorphic groundplan of Dictyoptera, since this condition is found in other dictyopteran members without exception. The embryo of *E. yasumatsui* is formed by the fusion of paired blastoderm region with higher cellular density. The formed embryo elongates and develops into its full elongation on the egg surface, undergoing the embryogenesis of short germ band type. The manners of embryo’s formation and elongation may be regarded as the potential apomorphic groundplan of Polyneoptera. The katatrepsis occurs, the dorsal closure proceeds, and finally the embryo acquires its definitive form. Throughout the embryonic development, the embryo of *E. yasumatsui* keeps its original position on the egg’s ventral side with its anteroposterior axis not reversed. The blastokinesis of Corydiidae is categorized in the “non-reversion type” together with Blaberoidea (= Corydiidae, “Blattellidae” and Blaberidae) and Mantodea, whereas the blastokineses of Blattoidea (= Blattidae and Cryptocercidae) and Isoptera are the “reversion-type”, in which the embryo’s anteroposterior axis is reversed during the blastokinesis. The information on major embryological features of *Eucorydia* such as the behavior of mycetome and development of appendages with reference to the formation of terga, sterna and spiracles is also given.

### Resolving an ancient rapid radiation: Biodiversity of the stick and leaf insects (Phasmatodea)

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Phasmatodea, commonly known as stick and leaf insects, represents a mesodiverse lineage of polyneopteran insects, standing out as one of the last traditional insect orders for which a robust, higher-level phylogenetic hypothesis is lacking. Recent studies demonstrated that often geographical distribution rather than traditional classification and morphological similarity reflects the evolutionary relationships among stick and leaf insects. Beyond the basal branching of Phasmatodea into the species-poor *Timema* (21 spp.) and the highly diverse Euphasmatodea



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(> 3.000 spp.), radiation of the major phasmatodean lineages is only poorly resolved. Molecular data suggests that there was an ancient rapid radiation at the origin of the Euphasmatodea, which occurred over a relatively short period in the Eocene when the principal extant subgroups emerged. Therefore, much of the early evolutionary history, such as the relationships between traditional subfamilies and some longstanding taxa like the Chilean *Agathemeria* is difficult to address. A genomic approach based on novel transcriptomic data is supposed to provide a robust phylogenetic backbone for Phasmatodea with all major lineages delineated. Preliminary data yield promising results. The early evolution of stick and leaf insects is also elucidated by a number of recently reported Mesozoic forms, which represent true stem-Phasmatodea predating co-evolution with angiosperm forests. The presence of stick insect fossils largely resembling Mesozoic taxa is expanded into the early Eocene, indicating a transitional phase in which they may have persisted during the radiation of Euphasmatodea. These ancient stick insects are not seen after the early Eocene and were obviously replaced by modern forms in a world of changing forest communities, climates, and plant-insect interactions.

### The Orthoptera Tree of Life: Elucidating patterns and processes of orthopteran evolution

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Orthoptera is the most diverse order among the polyneopteran groups and includes familiar insects, such as grasshoppers, crickets, katydids, and their kin. Due to a long history of conflicting classification schemes based on different interpretations of morphological characters, the phylogenetic relationships within Orthoptera are poorly understood and its higher classification has remained unstable. In this presentation, I present a robust phylogeny of Orthoptera based on comprehensive taxon and character sampling in order to test previous phylogenetic hypotheses and to provide a framework for a natural classification and a reference for studying the pattern of divergence and diversification. The analysis strongly supports the monophyly of suborders (Ensifera and Caelifera) as well as major superfamilies. Using fossil calibrations, divergence times for major orthopteran lineages are estimated, which suggests that the current diversity has been shaped by dynamic shifts of diversification rates at different geological times across different lineages. The analysis also finds that mitochondrial tRNA gene orders have been relatively stable throughout the evolutionary history of Orthoptera, but a major tRNA gene rearrangement occurred in the common ancestor of Tetrigoidea and Acridomorpha, thereby representing a robust molecular synapomorphy, which has persisted for 250 Myr.

### Phylogeny and origins of diversity in Dictyoptera

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The transition from omnivorous and solitary roaches to xylophagous and social termites is one of the most intriguing and unique events in the evolution of Polyneoptera. In contrast to the social groups within Hymenoptera it is most likely related to wood feeding. Historically, the phylogeny of Blattodea and Isoptera was poorly resolved due to a lack of morphological data, little interest and poor sampling of both in-group and outgroup taxa. Our team aims to illuminate the evolution of sociality through phylogenetic inference and other bioinformatic analyses using transcriptomes. We use transcriptomes from 46 blattodean terminals including Blaberoidea, Lamproblattidae, Noc-





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ticolidae, Tryonicidae, Blattidae, Corydiidae, Cryptocercidae, Mastotermitidae and other Termitoidea. The outgroup selection includes Mantodea and other neopterans. We use our data set to investigate changes in the morphology, the evolution of N-metabolic functional groups and the evolution of gut symbionts with the aim to better understand functional shifts correlated with the evolution towards a high-carbon, low-nitrogen wood diet. Preliminary phylogenetic analyses confirm that termites are nested within Blattodea. Analysis of N-metabolic functional gene groups shows that such analyses are difficult on such an old and diverse clade. Regardless, the data suggests a potentially wider distribution of *Blattabacterium* than previously thought and possible physiological compensation for dietary shifts in termites.

### Phylogeny of Blaberoidea (Blattodea): taxonomy and life history

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The superfamily Blaberoidea contains approximately 3500 of the 4500 known cockroach species (excluding termites) and exhibit large variation in life history strategies. Blaberoidea in the present sense contains two families, Ectobiidae and Blaberidae. However, Ectobiidae is paraphyletic with respect to Blaberidae and an ectobiid subfamily, Anaplectinae, was recently removed from Blaberoidea and placed as a family in Blattoidea (Djernæs et al., 2015). While various subsets of Blaberidae have been the subject of phylogenetic studies, no study has focused specifically on Blaberoidea or Ectobiidae. We reconstruct a molecular phylogeny of Blaberoidea to provide better estimates of the relationship among the ectobiid subfamilies and Blaberidae, as well as among the blaberid subfamilies. We also test the placement of Anaplectidae with an increased blaberoid taxon sampling. Blaberoidea (excl. Anaplectidae) and Blaberidae are confirmed as monophyletic while Ectobiidae is confirmed as paraphyletic. The ectobiid subfamilies are generally monophyletic although we find that Attaphilinae is deeply subordinate in Blattellinae. However, while Blaberidae is monophyletic, several blaberid subfamilies are not: Blaberinae and Zetoborinae are intermingled, but do form a generally monophyletic Blaberinae + Zetoborinae clade. Perisphaeriinae is split into two distantly related groups. Epilamprinae is split with the type genus only distantly related to most of the genera included in the subfamily. Panesthiinae is paraphyletic with respect to Geoscapheinae, but Panesthiinae incl. Geoscapheinae form a well-supported monophyletic group. Based on the phylogeny we explore several traits related to life history strategy: Body size, habitat choice, wingedness as well as oviposition and mating behaviour. We discuss the evolution of these traits and how they correlate with each other.

**Reference:** Djernæs M., Klass K.-D., Eggleton P. 2015. Identifying possible sister groups of Cryptocercidae + Isoptera: A combined molecular and morphological phylogeny of Dictyoptera. *Molecular Phylogenetics and Evolution* **84**: 284 – 303.



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### Revision in Neotropical praying mantises (Acanthoidea and Vatinae)

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The phylogenetic revision of the earless neotropical mantises was based on a DNA dataset of 9949 aligned nucleic acid characters comprising ten mitochondrial and nuclear genes. Our analyses largely resolved congruent relationships with high levels of support for higher-level taxonomic groups, while revealing multiple inconsistencies between the resolved topology and morphology-based classification systems. The polymorphic earless praying mantises, now granted superfamily status as the Acanthoidea **stat. n.**, comprises eight families including new subfamilies and tribes. Our new system resulted in the reassignment of various genera to new and existing higher-level taxa, the exclusion of old world genera otherwise traditionally classified among the Thespidae, Liturgusidae and Angelidae, the confirmation of *Stenophylla* Westwood, 1845 as member of this clade, and the revalidation of *Paradiabantia* Piza, 1973 **stat. rev.** We provide preliminary diagnoses for all suprageneric taxa using a combination of both external morphological characters and/or male genital features, all summarized in dichotomous keys. We also incorporate egg case structural variation as a novel character for taxon delineation. Our revision of the horned mantises, Vatinini, utilized on a combined molecular (1,945 characters) and morphological (96 characters) dataset for 33 of the 47 described taxa. We synonymized three genera, describe a new genus for a unique species, and erect a new tribe as well as remove non-neotropical members from Vatinae. We redescribe the genera, provide an identification key, and present images of representative taxa for all genera. We demonstrate an evolutionary shift towards crypsids in two independent lineages of Vatinae. The shift appears to be linked to the development of a cuticular leg lobe, which may be a precursor to additional leg lobe development and a shift towards a camouflage strategy. In addition, we demonstrate that serially homologous leg lobes and those occurring within the same leg segment are evolving together.

### Zoraptera – a phantom in insect evolution

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Zoraptera are a cryptic and enigmatic group of insects. The presently known diversity is very low (39 spp.) but several new species were recently described from different regions. The systematic placement was discussed controversially since the group was discovered 100 years ago. Affinities with Isoptera and Psocoptera were discussed in earlier studies. A sistergroup relationship with Acercaria (Psocodea, Thysanoptera, Hemiptera) was proposed by W. Hennig, for the first time based on a strictly phylogenetic argumentation. More recent studies consistently suggest a placement among the “lower neopteran orders” (Polyneoptera). This is mainly supported by embryological features. The precise placement is still controversial. Analyses of transcriptomic data (1KITE project) suggest a clade Zoraptera + Dermaptera as sistergroup of all other polyneopteran orders. However, this concept is not strongly supported. The intraordinal phylogeny is also largely unclarified. The extinct genus *Xenozorotypus* (Cretaceous) may be the sistergroup of all the remaining zorapterans. The general body morphology is very uniform, whereas the reproductive system differs strongly between species. This is likely due to different kinds of selection, i.e. sexual



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selection in the case of the genital organs. The mating pattern also differs profoundly within the order. A unique external sperm transfer occurs in *Zorotypus impolitus*. A species-level phylogeny and more investigations of the reproductive system should have high priority.

### Phylogenomics and morphology of the hemipteroid insect orders

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The hemipteroid Assembling the Tree of Life (AToL) project is in year three of the five-year project. The goals of this project are to reconstruct a backbone phylogeny of the hemipteroid insect orders (Psocodea, Thysanoptera, and Hemiptera) using phylogenomic and morphological data. A total of 163 transcriptomes and 56 genomes have been sequenced to date for this project. These data will be combined with over 90 transcriptomes sequenced by the 1KITE project for a first estimate of the phylogeny of this group from transcriptome data. In addition, over 300 morphological characters have been scored for representatives of this group and the phylogeny resulting from this data matrix largely agrees with previous assessments, although there are some key differences. These data will also be used to study the utility of genome organization for phylogenetics, and mitochondrial rearrangements are shown to have some phylogenetic signal. One of the main methodological advancements of this project has been the development of the software aTRAM; automated Target Restricted Assembly Method, which is a fast method for assembling genes from genomic data. aTRAM uses paired-end sequencing data to create an easily searchable library and quickly assembles loci of interest. This software has been used to construct phylogenomic data sets within hemipteroids and these have resulted in highly resolved and supported trees. The next steps for the methodological advances for this project are building pipelines for downstream processing of these data, particularly for alignment and building trees.

### Phylogeny and morphology of Dipsocoromorpha (Hemiptera: Heteroptera)

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Dipsocoromorpha, the minute litter bugs, are a poorly studied infraorder of morphologically diverse Heteroptera that currently includes only about 370 species in five families (Ceratocombidae, Dipsocoridae, Hypsipterygidae, Schizopteridae, and Stemmocryptidae). Litter bugs are small (1–2 mm) and mostly found in the wet tropics, accounting in part for the substantial undescribed genus- and species-level diversity in the group. Published phylogenies have included only three of the five families and few representatives, and the monophyly of the group remains to be corroborated. Family-level relationships within Dipsocoromorpha are largely untested. The current family-level classification, proposed in 1983 and based on morphological evidence, has not been investigated in a cladistic framework. In addition, family- and subfamily limits (e.g., Ceratocombidae, subfamilies within Schizopteridae) have become less clearly defined with the description of a number of new genera during the past two decades. The astounding



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ing diversity of structural features across the group is both intriguing (e.g., multiple origins of coleopteroidy), but also a challenge (e.g., homology concepts). As a part of an US National Science Foundation ARTS grant, >19,000 specimens of Dipsocoromorpha have been accumulated, mostly curated from EtOH residue samples. This collection has not only revealed enormous undescribed biodiversity, but has also enabled the generation of molecular and morphological data on a broad scale. We here further test the monophyly of Dipsocoromorpha (including for the first time the rare Hysipterygidae) and monophyly of and relationships within Ceratocombidae and Schizopteridae based on molecular data, while presenting examples of the extreme morphological diversity of the group using various imaging techniques.

### From termite assassin to transcriptome: exposing the phylogeny of assassin bugs (Hemiptera: Reduviidae)

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Reduvidae are the largest clade of non-holometabolous predatory insects (2 families, 27 subfamilies, ~7,000 species). The size of the group, the extraordinary morphological and ecological diversity, a significant but poorly documented fossil record, an emerging phylogenetic framework, and the importance as diseases vectors, make Reduvidae an ideal model for studying the evolutionary history of a megadiverse clade of predators and blood-feeders. Despite significant progress during the past decade, the systematic position of several assassin bug subfamilies has remained in the dark and relationships along the backbone of Higher Reduvidae are largely unresolved. Natural history data for a wealth of assassin bugs species have become available, but documentation of and transitions between euryphagy and stenophagy are hampered by the lack of prey data for many taxa. The objectives of this presentation are threefold: first, we present a transcriptomic study for Reduvidae that documents the importance of phylogenomic data for resolving the backbone phylogeny of Reduvidae. We further document the feasibility of generating a robust phylogenetic framework by combining transcriptomic and Sanger-sequencing data. Second, two enigmatic and elusive subfamilies of Reduvidae are incorporated into phylogenetic analyses for the first time, while impacting the phylogenetic position of an intriguing Baltic amber fossil. Third, a study focusing on the termite assassin subfamily Salyavatinae uses forensic methods to investigate prey range and documents prey conservatism in this group.

### Hopper Hype: an Auchenorrhyncha phylogeny update

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The higher-level phylogeny of the order Hemiptera remains a contentious topic in insect systematics. Consensus now suggests that the monophyletic order Hemiptera *sensu lato* (the largest non-holometabolous insect order, with approximately 82,000 described species) includes the following major monophyletic clades: Sternorrhyncha (scale insects, aphids, whiteflies, etc.; ~21 extant families), Heteroptera (true bugs, *sensu stricto*; ~54 extant families), Coleorrhyncha (sometimes called "moss bugs"; 1 extant family), Fulgoromorpha (planthoppers; ~20 extant families), and Cicadomorpha (leafhoppers, treehoppers, spittlebugs, and cicadas; ~12 extant families). However, relationships among these higher-level hemipteran lineages have not yet been definitively resolved, and specifically, the phylogenetic positions of Fulgoromorpha and Cicadomorpha (traditionally classified together as the monophyletic group



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Auchenorrhyncha) remain controversial. The “Auchenorrhyncha question” gained widespread attention in 1995 with the publication of three phylogenetic studies based on partial 18S rDNA sequence data. While not definitively refuting auchenorrhynchan monophyly, those analyses concluded that Fulgoromorpha and Cicadomorpha were likely separate lineages occupying independent (i.e., non-monophyletic) positions within the phylogeny of Hemiptera. Subsequent molecular phylogenetic investigations, based on more extensive taxonomic and data sampling, resulted in support for the monophyly of Auchenorrhyncha. Still more recent genomics-based analyses failed to recover Auchenorrhyncha as monophyletic. Which hypothesis is best supported by evidence? This presentation will summarize the alternative phylogenetic hypotheses, based on various lines of evidence, proposed on this question.

### BIG4 network: training insect systematists of the future

**ALEXEY SOLODOVNIKOV** (Natural History Museum of Denmark, Zoological Museum; [asolodovnikov@snm.ku.dk](mailto:asolodovnikov@snm.ku.dk))

BIG4 (Biosystematics, Informatics and Genomics of the big four insect groups) is a global consortium funded by the EU-based ‘Innovative Training Network’ program (<http://big4-project.eu>) and coordinated from the Natural History Museum of Denmark in the period of four years (2015–2018). BIG4 aims to train a new generation of systematic entomologists with broad profiles amalgamating classical aspects of biosystematics with the cross-disciplinary methodological innovations. Evolution of insects from the four biggest orders (1. beetles; 2. bees, ants and wasps; 3. flies and mosquitoes; 4. moths and butterflies) is at the core of BIG4. These ‘big four’ insect groups constitute about half of all living species on Earth and have an enormous impact on natural or anthropogenic ecosystems, even when not visible as such by a layman. The research and training program of BIG4 consists of 15 individual PhD projects, either taxonomically restricted to any of the ‘big four’ or cross-taxonomic. All projects overlap methodologically along such themes as: large data sets assembly and analyses; phylogenetics; genomics; advanced biodiversity data publishing, and citizen science. By arming students with a variety of methods and skills applicable in academic research and industry from the start of their career, BIG4 enhances knowledge, sustainable use and preservation of the fascinating insect diversity.

### Extinct diversity and integrated phylogeny of a megadiverse beetle lineage using data from µCT reconstruction of amber fossils

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One of the greatest challenges to accurate phylogeny reconstruction is the limited and usually non-representative sample of morphological and molecular diversity available from extant taxa, especially in lineages that have experienced high levels of extinction. Finely detailed, three-dimensional insect fossils preserved in amber hold great potential to overcome this challenge. However, fossilization in amber is a natural, imperfect process and important characters are often hidden by non-target inclusions or other structures of the specimen, and internal characters are typically unavailable when using light microscopy. The completeness of and signal within morphological character datasets can be greatly increased with reconstruction of these fossil taxa in 3-D using micro-CT. Here we apply this technique to unique Baltic amber fossils belonging to a lineage of the mega-diverse rove beetles, the tribe



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Staphylinini but not further assignable using light microscopy alone. The complementarity of these two techniques for acquiring phylogenetic data will be discussed.

### The phylogeny and evolution of beetles (Coleoptera) as revealed by new molecular phylogenetic and comparative genomic data

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In this talk I will present higher-level phylogenies for the order Coleoptera (beetles; >389,000 species) and some of its most species rich lineages, reconstructed using molecular data obtained by the Beetle Tree of Life Project, the 1KITE Beetle Project, and the 1K Weevils Project. These studies sample a few genes obtained via traditional methods, to thousands of genes obtained via high-throughput methods, e.g., transcriptome and genome sequencing, and anchored hybrid enrichment. Together, results from these studies provide new and notable insights into relationships and evolution in the order Coleoptera. I will close by briefly discussing the genomic basis and evolution of phytophagy (plant-feeding) in beetles, using the Asian longhorned beetle (*Anoplophora glabripennis*) as a model. The ALB genome encodes a diversity of genes that facilitate specialized plant feeding – a habit long associated with the apparent success of beetles. Together, these studies show how once separate fields of study are converging by way of new data and highly collaborative research efforts, to reveal the evolutionary history and genomic basis of beetle diversity.

### Molecular phylogeny of ant nest beetles (Coleoptera: Carabidae: Paussinae)

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Ant-nest beetles (*Paussus*) are the quintessential Trojan horses of the insect world. They hack the complex communication system of ants, allowing them to blend into the ant society and be treated as royalty, all the while preying upon the ants and the ants' brood and duping the ants into rearing their young (Geiselhardt et al. 2007; Luna de Carvalho 1987; Maurizi et al. 2012). Here we present results of the first molecular-based phylogeny of ant-nest beetles, which reveals that this symbiosis has produced one of the most stunning examples of rapid adaptive radiation documented to date (Moore & Robertson 2014). The most recent ancestor of a *Paussus* clade endemic to Madagascar is only 2.6 million years old. This species gave rise to a remarkably phenotypically diverse clade of 86 extant species with a net diversification interval of 0.38–0.81 million years, a rate of radiation faster than classic textbook examples of large, recent, rapid radiations such as *Anolis* lizards on Caribbean islands, cichlids of the East African Great Lakes, finches on the Galapagos Islands, and *Drosophila* and tetragnathid spiders on the Hawaiian Islands (Gillespie et al. 1994; Grant & Grant 2008; Kambysellis et al. 1995; Losos 2009; Turner et al. 2001). In order for *Paussus* to adapt to a new host ant species, the beetle's ability to perceive, deceive, and communicate with the new host must evolve quickly and in synchrony in both the larval and adult life stages, resulting in unusually strong selective pressure levied by their host ants. Data on host associations suggest that the history of host shifts may help explain both the striking phenotypic diversity within the Malagasy radiation and the evolution of phenotypically similar yet distantly related species in Madagascar and Africa.



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### 2015's state of knowledge on the phylogeny of Hymenoptera

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Hymenoptera are one of the “big four”, the mega-diverse orders of holometabolous insects. The order includes numerous groups of special relevance as biological control agents of pests or as pollinators of crops, or of special awareness in the public, like ants and bees. Some of the major evolutionary innovations of Hymenoptera are striking, even to the non-entomologist's eye, for example, the evolution of a parasitoid lifestyle, the evolution of a venomous stinger, of eusociality or of secondary phytophagy. Today, we observe incredibly species-rich lineages as well as species-poor lineages, yet the probably numerous keys to the evolutionary success of Hymenoptera are still not well understood. This is due to a still lacking phylogenetic resolution in the backbone of the Hymenoptera tree which makes reconstruction and interpretation of the evolutionary history of the group difficult.

To infer phylogenetic relationships, we *de novo*-sequenced in context of the international 1KITE project ([www.1kite.org](http://www.1kite.org)) whole-body transcriptomes of 270 different species of wasps, ants, and bees, covering major lineages of this group. We identified on average 2,400 single-copy protein-coding genes suitable for phylogenetic analysis. In this talk, we report on the phylogenetic analysis of these genes, show some first results obtained from these analyses and discuss the implications for our understanding of Hymenoptera evolution.

### The impact of Niels Peder Kristensen on insect phylogenetics

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Niels Peder Kristensen (NPK) was a towering figure in systematic entomology for four decades from 1975 onwards. Although the bulk of his original research was done on Lepidoptera, he was most widely known internationally as a world authority on hexapod phylogenetics. This reputation was founded with his (Kristensen 1975) review paper on the phylogeny of hexapod ‘orders’; he repeatedly updated this overview over the next quarter of a century, the last time in Kristensen (1999). NPK combined detailed knowledge of insect anatomy with a classical Hennigian approach to analyzing phylogenetically relevant data. He was instrumental in promoting W. Hennig's methodology in the Nordic countries in the 1960'ies. His breadth of knowledge of insect morphology was unsurpassed, allowing



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him to synthesize information from a wide range of character systems and taxa in his comprehensive phylogenetic reviews. These would later serve as a yardstick for evaluating molecular hexapod phylogenies from the 1990'ies onwards and as a source for morphological input to combined analyses. However, NPK also produced substantial original contributions to higher-level insect phylogenetics, culminating in the description of the new insect order Mantophasmatodea (Klass et al. 2002) in collaboration with K.-D. Klass, among others. Furthermore, he was an inspiration for students and colleagues across the world, sharing his knowledge and insights widely. He personally supervised a number of graduate students and post. docs and influenced many more through his publications and interactions. The Dresden Insect Phylogeny meeting series, initiated in 2003, was partly his brainchild, and he attended every meeting until the present one. We shall not see the likes of Niels Peder Kristensen again, but even now that he is gone we will continue to seek inspiration from his love for and dedication to our science.

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### The contributions of N. P. Kristensen to the understanding of Lepidoptera phylogeny

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The impact of the work of Niels Peder Kristensen on the understanding of Lepidoptera phylogeny cannot be underestimated. He championed the use of electron microscopy (both scanning and transmission) in comparative morphology of Lepidoptera and was among the first to analyze data in a cladistic framework. His phylogenetic hypothesis for Lepidoptera was the standard for the field up to the age of phylogenomics. His main passion in Lepidoptera was to understand the evolutionary history of the early lineages, those which he referred to as the "primitive" Lepidoptera. He described several new families, including one which was accepted for publication just before his untimely death. In addition to his scientific achievements, Niels was always greatly supportive of young researchers by actively inviting them to talk at conferences and showing sincere interest in their work. He is sorely missed.

### Phylogeny of Lepidoptera utilizing transcriptomes and hybrid enrichment data

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Butterflies and moths (Lepidoptera) are one of the most diverse insect orders, with more than 157,000 described species. They also constitute some of the most popular and charismatic insects and serve as a model group. However, many deep level relationships, especially among superfamilies, remain ambiguous. Here we update efforts on the Lepidoptera KITE project, and sample representative taxa from many superfamilies, construct a new transcrip-





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omic dataset, and present preliminary results on phylogenetic relationships of Lepidoptera. We also present results from a recently developed hybrid enrichment probe set, which targeted ~800 genes.

### A target capture approach to butterfly phylogeny (Lepidoptera)

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Next generation sequencing approaches within Papilionoidea (butterflies and skippers) are limited to very closely related species. Currently, most higher-level phylogenetic studies of Papilionoidea utilize 4 to 10 ‘standard’ loci, and these genes often do not provide robust support for deeper relationships within the superfamily. We used a target enrichment approach and Illumina sequencing to enrich 450 loci of length 300–2200 bp for 150 taxa covering all butterfly tribes and the Hedyliidae. To assess capture success and phylogenetic signal at a lower taxonomic level, we also sequenced 96 members of the subtribe Euptychiina (Satyrinae, Nymphalidae). This probe kit contains the most commonly used mitochondrial and nuclear loci (COI, Ef1- $\alpha$ , wg, GAPDH, Rps5, Rps2, IDH, MDH, CAD, ArgK, DDC), and can readily be combined with available sequence data. Preliminary results show that these 450 loci provide robust support for both higher and lower taxonomic levels.

### 1KITE: New insights on the phylogeny of Trichoptera from transcriptomes and targeted enrichment

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„Big data“; the collection of genomes or transcriptomes with high-throughput sequencing, has revolutionized today’s phylogenetics. One might also consider international efforts to sequence a single (barcode) locus from every species on earth another kind of big data. Kjer addresses the philosophical and analytical challenges of big data, and describes some of the solutions used in the 1KITE project to produce a well supported insect phylogeny from transcriptomes. There are many other sources of data as well, from genomes to single-locus “barcode” data. Some of these data sources such as barcodes combined with targeted PCR, are well suited to undergraduate teaching, or alpha taxonomy. Others, such as exome capture using degraded DNA from museum specimens, fill gaps in taxon sampling where transcriptomes are impossible to collect. Little attention has been directed toward coordinating diverse datasets into a unified picture of insect evolution, from the root to the tips of the tree. Kjer proposes a strategy to do that, using Trichoptera as an example. The strengths and weaknesses of each technology are discussed.



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### Molecular phylogenetics offers insight on the ecological diversification of aquatic insects

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Inland waters cover less than 1% of Earth's surface but harbor more than 6% of all insect species. Following more than 50 independent reinvasions of freshwater, nearly 100,000 species from 12 orders spend one or more life stages in freshwater habitats. Little is known about how this remarkable morphological and ecological diversity arose. Phylogenetic studies of selected taxa can provide insights into this diversification. We present examples from caddisflies, an order of > 15,000 species that have invaded all types of freshwater habitats and exhibit a wide range of ecologies.

The genus *Drusus* comprises ~100 species and exhibits different feeding types, including a unique predaceous drift-filtering foraging behavior. A six gene phylogeny clearly shows larval feeding groups to be monophyletic, and that the derived feeding type (grazing) and the unique feeding type (filtering) promoted morphological diversification.

With over 700 species *Rhyacophila* represents one of the most species-rich genera in Trichoptera. Some larvae of *Rhyacophila* possess abdominal and/or thoracic gills of varying complexity. Stream zonation preferences, respiration and osmoregulation have been hypothesized to correspond with gill shape. Using an anchored hybrid enrichment approach (AHE) we sequenced and analyzed ~520 nuclear loci from protein coding genes for a total of ~130k bp from 20 species of the *R. vulgaris*-group and 30 other *Rhyacophila* species. Our results show that within the *R. vulgaris*-group complex gill shapes are derived, and progressively evolved into increasingly complex shapes, while absence of abdominal gills represents the ancestral state. We discuss potential ecological implications of gill shape evolution in the *R. vulgaris*-group.

### The adult and pupal head of Trichoptera – ground plan pattern and the evolution of major morphological traits

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With app. 14,500 species, Trichoptera (caddisflies) comprise one of the most species rich insect orders with primarily aquatic larvae. The sistergroup relationship to the megadiverse Lepidoptera forming Amphiesmenoptera is well-supported and was never seriously challenged. The intraordinal relationships among the major trichopteran subgroups, Annulipalpia, Integripalpia and the most likely not monophyletic 'Spicipalpia' are controversially discussed. Especially the basal branching pattern is widely unresolved. Various analyses of molecular and/or morphological data yielded distinctly different results. This also impedes the accurate reconstruction of the trichopteran ground plan, which is needed for the interpretation of evolutionary transformations of morphological traits.

Adult and pupal head structures of representatives of all major trichopteran lineages were examined by using a combination of traditional (light microscopy, histology, scanning electron microscopy) and modern morphological techniques (micro-computed tomography, computer-based 3D-reconstruction, confocal laser scanning microscopy).



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Internal and external features were thoroughly evaluated in order to reconstruct the ground plan conditions for several cephalic character complexes. The homology of the trichopteran mouthparts was also discussed. The cephalic ground plan of Trichoptera contains a pi-shaped tentorium with short dorsal arms, moderately sized mandibles with three well-developed muscles, a small haustellum, five-segmented maxillary palps, and a distinct lacinia. The unusual configuration of the extrinsic dilator muscles of the salivarium is regarded as a potential autapomorphy of the order. The evolution of major morphological character complexes will be presented and discussed.

### Fleas, Flies, Scorpionflies: phylogenetic relationships of Antliophora based on transcriptomics

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Antliophora includes the megadiverse flies (Diptera) and the two smaller orders scorpionflies *sensu lato* (Mecoptera with ~ 550 described species) and fleas (Siphonaptera with ~ 2,200 described species). Fleas are ectoparasites with extreme host adaptations and can carry vectors of diseases. Mecoptera are much less specialized and quite diverse in their life histories. They play a crucial role in understanding the early evolution of Antliophora, and in some Permian deposits they comprise nearly half of all known insect fossils. Recent phylogenetic analyses of morphological and molecular data confirmed that Antliophora are monophyletic. However, the relationships among the three orders, the monophyly of Mecoptera and their intraordinal phylogeny remained a matter of debate. We present preliminary results on antliophoran relationships based on whole-body transcriptome data ("1KITE Antliophora" subgroup, [www.1kite.org](http://www.1kite.org)). Among ten representatives of Mecoptera we included crucial taxa like the wingless *Boreus* ("snow fleas"), the wingless Tasmanian endemic *Apteropanorpa*, and two species of the enigmatic Nannochoeristidae. Nannochoeristidae has been discussed as sister group with respect of all remaining mecopterans, or of Pistillifera, Boreidae, or even as closest relatives to (Diptera + Siphonaptera). In a recent study (1KITE) their placement varies with different analytical methods. In our ongoing analysis of antliophoran relationships we identified about 2,500 single-copy protein-coding genes suitable for phylogenetic analysis and present preliminary phylogenetic results using carefully designed datasets including partitioning by protein domains.

### Phylogenomics to resolve radiations in diverse fly lineages

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Molecular systematic studies from large gene harvests are providing exciting new phylogenetic resolution to many traditionally difficult and highly diverse taxa. As new genomes and transcriptomes are obtained for many insect groups, these genomic resources can be used to design gene probes for hybridization capture of orthologous genes from related taxa. Together with the 1KITE Antliophora group and a diverse team of collaborators, we are using full



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transcriptomes to investigate phylogeny across the Diptera and to resolve difficult areas of the tree due to rapid radiations, conflicting morphological evidence, or limited gene sampling. With Alan and Emily Lemmon at Florida State University, we developed an anchored hybrid enrichment probe set for Diptera based on comparative analysis of 15 fly transcriptomes from the 1KITE project and complete genomes. These probes have been used successfully to obtain large sequence data sets containing 300–600 genes from diverse families of flies, including Anthomyiidae, Drosophilidae, Syrphidae, Ephydriidae, Empididae, Tabanidae, Bombyliidae, and diverse families of Bibionomorpha and Schizophora. Here, I present new phylogenetic trees for Anthomyiidae, Syrphidae and Empidoidea based on anchored enrichment targeting over 550 genes. Our first trees using this method provide strong support that agree with morphological and taxonomic hypotheses and also challenge current classifications in several areas. New phylogenetic hypotheses for both Syrphidae and Anthomyiidae provide a new framework to understand the multiple origins of plant feeding and other specialized habits in these two diverse fly families and provide a valuable guide for additional NextGen sampling within Diptera.

### Malaise trap phylogenetics: affordable and fast assessment of species and phylogenetic diversity with NGS

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Many species-rich arthropod clades can be sampled efficiently with techniques like canopy fogging and Malaise-trapping. However, subsequent sample processing is challenging because species-level sorting based on morphology by parataxonomists yields unpredictable results, and taxonomic experts usually do not have the time to thoroughly examine specimen-rich samples. DNA barcoding could be an (imperfect) alternative, but traditional Sanger barcodes are too expensive. Here, we illustrate how NGS can be used to barcode individual insect specimens for ca. 50 cents per specimen and group them into operational taxonomic units (OTUs). Such OTUs are weak species hypotheses, but many can be converted into strong hypotheses based on genetic distinctness and/or morphological study of specimens which are preserved in “NGS barcoding”. Once species are delimited and imaged, they can be placed onto the Tree-of-Life using data from multiplexed PCRs using tagged primers. The proposed techniques will expedite the processing of large numbers of specimens and help with the discovery and phylogenetic placement of large numbers of species.



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### ***Stilbopteryx* meets *Pseudimares* – a challenging hypothesis (Neuroptera: Neuroptera: Myrmeleontidae)**

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The systematization of the Myrmeleontidae, the species-richest lace wing family of Neuroptera, comprising the subfamilies Myrmeleontinae, Palparinae and Stilbopteryginae, is still unsettled. The spectacular long-term monotypic genus *Pseudimares* Kimmins, 1933, from Iran, with *P. iris* having bewitched eye spots on all four wings, remains a mystery even after the recent discovery of a second species, *P. aphrodite* Aspöck & Aspöck, 2009, in Morocco. No eye spots of this beauty are known from any other extant Neuropteron. The male genital sclerites signalize a relationship to the South American genus *Dimares* Hagen, 1866, subfamily Palparinae, while the strikingly long legs rather range *Pseudimares* somewhere within the subfamily Myrmeleontinae. Our short-term molecular genetic analyses based on two mitochondrial genes comprising all material available at present placed *Pseudimares* near *Palpares*. Including all available Myrmeleontidae sequences from GenBank surprisingly gained the Australian genus *Stilbopteryx* Newmann, 1838, subfamily Stilbopteryginae, as the adelphotaxon of *Pseudimares*. Yet, this relationship is only weakly supported and certainly deserves further investigations. That *Stilbopteryx*, a Stilbopteryginae, might be in fact a member of Palparinae signalises the uncertainty of the present system within Myrmeleontidae. No doubt, morphological plausibility control is claimed. However, male genital sclerites, generally of most effective phylogenetic relevance, are in Myrmeleontidae in large parts camouflaged by intensive amalgamation on one hand or by bizarre structures on the other hand. Thus, further traits need to be analysed. Anyhow, a joint morphological and DNA-based approach will be the most promising way towards a solution.



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### 01 Comparative embryology of arctoperlarian Plecoptera

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Plecoptera is divided into two suborders Antarctoperlaria (four families) and Arctoperlaria (12 families) (Zwick 2000). Nine families of Arctoperlaria inhabit Japan. The basal position within Polyneoptera has been often bestowed to Plecoptera, but its affinity has been variously argued. For solving phylogenetic issues, the comparative embryological approach is one of the most useful methods. However, our embryological knowledge on Plecoptera remains fragmentary, being restricted to the relatively detailed studies on two arctoperlarian families (e.g. Miller 1939, 1940; Kishimoto & Ando 1985) and some brief reports on few other families of the same suborder. In such a background, to reconstruct the groundplan and phylogenetic affinity of Plecoptera, we have started a comparative embryological study of Plecoptera, as the first step, using nine all arctoperlarian families from Japan.

Based on the comparison of the embryogenesis of nine arctoperlarian families referring to the previous studies, plecopteran embryogenesis is characterized by: 1) the formation of the embryo at the posterior pole of the egg, 2) elongation of the embryo along the egg surface, 3) immersion of the embryo into the yolk at the middle developmental stage, with its cephalic and caudal ends left on the egg surface, and 4) blastokinesis involving the reversion of embryo's axis (excepting Scopuridae). These features may be considered to be the groundplan of Arctoperlaria. In Peltoperlidae, which have flattened eggs, the embryo shows the reversion accompanied with rotation of embryo during blastokinesis, as known in Pteronarcyidae, of which eggs are likewise flattened in shape (Miller 1939, 1940). However, the embryos in Scopuridae were revealed to suffer from neither reversion nor rotation during blastokinesis. Although this may be a potential apomorphy of the family, the phylogenetic reevaluation of it is a future subject.

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### 02 Diversity of egg structures and reproductive systems in Zoraptera

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Zoraptera is a least diverse insect order containing 39 extant species. Although multi-generic classifications of Zoraptera have been sometimes proposed, all extant species are presently classified into a single genus *Zorotypus*, due to a remarkable uniformity of the external morphology. Aiming at the intraordinal classification, morphological surveys for taxonomically useful characters should have high priority.

The egg structure is often used as a taxonomic character in insects, and we found that Zoraptera show striking variety in the reproductive systems in clear contrast to their external structural uniformity. We examined and compared egg structures and reproductive systems of several zorapteran species and could distinguish three groups in Zoraptera. The first group “A” is characterized by a two-layered chorion with uniform hexagonal surface pattern and



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small micropyles, posteriorly bifurcated ventral sclerite of the male genital organ (basal plate), slender spermathecal duct and spermatozoa of moderate length, comprising *Z. caudelli*, *Z. magnicaudelli*, *Z. gurneyi*, *Z. snyderi*, *Z. barberi*, *Z. huxleyi*, and *Z. weidneri*; group A can be further divided into “A-1” (first four species) and “A-2” (last three species) by the presence or absence of a coiled intromittent organ, respectively. The second group “B” is only represented by *Z. hubbardi* and characterized by a similar chorion but enlarged micropyles, large spermatheca, robust spermathecal duct, long spermatozoa, and the lack of basal plate and coiled intromittent organ. The third group “C” is only represented by *Z. impolitus*, and characterized by a one-layered chorion with a hexagonal pattern regionally different in sculpture, large micropyles, long spermatozoa, huge spermatheca, robust spermathecal duct, and the lack of basal plate and coiled intromittent organ. The large micropyles found in groups B and C, both of which have enlarged spermatozoa, are likely correlated with their spermatozoal size.

For more reliable intraordinal taxonomical reconstruction of Zoraptera, further morphological data are required in addition to those presented here, as well as a molecular species-level phylogeny. A robust phylogeny of Zoraptera will allow a reliable reconstruction of the evolution of the complex and variable character set related to the male and female genital system.

### 03 The “other” earwig: *Hemimerus* sp. and its cephalic adaptations towards commensalism

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All earwigs (Dermaptera) are very similar in their habitus. They are characterized by their flat and elongate bodies with typical pincers at the abdominal apex. The only distinct exceptions are the commensal Hemimeridae. They live in the fur of giant murid rats, where they feed on skin scales, secretions and fungi. This family differs morphologically so strongly from other earwigs, that they were even considered a separate order. However, recent molecular and morphological studies suggest that the highly specialized Hemimeridae are deeply nested in Dermaptera.

To study adaptive features related to the commensal lifestyle, we compared the head of *Hemimerus* sp. with cephalic structures of *Forficula auricularia* and *Diplatys* sp. *Hemimerus* shows several distinct modifications apparently linked with life in and on fur: the head capsule, which is oval in dorsal view in the remaining earwigs, is triangular and strongly compressed. The antennae are held close to the sides of the head. The compound eyes, which are obviously of minor importance in dense fur, are completely reduced, along with the optic lobes. As an adaptation to the specific diet, which requires no grinding, the mandibles are positioned further apart and lack a mola. Additionally, the maxillary and labial palps are smaller than in free-living earwigs.

Potential apomorphies of the dermapteran head include the 3-partite stipes, the prominent scapo-pedicellar joint and the paired distal sclerites on the praementum.



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### 04 First chromosomal study of Mantophasmatodea: Karyotype of *Karoophasma biedouwense* (Austrophasmatidae)

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We investigated for the first time the chromosomes of *Karoophasma biedouwense*, a species belonging to the recently discovered order Mantophasmatodea. Our study has revealed that males of this species display testes with numerous seminal tubes (follicles) as in other Polyneoptera and short tubular seminal vesicles embedded in a utricular gland. The karyotype consists of  $2n = 12A + X$  monocentric and biarmed, meta/submetacentric chromosomes (fundamental number of arms:  $FN = 26$ ) with blocks of heterochromatin around centromeres. The autosomes are classified into two size groups, one represented by a single, very large pair of autosomes and the other by five smaller pairs which constitute a continuous series gradually decreasing in size. Among "monocentric" orders of Polyneoptera, *K. biedouwense* shares its low chromosome number,  $2n = 13$ , only with some Orthoptera (Acridoidea, Grylloidea, Gryllacridoidea). Male meiosis is of the classical pre-reductional type and the X(0) sex determination system is probably an ancestral state. FISH with an 18S rDNA probe revealed multiple ribosomal clusters which most likely represent an apomorphic condition. The ancestral insect telomeric sequence (TTAGG)<sub>n</sub> in the terminal areas of chromosomes was identified.

### 05 Chromosome numbers & nuclear DNA content comparison in *Cimex* bed bugs

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Almost everyone knows about the existence of the human bed bug *Cimex lectularius* (Heteroptera) which is currently a serious human ectoparasite all over the world. However, the whole family Cimicidae comprises more than 100 other blood sucking species parasiting mainly birds and bats. Of the cimicids occurring in Europe, we managed to acquire also the uncommon *Cimex pipistrelli* from bats and very rare *C. hirundinis* from swallows.

Human bed bug has interesting intraspecific variability of the X sex chromosomes. We recorded the predominance of the basic karyotype ( $2n = 26 + X_1X_2Y$ ) with only two X sex chromosomes in males, but individuals with a huge variability of up to 20 X sex chromosomes were also recorded. The source of such extensive variability is considered to be caused by fragmentation of the X sex chromosome. In contrast, *C. pipistrelli* and *C. hirundinis* both have a simple karyotype ( $2n = 28 + X_1X_2Y$ ) and no intraspecific variability was recorded.

To test the hypothesis that the number of X chromosomes increase simply by fragmentation, we combined classical cytogenetic approach with the flow cytometry (we expected the stable DNA content even in individuals with different number of chromosome fragments). We analyzed karyotypes and the content of nuclear DNA of 300 specimens of *C. lectularius* from more than 60 localities in the Czech Republic. We found that the amount of the nuclear DNA in *C. lectularius* is variable and more chromosomal rearrangements than simple fragmentation have to occur in its karyotype. There is no correlation between chromosome number and volume of nuclear DNA. *Cimex pipistrelli* and *C. hirundinis* both have by 20% less nuclear DNA than *C. lectularius*.

Using the combination of this very unusual fusion of methods brought us closer to explanation of chromosome rearrangements origin in *Cimex lectularius* and also unique comparison of genome size among three closely relative





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cimicid species. This project was supported by the grants no. 277815/2015 of the Grant Agency of Charles University and of Ministry of Education, Youth and Sports of the Czech Republic no. SVV 260208/2015.

### 06 Cuticular structures of nymphal dorsoabdominal scent glands in the Pentatomomorpha

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Nymphal dorsoabdominal scent glands (DAGs hereinafter) are used not only for a determination but also in phylogenetic studies within the Heteroptera. However, only superficially described external DAGs' structures are used by most of the authors. States of the internal components of the glands are rarely known, though they are very important as well and very probably determine the functionality of the gland better than structures composing the external scent efferent system. Using scanning electron microscope and optical microscope, we studied both the internal cuticular structures (reservoir, ductuli of glandular units) and the external structures (ostiole, evaporatorium, peritreme) in nymphs from nine Pentatomomorpha families (Heterogastridae, Coreidae, Alydidae, Rhopalidae, Aradidae, Cydnidae, Plataspidae, Pentatomidae, Scutelleridae). The relationships of these families based on the nymphal DAGs' characters are discussed.

### 07 Features determining functional dorsoabdominal scent glands in Heteroptera adults – use in phylogeny of Pentatomomorpha

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Dorsoabdominal scent glands (= DAGs) are important phylogenetic character as well as way of chemical communication in the order Heteroptera. The originally larval DAGs could be persistent in a different degree also in adults. Proved persistence of functional DAGs in the adult Heteroptera is more frequent phenomenon than it was originally supposed. Characters formerly used as an evident proof of the persistence, e.g., scar of ostiole, open ostiole, reservoir, are not sufficient with regard to recent findings. The problem is that in these cases the functional glandular units of DAGs have not to be developed. For use of functional DAGs in adults as character in phylogenetic studies without any problem, it is necessary to find clearly evident character corroborating this functionality. The existence of ductuli (openings of conducting canals of the glandular units in reservoir) was chosen as such character. The external as well as internal cuticular structures of model Pentatomomorpha species were studied using optical and scanning electron microscopy methods. We tried to find out an occurrence of a possible relation of development of particular structures each to other in functional glands in the adults. The relation of developed ductuli to other structures, open ostiole, developed evaporatorium and others, was chosen as the model example to study.



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### 08 Morphological changes correlated with decreasing size in skeleton and musculature of the male genitalia in the higher Tephritoidea (Diptera: Tephritidae, Otitidae, Ulidiidae, and Platystomatidae)

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Among representatives of the superfamily Tephritoidea, the musculature of the male genitalia has been previously studied only in two species of Tephritidae, one species of Platystomatidae, one species of Pallopteridae, and three species of Ulidiidae. There are different views on the homology of some genital sclerites in the superfamily Tephritoidea; the study of the musculature is helpful in revealing this homology and specifying the functions of genital sclerites. The split of the hypandrium as one structure into three structures (the hypandrium and two lateral sclerites) is traced. The hypandrial origin of the lateral sclerites of the hypandrial complex is proved based on the localization of muscle attachment sites. The subepandrial origin of the inner lobes of the surstyli is revealed. It is shown for the first time that the genitalia of all studied families of Tephritoidea are asymmetrical and may become more asymmetrical with decreasing size. Secondary disappearance of the lateral sclerites can take place in Tephritidae if body length decreased. It is revealed that the structure most stable in size in Tephritoidea is the genital bursa, which at rest contains the coiled phallus. It is believed that in the higher Brachycera the male genitalia are rotated about their axis to 360° compared to their original state found in the primitive Nematocera. We have revealed for the first time differences in rotation of the male genitalia about their axis between representatives of the higher Tephritoidea. The degree of this rotation increases in the sequence of primitive to advanced Tephritoidea: 320° in Otitidae, 330° in Ulidiidae, 330° in Platystomatidae, and 360° in Tephritidae. This additional rotation is associated with the fusion of the pregenital segments (6–8). We have also revealed for the first time the state of connection between sternite 7 and the hypandrium (sternite 9). In species with the genitalia rotated to a greater degree, the pregenital muscles are more strongly reduced. We propose that the additional rotation of the male genitalia in Tephritoidea was associated with increased maneuverability of flight during copulation in the advanced families.

### 09 Evolution of hunting behaviour and morphology in the genus *Leptogenys* (Hymenoptera: Formicidae) from the Oriental region

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*Leptogenys* Roger, 1863 is the largest ponerine genus and contains over 300 species from the world's tropics and subtropics. Almost all species live in forests, hunting small ground animals. Among the Oriental species, different types of predatory behavior are observed. The members of the *L. processionalis* species group are regarded as army ants (sensu lato) and exhibit swarm raiding. They usually cut their prey into pieces that can be carried by one foraging worker. Larger prey pieces are rarely carried cooperatively. Some other species also have army ant characteristics, although their behaviour has not been reported in detail. The other species are solitary hunters or cooperative carriers. To explore the evolution of these hunting styles, we observed hunting behaviour of different *Leptogenys* species in Southeastern Asia. We revised the Oriental species taxonomically and chose focal species as representatives of each species group, examining in detail their mandible shape, which is considered an important character for cutting prey items. We reconstructed the phylogeny of Oriental species using Bayesian inference,



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combining mitochondrial and nuclear DNA datasets (about 2,500 bp, 80 OTUs). Our analysis revealed that all “army ant” species form a monophyletic clade comprised of three species groups (*processionalis*, *myops*, *currens*) except for one Philippine specie belonging to the *diminuta* species group. The mandibles of these army ant species have distinct teeth at the masticatory margin. Conversely, non-army ant species do not have teeth. Additionally, the relative length of the masticatory to the basal margin is significantly greater in army ants than in non-legionary species. We suggest that the development of teeth and the extension of the mandibular masticatory margin perform an adaptive function in cutting prey and may have played a role during the evolution of army ant syndrome in *Leptogenys*. The Philippine species is inferred to be a very derived member of the *diminuta* species group. Moreover, its morphology is similar to that of non-army ant species. We posit that this species evolved army ant-like behaviour relatively recently, perhaps by occupying the vacant niche made available by the absence of the three other army ant species-groups in the Philippines.

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## 10 Speciation and molecular divergence in a group of ant parasitoids

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Eucharitidae (Hymenoptera: Chalcidoidea) is the only family of insects known to specialize as parasitoids of a eusocial insect host. They attack the brood of five subfamilies, Ectatomminae, Formicinae, Myrmicinae, Myrmeciinae and Ponerinae. Species of *Orasema* (Oraseminae) are almost exclusively parasitoids of myrmicine ants, which include some of the most invasive and pestiferous species. *Orasema* are widespread and common in the Americas and widespread but relatively rare in Paleotropical regions. The subfamily is demonstrably monophyletic, but relationships among the four included genera are not so robust. In all of our results, the species of the sole New World genus *Orasema* are monophyletic. Our results differ for the Old World species, which can be either monophyletic or paraphyletic to the NW species. *Pheidole* is the only host known from the Old World, and the predominant host for *Orasema* in the New World. Recent studies suggest a NW origin for *Pheidole*, followed by a recent OW invasion. We compare the results from analyses of a taxon-rich traditional molecular analysis using ribosomal and mitochondrial genes, and a taxon poor but loci-rich data set from a combined Anchored Enrichment and Transcriptome data set. The AET data set (390 loci) provides strong support for a paraphyletic OW clade and a subsequent single and recent NW invasion. The timing, sequence of events and ecological diversification in the NW will be discussed.



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### 11 Crossing the borders of orders: head anatomy of *Coniopteryx pygmaea* (Insecta: Neuroptera: Coniopterygidae) and convergent miniaturization effects in insects

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*Coniopteryx pygmaea* Enderlein, 1906 with a body length of 1.5 mm is one of the smallest known lacewings. Several miniaturization effects were recognized in the course of the investigation of its head anatomy.

In many insect orders miniaturized forms evolved independently from larger ancestors. Structural, physiological and physical constraints lead to convergent modifications in the head anatomy: In the brain a certain number of neurons are required to retain sensory, motor and humoral control. Thus the relative size of the brain is increased (Beutel & Haas 1998). It occupies any available space in the head capsule and loses its dumbbell-shaped form which probably represents the ground plan condition in Ectognatha (Beutel et al. 2005). As the size of the head also limits the size of the compound eyes, number and length of ommatidia and the diameter of the facets are reduced (Fischer et al. 2014). Further, in miniaturized insects diffusion is largely sufficient for the distribution of haemolymph and oxygen which leads to a simplification of the circulatory and tracheal system. In most studied specimens miniaturization does not affect the total number of muscles but it does result in a smaller number of muscle subunits and muscle fibers (Polilov & Beutel 2009).

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### 12 Aenigmatineidae – a new family of microlepidoptera from Kangaroo Island, Australia, and its phylogenetic placement in Lepidoptera

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*Aenigmatinea glatzella* Kristensen & Edwards, 2015, a recently discovered species of microlepidoptera on the Kangaroo Island off southern Australia, is a fascinating moth. Immediately upon its discovery it was clear that *A. glatzella* belonged to one of the earliest lineages of Lepidoptera, but based on its morphology, it could not be placed in an existing family, and therefore a new family – Aenigmatineidae – was erected to accommodate it. We analyzed



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25 genetic loci to try to determine its relationships to other old lineages of lepidopterans and found that it is related to Neopseustidae and Acanthopteroctetidae. In addition to presenting the phylogenetic results, we provide an overview of the interesting morphological features present in *A. glatzella*, which are reshaping our understanding of the evolution of the earliest lepidopteran lineages.

### 13 Molecular phylogenetic analysis helps to reveal homoploid hybrid speciation events: a case study in *Agrodiaetus* blue butterflies (Lepidoptera, Lycaenidae)

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Homoploid hybrid speciation is a process by which a new reproductively-isolated, sexually reproducing species arises through hybridization and combination of parts of the parental genomes, but without an increase in ploidy. Empirical evidence for homoploid hybrid speciation is sufficiently scarce, especially among animals due to different reasons. One of the reasons is that the detection of homoploid hybrids individuals and species poses immense technical challenges and requires a multidisciplinary approach combining genetic, morphological, geographical and ecological data. However, molecular phylogenies *per se* can provide invaluable evidence to distinguish species of possible homoploid hybrid origin. In our study, we use intrageneric blue butterfly (*Polyommatus (Agrodiaetus)*) phylogeny on the basis of mitochondrial (gene COI) and nuclear (ITS2) molecular markers. We demonstrate that two distinct species of the *Agrodiaetus* blue butterflies (*P.(A.) karindus* and *P.(A.) morgani*, which differs in chromosome numbers, nuclear DNA (ITS2) and wing colouration have hybridized in the past. Furthermore, detailed phylogenetic analysis, coupled to cytogenetic (genomic *in situ* hybridization (GISH) and additional molecular data (AFLP) showed that interspecific hybridization between abovementioned species accompanied by the homoploid hybrid speciation and the appearance of new diploid hybrid species – *P. (A.) peilei*.

*Funding:* financial support for this study was provided by the grant from the Russian Science Foundation no. 14-14-00541 to the Zoological Institute of Russian Academy of Sciences. N.Shapoval was supported by the grant 1.50.1617.2013 of the Saint-Petersburg State University, Russia.

### 14 Inner maturity – the cephalothorax of *Stylops ovinae* (Strepsiptera)

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External and internal structures of the cephalothorax of females of *Stylops ovinae* (Stylopidae, Strepsiptera) were examined and documented in detail using scanning electron microscopy (SEM) and 3d reconstructions based on microtome sections. The results were compared with structural features of females of the basal Mengenillidae described in earlier studies. The cephalothorax of Stylopidae (Strepsiptera with endoparasitic females, ca. 95 % of all species) is generally a product of fusion comprising the head, all 3 thoracic segments and the 1st abdominal segment. In contrast to the sack-shaped and unsclerotized posterior part of the body it protrudes from the host's body (the solitary bee *Andrena vaga*) and is relatively rich in structural features. The transverse birth opening marks the border between the head and thorax and covers the brood channel pocket, which reaches deep into the lumen



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of the cephalothorax. The large Nasonov's glands produce and release pheromones for attracting the flying males. They are composed of numerous small lobes and fill out the largest part of the female cephalothorax. The loss of legs, antennae, compound eyes, and most components of the mouthparts, the greatly reduced muscle system, and the posterior shift of the main parts of the central nervous system are closely correlated with the obligatory endoparasitism, and also the retention of larval structures in the strongly simplified adult females.

### 15 The contribution of fossils to the phylogeny of Steninae (Coleoptera, Staphylinidae)

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One of the most striking examples of the evolutionary megaradiation is provided by rove beetle subfamily Steninae with more than 2700 species organized in only two recent genera, the mega-diverse *Stenus* Latreille, 1797 and much less species-rich *Dianous* Leach, 1819 (Lawrence & Newton 1982). With ca. 2500 described species, the genus *Stenus* is among the most diverse genera of organisms as a whole and at the same time fairly conservative in its morphology (Koerner et al. 2013). Steninae are distributed in all biogeographical regions except Antarctica and New Zealand, and occur in diverse habitats (Hansen 1997; Thayer 2005). Like most other rove beetle groups, Steninae show a typical slim habitus, with shortened elytra and a flexible abdomen. But they can be easily distinguished within Staphylinidae by their very peculiar habitus, in particular globular and protruding compound eyes correlated with active predation. The most obvious autapomorphic feature defining *Stenus* is an amazing prey-capture apparatus that is a harpoon-like protruding elongated labium with the paraglossae being modified into sticky pads. While in *Dianous* species, the labium is much shorter and does not form an adhesive prey-capture apparatus (Thayer 2005; Koerner et al. 2013). Despite the superficially obvious composition of subfamily, the relationship between *Stenus* and *Dianous* is not entirely clear and still remains disputable (e.g. Koerner et al. 2013). Also the presumed sister-relationship of Steninae with their closest related group, Euaesthetinae needs further investigation (e.g. Clarke & Grebennikov 2009; McKenna et al. 2014). One of the biggest drawback of all previous phylogenetic studies on these groups was that none of them fully used the potential of fossil record. Although all known fossils of Steninae come from the Cenozoic (Cai et al. 2014), the oldest known fossil Euaesthetinae are from the Cretaceous period (e.g. Clarke & Chatzimanolis 2009).

Here, I present a new odd extinct lineage of Steninae without distinct prey capturing apparatus, but very different either from *Dianous* or Euaesthetinae. These are 15 fossil specimens from one inclusion in the Cretaceous Burmese amber. This new finding is discussed in the context of possible scenario for the early evolution of Steninae prior to their modern radiation, and in terms of their phylogenetic relationships within Staphylinidae.

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### 16 Evolution of habitat shifts in “terrestrial” clades of hydrophilid beetles (Hydrophilidae: Rygmodinae and Sphaeridiinae)

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Subfamilies Rygmodinae and Sphaeridiinae together form approximately one third of the extant diversity within the family Hydrophilidae (Coleoptera: Polyphaga). Members of both these subfamilies inhabit wide spectrum of aquatic and terrestrial environments including specialized habitats such as phytotelmata, carrion or termite nests. So far, habitat shifts within these subfamilies have been only tested with a limited amount of taxa at the family level. Using a broader sampling and Bayesian and maximum likelihood methods, genus-level molecular phylogenetic analysis and divergence dating were performed. Dataset included 96 taxa, representing all major clades (genus groups) in both subfamilies, sequenced for two mitochondrial and two nuclear genes. Single shift from the aquatic to terrestrial environment in the Middle Jurassic was suggested, thus revealing both subfamilies and all tribes as ancestrally inhabiting decaying plant material and leaf litter. Secondary returns to aquatic habitats were suggested for two lineages of the Rygmodinae and several lineages belonging to tribes Coelostomatini and Megasternini. Single shift to flowers was revealed in the subfamily Rygmodinae. Similarly, single independent shifts to inquiline life style in tribes Omicrini and Megasternini were revealed. In contrast, shift to dung + carrion occurred multiple times in the subfamily Rygmodinae and tribe Megasternini, and once in an ancestor of the tribe Sphaeridiini. Results of diversification analysis agree with those performed at family level, with a single increase revealed in the Megasternini and not corresponding to any habitat shift. Morphological characters supposed to be adaptations to aquatic life style (ventral hydrophobic pubescence, presence of trichobothria) were coded for all terminal taxa and tested for their correlation with habitat and for possible correlated evolution, in both cases using phylogenetic comparative methods. Results showed similar trait values in closely related taxa rather than in taxa sharing the same habitat, and little correlation between particular characters.

### 17 Leptodirines (Staphylinoidea: Leiodidae: Cholevinae) possess pore plates on the terminal tarsomeres

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Leptodirini is the most species-rich and most intensively studied tribe of Leiodidae. They comprise around 900 known species in ca. 240 genera and represent one of the most spectacular radiations of beetles in the subterranean environment. The tribe is recognized as monophyletic but the phylogenetic relationships of its seven subtribes remain largely unclear. Moreover, the monophyly of these subgroups was never demonstrated. A recent survey of distal leg elements of leiodids revealed a set of pore plates (PPs) on the cuticular surface of the terminal tarsomere of Leptodirini, probably associated with glands. Here we describe the distribution in the tribe and provide a documentation with SEM micrographs. We identified PPs in at least two members of five of the six studied subtribes of Leptodirini: Anthroherponina (2), Bathysciina (4), Bathysciotina (2), Leptodirina (4) and Pholeuina (2). The structure



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is lacking in the subtribe Spelaeobatina and in all other leioidids examined (representatives of 15 cholevine subtribes and 6 non-cholevine leioidids). Two distinct structural patterns of cuticle perforation were observed. In Leptodirina and *Remyella* (Anthroherponina) the cuticle is perforated by irregular aggregate slits, while the PPs are characterized by aggregate circular perforations in the remaining leptodirines. The PPs are distributed on the lateral and dorsal surfaces of the terminal tarsomere of all legs, mostly associated to the base of the tarsal setae. Betz (2003) reported similar structural modifications on the tarsi of *Stenus* (Staphylinidae). He demonstrated their association to a unicellular gland of uncertain function, but likely contributing to the tarsal adhesive performance. The PPs of Leptodirini are a new character system for the group and likely of phylogenetic and taxonomic value. Moreover, they are interesting in a functional context. Future investigations using histology and TEM will help to verify PP-associated glands and reveal their ultrastructure.

**Reference:** Betz O. 2003. Structure of the tarsi in some *Stenus* species (Coleoptera, Staphylinidae): external morphology, ultrastructure, and tarsal secretion. *Journal of Morphology* **255**: 24–43.

### 18 The use of sex pheromones as a tool for integrative taxonomy and phylogeny – An example from the cryptic click beetle complex *Idolus* (Coleoptera: Elateridae)

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Here we report on the discovery of new species within the click beetle genus *Idolus* in Central Europe by analysis of sex pheromone composition. Analyses of mitochondrial markers suggest the presence of four different species in Central Europe. In contrast, chemical analysis revealed five different species based on the specific composition of their sex pheromones and that these five species can be clustered in two groups, one characterised by geranyl esters and the other by neryl esters. Morphological studies using a large number of specimens collected in pheromone traps likewise revealed a separation in five species. This was supported by subsequent analyses of nuclear markers, which also revealed monophyly of the neryl esters group.

This highlights the importance of sex pheromones. Only by studying the pheromone composition and using the identified compounds in field traps, we were able to collect large numbers of specimens of each type. This enabled their separation based on morphological differences. Furthermore, because sex pheromones are required for successful mating, they enable predictions about sexual isolation and the species status of a taxon. Therefore, we advocate for an increase in pheromone investigations especially for integrative taxonomy to verify the taxonomic status of cryptic species and to study the phylogenetic position and evolution of taxa.

### 19 Phylogenetic relationships and evolution of host plant use in the Palearctic Apioninae (Curculionoidea, Coleoptera)

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Apioninae is a group of relatively small weevils (1–5 mm) with long non-geniculate antenna, elongated trochanter and a typical pear-like body shape. They are distributed worldwide with about 1900 described species. Taxonomic





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and systematic examination of Apioninae is constantly challenged by their relatively uniform appearance and almost all Palearctic apionines were traditionally assigned to one genus, *Apion* HERBST. However, apionine weevils are generally monophagous or oligophagous with their larvae developing in flowers, seeds, stems or roots. Most Palearctic taxa live on Asteraceae and Fabaceae, but many are associated with other plant families, like Lamiaceae, Malvaceae and Polygonaceae and some others. According to the host associations in addition to morphological characters, subgenera of *Apion* HERBST have been defined and many of these have now been erected to genera. In this context, we want to target the following questions: 1) Is host plant use in Apioninae generally conserved? 2) Are specific host plants associated with enlarged species richness? 3) Does different larval host tissue use in species feeding on similar hosts, reflect mechanisms of competition prevention? We compiled a comprehensive molecular data set, based on five ribosomal RNA and protein coding genes, representing all Palearctic apionine tribes. Based on this data, tree reconstruction was conducted and divergence times of the tribes were estimated. Our phylogenetic analyses proposes all tribes being monophyletic, except of Oxystomatini and Aplemonini are the sister group to all remaining apionine tribes. Divergence time estimations indicate an “ancient-rapid-radiation” in Palearctic Apioninae, followed by their occurrence in the Upper Cretaceous. Host plant use is generally conserved, with Fabaceae being colonised at least two times. We could also show several genera in Exapiini and Oxystomatini being polyphyletic, making a future taxonomic revision of these groups necessary.

### 20 Phylogeny and phylogeography of *Liophloeodes* (Coleoptera: Curculionidae) populations

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*Liophloeodes* Weise, 1894 is a subgenus of weevils belonging to genus *Liophloeus*. It includes 5 very similar (but with high intraspecific variation) bisexual species with only one diagnostic trait: shape of aedeagus. Moreover, also this trait exhibits high variation within particular species. *Liophloeodes* weevils prefer wet and cold biotopes, thus most populations inhabit mountain and sub-mountain areas (Carpathians, Sudetes, mountains of Balkans, Alps). According to their ranges and similarity in appearance and ecological preferences, it is possible that they are young species, whose evolution was connected with mountainous (or sub-mountainous) refugia. In my research, I studied the phylogeny of *Liophloeodes* populations from Carpathians, Sudetes, Alps and Balkans. I used three DNA markers: *COI* (mtDNA marker), *EF-1alpha* (nDNA marker) and *wsp* (*Wolbachia* marker) and constructed phylogenetic trees. I also made an attempt to resolve phylogeographical routes of these species and find out from which refugia they came out during climate changes.

### 21 Phylogenetic analyses reveal complex evolutionary patterns in the flower chafer genus *Eudicella* (Scarabaeidae: Cetoniinae)

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*Eudicella* is a diverse genus of flower chafers distributed widely in sub-Saharan Africa. The genus has been split by different authors into either two or three subgenera (*Eudicella* White, *Cyprolais* Thomson and *Ceratorhina* Westwood, *sensu* Allard). Despite the revision of many intraspecific taxa in *Eudicella s.str.*, the genus is lacking an overall



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taxonomic revision. Furthermore, no study has addressed the evolutionary history of these beetles. Here, we use a combination of molecular and morphological analyses to clarify the subgeneric composition of the genus as well as getting insights into its evolution.

Two mitochondrial (COI, 16S) and one nuclear marker (28S) were sequenced to infer the phylogenetic relationships among taxa; divergence times were estimated and the ancestral biogeography of the genus was inferred by statistical-Dispersal Vicariance Analysis (S-DIVA). Morphology and molecular data suggest that *Eudicella* is split into four well-defined taxonomic groups, which we suggest to treat as subgenera. The relationships among the subgenera, however, are not well resolved. S-DIVA suggested East Africa as ancestral distribution for all subgenera. Moreover, divergence time estimates suggest that *Eudicella* radiated within a timeframe of extreme climate variability during the Pleistocene in East Africa.

### 22 Countless forms of cockroach wings – the beauty of reduction

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Wings and active flight are recognized as one of the most iconic evolutionary innovations in insects. Nevertheless, a great number of representatives of diverse taxa exhibit a certain degree of wing reduction. Cockroaches (Blattodea), excluding termites, are the insect order with one of the highest occurrences of forms with reduced wings. Roff (1990) states, that wing reduction is present in more than half of all described cockroach species. Although Rehn (1932), inspired by Chopard (1924), discussed the variability of wing reduction among the Blattidae, there is no such study through the whole order reflecting current knowledge on cockroach systematics.

We have examined cockroach material in several European museum collections and from material in NHM London solely, we have gained data on wing states for more than 1200 species (approximately 27 % of all described species) representing 281 genera (55 % of all described genera). Cockroaches have achieved practically all possible wing conditions and combinations ranging from fully developed to completely absent wings in both sexes. However, it is always females which precede males in wing reduction leading to the frequently occurring sexual wing dimorphism (e.g. Perisphaeriinae are almost exclusively dimorphic in their wing condition). Generally speaking, all examined members of the same genera share their wing state. In few exceptions where different wing states combine in one genera, taxonomic re-examination of genera would be desired.

Data from other museum collections will be analyzed too and description papers should be examined in the future to obtain complete dataset.

The project was supported by GAUK 1700-243-253471 and Mobility Fund of Charles University.

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### 23 The steps towards an inconspicuous vein fusion documented in *Stenosmylinae* forewings (Neuroptera: Osmyliidae)

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Based on respective numbers of branches in fore- and hind wing, and on the morphology of fossil species, it has been assumed that a fusion of the posterior branch of the posterior Media (MP2) with the anterior Cubitus (CuA) was acquired convergently in fore- and hind wings in several families of Neuroptera (Insecta), including the Osmyliidae (Shi et al. 2012). The corresponding conjectures of topographic homology (THCs) had to assume inconspicuous vein fusion, but without intermediate condition being reported. Based on inter-specific, intra-specific and intra-individual variations observed in forewings of a selection of *Stenosmylinae* species (Osmyliidae), we herein document a complete transformation series ranging from the condition 'MP2 and CuA approximating' to 'MP2 and CuA fully fused, without distinct origin of MP2', with intermediate conditions in which the origin of MP2 has a cross-vein-like appearance. The relevance of series of conspecific specimens to investigate problematic THCs is emphasized.

**Reference:** Shi C., Béthoux O., Shih C., Ren D. 2012. *Guyiling jianboni* gen. et sp.n., an antlion-like lacewing, illuminating homologies and transformations in Neuroptera wing venation. *Systematic Entomology* **37**(3): 617–631.

### 24 Testing monophyly of megadiverse *Spilomelinae* (Lepidoptera: Pyraloidea)

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With about 4,000 species, *Spilomelinae* are the most speciose subgroup of snout moths (Pyraloidea) and contain many species of economic importance, including invasive pests. Yet, the monophyly of the group as such is still in doubt as *Spilomelinae* are largely defined by ambiguous and absence characters and have repeatedly been claimed to be polyphyletic. Moreover, *Pyraustinae* are regarded as either close or distant relatives, and some genera like *Udea* assigned to either of the subfamilies, depending on author opinions. In order to test these different hypotheses, we compiled molecular data of six genes as well as morphological data of 76 characters derived from adults of 78 *Spilomelinae* and 18 *Pyraustinae*, and analyzed them phylogenetically. Our new, yet to be published results confirm a sister-group relationship of *Spilomelinae* and *Pyraustinae*. Furthermore, *Spilomelinae* only form a natural group with the inclusion of the ant-associated *Niphopyralis*, formerly placed in *Wurthiinae*, and the exclusion of *Sufetula*, now placed in the recently revised *Lathrotelinae*. We identify a number of genus groups within *Spilomelinae* and present morphological and ecological features that might serve as diagnostic characters. This is the first phylogenetic analysis comprising the so far recognized major subgroups of *Spilomelinae*, providing arguments for a tribal subdivision of the group.



## Abstracts — Poster Presentations

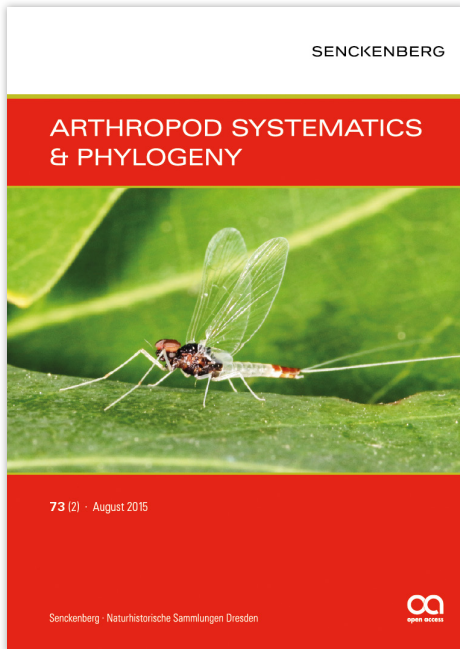
### 25 **Transcriptomic and phenotypic data related to the geographic distribution of two spurge hawk moth lineages of the *Hyles euphorbiae* complex (Lepidoptera: Sphingidae)**

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Spurge hawk moths of the *Hyles euphorbiae* complex (HEC) comprise two major genetic lineages across a large distribution range: The central European *H. euphorbiae* and the northern African *H. tithymali*. Both have their specific distribution, but readily interbreed forming a hybrid zone in southern Europe where the lineages meet. Thus, the HEC is a well suited model to test for functional differences in ecology and physiology that lead to lineage separation in spite of obvious inter-lineage fertility. Differences in cold adaptation and content of tetradecanoylphorbolacetat (TPA) in spurge food plants (Euphorbiaceae) have been suggested as such separating factors. Recently, we sequenced *H. euphorbiae* transcriptomic data (Illumina; 1KITE project) of cold treated overwintering (diapause) pupae and L5 instar larvae having fed on TPA, to identify genomic biomarkers relating to each treatment. Moreover, we determined *H. euphorbiae* and *H. tithymali* phenotypes differing in cold-hardiness and TPA detoxification potential under laboratory conditions, to define ecological niches. These data will be further used to study differential gene expression with respect to functional lineage sorting in the HEC.



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is the successor of Entomologische Abhandlungen, formerly published by the Museum of Zoology Dresden, Germany.

There are three issues per year. Individual papers may be published electronically prior to the print version.

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**Impact Factor (2014): 1,37**

Journal Citation Reports©, Thomson Reuters

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