

September 20–22, 2019

Senckenberg
Naturhistorische Sammlungen Dresden

Königsbrücker Landstraße 159
01109 Dresden

9th Dresden Meeting on **Insect Phylogeny**

This meeting is supported by
the German Research Foundation



Organisation staff

Main organiser

Klaus-Dieter Klass

Logistics

Sigrid Beutner

Roland Schmidt

Birgit Walker

Logistics assistance

Antonia Mühle

Marieke Michaela Scheide

Technical support/IT

Andreas Weck-Heimann

Michael Weingardt

Conference Logo and Layout

Markward Herbert Fischer

Financial support



Deutsche Forschungsgemeinschaft
German Research Foundation

GZ KL 1162/12-1





Oral Presentations · Friday, September 20

Chair of *morning* session: **AKITO KAWAHARA** · Chair of *afternoon* session: **RUDOLF MEIER**

07:30	Reception Desk open
09:10–09:25	Opening KLAUS-DIETER KLASS (Senckenberg Natural History Collections Dresden, Museum of Zoology, Königsbrücker Landstrasse 159, 01109 Dresden, Germany)
09:25–10:15	The early evolution of insect genitalia KLAUS-DIETER KLASS (Senckenberg Natural History Collections Dresden, Museum of Zoology, Königsbrücker Landstrasse 159, 01109 Dresden, Germany; klaus.klass@senckenberg.de) — NATALIA A. MATUSHKINA (Department of Ecology and Zoology, Institute of Biology and Medicine, Taras Shevchenko National University of Kyiv, Ukraine; odonataly@gmail.com)
10:15–10:45	Skeleto-muscular evolution of male insect genitalia, with emphasis on the Endopterygota BRENDON E. BOUDINOT (Department of Entomology & Nematology, University of California, Davis, One Shields Ave, Davis, CA 95618 USA; boudinotb@gmail.com)
10:45–11:10	Coffee Break
11:10–11:40	Museomics: opening the floodgates to sequencing genomes of all species NIKLAS WAHLBERG (Department of Biology, Lund University, Sweden)
11:40–12:10	From Hennig to 1KITE – what have we learned? ROLF G. BEUTEL (Institut für Zoologie und Evolutionsforschung, Friedrich-Schiller-Universität Jena, 07743 Jena, Germany)
12:10–12:40	Reviewing and reanalyzing the Palaeoptera problem KAREN MEUSEMANN (Evolutionary Biology & Ecology, Institute for Biology, University of Freiburg, Germany; Center of Molecular Biodiversity, Zoologisches Forschungsmuseum Koenig, Bonn) — SABRINA SIMON (Biosystematics, Wageningen University & Research, The Netherlands)
12:40–14:00	Lunch Break
14:00–14:30	The phylogenetics and divergence times of Odonata: dragonflies and damselflies JESSICA WARE (Rutgers University, Department of Biological Sciences, Newark, NJ, USA) — MANPREET KOHLI (Rutgers University, NJ, USA) — CAROLA GREVE (LÖEWE Centre for Translational Biodiversity Genomics, Germany) — OLIVIER BETHOUX (Muséum National d'Histoire Naturelle, Paris, France) — RYUICHIRO MACHIDA (University of Tsukuba, Japan) — OLIVER NIEHUIS (Albert-Ludwigs-Universität Freiburg, Germany) — JES RUST , Steinmann-Institut (Universität Bonn, Germany) — TORSTEN WAPPLER (Hessisches Landesmuseum Darmstadt, Germany) — HARALD LETSCH (University of Vienna, Austria)
14:30–14:45	Odonata phylogeny: A work in progress to combing fossil and extant taxa SETH M. BYBEE (Department of Biology, Brigham Young University, Provo, UT, USA) — ROBERT J. ERICKSON (Department of Biology, Brigham Young University, Provo, UT, USA)
14:45–15:15	Phylogeny of principal lineages of Polyneoptera BENY WIPFLER (Forschungsmuseum Alexander Koenig, Bonn, Germany) — SABRINA SIMON (Wageningen University, Wageningen, Netherlands)



Oral Presentations · Friday, September 20

Chair of *morning* session: **AKITO KAWAHARA** · Chair of *afternoon* session: **RUDOLF MEIER**

15:15–15:40

Coffee Break

15:40–16:10

The phylogeny and biogeography of stoneflies (Plecoptera, Insecta): evidence for a Pangaeen origin and an Early Mesozoic radiation

HARALD LETSCH (Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Vienna, Austria) — **SABRINA SIMON** (Wageningen University, Wageningen, Netherlands) — **PAUL FRANDSEN** (Brigham Young University, Provo, USA) — **XIN ZHOU** (China Agricultural University, Beijing, China) — **BENJAMIN WIPFLER** (Forschungsmuseum Alexander Koenig, Bonn, Germany)

16:10–16:40

A tree of twigs and leaves: Revealing the role of biogeography in stick insect evolution (Phasmatodea)

SARAH BANK (Dept. Animal Evolution and Biodiversity, Georg-August-Universität Göttingen, Göttingen, Germany) — **SVEN BRADLER** (Dept. Animal Evolution and Biodiversity, Georg-August-Universität Göttingen, Göttingen, Germany)



Oral Presentations · Saturday, September 21

Chair of *morning* session: **SABRINA SIMON** · Chair of *afternoon* session: **ANDREAS ZWICK**

09:00–09:35	Phylogeny of Mantophasmatodea REINHARD PREDEL (University of Cologne, Institute for Zoology) — LAPO RAGIONIERI (University of Cologne, Institute for Zoology) — ÁLVARO ZÚÑIGA-REINOSO (University of Cologne, Institute for Zoology) — STEFFEN ROTH (University Museum of Bergen, The Natural History Collections)
09:35–10:05	Phylogenetic synecdoche demonstrates optimality of subsampling and improves recovery of the Blaberodea phylogeny DOMINIC A. EVANGELISTA (Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, UA, 57 rue Cuvier, CP50, 75005 Paris, France; 2. Department of Ecology and Evolutionary Biology, The University of Tennessee, Dabney Hall, 1416 Circle Dr., Knoxville, TN 37996, USA) — SABRINA SIMON (Biosystematics Group, Wageningen University and Research, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands) — MEGAN M. WILSON (Federated Department of Biological Sciences, Rutgers, The State University of New Jersey and NJIT, 195 University Ave, Newark, NJ 07102, USA) — AKITO Y. KAWAHARA (Florida Museum of Natural History, University of Florida, Gainesville, FL 32611, USA) — MANPREET K. KOHLI (Federated Department of Biological Sciences, Rutgers, The State University of New Jersey and NJIT, 195 University Ave, Newark, NJ 07102, USA) — JESSICA L. WARE (Federated Department of Biological Sciences, Rutgers, The State University of New Jersey and NJIT, 195 University Ave, Newark, NJ 07102, USA) — BENJAMIN WIPFLER (Center for Taxonomy and Evolutionary Research, Zoological Research Museum Alexander Koenig (ZFMK), Adenauerallee 160, 53113 Bonn, Germany) — OLIVIER BÉTHOUX (CR2P (Centre de Recherche en Paléontologie – Paris), MNHN – CNRS – Sorbonne Université, UPMC Univ Paris 06, MNHN, CNRS, Paris, France; Muséum national d'Histoire naturelle, 57 rue Cuvier, CP38, 75005 Paris, France) — PHILIPPE GRANDCOLAS (Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, UA, 57 rue Cuvier, CP50, 75005 Paris, France) — FRÉDÉRIC LEGENDRE (Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, UA, 57 rue Cuvier, CP50, 75005 Paris, France)
10:05–10:20	Updating our knowledge about the diversity of Neotropical cockroaches: a molecular phylogenetic approach ANDRÉZ VÉLEZ-BRAVO (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; avelez82@gmail.com) — JUAN M. DAZA-ROJAS (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; jumadaza@gmail.com)
10:20–10:45	Coffee Break
10:45–11:15	The last two decades of termite phylogenetics: where do we go from here? JESSICA L. WARE (Rutgers University Newark, 195 University Avenue, Newark, NJ, 07102, USA) — MEGAN M. WILSON (Rutgers University Newark, 195 University Avenue, Newark, NJ, 07102, USA)
11:15–11:30	Studies on the phylogeny of the genus <i>Psammodermes</i> (Isoptera: Rhinotermitidae) FELICITAS GUNTER (Research Unit Biodiversity, Evolution and Ecology, University of Hamburg, Germany) — BARBARA RUDOLPH (Research Unit Biodiversity, Evolution and Ecology, University of Hamburg, Germany) — NORBERT JÜRGENS (Research Unit Biodiversity, Evolution and Ecology, University of Hamburg, Germany)
11:30–12:00	Recent advances in paraneopteran phylogenomics: exploring sources of instability and conflict in a highly diverse insect group RACHEL K. SKINNER (University of Illinois at Urbana-Champaign, Department of Entomology, Urbana, Illinois, United States of America) — CHRISTOPHER H. DIETRICH (Illinois Natural History Survey, Urbana, Illinois, United States of America) — KAREN MEUSEMANN (University of Freiburg, Department of Ecology and Evolutionary Biology, Freiburg, Baden-Württemberg, Germany) — ERIC GORDON (University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, Connecticut, United States of America) — KEVIN P. JOHNSON (Illinois Natural History Survey, Urbana, Illinois, United States of America)



Oral Presentations · Saturday, September 21

Chair of *morning* session: **SABRINA SIMON** · Chair of *afternoon* session: **ANDREAS ZWICK**

12:00–12:10	We make a photo! (Please assemble in the backyard just outside the lecture hall)
12:10–13:30	Lunch Break
13:30–14:00	Advancing the resolution of the fly tree of life MICHELLE D. TRAUTWEIN (California Academy of Sciences, San Francisco, CA, USA; michelletrautwein@gmail.com) — BRIAN M. WIEGMANN (North Carolina State University, Department of Entomology, Raleigh, NC, 27695, USA; bwiegman@ncsu.edu)
14:00–14:30	Toward well-supported and species-rich trees: Utilizing legacy data, reactivating legacy DNA, and data layering RUDOLF MEIER (Department of Biological Sciences, National University of Singapore, Singapore)
14:30–14:45	Origin of the male terminalia in Eremoneura (Diptera) TADEUSZ ZATWARNICKI (Institute of Biology, Opole University, ul. Oleska 22, 45-052 Opole, Poland)
14:45–16:00	Coffee Break & Poster Session
16:00–16:30	Crucial points in acalyprate fly phylogeny with an emphasis on Sciomyzoidea and Sphaeroceroidea KEITH M. BAYLESS (Australian National Insect Collection, CSIRO National Research Collections Australia (NRCA), Acton, ACT, Canberra, Australia) — DAVID K. YEATES (Australian National Insect Collection, CSIRO National Research Collections Australia (NRCA), Acton, ACT, Canberra, Australia)
16:30–17:00	The phylogeny of Trichoptera PAUL B. FRANSEN (Brigham Young University, Provo, USA) — 1KITE TRICHOPTERA Subgroup
20:00–...	Social evening (in the lecture hall) Please pay 15 € at the reception desk (best when you arrive at the meeting on Friday morning)



Oral Presentations · Sunday, September 22

Chair of *morning* session: **NIKLAS WAHLBERG** · Chair of *afternoon* session: **ROLF BEUTEL**

09:00–09:30	Phylogenomics of Lepidoptera – a perspective from Down Under ANDREAS ZWICK (ANIC, CSIRO, Canberra, Australia) — DIANA HARTLEY (ANIC, CSIRO, Canberra, Australia) — MARIANNE HORAK (ANIC, CSIRO, Canberra, Australia) — LUISA TEASDALE (ANIC, CSIRO, Canberra, Australia)
09:30–09:55	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths AKITO Y. KAWAHARA (Florida Museum of Natural History) — 1KITE LEPIDOPTERA Group
09:55–10:10	Using museomics to investigate the evolutionary relationships of Tineoidea VICTORIA TWORT (Luomus, Finnish Museum of Natural History, Zoology Unit, University of Helsinki) — CHRIS WHEAT (Department of Zoology, Stockholm University) — NIKLAS WAHLBERG (Department of Biology, Lund University) — LAURI KAILA (Luomus, Finnish Museum of Natural History, Zoology Unit, University of Helsinki)
10:10–10:25	Whole genome sequencing for phylogenetics of old genomic DNA extracts: Erebiidae moths as an example H.R. GHANAVI (Department of Biology, Lund University, Lund, Sweden; hamid.ghanavi@biol.lu.se) — V. TWORT (Department of Biology, Lund University, Lund, Sweden) — T. HARTMAN (Department of Biology, Lund University, Lund, Sweden) — N. WAHLBERG (Department of Biology, Lund University, Lund, Sweden)
10:25–10:50	Coffee Break
10:50–11:05	A multispecies coalescent approach in higher-level systematics: Morphology and DNA inform the species-level phylogeny of “basal” tribes in the butterfly subfamily Satyriinae (Nymphalidae: Haeterini & Brassolini) PÁVEL MATOS (Institute of Entomology, Biology Centre CAS, České Budějovice, Czech Republic) — NIKLAS WAHLBERG (Department of Biology, Lund University, Sweden) — CARLA PENZ (Department of Biological Sciences, University of New Orleans, USA)
11:05–11:45	Phylogeny and evolution of Hymenoptera, with focus on the parasitoid wasps RALPH S. PETERS (Zoologisches Forschungsmuseum Alexander Koenig, Arthropoda Department, Adenauerallee 160, 53113 Bonn, Germany)
11:45–12:15	The phylogeny of cuckoo wasps (Hymenoptera: Chrysididae) inferred from transcriptomes, DNA target enrichment data, and Sanger DNA sequences OLIVER NIEHUIS (Department of Evolutionary Biology and Ecology, Albert Ludwig University, Hauptstraße 1, 79104 Freiburg, Germany)
12:15–13:35	Lunch Break


Oral Presentations · Sunday, September 22

 Chair of *morning* session: **NIKLAS WAHLBERG** · Chair of *afternoon* session: **ROLF BEUTEL**

13:35–14:05	<p>Apoidea reloaded: phylogenomic relationships of apoid wasps and bees, its implications, and future perspectives</p> <p>MANUELA SANN (University of Freiburg, Institute of Biology I (Zoology), Evolutionary Biology and Animal Ecology, Hauptstr. 1, 79104 Freiburg, Germany) — OLIVER NIEHUIS (University of Freiburg, Institute of Biology I (Zoology), Evolutionary Biology and Animal Ecology, Hauptstr. 1, 79104 Freiburg, Germany) — RALPH S. PETERS (Center of Taxonomy and Evolutionary Research, Arthropoda Department, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — CHRISTOPH MAYER (Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — ALEXEY KOZLOV (HITS gGmbH, Heidelberg Institute for Theoretical Studies, Schloss-Wolfsbrunnengweg 35, 69118 Heidelberg, Germany) — LARS PODSIADLOWSKI (Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — SARAH BANK (Georg-August-Universität Göttingen, Animal Evolution and Biodiversity, Untere Karspüle 2, 37073 Göttingen, Germany) — KAREN MEUSEMANN (University of Freiburg, Institute of Biology I (Zoology), Evolutionary Biology and Animal Ecology, Hauptstr. 1, 79104 Freiburg, Germany) — BERNHARD MISOF (Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — CHRISTOPH BLEIDORN (Georg-August-Universität Göttingen, Animal Evolution and Biodiversity, Untere Karspüle 2, 37073 Göttingen, Germany) — MICHAEL OHL (Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Invalidenstraße 43, 10115 Berlin, Germany)</p>
14:05–14:20	<p>The evolution of head morphology in ants: analysis of an understudied character complex</p> <p>ADRIAN RICHTER (Entomology group, Institut für Zoologie und Evolutionsforschung, Friedrich-Schiller-University Jena, Germany) — ROBERTO A KELLER (MUHNAC/cE3c eCentre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências da Universidade de Lisboa, Portugal; Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Japan) — EVAN ECONOMO (Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Japan) — FRANCISCO HITA GARCIA (Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Okinawa, Japan) — JOHAN BILLEN (Laboratory of Socioecology and Social Evolution, Zoological Institute, University of Leuven, Belgium) — ROLF BEUTEL (Entomology group, Institut für Zoologie und Evolutionsforschung, Friedrich-Schiller-University Jena, Germany)</p>
14:20–14:35	<p>The evolution of floral host preference in longhorn bees of the genus <i>Eucera</i> (Hymenoptera, Apidae, Eucerini): is association with pollen from bee-flowers advantageous?</p> <p>ACHIK DORCHIN (The Steinhardt Museum of Natural History, Tel Aviv University) — DAFNA LANGGUT (Institute of Archaeology and The Steinhardt Museum of Natural History, Tel Aviv University) — FRANK NEUMANN (Evolutionary Studies Institute, University of the Witwatersrand) — NICOLAS VEREECKEN (Université libre de Bruxelles (ULB))</p>
14:35–14:50	<p>Diverse palaeofauna of Neuropterida from the mid-Cretaceous of Myanmar and its phylogenetic significance</p> <p>XINGYUE LIU (Department of Entomology, China Agricultural University, Beijing 100193, China)</p>
14:50–15:05	<p>Testing the placement of beetle fossils via topology-constrained phylogenetic analyses</p> <p>MARTIN FIKÁČEK (National Museum & Charles University, Prague, Czech Republic) — ROLF G. BEUTEL (Friedrich-Schiller-University Jena, Germany) — CHENYANG CAI (Nanjing Institute of Geology and Palaeontology, China & University of Bristol, UK) — JOHN F. LAWRENCE (Australian National Insect Collection, Canberra, Australia) — ALFRED F. NEWTON (Field Museum of Natural History, Chicago, USA) — ALEXEY SOLODOVNIKOV (Zoological Museum, Copenhagen, Denmark) — ADAM ŚLIPIŃSKI (Australian National Insect Collection, Canberra, Australia) — MARGARET K. THAYER (Field Museum of Natural History, Chicago, USA) — SHŪHEI YAMAMOTO (Field Museum of Natural History, Chicago, USA)</p>



Oral Presentations · Sunday, September 22

Chair of *morning* session: **NIKLAS WAHLBERG** · Chair of *afternoon* session: **ROLF BEUTEL**

15:05–15:30	Coffee Break
15:30–16:00	The phylogeny and evolution of beetles DUANE MCKENNA (University of Memphis, Department of Biological Sciences; University of Memphis, Center for Biodiversity Research) — SEUNGGWAN SHIN (University of Memphis, Department of Biological Sciences; University of Memphis, Center for Biodiversity Research) — 1KITE BEETLE CONSORTIUM
16:00–16:30	Coleoptera: Evolution of soft-bodied and neotenic forms in Elateroidea LADISLAV BOCAK (Palacky University, Faculty of Science, Olomouc, Czech Republic) — DOMINIK KUSY (Palacky University, Faculty of Science, Olomouc, Czech Republic) — MICHAL MOTYKA (Palacky University, Faculty of Science, Olomouc, Czech Republic) — MATEJ BOCEK (Palacky University, Faculty of Science, Olomouc, Czech Republic)
16:30–16:45	The smallest beetles and their evolutionary transformations (Ptiliidae, Staphylinoidea) MARGARITA I. YAVORSKAYA (Department Biologie II, LMU München, Biozentrum, Großhaderner Str. 2, 82152 Planegg-Martinsried; yavorskaya@biologie.uni-muenchen.de) — ALEXEY POLILOV — IGNACIO RIBERA — VASILY V. GREBENNIKOV — ROLF G. BEUTEL
16:45–16:55	Closure KLAUS-DIETER KLASS (Senckenberg Natural History Collections Dresden, Museum of Zoology, Königsbrücker Landstrasse 159, 01109 Dresden, Germany)



Poster Presentations

Position	Presentation
01	<p>Past climatic changes and their effects on the phylogenetic pattern of the Gondwanan relict <i>Maindronia</i> (Insecta: Zygentoma) in the Chilean Atacama Desert</p> <p>ÁLVARO ZÚÑIGA-REINOSO (University of Cologne, Institute for Zoology; azunigar@uni-koeln.de) — REINHARD PREDEL (University of Cologne, Institute for Zoology; rprede@uni-koeln.de)</p>
02	<p>Were immatures of Late Paleozoic Palaeodictyoptera strictly terrestrial?</p> <p>JAKUB PROKOP (Department of Zoology, Charles University, Praha, Czech Republic) — EWA KRZEMIŃSKA (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland) — WIESŁAW KRZEMIŃSKI (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland) — KATEŘINA ROSOVÁ (Department of Zoology, Charles University, Praha, Czech Republic) — MARTINA PECHAROVÁ (Department of Zoology, Charles University, Praha, Czech Republic) — ANDRÉ NEL (Muséum national d'Histoire naturelle, Sorbonne Universités, Paris, France) — MICHAEL S. ENGEL (Division of Entomology, Natural History Museum, and Department of Ecology & Evolutionary Biology, University of Kansas, Lawrence, Kansas, USA & Division of Invertebrate Zoology, American Museum of Natural History, New York, USA)</p>
03	<p>Cryptic diversity in cockroaches: Phylogeny of the genus <i>Xestoblatta</i> (Blattodea: Ectobiidae) and the recognition of two new genera in the Neotropical region</p> <p>ANDRÉZ VÉLEZ-BRAVO (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; avelez82@gmail.com) — JUAN M. DAZA-ROJAS (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; jumadaza@gmail.com)</p>
04	<p>Recategorization of cockroach mating behaviour</p> <p>ZUZANA KOTYKOVÁ VARADÍNOVÁ (Department of Zoology, Charles University; Department of Zoology, National Museum) — MICHAEL KOTYK (Department of Zoology, Charles University) — TOMÁŠ DVOŘÁK (Department of Zoology, Charles University)</p>
05	<p>Karyotype evolution of Oxyhaloinae cockroaches</p> <p>MAREK JANKÁSEK (Department of Zoology, Charles University) — ZUZANA KOTYKOVÁ VARADÍNOVÁ (Department of Zoology, Charles University; Department of Zoology, National Museum) — FRANTIŠEK ŠTÁHLAVSKÝ (Department of Zoology, Charles University)</p>
06	<p>Relationships within <i>Poecilimon ornatus</i> species group (Orthoptera)</p> <p>MACIEJ KOCIŃSKI (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland; e-mail: kocinski@isez.pan.krakow.pl) — DRAGAN CHOBANOV (Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 1 Tsar Osvoboditel Boul., 1000 Sofia, Bulgaria) — BEATA GRZYWACZ (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland)</p>
07	<p>Notes on the molecular relationships within the genus <i>Aerotegmina</i> (Orthoptera: Tettigoniidae: Hexacentrinae)</p> <p>BEATA GRZYWACZ (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland) — MACIEJ KOCIŃSKI (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland) — KLAUS-GERHARD HELLER (Grillenstieg 18, 39120 Magdeburg, Germany) — CLAUDIA HEMP (University of Bayreuth, Dept. Plant Systematics, 95440 Bayreuth, Germany)</p>
08	<p>Phylogeny and species delimitation within the <i>Platycleis albopunctata</i> group (Orthoptera: Tettigoniidae) – a preliminary study</p> <p>SZYMON CZYŻEWSKI (Department of Entomology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland)</p>



Poster Presentations

Position	Presentation
09	<p>Highly divergent DNA barcodes in the butterfly <i>Colias palaeno</i> (Lepidoptera: Pieridae): evidence of cryptic species, interspecific hybridization or <i>Wolbachia</i> infection?</p> <p>NAZAR SHAPOVAL (Zoological Institute of Russian Academy of Sciences, Russia) — GALINA KUFTINA (Altai State University, Russia) — ROMAN YAKOVLEV (Altai State University, Russia) — ANATOLY KRUPITSKY (Moscow State University, Russia; Severtsov Institute of Ecology and Evolution, Russia)</p>
10	<p>Preliminary results of research on a morphologically uniform genus <i>Apisa</i> (Lepidoptera: Erebiidae: Arctiinae)</p> <p>ANNA PRZYSTALKOWSKA (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland; przystalkowska@isez.pan.krakow.pl) — ŁUKASZ PRZYBYŁOWICZ (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland) — SEBASTIAN TAR CZ (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland)</p>
11	<p>Intra- and interspecific divergences within the genus <i>Trypocoprís</i> Motschulsky, 1858 evaluated through shape variation of morphological traits</p> <p>ROGGERO ANGELA (University of Torino, Dpt. of Life Sciences and Systems Biology, Torino, Italy) — COLLA FABRIZIO (Civico Museo di Storia Naturale di Trieste, Trieste, Italy) — ZANIN GAIA (Civico Museo di Storia Naturale di Trieste, Trieste, Italy) — ROLANDO ANTONIO (University of Torino, Dpt. of Life Sciences and Systems Biology, Torino, Italy) — PALESTRINI CLAUDIA (University of Torino, Dpt. of Life Sciences and Systems Biology, Torino, Italy)</p>
12	<p>Phylogeny and systematics of New World Bess Beetles (Coleoptera: Passalidae: Passalinae)</p> <p>CRISTIAN FERNANDO BEZA-BEZA (Department of Biological Sciences, University of Memphis, Memphis, TN; cfbeza@memphis.edu) — LARRY JIMÉNEZ-FERBANS (Facultad de Ciencias Básicas, Universidad del Magdalena, Carrera 32 No 22 – 08, Santa Marta, Colombia, P.C. 470004; ljimenezf@unimagdalena.edu.co.) — DUANE MCKENNA (Department of Biological Sciences, University of Memphis, Memphis, TN; dmckenna@memphis.edu)</p>
13	<p>Vicariance and long-distance dispersal shaped the distribution of ‘Gondwanan’ water scavenger beetles</p> <p>MATTHIAS SEIDEL (Department of Zoology, Faculty of Science, Charles University & National Museum, Prague, Czech Republic) — VÍT SÝKORA (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — RICHARD A. B. LESCHEN (Manaaki Whenua, New Zealand Arthropod Collection, Auckland, New Zealand) — MARTIN FIKÁČEK (Department of Zoology, Faculty of Science, Charles University & National Museum, Prague, Czech Republic)</p>
14	<p>Molecular phylogeny of terrestrial water scavenger beetle tribe Megasternini (Hydrophilidae: Sphaeridiinae) reveals repeated and bidirectional continental interchange during the Eocene</p> <p>EMMANUEL ARRIAGA-VARELA (Charles University & National Museum, Prague, Czech Republic) — MARTIN FIKÁČEK (National Museum & Charles University, Prague, Czech Republic) — DANIEL MARQUINA (Swedish Museum of Natural History & Stockholm University, Stockholm, Sweden)</p>
15	<p>Origin, evolution and biogeography of New Zealand riffle beetles (Elmidae)</p> <p>VÍT SÝKORA (Charles University, Prague, Czech Republic) — MARTIN FIKÁČEK (National Museum & Charles University, Prague, Czech Republic) — RICHARD A.B. LESCHEN (Landcare Research, Auckland, New Zealand) — CRYSTAL A. MAIER (Harvard Museum of Comparative Zoology, Cambridge, USA) — MATTHIAS SEIDEL (National Museum & Charles University, Prague, Czech Republic) — WILLIAM D. SHEPARD (Essig Museum of Entomology, Berkeley, USA) — CHERYL B. BARR (Essig Museum of Entomology, Berkeley, USA) — MIGUEL ARCHANGELSKY (Universidad Nacional de La Patagonia, Esquel, Argentina) — NICOLÁS R.M. ROMÁN (Universidad Nacional de La Patagonia, Esquel, Argentina)</p>



Poster Presentations

Position	Presentation
16	<p>Excitators: female-specific, presumably secretory structures in marsh beetles (Coleoptera: Scirtidae) – diversity and evolutionary significance</p> <p>RAFAL RUTA (Department of Biodiversity and Evolutionary Taxonomy, University of Wrocław, Przybyszewskiego 65, 51-148 Wrocław, Poland; rafal.ruta@uwr.edu.pl)</p>
17	<p>Tiny critters from giant mountains: evolution of moss-inhabiting flea beetles (Coleoptera: Chrysomelidae)</p> <p>ALBERT FRANTIŠEK DAMAŠKA (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — MARTIN FIKÁČEK (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic; National Museum, Prague, Czech Republic)</p>
18	<p>Phylogeny of the <i>Ropalopus ungaricus</i> / <i>insubricus</i> group (Coleoptera: Cerambycidae: Callidiini) of the West Palearctic region</p> <p>LECH KARPIŃSKI (Museum and Institute of Zoology, Polish Academy of Sciences, Warsaw, Poland) — WOJCIECH T. SZCZEPAŃSKI (Department of Zoology, Faculty of Biology and Environmental Protection, University of Silesia, Katowice, Poland)</p>
19	<p>Transcriptome analyses provide an updated phylogeny of the family Cerambycidae and insights into the distribution of plant cell wall degrading enzymes in these beetles</p> <p>NA RA SHIN (Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany) — SEUNGWAN SHIN (University of Memphis, Department of Biological Sciences, TN, USA) — ROY KIRSCH (Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany) — PETR SVACHA (Institute of Entomology, Biology Centre, Czech Academy of Sciences, Ceske Budejovice, Czech Republic) — OLIVIER DENUX (French National Institute for Agricultural Research, Paris, France) — SYLVIE AUGUSTIN (French National Institute for Agricultural Research, Paris, France) — VINCENT LOMBARD (AFMB UMR 7257 Case 932, Campus de Luminy, Marseille, France) — BERNARD HENRISSAT (AFMB UMR 7257 Case 932, Campus de Luminy, Marseille, France) — DUANE MCKENNA (University of Memphis, Department of Biological Sciences, TN, USA) — YANNICK PAUCHET (Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany)</p>
20	<p>Integration of molecular and morphological data for species delimitation within <i>Otiorhynchus tenebricosus</i> (Herbst, 1784) complex (Coleoptera: Curculionidae)</p> <p>MAJA PRZYBYCIEŃ (Department of Entomology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland)</p>
21	<p>Climate and host plant associations shaped the evolution of ceutorhynch weevils (Coleoptera: Curculionidae: Ceutorhynchinae) throughout the Cenozoic</p> <p>HARALD LETSCH (Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Vienna, Austria) — BRIGITTE GOTTSBERGER (University of Vienna, Austria) — CHRISTIAN METZL (University of Vienna, Austria) — JONAS ASTRIN (Forschungsmuseum Alexander Koenig, Germany) — ARIEL FRIEDMAN (Tel Aviv University, Israel) — DUANE MCKENNA (University of Memphis, USA) — KONRAD FIEDLER (University of Vienna, Austria)</p>



The early evolution of insect genitalia

KLAUS-DIETER KLASS (Senckenberg Natural History Collections Dresden, Museum of Zoology, Königsbrücker Landstrasse 159, 01109 Dresden, Germany; klaus.klass@senckenberg.de) — **NATALIA A. MATUSHKINA** (Department of Ecology and Zoology, Institute of Biology and Medicine, Taras Shevchenko National University of Kyiv, Ukraine; odonataly@gmail.com)

The pairs of gonapophyses of abdominal segments 8 and 9 are an original constituent of the genitalia of Insecta (= Ectognatha) in both sexes. The gonapophyses of both segments are evolutionarily quite stable in females, but in males they are variously present or absent in subgroups of Archaeognatha and Zygentoma. Stability in females likely results from a channel-like function requiring both pairs, for sperm uptake and egg deposition, the latter function being maintained deeply into the Pterygota. In males, the function of sperm thread spinning requires only one pair, and this function becomes lost with direct copulation in Pterygota. Yet, in Archaeognatha the male and female morphologies of gonapophyses and other parts of the genitalia share many details, many indicating an original channel-like function (Klass & Matushkina 2012, 2018). This leads to the hypothesis that the gonapophyseal apparatus initially had a non-genitalic function: water-uptake, which is also the function of the homonomous structures of the pregenital segments, the coxal vesicles. A group of stiffened, channel-forming gonapophyses could take up water from deeper crevices, where it persists longer than in flat moulds that can be reached by coxal vesicles. Genital functions were adopted later in the insect stem lineage, and those in the female still reflect the original functions involved in water uptake: entering a crevice (initially for reaching water, now for egg laying) and taking up fluid (initially water, now deposited sperm). This hypothesis may also explain the frequent parallel loss of male gonapophyses 8 in Archaeognatha, and also the fact that the female genital opening (on hind rim of segment 7) is originally not in a place from where eggs could easily enter the gonapophyseal channel (the ovipositor); accessory structures are needed for this (originally likely the 7th-segmental genital lobe and mesally projecting parts of 8th-segmental coxal lobes). In most Pterygota the female genital opening is apparently “shifted” posteriorly to segment 8. Abdominal morphology in an orthopteran shows, however, that there is no shift, but a growth process dragging the lateral bases of the genital lobe posteriorly to deeply “invade” segment 8. This eventually allows laterocoxal sclerotisations of segment 8 to fuse with the 7th-segmental genital lobe sclerotisation, thus forming the subgenital plate as seen in Pterygota, which is then bisegmental. The evaluation of ontogenetic data suggests that the penis of Insecta is derived from the gonapophyses of abdominal segment 10 (then representing the limbs of segment 10), which have undergone a shift to the anterior (like gonapophyses 9) and usually a median fusion. However, there are conflicts in this hypothesis, e.g. the course of a ventral transverse ridge (ventral antecosta 10?) in some female Odonata, which traverses posterior to the sclerite likely corresponding to the male penial sclerotisation.

References: Klass K.-D., Matushkina N.A. 2012: The exoskeleton of the female genitalic region in *Petrobiellus tokunagai* (Insecta: Archaeognatha): insect-wide terminology, homologies, and functional interpretations. *Arthropod Structure & Development* 41: 575–591. — Klass K.-D., Matushkina N.A. 2018: The exoskeleton of the male genitalic region in Archaeognatha, with hypotheses on the early evolution and the morphological interpretation of genitalia in insects. — *Arthropod Systematics & Phylogeny* 76: 235–294.



Skeletomuscular evolution of male insect genitalia, with emphasis on the Endopterygota

BRENDON E. BOUDINOT (Department of Entomology & Nematology, University of California, Davis, One Shields Ave, Davis, CA 95618 USA; boudinotb@gmail.com)

No consensus exists for the homology and terminology of the male genitalia of the Hexapoda despite widespread acknowledgment of systematic value and well over a century of debate. Based on dissections and the literature, I compared genital skeletomusculature across the Hexapoda in contrast with the Remipedia, the closest pancrustacean outgroup. I found the pattern of origin and insertion for extrinsic and intrinsic genitalic and appendicular musculature to be consistent among the Ectognatha, Protura, and the Remipedia; from these consistencies, I have inferred a groundplan for the Hexapoda, and have provided an extended and explicitly diagrammed theory of genitalic homologies and evolution for all insect orders (Boudinot 2018). In the present talk, I will explain the fundamental concepts derived from this study, and I will illustrate via fine-grained transition series the evolutionary patterns leading to the Endopterygota and clades therein.

Reference: Boudinot B.E. 2018. A general theory of genital homologies for the Hexapoda (Pancrustacea) derived from skeletomuscular correspondences, with emphasis on the Endopterygota. *Arthropod Structure & Development* 47: 563–613

Museomics: opening the floodgates to sequencing genomes of all species

NIKLAS WAHLBERG (Department of Biology, Lund University, Sweden)

The costs of sequencing whole genomes has decreased drastically in the last few years, opening up new opportunities in phylogenomics. Large scale projects have been envisaged, with an aim of sequencing the genomes of all species on the planet. However, such projects lack realism as the taxonomic impediment will make it so that getting fresh specimens for the majority of species will not be feasible. Sequencing curated, identified specimens in natural science collections, including types, has become a viable option. I show the utility of sequencing highly fragmented genomes of museum specimens for phylogenomics and discuss implications of such methods for the grand goals of sequencing the genomes of all species.

From Hennig to 1KITE – what have we learned?

ROLF G. BEUTEL (Institut für Zoologie und Evolutionsforschung, Friedrich-Schiller-Universität Jena, 07743 Jena, Germany)

Haeckel's attempt to classify insects based on the mode of food uptake resulted in a very unorthodox phylogeny from today's perspective, combining for instance Orthoptera and Coleoptera, and Diptera and Hemiptera. In contrast to this, a very remarkable insect phylogeny was presented by Carl Börner (1904), lacking a consistent methodology, but nevertheless displaying a pattern very close to recent concepts. In the mid-20th century Willi Hennig



Abstracts · Oral Presentations

revolutionized phylogenetics. His “Stammesgeschichte der Insekten” (1969) was a major breakthrough in insect systematics. Most of what he suggested was confirmed by recent studies based on extensive morphological or molecular data. The first cladistic analysis of morphological characters, published in 2001, largely confirmed phylogenetic hypotheses presented by Hennig and also Niels Peder Kristensen. In contrast, earlier molecular studies, mainly based on ribosomal genes, yielded unorthodox results, in distinct conflict with previous phylogenetic concepts. Recent phylogenomic studies (1KITE project) again largely confirm Hennig’s views, with very few exceptions, for instance the basal placement of Hymenoptera in Holometabola. The interordinal relationships in the main lineages Polyneoptera, Hemiptera and Holometabola are now largely resolved. Persistent problems are the relationships of the entognathous orders (Collembola, Protura, Diplura), the “Palaeoptera problem” (Odonata, Ephemeroptera, Neoptera), the monophyly of Paraneoptera (Psocodea, Thysanoptera, Hemiptera), and the Mecoptera. The impression that new insights since Hennig are limited is misleading. The methodological progress is enormous. The handling of extremely large data sets and the refinement of analytical methods are remarkable achievements. Aside from this, 1KITE yielded a robust time frame for insect evolution, with estimations of the time of origin for all major lineages. Major future challenges are exploring insect evolution in the dimension of time, documenting the rapidly declining diversity, and developing concepts of preservation. These aims should be tackled with a close cooperation between taxonomists, morphologists, palaeontologists, molecular systematics, and ecologists.

Reviewing and reanalyzing the Palaeoptera problem

KAREN MEUSEMANN (Evolutionary Biology & Ecology, Institute for Biology, University of Freiburg, Germany; Center of Molecular Biodiversity, Zoologisches Forschungsmuseum Koenig, Bonn) — **SABRINA SIMON** (Biosystematics, Wageningen University & Research, The Netherlands)

The phylogenetic relationships of the winged insect lineages mayflies (Ephemeroptera), damselflies and dragonflies (Odonata), and all other winged insects (Neoptera) are still controversially debated: three hypotheses are supported by different datasets: Palaeoptera, Metapterygota and Chiasmomyaria. We reanalyzed the relationships of these lineages („Paleoptera problem”) with special focus on potential alternative and / or confounding signal within phylogenomic datasets. We therefore compiled new datasets mainly based on transcriptomes published by Misof et al. (2014) and including data from whole genomes. We evaluated in-depth confounding and alternative signal present in the datasets using various methodological approaches.

Despite overall support for the Palaeoptera hypothesis, we also found considerable signal for Chiasmomyaria, which is not easily detectable by standardized phylogenetic tree inference approaches. Analyses of the accumulation of signal across partitions showed that signal accumulates gradually. In case signal only slightly supported one over the other hypothesis, topologies switched from statistically strongly supported Palaeoptera to statistically strongly supported Chiasmomyaria.

Reference: Misof B., Liu S., Meusemann K. et al. 2014: Phylogenomics resolves the timing and pattern of insect evolution. *Science* 346: 763–767.



The phylogenetics and divergence times of Odonata: dragonflies and damselflies

JESSICA WARE (Rutgers University, Department of Biological Sciences, Newark, NJ, USA) — **MANPREET KOHLI** (Rutgers University, NJ, USA) — **CAROLA GREVE** (LOEWE Centre for Translational Biodiversity Genomics, Germany) — **OLIVIER BETHOUX** (Muséum National d'Histoire Naturelle, Paris, France) — **RYUICHIRO MACHIDA** (University of Tsukuba, Japan) — **OLIVER NIEHUIS** (Albert-Ludwigs-Universität Freiburg, Germany) — **JES RUST**, Steinmann-Institut (Universität Bonn, Germany) — **TORSTEN WAPPLER** (Hessisches Landesmuseum Darmstadt, Germany) — **HARALD LETSCH** (University of Vienna, Austria)

There are over 6000 species of Odonata, distributed worldwide. Dragonflies and damselflies (Insecta: Odonata) are likely sister to the Ephemeroptera, forming a clade called the Palaeoptera. Here we present a well-resolved phylogenetic tree, including 103 ingroup species that comprehensively tests the interfamilial relationships within the group using transcriptomics for the first time in odonate systematics. We find that the Zygoptera, the earliest branching lineage in the order, has well resolved relationships among the Lestoidea, Coenagrionoidea and Calopterygoidea. Anisoptera is the sister group to Epiophlebiidae. Within Anisoptera, Gomphidae and Cavilabiata are not recovered as sister taxa, but Gomphidae is sister to Petaluridae, which has implications for our understanding of the evolution of exophytic oviposition. Our divergence time estimations further indicated that Odonata emerged in the Upper Triassic and both Anisoptera and Zygoptera appeared in the Middle Jurassic.

Odonata phylogeny: A work in progress to combing fossil and extant taxa

SETH M. BYBEE (Department of Biology, Brigham Young University, Provo, UT, USA) — **ROBERT J. ERICKSON** (Department of Biology, Brigham Young University, Provo, UT, USA)

Relationships along the backbone of extant Odonata have been difficult to resolve with high support. We present phylogenetic results from both Transcriptome and AHE data. Further, the relationships between both extant and fossil odonates, as well as closely related odonatoid fossils add additional complexity to odonate phylogenetic reconstruction. To date no cladistic, large-scale phylogenetic reconstruction of both extant and fossil odonates has been attempted. We take the first steps by combining 233 morphological characters for > 300 taxa (~200 fossil and ~125 extant) and 478 molecular loci to reconstruct a phylogeny of Odonata that includes both fossil odonates and odonatoids. Including fossils allows for a rigorous test of the taxonomic classification for both fossil and extant Odonata and allow for an exploration of homoplasy among sets of morphological characters (e.g., wing venation) in the presence of molecular data.



Abstracts · Oral Presentations

Phylogeny of principal lineages of Polyneoptera

BENY WIPFLER (Forschungsmuseum Alexander Koenig, Bonn, Germany) — **SABRINA SIMON** (Wageningen University, Wageningen, Netherlands)

The talk provides a review of the phylogeny and major important major evolutionary transitions within Polyneoptera. Phylogenomic approaches support the monophyly of Polyneoptera and a stable internal topology with Dermaptera + Zoraptera as sistergroup to a clade Plecoptera + (Orthoptera + (Dictyoptera + (Xenonomia + Eukinolabia))). The last common ancestor of the group showed several adaptations towards a ground orientated life style such as sclerotized front wings or specialized attachment structures at the tarsi (euplantulae). Within the group various modifications to this ground plan appeared and include for example the reduction of the sclerotized front wings in Embioptera or Zoraptera or the secondary transition to a life in bushes or trees in groups like Mantophasmatodea, Mantodea or Phasmatodea that is associated with a plant diet or a predatory life style. Prognathous mouthparts evolved several times independently within Polyneoptera. Social behavior in various different forms is found in many groups but apparently was not part of the polyneopteran ground plan. The last common ancestor of Polyneoptera was terrestrial throughout its entire life which implies that the aquatic nymph of stoneflies evolved independently from those of mayflies and dragonflies.

The phylogeny and biogeography of stoneflies (Plecoptera, Insecta): evidence for a Pangean origin and an Early Mesozoic radiation

HARALD LETSCH (Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Vienna, Austria) — **SABRINA SIMON** (Wageningen University, Wageningen, Netherlands) — **PAUL FRANDBSEN** (Brigham Young University, Provo, USA) — **XIN ZHOU** (China Agricultural University, Beijing, China) — **BENJAMIN WIPFLER** (Forschungsmuseum Alexander Koenig, Bonn, Germany)

Combined transcriptomic (16 species – 678–2997 characters (genes)) and traditional multi gene (498 species – 7 genes) data sets were used for phylogenetic and biogeographical analyses. The monophyly of Antartcopterla, as well as Systellognatha and Euholognatha was confirmed, whereas Arctoperlaria (Systellognatha+Euholognatha) was only weakly supported. Within Systellognatha, the family relationships were resolved unequivocally, but in Euholognatha several relationships remain unresolved. Subsequent dating analyses indicated a Pangean origin of Plecoptera in the Early Triassic, shortly before the Permian-Triassic extinction event. The radiation of many families started in the Middle Jurassic. Biogeographical reconstructions show a widespread colonization of the Pangean supercontinent and indicate an early southern radiation of Antartcopterlaria on the later Gondwana subcontinent and a northern radiation of both Systellognatha and Euholognatha in Laurasia. Our analyses further support the Pangean origin of the ancestors of the “south forestflies” (Notonemouridae), which are nowadays only found in South America, South Africa, Australia and New Zealand. This contradicts the hypothesis of a Cretaceous origin of Notonemouridae in Eurasia and their distribution in the southern hemisphere via long-distance dispersal.



A tree of twigs and leaves: Revealing the role of biogeography in stick insect evolution (Phasmatodea)

SARAH BANK (Dept. Animal Evolution and Biodiversity, Georg-August-Universität Göttingen, Göttingen, Germany) — **SVEN BRÄDLER** (Dept. Animal Evolution and Biodiversity, Georg-August-Universität Göttingen, Göttingen, Germany)

Phasmatodea are large tropical herbivorous insects known for their extreme forms of plant mimicry, which includes striking imitation of either twig, leaf, bark or moss. Phasmatodeans developed a vast morphological diversity over time, and in the past solely anatomical traits have been considered to justify the proposal of new species and taxonomic groups. Traditional taxonomy is devoid of formal cladistic analyses and consequently burdened with unmethodical classification. More recently, molecular studies have started to revise these traditional concepts and revealed that morphological resemblance is not necessarily the result of common ancestry but of convergent adaptations in geographic isolation. The dispersal capability of stick and leaf insects is considered to be rather limited, yet they have spread over all (sub)tropical regions worldwide, and their geographical distribution has been demonstrated to be informative towards their phylogenetic relationships on nearly all taxonomic levels. In order to resolve the deep nodes of phasmid systematics, which apparently are the result of a rapid ancient radiation in the Eocene, we inferred a phylogeny based on >2000 orthologous genes obtained from transcriptomic data. Our results are in line with previous analyses corroborating Timematodea as sister group to all remaining Phasmatodea (Euphasmatodea), and Aschiphasmatodea as sister to all remaining euphasmids, the Neophasmatodea. Within Neophasmatodea unexpectedly novel clades were identified that represent a split into a major New World and Old World clade, namely, the Occidophasmata and Oriophasmata. Divergence time analyses in combination with a thorough ancestral range reconstruction furthermore show only a single dispersal event of phasmatodeans to Madagascar and to the Australian region and propose a Southeast Asian or Nearctic-Neotropical origin of the whole group. Within Oriophasmata, we present new phylogenetic trees based on a nearly complete taxon sampling for the true leaf insects (Phylliinae) and the ground-dwelling Heteropterygidae, both of which are considered of being pivotal taxa for understanding Phasmatodea evolution. We demonstrate how a robust phylogeography is the key factor in understanding the phasmatodean tree of life, allowing us to make assumptions on significant evolutionary patterns and processes.

Phylogeny of Mantophasmatodea

REINHARD PREDEL (University of Cologne, Institute for Zoology) — **LAPO RAGIONIERI** (University of Cologne, Institute for Zoology) — **ÁLVARO ZÚÑIGA-REINOSO** (University of Cologne, Institute for Zoology) — **STEFFEN ROTH** (University Museum of Bergen, The Natural History Collections)

The insect order Mantophasmatodea has been described by Klass et al. (2002), based on two museum specimens collected in Namibia and Tanzania a long time ago. In the following years, a surprising abundance and species diversity was found especially in southern Africa. Most species have been provisionally grouped into three families (e.g. Damgaard et al. 2008): Tanzaniophasmatidae with a single species from Tanzania, Austrophasmatidae (9 de-



Abstracts · Oral Presentations

scribed species from South Africa), and Mantophasmatidae (5 described species from Namibia). In addition, several genera were described without clear assignment to one of these families (e.g. Wipfler et al. 2011, 2019). To resolve existing ambiguities in intraordinal relationships of Mantophasmatodea, we performed transcriptomic analyses of all described species of Mantophasmatodea and several not yet described taxa. Subsequently, we identified for each species the translated protein precursors of 32 different neuropeptide genes. Phylogenetic analysis of the concatenated datasets revealed a very well-supported topology of Mantophasmatodea. In fact, most nodes were recovered with maximal support. Our data support the restructuring of the family Mantophasmatidae, the invalidation of Tanzaniophasmatidae, the integration of the genera *Striatophasma*, *Minutophasma*, and *Kuboesphasma* in the family Austrophasmatidae and the description of two new families of Mantophasmatodea. In addition to the elucidation of the phylogenetic relationships of all genera of Mantophasmatodea we discuss the speciation/species descriptions of the widespread Namibian genus *Mantophasma*.

References: Klass K.-D., Zompro O., Kristensen N.P., Adis J. 2002: Mantophasmatodea: A new insect order with extant members in the Afrotropics. *Science* 296: 1456–1459. — Damgaard J., Klass K.-D., Picker, M.D., Buder G. 2008: Phylogeny of the Heelwalkers (Insecta: Mantophasmatodea) based on mtDNA sequences, with evidence for additional taxa in South Africa. *Molecular Phylogenetics and Evolution* 47: 443–462. — Wipfler B., Pohl H., Predel R. 2012: Two new genera and species of Mantophasmatodea (Insecta, Polyneoptera) from Namibia. *ZooKeys* 166: 75–98. — Wipfler B., Theska T., Predel R. 2018: Mantophasmatodea from the Richtersveld in South Africa with description of two new genera and species. *ZooKeys* 746: 137–160.

Phylogenetic synecdoche demonstrates optimality of subsampling and improves recovery of the Blaberoidea phylogeny

DOMINIC A. EVANGELISTA (Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, UA, 57 rue Cuvier, CP50, 75005 Paris, France; 2. Department of Ecology and Evolutionary Biology, The University of Tennessee, Dabney Hall, 1416 Circle Dr., Knoxville, TN 37996, USA) — **SABRINA SIMON** (Biosystematics Group, Wageningen University and Research, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands) — **MEGAN M. WILSON** (Federated Department of Biological Sciences, Rutgers, The State University of New Jersey and NJIT, 195 University Ave, Newark, NJ 07102, USA) — **AKITO Y. KAWAHARA** (Florida Museum of Natural History, University of Florida, Gainesville, FL 32611, USA) — **MANPREET K. KOHLI** (Federated Department of Biological Sciences, Rutgers, The State University of New Jersey and NJIT, 195 University Ave, Newark, NJ 07102, USA) — **JESSICA L. WARE** (Federated Department of Biological Sciences, Rutgers, The State University of New Jersey and NJIT, 195 University Ave, Newark, NJ 07102, USA) — **BENJAMIN WIPFLER** (Center for Taxonomy and Evolutionary Research, Zoological Research Museum Alexander Koenig (ZFMK), Adenauerallee 160, 53113 Bonn, Germany) — **OLIVIER BÉTHOUX** (CR2P (Centre de Recherche en Paléontologie – Paris), MNHN – CNRS – Sorbonne Université, UPMC Univ Paris 06, MNHN, CNRS, Paris, France; Muséum national d'Histoire naturelle, 57 rue Cuvier, CP38, 75005 Paris, France) — **PHILIPPE GRANDCOLAS** (Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, UA, 57 rue Cuvier, CP50, 75005 Paris, France) — **FRÉDÉRIC LEGENDRE** (Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, UA, 57 rue Cuvier, CP50, 75005 Paris, France)

Phylogenomics seeks to use next-generation data to robustly infer an organism's evolutionary history. Yet, the practical caveats of phylogenomics motivates investigation of improved efficiency, particularly when quality of phylogenies are questionable. To achieve improvements, one goal is to maintain or enhance the quality of phylogenetic inference while severely reducing dataset size. We approach this goal by designing an optimized subsample of data

**Abstracts · Oral Presentations**

with an experimental design whose results are determined on the basis of phylogenetic synecdoche – a comparison of phylogenies inferred from a subsample to phylogenies inferred from the entire dataset. We examine locus mutation rate, saturation, evolutionary divergence, rate heterogeneity, selection, and a priori information content as traits that may determine optimality. Our controlled experimental design is based on 265 loci for 102 blaberoidean cockroaches and 22 outgroup species. High phylogenetic utility is demonstrated by loci with high mutation rate, low saturation, low sequence distance, low rate heterogeneity, and low selection. We found that some phylogenetic information content estimators may not be meaningful for assessing information content a priori. We use these findings to design concatenated datasets with an optimized subsample of 100 loci. The tree inferred from the optimized subsample alignment was largely identical to that inferred from all 265 loci but with less evidence of long branch attraction and improved statistical support. In sum, optimized subsampling can improve tree quality while reducing data collection costs and yielding 4–6 × improvements to computation time in tree inference and bootstrapping. The systematic results provide support for a revised classification scheme of Blaberoidea, which we propose to contain four monophyletic clades (Ectobiidae, Pseudophyllodromiidae, Blattellinae, and Blaberidae). Further research into the phylogeny of Blaberidae shows some resolution but ultimately demonstrates the difficulty of resolving this rapid radiation.

Updating our knowledge about the diversity of Neotropical cockroaches: a molecular phylogenetic approach

ANDRÉZ VÉLEZ-BRAVO (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; avelez82@gmail.com) — **JUAN M. DAZA-ROJAS** (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; jumadaza@gmail.com)

The Neotropics is the biogeographic region with the highest richness of cockroaches, harboring more than 30% out of 4.800 species currently known (Beccaloni 2014). In the early 1900s, entomological expeditions throughout the Neotropics were common, and as a consequence, also the first studies regarding cockroach diversity. Since then, new checklists of species by countries, taxonomic revisions and description of new lineages have been published but without any phylogenetic support. Here, we have inferred for the first time, phylogenetic trees for several groups of Neotropical cockroaches. We combined DNA sequences from mitochondrial and nuclear regions of specimens collected in the Caribbean, Central America and northern South America. This new molecular data available allowed to include new neotropical groups in the cockroaches tree of life. These phylogenetic hypotheses also reject the monophyly of genera such as *Imblattella*, *Nyctibora* and *Xestoblatta* and uncover huge cryptic diversity. For instance, genetic data suggest more species for *Imblattella* than have been currently described for this genus. The advance towards the generation of phylogenetic hypotheses will not only offer clues for the generation of a taxonomy with phylogenetic sense, the discover of cryptic diversity, but also allow to understand how the diversity of this insects was generated and distributed throughout a region with a complex geological and climatic history.

Reference: Beccaloni G.W. 2014: Cockroach Species File Online. Version 5.0/5.0. World Wide Web electronic publication. <<http://Cockroach.SpeciesFile.org>> [accessed 18 June 2019].



The last two decades of termite phylogenetics: where do we go from here?

JESSICA L. WARE (Rutgers University Newark, 195 University Avenue, Newark, NJ, 07102, USA) — **MEGAN M. WILSON** (Rutgers University Newark, 195 University Avenue, Newark, NJ, 07102, USA)

Termites, social, myopic roaches, comprise a small group of cellulose feeding organisms distributed globally. Here, we review the past and present phylogenetic hypotheses for termites, providing new insights into their topology based on morphology, AHE and transcriptomic data. In particular, we focus on non-termitidae systematics, but additionally highlight a unique Termitidae with a remarkable defensive behaviour.

Studies on the phylogeny of the genus *Psammotermes* (Isoptera: Rhinotermitidae)

FELICITAS GUNTER (Research Unit Biodiversity, Evolution and Ecology, University of Hamburg, Germany) — **BARBARA RUDOLPH** (Research Unit Biodiversity, Evolution and Ecology, University of Hamburg, Germany) — **NORBERT JÜRGENS** (Research Unit Biodiversity, Evolution and Ecology, University of Hamburg, Germany)

According to the current state of knowledge, the genus *Psammotermes* Desneux 1902 comprises six accepted species, which are found in Africa, Madagascar and India. One of these species is *Psammotermes allocerus* Silvestri 1908 which was underrepresented in previous phylogenetic studies. We studied numerous populations from Angola, Namibia and South Africa which hitherto would have been assigned as one species. These populations forage on dead wood, but also on grasses. A subset of populations causes the famous “fairy circles” (circular patches bare of vegetation at the Namib desert margins) by localized foraging on grass roots. Our results of detailed morphological studies on soldier traits measured among others with the “Geometric Morphometric Method” supports the assumption that *P. allocerus* cannot be regarded as one species. Additionally, we present the “intraspecific” phylogeny based on combined analysis of COI and COII markers, with Haplotype, Barcode Gap and *structure* analyses and summarize that *P. allocerus* consists of several cryptic species and we discuss the position of this cryptic species complex in relation to other *Psammotermes* species.



Recent advances in paraneopteran phylogenomics: exploring sources of instability and conflict in a highly diverse insect group

RACHEL K. SKINNER (University of Illinois at Urbana-Champaign, Department of Entomology, Urbana, Illinois, United States of America) — **CHRISTOPHER H. DIETRICH** (Illinois Natural History Survey, Urbana, Illinois, United States of America) — **KAREN MEUSEMANN** (University of Freiburg, Department of Ecology and Evolutionary Biology, Freiburg, Baden-Württemberg, Germany) — **ERIC GORDON** (University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, Connecticut, United States of America) — **KEVIN P. JOHNSON** (Illinois Natural History Survey, Urbana, Illinois, United States of America)

The hemipteroid insects (Insecta: Paraneoptera), comprising more than 121,000 species across the orders Hemiptera, Thysanoptera, and Psocodea, are one of the most diverse insect groups, but their evolutionary relationships have been historically difficult to resolve confidently. Recent transcriptome-based phylogenies of Paraneoptera and the included hemipteran suborder Auchenorrhyncha have yielded several unexpected or conflicting relationships that received high bootstrap support but were inconsistently supported using alternative metrics. An initial transcriptome-based phylogenomic analysis of extant hexapods recovered Psocodea as the sister taxon of Holometabola, rendering Paraneoptera paraphyletic. A follow-up study including greater taxon sampling within Paraneoptera also recovered Psocodea+Holometabola with high bootstrap support. However, the majority of quartets in a four-cluster likelihood mapping analysis of the same data supported a monophyletic Paraneoptera, suggesting that paraphyly of Paraneoptera is not a robust result. To further evaluate the potential sources of phylogenetic instability in the placement of Psocodea, we analyzed more than 1.9 million base pairs of nucleotide data from the most recent analysis using both concatenated and previously unperformed coalescent analyses. Both analyses again recovered Psocodea+Holometabola with high support but the coalescent analysis suggested a high degree of gene tree conflict for this relationship. Taxon removal experiments indicate that the recovered topology is highly sensitive to taxonomic sampling and additional observations suggest that branch lengths within certain clades may be correlated with the frequency of Psocodea + Holometabola in quartet likelihood mapping. Our analyses add to the growing body of literature demonstrating that bootstrap values can be misleadingly high and may mask significant data conflict in phylogenomic data sets. Our study also implies that even with maximum likelihood models, relative branch lengths may still have a very strong influence on the tree topology even with dense taxon sampling and large sequence data sets.

Within Auchenorrhyncha, relationships between and within the four superfamilies Fulgoroidea, Cicadoidea, Cercopoidea, and Membracoidea have been contentious. Our recent study incorporating sequence data of 2139 orthologs from 84 auchenorrhynchan species representing 27 families used both maximum likelihood and multispecies coalescent analyses to reconstruct the evolutionary history in this group using amino acid, nucleotide, and degeneracy-coded nucleotide ortholog data. Although many relationships at the superfamily level were consistent between analyses, several differing, highly supported topologies were recovered using different datasets and reconstruction methods, most notably the differential placement of Cercopoidea as sister either to Cicadoidea or Membracoidea. To further interrogate the recovered topologies, we explored the contribution of genes as partitioned by third-codon-position guanine-cytosine (GC) content and heterogeneity. We found consistent support for several relationships, including Cercopoidea + Cicadoidea, most often in genes that would be expected to be enriched for the true species tree if recombination-based dynamics in GC content have contributed to the observed GC heterogeneity. Our results provide a generally well-supported framework for future studies of auchenorrhynchan phylogeny and suggest that



Abstracts · Oral Presentations

transcriptome sequencing is likely to be a fruitful source of phylogenetic data for resolving its clades. However, we caution that future work should account for the potential effects of GC content heterogeneity on relationships recovered in this group.

Advancing the resolution of the fly tree of life

MICHELLE D. TRAUTWEIN (California Academy of Sciences, San Francisco, CA, USA; michelletrautwein@gmail.com) — **BRIAN M. WIEGMANN** (North Carolina State University, Department of Entomology, Raleigh, NC, 27695, USA; bwiegman@ncsu.edu)

Large phylogenomic data sets have greatly improved the resolving power of fly molecular systematic analyses. Complex species radiations, adequate sampling of characters and taxa, and challenging analytical issues all remain critically important for reconstructing fly phylogeny. Working together with a large international team of dipterists (1Kite Antliophora Team), we have compiled large data sets from transcriptomes, genomes, and hybrid enrichment to investigate fly relationships at multiple levels of the hierarchy. Our new data analyses provide information that definitively resolves many key nodes in fly phylogeny. Using these data, we also examine the effects of alternative methods to evaluate information content and rate variation in harvested loci. New insights into the origin and evolution of the earliest fly lineages, the relationships among lower brachyceran families, the phylogeny of acalyprate Schizophora, and the diversification of mosquitoes are presented as examples of the challenges and resolving power of these data. The on-going search for new data strategies is key to successfully implementing phylogenomics research. With the new big data paradigm inspiring our dipterological collaborations, we seek biologically plausible phylogenetic hypotheses that provide reliable context for investigating the evolution of flies.

Toward well-supported and species-rich trees: Utilizing legacy data, reactivating legacy DNA, and data layering

RUDOLF MEIER (Department of Biological Sciences, National University of Singapore, Singapore)

Planet Earth is likely to be home to 10 million animal species. It is likely that < 1% of these species have ever been included in a phylogenetic analysis. This impedes with understanding the evolution of animals but also interferes with the use of phylogenetic information for conservation purposes (e.g., habitat assessment based on phylogenetic diversity). In my lab, we are interested in generating species-rich trees for Diptera by applying a step-wise procedure that is based on the principle that one should determine empirically how much data are needed for resolving a particular set of relationships. This is why we start with legacy Sanger data. For scalability reasons, we then continue by collecting mt genomes and 28S rDNA for species for which we have “legacy DNA” and new species that are discovered using NGS barcodes. Lastly, we identify which clades require more data and obtain these data for representative species via transcriptomics or genome skimming. All data are then combined in a quest for trees that are species-rich and well-supported. I will discuss the success of this approach for sepsids, calyprates, and the Diptera of Singapore.



Crucial points in acalyprate fly phylogeny with an emphasis on Sciomyzoidea and Sphaeroceroidea

KEITH M. BAYLESS (Australian National Insect Collection, CSIRO National Research Collections Australia (NRCA), Acton, ACT, Canberra, Australia) — **DAVID K. YEATES** (Australian National Insect Collection, CSIRO National Research Collections Australia (NRCA), Acton, ACT, Canberra, Australia)

Prior attempts to decipher the evolutionary relationships between the major lineages of schizophoran flies have been obstructed by the magnitude of challenge in terms of species diversity and high diversification rates. Five of the ten acalyprate superfamilies are likely non-monophyletic, and the interrelationships between Acalypratae and Calypratae are unclear. Recent competing hypotheses place Conopidae, Diopsoidea, or Calypratae+Ephydroidea as sister to the remaining Schizophora. Our approach of analyzing thousands of genes from combinations of transcriptomic and Anchored Hybrid Enrichment exome data offers a window into the first robustly supported evolutionary tree of acalyprate flies. Calypratae is recovered deep within the acalyprates, allied with Ephydroidea, rendering the acalyprates non-monophyletic. Schizophoran flies can be grouped into five major lineages, which either roughly correspond with traditional clades or are corroborated by morphological synapomorphies. A lineage including Sciomyzoidea, Lauxanioidea, and Conopidae ("Sciomyzoidea s.l.") is resolved to be the sister group to the rest of Schizophora, and a modified Sphaeroceroidea (= Heteromyzoidea) is likely sister to the other acalyprates and Calypratae. This phylogenomic approach offers compelling hypotheses for the relationships within these early diverging clades. Sensitivity analyses exploring parameter space and taxonomic subsamples demonstrate that within these clades, Lauxanioidea, Conopidae, and Heleomyzidae (= Heteromyzidae) are not monophyletic. The placement of Sepsidae and Ropalomeridae within Sciomyzoidea is rejected. Sciomyzoidea s.l. and Sphaeroceroidea s.l. contain several ecologically specialized families with evidence of southern connections between Chile, New Zealand, and Australia. Five families of Sciomyzoidea contain littoral species that feed on kelp and other detritus washed up on beaches. This life history likely evolved or was lost multiple times within Sciomyzoidea s.l., as did parasitoidism. Teratomyzidae, the only insect family ecologically specialized to feed on ferns, occupy an isolated position within Sphaeroceroidea s.l. Most species of fern flies are undescribed due to narrow geographic distribution and host specificity. Revisionary syntheses integrating phylogenomics, morphology, and ecology are underway on fern flies to contextualize the evolution of this unique trait. Compelling novel hypotheses based on analyses of large datasets of these flies, examined in light of natural history and functional morphology, yielded a broad and robust view into their evolution through time and morphological space. This approach demonstrates that context is everything in acalyprate flies. A robust understanding of the evolution of the entire group was necessary to form testable hypotheses and discover evolutionary patterns in previously obscure critical lineages.



Origin of the male terminalia in Eremoneura (Diptera)

TADEUSZ ZATWARNICKI (Institute of Biology, Opole University, ul. Oleska 22, 45-052 Opole, Poland)

Internal structures and gonocoxites of the male hypopygium in Eremoneura are strongly modified, compared to the basic condition of lower Diptera. There are two hypotheses on the origin of clasping lobes in both Orthogynya and Cyclorrhapha. According to “classical hypothesis” (Crampton 1936) clasping lobes are secondary structures (“surstyli”), and according to current revised version originated from epandrium (IX. tergite). There is no evidence for such a replacement of structures. According to the second hypothesis, called “hinge hypothesis” proposed by Zatwarnicki (1996), gonostyli continue their function in Eremoneura, being attached to the epandrium, so clasping lobes are homologous in all Diptera.

The phylogeny of Trichoptera

PAUL B. FRANSDEN (Brigham Young University, Provo, USA) — **1KITE TRICHOPTERA SUBGROUP**

With more than 16,000 species spread throughout 51 extant families, caddisflies (Insecta: Trichoptera) represent the largest strictly aquatic insect order. Caddisflies are reciprocally monophyletic with Lepidoptera (moths and butterflies), but, contrary to most lepidopterans, they inhabit freshwater ecosystems as larvae. A well-resolved phylogenetic tree is of vital importance in deciphering the underwater diversification of this group. However, despite years of careful phylogenetics research, the deep splits within Trichoptera have been difficult to resolve. In particular, the relationships among the so-called “spicipalpian” families (Hydroptilidae, Ptilocolepidae, Rhyacophilidae, Hydrobiosidae, and Glossosomatidae) and the monophyletic Annulipalpia and the tube-case making Integripalpia were unclear. Here we use the first trichopteran phylogenomics data set, consisting of a combination of *de novo* transcriptomes and targeted enrichment data to resolve the deep splits within Trichoptera. We find that the “spicipalpian” families form a clade with the tube-case makers, which we now collectively refer to as Integripalpia. The first diverging lineage in Integripalpia consists of the micro-caddisflies, Hydroptilidae and Ptilocolepidae, followed by a new clade consisting of the free-living caddisfly families (Hydrobiosidae and Rhyacophilidae) and the tortoise-case makers (Glossosomatidae), which leads up to the tube-case makers. We confirm the reciprocal monophyly of the two tube-case making infra-orders, Plenitentoria and Brevitentoria. The fixed-retreat makers, Annulipalpia, are monophyletic and the net-spinners (Hydropsychoidea) are sister to the rest of Annulipalpia. We hope this well-resolved phylogeny will enable the interpretation of important traits within Trichoptera such as the evolution of underwater silk use and the mode of their diversification under water.



Phylogenomics of Lepidoptera – a perspective from Down Under

ANDREAS ZWICK (ANIC, CSIRO, Canberra, Australia) — **DIANA HARTLEY** (ANIC, CSIRO, Canberra, Australia) — **MARIANNE HORAK** (ANIC, CSIRO, Canberra, Australia) — **LUISA TEASDALE** (ANIC, CSIRO, Canberra, Australia)

Our understanding of the evolution of Lepidoptera has greatly advanced during the past decade, with molecular data leaping from a few genes to hundreds and thousands of loci through hybrid enrichment and transcriptome sequencing. In contrast, the taxon sampling of such larger molecular studies is still very limited and not representative for the 160,000 named species of the order. Furthermore, taxa from the southern hemisphere are typically understudied, and key lineages are not included in deep-level phylogenomic analyses.

We present the results from a phylogenomic study that extends existing transcriptomes with data from 300 mainly Australian species of moths. We discuss relationships between superfamilies and families from a more Australian perspective, with emphasis on lineages previously not included and on relationships in the superfamily Tortricoidea. We also present the development of a high-throughput collection genomics approach and how it will direct deep-level phylogenomics in future, in particular for less studied yet diverse moth faunas like the one of Australia.

Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths

AKITO Y. KAWAHARA (Florida Museum of Natural History) — **1KITE LEPIDOPTERA GROUP**

Butterflies and moths (Lepidoptera) are one of the major super-radiations of insects, comprising nearly 160,000 described extant species. As herbivores, pollinators, and prey, Lepidoptera play a fundamental role in almost every terrestrial ecosystem. Lepidoptera are also indicators of environmental change and serve as model organisms for research on mimicry and genetics. They have been central to the development of co-evolutionary hypotheses, such as butterflies with flowering plants, and moths' evolutionary arms race with echolocating bats. However, these questions remain unanswered because a robust lepidopteran phylogeny and timing of evolutionary novelties are lacking. To address these issues, we inferred a comprehensive, dated phylogeny of Lepidoptera with an unparalleled scale of data: 2,098 orthologous protein-coding genes from 186 species representing nearly all superfamilies, including carefully evaluated synapomorphy-based fossils. The earliest lepidopterans originated in the Late Carboniferous (~ 300 million years ago [Ma]) and fed on early land plants. Lepidoptera evolved a key morphological innovation, the tube-like proboscis, in the Middle Triassic (~ 241 Ma), which likely allowed lepidopterans to diversify and acquire nectar from the many flowering plants in the Cretaceous. Our results demonstrate that moths were likely nocturnal before the Jurassic (~ 200 Ma) and day-flying butterflies first appeared in the Late Cretaceous (~ 98 Ma). Contrary to popular belief, moth hearing organs evolved multiple times prior to entering an evolutionary arms race with bats, perhaps initially functioning for auditory surveillance before being co-opted for bat sonar detection. Our study provides a highly relevant framework for future comparative studies on butterfly and moth evolution.



Using museomics to investigate the evolutionary relationships of Tineoidea

VICTORIA TWORT (Luomus, Finnish Museum of Natural History, Zoology Unit, University of Helsinki) — **CHRIS WHEAT** (Department of Zoology, Stockholm University) — **NIKLAS WAHLBERG** (Department of Biology, Lund University) — **LAURI KAILA** (Luomus, Finnish Museum of Natural History, Zoology Unit, University of Helsinki)

Natural history museums are a diverse biobank of the extant and extinct diversity that surrounds us. The utilisation of such material for genetic research allows us to expand the scope of questions and taxa available for investigation. Museomics is one such field that is starting to utilise these diverse biobanks to further our scientific knowledge. Low coverage whole genome sequencing of 100 species of the Tineoid family assemblage from museum specimens has been carried out, in order to investigate the phylogenetic relationships among this group. *De novo* genome assembly resulted in fragmented assemblies, however the recovery of 332 genes of interest (manually curated gene set for Lepidoptera) was high. The resulting data has been combined with our existing Lepidoptera dataset, encompassing a diverse range of taxa. The current phylogeny based on our phylogenomic analysis will be discussed.

Whole genome sequencing for phylogenetics of old genomic DNA extracts: Erebidae moths as an example

H.R. GHANAVI (Department of Biology, Lund University, Lund, Sweden; hamid.ghanavi@biol.lu.se) — **V. TWORT** (Department of Biology, Lund University, Lund, Sweden) — **T. HARTMAN** (Department of Biology, Lund University, Lund, Sweden) — **N. WAHLBERG** (Department of Biology, Lund University, Lund, Sweden)

The development of Next Generation Sequencing (NGS) methods was a major advance in molecular biology, which has influenced nearly every branch of current biology. One of the main reasons for the success of this technology is the large volume of data generated which is practically impossible using traditional methods. However, despite the wide applicability of this technique, some fields are yet to utilise its full potential. Phylogenetics is one of the fields that has been revolutionised with the appearance of these new methods, but many factors limit their use. One of the problems in phylogenetic analyses apart from the high cost of these methods for large sample sizes is the need for high quality DNA. Some colleagues arguably advocate that the big depth of data obtained for each sample compensates for the low sample size. In cases where large sample sizes are still needed, researchers usually try to overcome the big cost of NGS methods by marking each sample with a unique marker (indexing) and mixing different samples (pooling). This method reduces considerably the costs. In the present approach, the same indexing principle is used using old genomic DNA extracts. We are applying this new approach to the study of the phylogeny of Erebid moths, one of the largest families of Lepidoptera. The current phylogenetic relationships among this family are poorly studied and hence lacking resolution. Using 40 genomes, we obtained a resolved phylogeny focusing on the deepest nodes of the group to resolve the relationships between the major lineages of this family.



A multispecies coalescent approach in higher-level systematics: Morphology and DNA inform the species-level phylogeny of “basal” tribes in the butterfly subfamily Satyrinae (Nymphalidae: Haeterini & Brassolini)

PÁVEL MATOS (Institute of Entomology, Biology Centre CAS, České Budějovice, Czech Republic) — **NIKLAS WAHLBERG** (Department of Biology, Lund University, Sweden) — **CARLA PENZ** (Department of Biological Sciences, University of New Orleans, USA)

The multispecies coalescent (MSC) is theoretically and empirically more robust than concatenation-based phylogenetic inference. Its conceptual framework relies on modeling a species tree in the light of gene trees evolution, while taking into account population-level coalescence and species-level diversification. These properties allow the MSC to infer confident species relationships and their divergence times by jointly modeling incomplete lineage sorting and the probabilities of speciation. However, this flexibility has scarcely been tested in higher level insect systematics. Here we evaluated the MSC in two early diverging tribes of the butterfly subfamily Satyrinae, the Haeterini and Brassolini. We used a multi-disciplinary dataset (morphology + molecular) informed by taxonomic understanding modeled as prior distributions in Bayesian phylogenetics to resolve the systematics of these two tribes. First, we evaluated species boundaries in the light of MSC and taxonomic opinion (lumping, splitting, and misclassification). We provide evidence that the MSC standardizes taxonomic opinion by recognizing cryptic species and divergent subpopulations within single species (Matos-Maraví et al. 2019a). Second, we evaluated the performance of MSC when both molecular and morphology evolution are jointly modeled (Matos-Maraví et al. 2019b). By taking into account evolutionary processes such as incomplete lineage sorting and gene tree incongruence, we revealed a robust species-level phylogeny of early diverging Satyrinae tribes. We conclude that the MSC will provide a robust framework for higher level insect systematics in the light of phylogenomic datasets, the fossil record incorporated into morphological datasets, and species delimitation using DNA sequences, all in a single probabilistic framework. Resolving the phylogenetic diversification in early diverging lineages of the subfamily Satyrinae is important to understand its early evolution and ancestral states such as larval host plants and geographical ranges.

References: Matos-Maraví P, Wahlberg N., Antonelli A., Penz C.M. 2019a: Species limits in butterflies (Lepidoptera: Nymphalidae): reconciling classical taxonomy with the multispecies coalescent. *Systematic Entomology*: in press. DOI: 10.1111/syen.12352. — Matos-Maraví P, Wahlberg N., Freitas AVL, DeVries P., Antonelli A., Penz C.M. 2019b: Mesoamerica is a cradle and the Brazilian Atlantic Forest is museum of Neotropical butterfly diversity (Lepidoptera: Nymphalidae: Brassolini). In preparation.

Phylogeny and evolution of Hymenoptera, with focus on the parasitoid wasps

RALPH S. PETERS (Zoologisches Forschungsmuseum Alexander Koenig, Arthropoda Department, Adenauerallee 160, 53113 Bonn, Germany)

While great progress has been made in recent years to infer the Hymenoptera tree of life, many of the parasitoid wasp taxa are still inadequately studied or excluded from large phylogenetic studies.

However, as the parasitoid wasps are arguably the most diverse arthropod group on this planet, displaying an astonishing richness in species, forms, and life histories, a thorough understanding of the evolutionary history of the



Abstracts · Oral Presentations

group is necessary to approach the ultimate goal of explaining biodiversity. In this talk, I will review the status quo of our knowledge of the evolutionary history of parasitoid wasps, summarize the most important open questions that need to be addressed, and give an outlook on future and ongoing studies that aim at closing the most severe gaps.

In this context, I will present our latest studies on one of the megadiverse parasitoid wasp superfamilies – Chalcidoidea – that target the evolution and re-classification of the group, based on analyses of phylogenomic data. Within Chalcidoidea, analyses have helped to resolve relationships that had so far been unknown or controversial. However, we also still see unresolved relationships and significant conflict within data sets as well as incongruence between phylogenomic results and evidence from other data sources.

My talk will be on behalf of a large group of contributors, presenting results from collaborative efforts.

The phylogeny of cuckoo wasps (Hymenoptera: Chrysididae) inferred from transcriptomes, DNA target enrichment data, and Sanger DNA sequences

OLIVER NIEHUIS (Department of Evolutionary Biology and Ecology, Albert Ludwig University, Hauptstraße 1, 79104 Freiburg, Germany)

Cuckoo wasps (Hymenoptera: Chrysididae) are a species-rich family of obligate brood parasites (i.e., parasitoids and kleptoparasites) whose hosts range from sawflies, wasps and bees, to walking sticks and moths. Their brood parasitic lifestyle has led to the evolution of fascinating adaptations, including chemical mimicry of host odors by some species. Long-term nomenclatural stability of the higher taxonomic units (e.g., genera, tribes, and subfamilies) in this family and a thorough understanding of the family's evolutionary history critically depend on a robust phylogeny. In a recently published study (Pauli et al. 2019), we analyzed Sanger DNA sequences of eleven protein-coding genes (ten of which are nuclear-encoded) to infer the phylogenetic relationships among 186 cuckoo wasp species representing almost all major lineages of the family. However, the available data proved insufficient to resolve the backbone of the phylogenetic tree and hence to shed light on the early diversification of the family. Here I present results from phylogenetically analyzing amino acid sequence data of 492 single-copy genes of 94 Chrysoidea and 45 outgroup species obtained by combining transcriptomic and target DNA enrichment data. The resulting phylogenetic backbone tree of Chrysididae is fully resolved and robust and challenges earlier ideas on the evolution of the family. Using the backbone topology as constraint, we subsequently obtained an almost completely resolved phylogeny of 196 cuckoo wasp and 104 outgroup species by combining the new phylogenomic with the published Sanger sequence data in one analysis. I will discuss evolutionary and taxonomical implications of the phylogenetic results and highlight the current uncertainty of the exact phylogenetic position of the family Dryinidae, previously included in the superfamily Chrysoidea.

Reference: Pauli T. et al. 2019: Phylogenetic analysis of cuckoo wasps (Hymenoptera: Chrysididae) reveals a partially artificial classification at the genus level and a species-rich clade of bee parasitoids. *Systematic Entomology* 44: 322–335.



Apoidea reloaded: phylogenomic relationships of apoid wasps and bees, its implications, and future perspectives

MANUELA SANN (University of Freiburg, Institute of Biology I (Zoology), Evolutionary Biology and Animal Ecology, Hauptstr. 1, 79104 Freiburg, Germany) — **OLIVER NIEHUIS** (University of Freiburg, Institute of Biology I (Zoology), Evolutionary Biology and Animal Ecology, Hauptstr. 1, 79104 Freiburg, Germany) — **RALPH S. PETERS** (Center of Taxonomy and Evolutionary Research, Arthropoda Department, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — **CHRISTOPH MAYER** (Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — **ALEXEY KOZLOV** (HITS gGmbH, Heidelberg Institute for Theoretical Studies, Schloss-Wolfsbrunnengasse 35, 69118 Heidelberg, Germany) — **LARS PODSIADLOWSKI** (Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — **SARAH BANK** (Georg-August-Universität Göttingen, Animal Evolution and Biodiversity, Untere Karspüle 2, 37073 Göttingen, Germany) — **KAREN MEUSEMANN** (University of Freiburg, Institute of Biology I (Zoology), Evolutionary Biology and Animal Ecology, Hauptstr. 1, 79104 Freiburg, Germany) — **BERNHARD MISOF** (Center for Molecular Biodiversity Research, Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany) — **CHRISTOPH BLEIDORN** (Georg-August-Universität Göttingen, Animal Evolution and Biodiversity, Untere Karspüle 2, 37073 Göttingen, Germany) — **MICHAEL OHL** (Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Invalidenstraße 43, 10115 Berlin, Germany)

Apoid wasps and bees (Apoidea) are an ecologically and morphologically diverse group of Hymenoptera. Major problems for our understanding of the evolutionary history of Apoidea have been the difficulty to trace the phylogenetic origin and to reliably estimate the geological age of bees. To address these issues, a comprehensive phylogenetic data set was compiled by simultaneously analyzing target DNA enrichment data and transcriptomic sequence data, comprising 195 single-copy protein-coding genes and covering almost all major lineages of apoid wasps and bee families. The comprehensive phylogeny allowed to trace the evolutionary origin of bees and revealed the Ammoplanidae as possibly the closest extant relatives of bees. In addition, the inferred phylogenetic relationships of apoid wasps require the implementation of a new classification to establish a natural system of Apoidea. To fill continuing gaps in our knowledge of the phylogeny of Apoidea I applied a genome skimming approach on key taxa that have not been considered in the previous phylogenetic study i.e. *Heterogyna*, *Eremiasphecium*, and *Entomosericus*. In my talk, I will present the results of the newly re-analyzed phylogenetic data set.

When studying the evolution of Hymenoptera reliable phylogenetic studies of representative groups are needed to provide new perspectives for future comparative and functional genomics, transcriptomics, and phylogenomics. The phylogenetic relationships of apoid wasps, for example, not only illuminate the most recent common ancestor of bees but also allow to trace the evolutionary origin of bees. The latter was accompanied by one of the most fundamental dietary transitions within the Hymenoptera, namely the shift from phyto-zoophagous to pollenivorous nutrition. The ammoplanids' biology thus indicates how the transition from a phyto-zoophagous to an exclusively pollenivorous nutrition could have taken place.

Finally, Hymenoptera are a highly suitable group to study dietary capabilities and adaptations to different food sources due to their two remarkable dietary transitions that have occurred during their evolution. On the one hand the switch from phytophagy to phyto-zoophagy which was concomitant with the evolution of parasitoidism, and the switch from phyto-zoophagy to pollenivory on the other, which mainly gave rise to the evolution of bees. In my talk, I will discuss new and future projects to study genomic adaptations and transcriptional versatility in representative Hymenoptera with specific food habits.



The evolution of head morphology in ants: analysis of an understudied character complex

ADRIAN RICHTER (Entomology group, Institut für Zoologie und Evolutionsforschung, Friedrich-Schiller-University Jena, Germany) — **ROBERTO A KELLER** (MUHNAC/cE3c eCentre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências da Universidade de Lisboa, Portugal; Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Japan) — **EVAN ECONOMO** (Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Japan) — **FRANCISCO HITA GARCIA** (Biodiversity and Biocomplexity Unit, Okinawa Institute of Science and Technology Graduate University, Onna-son, Okinawa, Japan) — **JOHAN BILLEN** (Laboratory of Socioecology and Social Evolution, Zoological Institute, University of Leuven, Belgium) — **ROLF BEUTEL** (Entomology group, Institut für Zoologie und Evolutionsforschung, Friedrich-Schiller-University Jena, Germany)

With currently 13.555 valid species, ants are the largest clade of eusocial insects. They occur in almost all terrestrial habitats and play a crucial role in various ecosystems. With their enormous diversity in behavior, dietary specializations and morphology, they are a highly attractive subject in evolutionary biology and related disciplines. However, despite of numerous studies dedicated to the group, morphological research has been neglected to an astonishing degree. As organisms interact with their environment through their morphological structures, a detailed knowledge of the phenotype and its variations is crucial for understanding the phylogeny and evolution, but also important in a wider biological context, including functional morphology or behavior. In recent years, molecular studies yielded many insights into the phylogeny of Formicidae. However, since anatomical data are presently lacking for most clades, evolutionary interpretations are often very limited. In this project we will improve this situation by systematically producing detailed morphological documentations for carefully selected representatives of ants, starting with the head as the most complex body region. Combined with a robust phylogeny, this will allow a reliable reconstruction of the evolution on the phenotypic level. Preliminary results suggest important and previously undocumented differences of the endoskeleton, the foregut and its musculature, and glands across ant lineages. It is apparent that the observed features have functional implications in most cases. However, more work needs to be done to reconstruct evolutionary pathways in a broader phylogenetic context in Formicidae, including also stemgroup members of the family.

The evolution of floral host preference in longhorn bees of the genus *Eucera* (Hymenoptera, Apidae, Eucerini): is association with pollen from bee-flowers advantageous?

ACHIK DORCHIN (The Steinhardt Museum of Natural History, Tel Aviv University) — **DAFNA LANGGUT** (Institute of Archaeology and The Steinhardt Museum of Natural History, Tel Aviv University) — **FRANK NEUMANN** (Evolutionary Studies Institute, University of the Witwatersrand) — **NICOLAS VEREECKEN** (Université libre de Bruxelles (ULB))

Flowers with specialised pollination mechanism with concealed pollen, such as in the Fabaceae and Lamiaceae, are pollinated primarily by bees and are often referred to as 'bee flowers'. While some long-tongued bees show



preference to bee flowers with restricted pollen, other species specialise on pollen accessible flowers or are floral generalists. Recent studies suggested that pollen is not an easy-to-use resource, such that changes in floral host preference would strongly depend on physiological and neurological constraints of bees. It can be therefore hypothesised that exploitation of restricted pollen from bee flowers consisted a significant event in bee evolution, opening a new ecological niche that has resulted in increased diversification of the associated bee lineages. So far, no empirical evidence for increased diversification rates has been demonstrated in bees in association with exploitation of restricted pollen from bee flowers.

This study uses phylogenetic inference and determination of pollen grains collected by ca. 390 females from ca. 80 species to trace the evolution of floral host preference in longhorn bees of the widely distributed genus *Euclera*. Based on the pollen spectrum collected, each species is assigned to one of the floral preference categories: 1. pollen accessible flowers; 2. pollen restricted flowers; or 3. generalist with regard to pollen accessibility. Reconstruction of ancestral floral preferences using Bayesian methods show that early diverging *Euclera* lineages are mostly associated with accessible pollen whereas more recently diverging lineages are capable of utilising both accessible and restricted pollen or prefer restricted pollen. We use different approaches, including character state dependent speciation-extinction (SSE), method-of-moments, and Phylogenetic Generalised Least Squares (PGLS), to test the hypothesis that a main switch event from utilising accessible pollen to restricted pollen from bee flowers has increased the rate of diversification in *Euclera* bees.

Diverse palaeofauna of Neuropterida from the mid-Cretaceous of Myanmar and its phylogenetic significance

XINGYUE LIU (Department of Entomology, China Agricultural University, Beijing 100193, China)

The Neuropterida (lacewings and allies) from the mid-Cretaceous of Myanmar were extraordinarily diverse, currently with three orders, 21 families, 68 genera, and 77 species, documented by the Burmese amber. This biota of Neuropterida display highly diversified and specialized traits in their early evolution of adaptation, but further provide significant evidence for understanding the phylogeny of this group. Here I present two cases of the phylogeny and evolution of the Burmese amber lacewings. First, the long-proboscid lacewings previously either considered as Dilaridae or Psychopsoidea were clarified to belong to the extinct psychopoid family Kalligrammatidae, which is one of the significant Mesozoic pollinating insects, based on the morphology-based phylogenetic analysis. Furthermore, high nich diversity of Mesozoic pollinating insects was revealed in light of the diversified proboscis length in Kalligrammatidae and other Mesozoic pollinating insects. Second, a diverse palaeofauna of the Burmese amber Mantispidae was discovered. The new mantispids shed new light on the deep phylogeny as well as the evolution of the raptorial forelegs of this family.



Testing the placement of beetle fossils via topology-constrained phylogenetic analyses

MARTIN FIKÁČEK (National Museum & Charles University, Prague, Czech Republic) — **ROLF G. BEUTEL** (Friedrich-Schiller-University Jena, Germany) — **CHENYANG CAI** (Nanjing Institute of Geology and Palaeontology, China & University of Bristol, UK) — **JOHN F. LAWRENCE** (Australian National Insect Collection, Canberra, Australia) — **ALFRED F. NEWTON** (Field Museum of Natural History, Chicago, USA) — **ALEXEY SOLODOVNIKOV** (Zoological Museum, Copenhagen, Denmark) — **ADAM ŚLIPIŃSKI** (Australian National Insect Collection, Canberra, Australia) — **MARGARET K. THAYER** (Field Museum of Natural History, Chicago, USA) — **SHŪHEI YAMAMOTO** (Field Museum of Natural History, Chicago, USA)

Dated phylogenies are usually constructed using fossils to calibrate the age of selected nodes. This method implies *a priori* confidence in the correct phylogenetic assignment of these fossils which is problematic because of their fragmentary preservation. In beetles, it is further impeded by a compact body structure concealing many characters and causing a high amount of homoplasy which complicates morphology-based phylogenetic analyses. Tests of the phylogenetic placement of such fossils require an analysis combining morphology with molecular data which is robust to a large number of missing characters. We propose a topology-constrained approach for such tests: the analysis is based on morphology but the tree topology of modern taxa is fixed based on the molecular studies. The fossil is allowed to move across the constrained topology. Maximum parsimony (MP) and Bayesian inference (BI) may be used; BI allows exploration of alternative placements including those with lower than maximum posterior probability and proves useful for considering alternative placements of fragmentary fossils. We tested this approach using the morphological matrix provided by the *Beetle Tree of Life* project: ten extant beetles with randomly deleted characters revealed that the accuracy stays high when at least 20% of non-genital characters (61 chars) are coded, and starts to drop with 5–10% of characters coded; both MP and BI perform in a similar way. BI reveals very few alternative placements even for taxa with 5% of characters coded, some of which are close to the correct taxon position. We used this approach to analyse the phylogenetic position of *Leehermania*, a Late Triassic fossil considered as the oldest staphylinid (and hence polyphagan) beetle. BI identifies two alternative placements of *Leehermania*: in suborder Myxophaga or close to the family Ptiliidae in Polyphaga. Additional morphological analysis excludes the latter and identifies *Leehermania* as an extinct lineage within Myxophaga, closest to the modern family Hydroscaphidae.



The phylogeny and evolution of beetles

DUANE MCKENNA (University of Memphis, Department of Biological Sciences; University of Memphis, Center for Biodiversity Research) — **SEUNGGWAN SHIN** (University of Memphis, Department of Biological Sciences; University of Memphis, Center for Biodiversity Research) — **1KITE BEETLE CONSORTIUM**

We inferred the phylogeny of beetles (Coleoptera) using 4,818 genes for 146 species and estimated timing and rates of beetle diversification using 89 genes for 521 species representing all major lineages. Phylogenomic analyses of these uniquely comprehensive datasets resolved previously controversial beetle relationships, dated the origin of Coleoptera to the Carboniferous, and supported the co-diversification of beetles and angiosperms. Moreover, we showed that genes obtained from bacteria and fungi via horizontal gene transfers were key to the Mesozoic diversification of herbivorous beetles. Beetle diversity thus appears to have resulted from multiple factors, including a low rate of lineage extinction over a long evolutionary history, co-diversification with angiosperms, and adaptive radiations of herbivorous beetles following horizontal transfers of microbial genes.

Coleoptera: Evolution of soft-bodied and neotenic forms in Elateroidea

LADISLAV BOCAK (Palacky University, Faculty of Science, Olomouc, Czech Republic) — **DOMINIK KUSY** (Palacky University, Faculty of Science, Olomouc, Czech Republic) — **MICHAL MOTYKA** (Palacky University, Faculty of Science, Olomouc, Czech Republic) — **MATEJ BOCEK** (Palacky University, Faculty of Science, Olomouc, Czech Republic)

Elateroid beetles comprise a morphologically diverse assemblage of well-sclerotized and soft-bodied families. These lineages had been placed in Elateroidea (e.g., Elateridae, Eucnemidae, Artematopodidae) and Cantharoidea (Cantharidae, Lampyridae, Lycidae etc.). Later, these superfamilies were merged in the widely defined Elateroidea, but the cantharoids were still considered monophyletic. Although earlier a sole source of phylogenetic information, phenotypic differences do not necessarily indicate distant relationships and they can be affected by ontogenetic reprogramming. Using robust molecular phylogenies inferred from transcriptomes and whole genome sequences, we can recover the backbone Elateroidea relationships and revise the formal classification. At the deepest level, the enigmatic Rhinorhipidae of a putative Lower Mesozoic origin are the sister to all other elateriform superfamilies and are definitively excluded from the Elateroidea. Soft-bodied families are distributed across the whole Elateroidea tree and their monophyly does not get any support. Additionally, three traditionally defined families, Drilidae, Omalisidae and Plastoceridae, are all nested in Elateridae. Several morphological traits repeatedly evolved in unrelated lineages and the morphology- and DNA-based topologies are irreconcilable.

Similarly, the transcriptome and genome sequencing solved radiation of net-winged beetles (Lycidae) and provided a new insight in the parallel evolution of morphological traits and neotenic females. We inferred at least six independent origin of neotenic females in Lycidae and shared morphological modifications in males. The neotenic have a tendency to produce large-bodied females, they occur in very limited ranges, are species poor, and the male bodies are often miniaturized. Their biological characteristics make them a strong indicator of the tectonical and ecological stability of the regions where they occur.



The smallest beetles and their evolutionary transformations (Ptiliidae, Staphylinoidea)

MARGARITA I. YAVORSKAYA (Department Biologie II, LMU München, Biozentrum, Großhaderner Str. 2, 82152 Planegg-Martinsried; yavorskaya@biologie.uni-muenchen.de) — **ALEXEY POLILOV** — **IGNACIO RIBERA** — **VASILY V. GREBENNIKOV** — **ROLF G. BEUTEL**

Ptiliidae (Staphylinoidea) is a beetle family that includes the smallest (0,325 mm) non-parasitic insects with the adult body length generally below 1 mm. We addressed the phylogenetic relationships within the group for the first time with a combination of molecular data and adult morphological characters. After a thorough evaluation of the data, we propose that Ptiliidae should be taxonomically divided into two subfamilies: Nossidiinae and Ptiliinae. The latter is currently composed of seven tribes: Acrotrichini, Cephaloplectini, Discheramocephalini, Nanosellini, Ptenidiini, Ptiliini and Ptinellini, although the monophyly and taxonomic status is still uncertain in some cases. Important morphological innovations evolved in the stem group of Hydraenidae + Ptiliidae, including partly internalized mouthparts suitable for saprophagy and sporophagy, a labral-mandibular locking device, a specific elytral locking mechanism with elongated alacristae, wings with fringes of hairs, and an unusual spermathecal pump. A complex feature of Ptiliidae linked with miniaturization is the transformation of the alae into “feather wings”, with a highly efficient flight mechanism unique in beetles. Nanosellini include the smallest ptiliid species and display features correlated with extremely small body size, such as simplification of the endoskeleton of the head and thorax, far-reaching reduction of the wing venation, and a reduced number of antennomeres.



01 Past climatic changes and their effects on the phylogenetic pattern of the Gondwanan relict *Maindronia* (Insecta: Zygentoma) in the Chilean Atacama Desert

ÁLVARO ZÚÑIGA-REINOSO (University of Cologne, Institute for Zoology; azunigar@uni-koeln.de) — REINHARD PREDEL (University of Cologne, Institute for Zoology; rpredel@uni-koeln.de)

The silverfish family Maindroniidae (Insecta: Zygentoma) consists of three described species from desert biomes in Sudan, the Arabian Peninsula and Chile. This distribution is remarkable for closely related arthropods, suggesting a Gondwanan relict group. Extensive collecting efforts in Chile show a surprisingly widespread distribution in the Atacama. These insects were even found in hyperarid areas where no other metazoans could be observed. *Maindronia* can thus be considered as the most adapted desert animal in the Atacama, which in turn is one of the driest deserts in the world. The common habitat preference in the Chilean Atacama, and evidently also in Sudan, suggests that hyperarid environments have always been present, at least locally, in South America over the past 120 million years. Likely, Chilean *Maindronia* have evolved with and within the Atacama Desert. This scenario clearly differs from that shown for other animals or plants that have more recently migrated into suitable environments in the Atacama. Phylogenetic analyses show the presence of at least five clades derived from a single ancestor and diverging in the last 15 million years. The divergence times of the clades can be attributed to palaeoclimatic changes; mostly periods of extreme hyperaridity.

02 Were immatures of Late Paleozoic Palaeodictyoptera strictly terrestrial?

JAKUB PROKOP (Department of Zoology, Charles University, Praha, Czech Republic) — EWA KRZEMIŃSKA (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland) — WIESŁAW KRZEMIŃSKI (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland) — KATEŘINA ROSOVÁ (Department of Zoology, Charles University, Praha, Czech Republic) — MARTINA PECHAROVÁ (Department of Zoology, Charles University, Praha, Czech Republic) — ANDRÉ NEL (Muséum national d'Histoire naturelle, Sorbonne Universités, Paris, France) — MICHAEL S. ENGEL (Division of Entomology, Natural History Museum, and Department of Ecology & Evolutionary Biology, University of Kansas, Lawrence, Kansas, USA & Division of Invertebrate Zoology, American Museum of Natural History, New York, USA)

Palaeodictyopterid insects, with their specialized haustellate mouthparts, constitute a significant proportion of Late Paleozoic insect diversity. The currently dominant hypothesis presumes that their immature stages occupied strictly terrestrial habitats, although 19th and early 20th century authors hypothesized them to have had specializations for amphibious or aquatic life-histories. We re-examined the morphology of immature stages and adults of several species by various microscopic techniques. Our results reveal that some members of Palaeodictyoptera had aquatic or semiaquatic larval specializations during at least a brief period of their postembryonic development. Moreover, we found bifid lateral abdominal structures which were possibly functional or rudimentary tracheal gills retained by some adults of Megaseoptera. Accordingly, amphibious life-strategies played a significant role in the life of certain lineages within this early diverging group of Pterygota.



03 Cryptic diversity in cockroaches: Phylogeny of the genus *Xestoblatta* (Blattodea: Ectobiidae) and the recognition of two new genera in the Neotropical region

ANDRÉZ VÉLEZ-BRAVO (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; avelez82@gmail.com) — **JUAN M. DAZA-ROJAS** (Grupo Herpetológico de Antioquia (GHA), Universidad de Antioquia (UdeA), Medellín, Colombia; jumadaza@gmail.com)

Xestoblatta is a cockroach genus with 45 known species and distributed from southern Mexico to southern Brazil. Since its description, Hebard (1916) and other authors have recognized the existence of high intrageneric morphological variability mostly the specialization of the male abdominal tergites and number of branches of the unlar vein. Recently, we have found strong evidence to reject the monophyly of *Xestoblatta*. Therefore, the existence of incongruence between the morphological and molecular evidence in *Xestoblatta* is possible. We carried out a phylogenetic analysis for the genus *Xestoblatta* to test its monophyly using DNA sequences from mitochondrial and nuclear regions. The results show a non monophyletic *Xestoblatta* with three well-supported but not closely related clades. Combining genetic data, external morphological characters and the configuration of the male genital sclerites we propose a new taxonomic arrangement. *Xestoblatta sensu stricto* is defined and the remaining species are relocated in two new genera.

Reference: Hebard M. 1916: Studies in the Group Ischnopterites (Orthoptera, Blattidae, Pseuomopinae). Transactions of the American Entomological Society 42: 337–383.

04 Recategorization of cockroach mating behaviour

ZUZANA KOTYKOVÁ VARADÍNOVÁ (Department of Zoology, Charles University; Department of Zoology, National Museum) — **MICHAEL KOTYK** (Department of Zoology, Charles University) — **TOMÁŠ DVOŘÁK** (Department of Zoology, Charles University)

Highly ritualized sexual behaviour of cockroaches is spectacular phenomenon. Traditionally, three different mating patterns are recognised. To better understand their evolutionary relationships, we explored diversity of courtship and mating behaviour in family Blaberidae, which is the only cockroach family where all three types are present. We report descriptions of mating patterns in 21 Blaberidae species, 16 of them haven't been examined before. Qualitative behavioural elements of our data and additional 17 species from the literature were analysed with multidimensional statistical methods. As opposed to three traditionally recognized mating types, only two clusters were consistently supported by analyses and biological interpretations. Therefore, we propose to distinguish two types of cockroach mating patterns: ancestral type which is identical with type A and derived types which include former types B and C as well as other cases which are not clearly attributable to ancestral type. Derived types then originated multiple times independently from the ancestral type.



05 Karyotype evolution of Oxyhaloinae cockroaches

MAREK JANKÁSEK (Department of Zoology, Charles University) — **ZUZANA KOTYKOVÁ VARADÍNOVÁ** (Department of Zoology, Charles University; Department of Zoology, National Museum) — **FRANTIŠEK ŠTAHLAVSKÝ** (Department of Zoology, Charles University)

Cockroaches of Afrotropical subfamily Oxyhaloinae (Blattodea: Blaberidae) are widely known due to the popularity of Madagascar hissing cockroaches as pet species. It is thus surprising that evolutionary relationships and cytogenetical characteristics of this group haven't been studied in detail yet. We analysed the phylogeny of 24 Oxyhaloinae species representing all three traditionally recognized tribes (Oxyhaloini, Nauphoetini, Gromphadorhini) and 3 incertae sedis genera based on three mitochondrial (12S, 16S, COI) and three nuclear (18S, 28S, H3) markers. Karyotypes of 12 species are described for the first time and additional karyotype information for other 4 species are provided. Surprisingly, intraspecific chromosome number polymorphism was observed in two species. The first application of molecular-cytogenetic methods within Blattodea in form of fluorescent in situ hybridization using 18S rDNA probe revealed intraspecific 18S rDNA loci number variation in four species. All cytogenetic characteristics are discussed in the context of obtained phylogenetic hypothesis and put in a frame of recent knowledge.

06 Relationships within *Poecilimon ornatus* species group (Orthoptera)

MACIEJ KOCIŃSKI (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland; e-mail: kocinski@isez.pan.krakow.pl) — **DRAGAN CHOBANOV** (Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 1 Tsar Osvoboditel Boul., 1000 Sofia, Bulgaria) — **BEATA GRZYWACZ** (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland)

Poecilimon Fischer, 1853 is one of the largest genera of the subfamily Phaneropterinae (Orthoptera, Tettigoniidae). It consists of 142 species distributed in the Palaearctic area with the highest number of endemic species in the Aegean and Pontic areas. All species are micropterous, short-winged and unable to fly. One of the least known species groups within the genus is *Poecilimon ornatus*. The most dispersed taxon in the group is *Poecilimon affinis* with numerous subspecies. This species is distributed in mountainous areas from northern Greece, through the central and western Balkans to the Carpathians in Romania and in an isolated spot in Ukraine. *P. ornatus* group consists of 13 taxa (five taxa currently having subspecies status and two species status are here named *P. affinis* complex). Species from *P. ornatus* group have been described mainly based on morphological characteristics, as well as the type of singing. In order to confirm the large variation within the group and to clarify the discrepancies between the published data, we conducted the genetic studies. A total of 7 taxa belonging to *P. affinis* complex, 10 species of *P. ornatus* group (outside the complex) and 5 species outside the group as outgroup were used in the present analyses. The total alignment of DNA fragment consisted of 830 (COI) and 450 (ITS1) base pairs. Genes were sequenced to establish a phylogenetic tree by using Maximum Likelihood estimation and Bayesian Inference analyses. The species that we initially identified as a complex do not form a monophyletic group, but we noticed a high genetic variability between *P. affinis* species. Additionally, we can suppose that *P. gracilis* is the most basal species compared to the other taxa in *P. ornatus* group.



07 Notes on the molecular relationships within the genus *Aerotegmina* (Orthoptera: Tettigoniidae: Hexacentrinae)

BEATA GRZYWCZAK (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland) — **MACIEJ KOCIŃSKI** (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland) — **KLAUS-GERHARD HELLER** (Grillenstieg 18, 39120 Magdeburg, Germany) — **CLAUDIA HEMP** (University of Bayreuth, Dept. Plant Systematics, 95440 Bayreuth, Germany)

Aerotegmina Hemp, 2001 is an East African genus, which belongs to the subfamily Hexacentrinae. Species of this genus are found in the canopy of montane forests, in submontane and lowland forest on old and young mountains in eastern Africa. Currently, this flightless genus contains five species with a low mobility. The genus is characterized by strongly inflated wings used for acoustical communication. The phylogenetic relationship within these species is still unclear. In our study, we investigated the affinity within *Aerotegmina* for the first time using molecular methods. We combined molecular data from two mitochondrial (COI and 16S) and one nuclear gene (H3). *Aerotegmina* was supported as a monophyletic group. The species from the South Pare Mountains and the Taita Hills, both belonging to the geologically old mountain chain of the Eastern Arc form a sister group and are the most basal taxa of the genus. Sister group to these morphologically and molecularly basal species is the wide-spread *A. kilimandjarica*. *A. shenganae*, *A. taitensis* and *A. kilimandjarica* are all distributed in northern Tanzania up to central Kenya and exhibit a completely different morphology (being considerably smaller) compared to the large *Aerotegmina* species *A. megaloptera* and *A. vociferator* restricted to the Nguru and Udzungwa Mountains further south. The different morphology agrees with their molecular relationship, both groups being well separated molecularly.

08 Phylogeny and species delimitation within the *Platycleis albopunctata* group (Orthoptera: Tettigoniidae) – a preliminary study

SZYMON CZYŻEWSKI (Department of Entomology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland)

Platycleis Brunner von Wattenwyl, 1893 is a genus group of Orthoptera belonging to the family Tettigoniidae. It includes numerous similar species with occurrence restricted to Palearctic and with one of the best morphological traits being the shape of the female subgenital plate. They inhabit dry habitats such as xerothermic grasslands and steppes. Conducted research comprised studying the phylogeny of *Platycleis albopunctata* group. Using four DNA markers, H3 (nDNA marker), ITS2 (nDNA marker), ND1 (mtDNA marker), we constructed phylogenetic trees of the genus group *Platycleis* and of *P. albopunctata* group which consists of several subspecies, focusing on two subspecies most wide spread in Europe, *P. a. albopunctata* and *P. a. grisea*. Molecular analyses, done on specimens from southern Poland, have shown significant differences between the two examined subspecies. Comparing exclusively the H3 marker seems to indicate an even larger difference, with *P. grisea* being closer to another species from the same genus, *P. affinis* which differs morphologically even more from the examined subspecies. As the two latter species occur together in the steppes of the Pannonian Basin, this could suggest hybridization to have occurred, but to verify this assumption requires further research.



09 Highly divergent DNA barcodes in the butterfly *Colias palaeno* (Lepidoptera: Pieridae): evidence of cryptic species, interspecific hybridization or *Wolbachia* infection?

NAZAR SHAPOVAL (Zoological Institute of Russian Academy of Sciences, Russia) — **GALINA KUFTINA** (Altai State University, Russia) — **ROMAN YAKOVLEV** (Altai State University, Russia) — **ANATOLY KRUPITSKY** (Moscow State University, Russia; Severtsov Institute of Ecology and Evolution, Russia)

DNA barcoding is an effective and widely used tool in biodiversity researches. Mitochondrial DNA barcodes serve as valuable markers for species identification, exploring boundaries among taxa, detecting cryptic diversity and solving existing taxonomic problems.

However, numerous studies have demonstrated that mtDNA-based phylogenies are not always congruent with phylogenies inferred from the nuclear DNA. This phenomenon is called mito-nuclear discordance. Several mechanisms have been shown to generate mito-nuclear discordance, such as incomplete lineage sorting, mitochondrial introgression, natural selection or genetic sweeps mediated by *Wolbachia* infection.

During the complex investigation of the Palaearctic Lepidoptera we have found striking example of mito-nuclear discordance in the taxonomically well-studied species - Moorland clouded yellow, *Colias palaeno* (Linnaeus, 1761). We sequenced a standard barcoding region (the 658 bp fragment of COI gene) for 850 specimens that spans the whole species distribution range. Analysis of DNA barcodes revealed five deeply diverged mitochondrial lineages, that were characteristic of the species level. These lineages occur in sympatry and recovered as separate entities on the phylogenetic tree, with minimum uncorrected pairwise distances of the COI gene among them ranged from 1,5% to 9%, which exceed typical interspecific COI distances reported for butterflies. In contrast to these results, we have found that *Colias palaeno* is genetically homogenous with respect to studied nuclear genes. The recovered mitochondrial lineages did not correspond neither to the phenotypic traits, nor to the clustering of nuclear genes. Thus, we found no clear evidence of cryptic species within *Colias palaeno*. Further investigation revealed strong association of the mitochondrial clades with two different *Wolbachia* strains, supporting the hypothesis that the mito-nuclear discordance resulted from selection on the mitochondrial genome due to selective sweeps by *Wolbachia* strains. We conclude that *Wolbachia* infection has played a key role in the evolution of mitochondrial genomes of *Colias palaeno*.

The financial support for this study was provided by the grants from the Russian Foundation for Basic Research No. 18-34-00756, 17-04-00828, 17-04-00754. The work was conducted within the framework of the state task No. 6.2884.2017/4.6 Ministry of Education and Science of Russian Federation.



10 Preliminary results of research on a morphologically uniform genus *Apisa* (Lepidoptera: Erebidae: Arctiinae)

ANNA PRZYSTALKOWSKA (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland; przystalkowska@isez.pan.krakow.pl) — **ŁUKASZ PRZYBYŁOWICZ** (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland) — **SEBASTIAN TAR CZ** (Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland)

The subject of the current research are Afrotropical and Palearctic (Arabian Peninsula) moths belonging to genus *Apisa* Walker, 1855 within the Syntomini tribe and family Erebidae. Studied genus is divided to three subgenera (*Apisa*, *Dufraneella* Kiriakoff, 1953, *Parapisa* Kiriakoff, 1952). Up to date it was not subject to modern taxonomic revision. Currently the nine species are described, however their biology is very poorly known. The main problem is the extraordinary morphological uniformity of specimens of the genus *Apisa*. As a complement to morphological analyzes, we use molecular techniques such as DNA barcoding. Application of combined techniques enables better understanding of the studied group. Because of that, it is possible to systematize the current knowledge and distinguish a number of new species. So far, we have got COI mtDNA sequences from more than 50 specimens. The system of clades on the phylogenetic tree partially confirmed compliance with some morphotypes marked on the basis of morphology. Within the genus there may be cryptic species, and the genus itself has more taxa than previously described.

As a result of conducted morphological, biogeographical and molecular analyzes, at least two new species will be described. The male genital organs with vesica in details are illustrated for the first time.

The majority of determinations are carried out on the male genital structures which are richer in the informative structures and also more diverse. Here we go to another difficulty in assigning females to appropriate species. Female reproductive organs are less in characteristics features so the morphological designation is almost impossible.

The research is conducted on specimens deposited in collection of ISEA PAS, borrowed from museums in the Great Britain, German, Belgium, Italy, USA, and from private collectors.

11 Intra- and interspecific divergences within the genus *Trypocopris* Motschulsky, 1858 evaluated through shape variation of morphological traits

ROGGERO ANGELA (University of Torino, Dpt. of Life Sciences and Systems Biology, Torino, Italy) — **COLLA FABRIZIO** (Civico Museo di Storia Naturale di Trieste, Trieste, Italy) — **ZANIN GAIA** (Civico Museo di Storia Naturale di Trieste, Trieste, Italy) — **ROLANDO ANTONIO** (University of Torino, Dpt. of Life Sciences and Systems Biology, Torino, Italy) — **PALESTRINI CLAUDIA** (University of Torino, Dpt. of Life Sciences and Systems Biology, Torino, Italy)

Most of the dung beetles are facilitated in dispersal, and search for partner or food because they are good flyers. Shape, size and structure of hindwings are therefore functionally important in these Coleoptera. Recent studies (Bai et al. 2011) suggested that these traits may also be useful in systematics and phylogenetics analyzes, as it is



the case of Drepanocerina and Onthophagina taxa where differentiated patterns of shape variation were shown for the hindwings (Palestrini et al. 2016). The small Palearctic *Trypocapris* genus includes at present seven species, with several subspecies commonly established on the ground of chromatic differences. Previous molecular studies (Carisio et al. 2004) highlighted how interspecific and intraspecific differences were supported by genetic divergence in this genus. We here applied the geometric morphometrics approach on various anatomical traits to verify whether morphological variation can detect systematic divergence and mirrors genetic divergences. Specimens of *Trypocapris vernalis* (Linnaeus, 1758), *T. pyrenaicus* (Charpentier, 1825), *T. alpinus* (Sturm & Hagenbach, 1825), *T. fulgidus* (Motschulsky, 1845) and *T. amedei* (Fairmaire, 1861) from several European localities were examined in the present research. Results evidenced that the overall shape variation of the hindwings discriminated the five *Trypocapris* species, confirming thus the interspecific divergence. Differences among guilds of *T. vernalis* specimens from the Eastern Adriatic Coast (localities from Eastern Italy, Slovenia, Croatia and Albania) were assessed after these specimens were classified on the basis of the chromatic characteristics. Inter-guilds differences were also detected for the shape of the head, epipharynx and pronotum, suggesting therefore that chromatic and morphological divergences represent differences at the subspecific level. A combined phylogenetic analysis (Goloboff & Catalano 2016) has thence been carried out to reconstruct the relationships within the *Trypocapris* species and subspecies using the characters examined in this study.

References: Bai M., McCullough E., Song K.-Q., Liu W.-G., Yang X.-K. 2011: Evolutionary constraints in hind wing shape in Chinese dung beetles (Coleoptera: Scarabaeinae). *PLoS ONE* 6: e21600. — Carisio L., Cervella P., Palestrini C., Delpero M., Rolando A. 2004: Biogeographical patterns of genetic differentiation in dung beetles of the genus *Trypocapris* (Coleoptera, Geotrupidae) inferred from mtDNA and AFLP analyses. *Journal of Biogeography* 31: 1149–1162. — Goloboff P.A., Catalano S.A. 2016: TNT version 1.5, including a full implementation of phylogenetic morphometrics. *Cladistics* 32: 221–238. — Palestrini C., Roggero A. 2016. Hindwings and elytra: shape and size evolution in dung beetles. 1st UIZ-SIE-SIB Congress, Milano, p.354.

12 Phylogeny and systematics of New World Bess Beetles (Coleoptera: Passalidae: Passalinae)

CRISTIAN FERNANDO BEZA-BEZA (Department of Biological Sciences, University of Memphis, Memphis, TN; cfbeza@memphis.edu) — **LARRY JIMÉNEZ-FERBANS** (Facultad de Ciencias Básicas, Universidad del Magdalena, Carrera 32 No 22 – 08, Santa Marta, Colombia, P.C. 470004; ljimenezf@unimagdalena.edu.co). — **DUANE MCKENNA** (Department of Biological Sciences, University of Memphis, Memphis, TN; dmckenna@memphis.edu)

The family Passalidae (Coleoptera: Scarabaeoidea) contains approximately 700 species distributed mainly in the Pan-tropical region, with around the 50% of its species confined to the New World (Reyes-Castillo 2003). Taxonomically, the family is divided in two subfamilies: Aulacocyclinae (Oriental and Australian regions) and Passalinae (Pan-tropical). Passalinae is comprised of five tribes: Solenocyclini (Africa-Madagascar), Leptaulacini (India-Southeast Asia to New Guinea), Macrolini (India-Southeast Asia to Australia) and, in the Neotropical region, Passalini and Proculini. The two Neotropical tribes together contain approximately 400 species in 26 genera. Passalini contains six genera, most of which occur only in South America. and Proculini contains 20 genera, most of which occur only in Mesoamerica. The phylogenetic relationships between Passalini and Proculini nonetheless remain unclear. For



Abstracts · Poster Presentations

example, in some phylogenetic analyses Proculini renders Passalini paraphyletic (Gillogly 2004, Boucher 2006, Jiménez-Ferbans 2014), in other analyses, each tribe is monophyletic (Boucher 2006, Fonseca et al. 2011). Moreover, the relationships of genera within Passalini and Proculini have been little-studied. The limits between the genera are often diffuse, and until now no study has conducted an analysis with all 26 New World genera of Passalidae. Here we reconstruct the phylogeny of the genera of Passalini (5/6) and Proculini (20/20), employing morphological and molecular data (genes CAD, Wingless, and 28S). The matrix included 93 ingroup and 8 outgroup species. Outgroups included representatives of the passalid subfamily Aulacocyclusinae, and within Passalinae, the tribes Macrolini, Leptaulacini, and Solenocyclusini. We used *Geotrupes* sp. (Geotrupidae) to root the trees. We conducted parsimony, Bayesian, and maximum likelihood analyses on individual and concatenated alignments. In all analyses, Proculini and Passalini were recovered as monophyletic. Passalini: *Passalus* was not monophyletic and at least one of the genera previously synonymized must be revalidated. In Proculini, most genera in which the monophyly was tested were recovered as independent lineages; however, *Pseudacanthus*, *Vindex*, *Petrejoides*, and *Popilius* were not monophyletic. We recovered three main clades within Proculini (*Proculus*, *Vindex*, and *Chondrocephalus*). These clades are similar to the clades recovered by Boucher (2006), and the larval groupings suggested by Schuster (1992).

References: Boucher S. 2006: Évolution et phylogénie des coléoptères Passalidae (Scarabaeoidea). Les taxons du groupe famille la tribu néotropical de Proculini et son complexe *Veturius*. *Annales de la Société Entomologique de France* 41: 239–603. <https://doi.org/10.1080/00379271.2005.10697444> — Fonseca C.R.V., Barbosa M.L.L., Farnandez M.F.S. 2011: A hypothetical evolutionary history of passalid beetles narrated by the comparative anatomy of the hindgut (Coleoptera: Passalidae). *Zootaxa* 3012: 1–20. — Gillogly, A. 2005: Review of the genus *Popilius* and preliminary phylogeny of Passalidae (Coleoptera), PhD thesis, College Station, Texas, USA: Texas A&M University. — Jiménez-Ferbans, L., González, D., Reyes-Castillo, P. 2016: Phylogeny and species delimitation in the group *Rhodocanthopus* of the genus *Passalus* (Coleoptera: Passalidae) inferred from morphological and molecular data, with description of two new species. *Arthropod Systematics and Phylogeny* 74: 255–266. — Reyes-Castillo P. 2003: Familia Passalidae. Pp. 135–187 in: Morón M.A. (ed.), *Atlas de los escarabajos de México Coleoptera: Lamellicornia*. Vol. II. Familias Scarabaeidae, Trogidae, Paissalidae y Lucanidae. Vol. II. Argania Editó, Barcelona. — Schuster, J.C. 1992. Passalidae: State of larval taxonomy with description of new world species. *The Florida Entomologist* 75: 357–369.

13 Vicariance and long-distance dispersal shaped the distribution of ‘Gondwanan’ water scavenger beetles

MATTHIAS SEIDEL (Department of Zoology, Faculty of Science, Charles University & National Museum, Prague, Czech Republic) — **VÍT SÝKORA** (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — **RICHARD A. B. LESCHEN** (Manaaki Whenua, New Zealand Arthropod Collection, Auckland, New Zealand) — **MARTIN FIKÁČEK** (Department of Zoology, Faculty of Science, Charles University & National Museum, Prague, Czech Republic)

Cylominae is an enigmatic subfamily of water scavenger beetles (Coleoptera: Hydrophilidae) with a disjunct Southern Hemisphere distribution. Here we present the first comprehensive molecular phylogeny of this subfamily and explore the historical biogeography and processes that led to the current distribution of the group in Australia, New Zealand, austral South America, and South Africa. Our results reveal the subfamily to consist of two principal clades whose reciprocal monophyly is supported by larval morphology; these clades correspond to the two former tribes Cylomini (now containing 14 genera) and Andotypini (now containing 9 genera). Four genera from New Zealand remain undescribed. Our study demonstrates that Cylominae originated in the Early Cretaceous in temperate



southern Gondwana and subsequently reached their current distribution by a combination of vicariance and long-distance dispersal events. Most interestingly, the presence of the subfamily in South Africa is revealed as a result of a long-distance dispersal postdating the separation of the African continent from Southern Gondwana by more than 50 million years. The New Zealand fauna originated by a mixture of vicariance and long-distance dispersal, all genera arriving prior to the Oligocene bottleneck.

14 Molecular phylogeny of terrestrial water scavenger beetle tribe Megasternini (Hydrophilidae: Sphaeridiinae) reveals repeated and bidirectional continental interchange during the Eocene

EMMANUEL ARRIAGA-VARELA (Charles University & National Museum, Prague, Czech Republic) — **MARTIN FIKÁČEK** (National Museum & Charles University, Prague, Czech Republic) — **DANIEL MARQUINA** (Swedish Museum of Natural History & Stockholm University, Stockholm, Sweden)

Megasternini (Coleoptera: Hydrophilidae: Sphaeridiinae) is the most diverse tribe in the family with nearly 600 described saprophagous species distributed all over the globe. In this study we used sequences of eight gene regions, five nuclear (*histone 3*, *wingless*, *topoisomerase 1*, *18s*, *28s*) and three mitochondrial (*cytochrome oxidase I and II*, and *12S*), in order to investigate the phylogenetic relationships and historical biogeography of members of tribe Megasternini. Analyses employed are Maximum likelihood (ML) (IQtree), Bayesian inference (BI) including divergence dating based on a relaxed-clock model (MrBayes) and ancestral area estimation analyses (BioGeoBears). Results of the analyses of BI and ML resulted in similar tree topologies, although with low posterior probability support in basal divergences on the BI tree. The resulting topology from BI is adopted to revise the suprageneric classification and historical biogeography of the tribe. Our results support the division of the tribe in two main lineages that are defined by morphological characters: subtribes Megasternina and Oosternina new subtribe. We identify 12 clades, two in Oosternina and nine in Megasternina. The main morphological patterns among the members of these clades are discussed. Genera *Cercyon* Leach, *Oosternum* Sharp, *Cetiocyon* Hansen, *Australocyon* Hansen and *Pelosoma* were not recovered as monophyletic, with species of *Cercyon*, the most diverse genus in the tribe found all over the tree. Our results suggest that a taxonomical reorganization of the generic concepts in the tribe is needed. The ancestral area reconstruction estimation show a series parallel intercontinental dispersion events in different directions happening between 55–50 Mya corresponding to the hyperthermal conditions of the early Eocene that allowed massive biotic interchange between landmasses. Interchange between the Oriental region and the New World happened in opposite directions during this period. The climatic changes that occurred during the Eocene had a differential effect on the diversification patterns in both subtribes.



15 Origin, evolution and biogeography of New Zealand riffle beetles (Elmidae)

Vít SÝKORA (Charles University, Prague, Czech Republic) — **MARTIN FIKÁČEK** (National Museum & Charles University, Prague, Czech Republic) — **RICHARD A.B. LESCHEN** (Landcare Research, Auckland, New Zealand) — **CRYSTAL A. MAIER** (Harvard Museum of Comparative Zoology, Cambridge, USA) — **MATTHIAS SEIDEL** (National Museum & Charles University, Prague, Czech Republic) — **WILLIAM D. SHEPARD** (Essig Museum of Entomology, Berkeley, USA) — **CHERYL B. BARR** (Essig Museum of Entomology, Berkeley, USA) — **MIGUEL ARCHANGELSKY** (Universidad Nacional de La Patagonia, Esquel, Argentina) — **NICOLÁS R.M. ROMÁN** (Universidad Nacional de La Patagonia, Esquel, Argentina)

New Zealand is known for its long isolation and complex geological and climatic history which greatly influenced biota of the archipelago. This resulted in a mosaic of surviving ancient Gondwanan relics and later colonizers that sometimes evolved into unusual forms. Although generally rather poor in diversity, this is also the case of New Zealand aquatic beetle fauna as it still includes groups that were able to undergo adaptive radiations to fill open niches. One such group are beetles of the family Elmidae. They are represented in New Zealand by single genus *Hydora* belonging to the traditionally recognized subfamily Larinae. *Hydora* represents the most abundant beetle taxon in New Zealand running waters. However, its diversity, ecology and evolution have never been studied. The aim of our work is to reconstruct dated phylogeny and biogeography of *Hydora* and other related Gondwanan elmid genera to be able to understand its origin and evolution. Our preliminary results suggest that New Zealand *Hydora* is of ancient Gondwanan origin and its diversity is approximately three times higher than currently described ten species (8 in New Zealand, 2 in South America and 1 in Australia). Unlike most larinae, both adults and larvae adapted to diverse microhabitats (gravel, submerged moss etc.), which is also reflected in their diverse morphology. This fact, together with the geological history of New Zealand, likely contributed to high species diversity of *Hydora*, a condition that is rather unusual among larine riffle beetles.

16 Excitators: female-specific, presumably secretory structures in marsh beetles (Coleoptera: Scirtidae) – diversity and evolutionary significance

RAFAL RUTA (Department of Biodiversity and Evolutionary Taxonomy, University of Wrocław, Przybyszewskiego 65, 51-148 Wrocław, Poland; rafal.ruta@uwr.edu.pl)

Scirtidae (Coleoptera: Scirtoidea) is a family of beetles with ca. 1900 species and 71 genera worldwide. The group is understudied in many aspects, including its phylogeny, taxonomy, and morphology. In most phylogenetic analyses of Coleoptera, Scirtoidea seem to represent old evolutionary lineage, a sister group to remaining Polyphagan beetles (e.g. McKenna et al. 2015), although in a recent study (Beutel et al. 2019) Scirtoidea are not placed at the base of Polyphaga. Champion (1897) was the first researcher who noted presence of peculiar structures on elytra of females of some Central American species of *Contacyphon* Gozis, and immediately recognized their similarity with structures present in males of Malachiinae. In a study by Ruta (2008), the term excitator (by analogy to the name of similar structures in Malachiinae) was attributed to structures in Scirtidae, as it is highly plausible that modified portions of elytra secrete sexual pheromones. During subsequent studies, excitators were found in numerous genera of Scirtidae, mostly on elytra, but rarely also on the pronotum and likely also on the head. Excitators are absent in



monotypic subfamilies Nipponocyphoninae Lawrence & Yoshitomi and Stenocyphoninae Lawrence, and are present in numerous genera of Scirtinae, what suggests that they either evolved independently multiple times, or were lost in some lineages of marsh beetles.

References: Beutel R.G., Pohl H., Yan E.V., Anton E., Liu S.-P., Šlipiński A., McKenna D., Friedrich F. 2019: The phylogeny of Coleopteridae (Hexapoda) – morphological characters and molecular phylogenies. *Systematic Entomology* 44: 75–102. — Champion G.C. 1897: Helodinae. *Biologia Centrali-Americana. Insecta. Coleoptera. Vol. III. Part 1. Serricornia*: 600–622, 661–662. — McKenna D., Wild A.L., Kojun K., Bellamy Ch.L., Beutel R.G., Caterino M.S., Farnum Ch.W., Hawks D.C., Ivie M.A., Jameson M.L., Leschen R.A.B., Marvaldi A., McHugh J.V., Newton A.F., Robertson J.A., Thayer M.K., Whiting M.F., Lawrence J.F., Šlipiński A., Maddison D.R., Farrell B.D. 2015: The beetle tree of life reveals that Coleoptera survived end-Permian mass extinction to diversify during the Cretaceous terrestrial revolution. *Systematic Entomology* 40: 835–880. — Ruta R. 2008. Contribution to the knowledge of Seychellois Scirtidae (Coleoptera: Scirtoidea). *Zootaxa* 1913: 49–68.

17 Tiny critters from giant mountains: evolution of moss-inhabiting flea beetles (Coleoptera: Chrysomelidae)

ALBERT FRANTIŠEK DAMAŠKA (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic) — **MARTIN FIKÁČEK** (Department of Zoology, Faculty of Science, Charles University, Prague, Czech Republic; National Museum, Prague, Czech Republic)

Flea beetles (Aلتicini) are a highly diversified group of leaf beetles (Chrysomelidae) with about 8 000 known species from about 560 genera distributed worldwide except Antarctica. The major life strategy of flea beetles is external feeding on vascular plants, similarly to other leaf beetles. However, studies published during last years revealed existence of numerous different flea beetle genera feeding on mosses. Moss-inhabiting flea beetles are usually highly specialized and share similar morphological characteristics, including flightlessness, compact body shape and modified antennae. However, their phylogenetic position remained unknown. In this study, we performed a phylogenetic analysis of 14 known moss- and leaf litter inhabiting flea beetle genera, included into a large dataset of various genera of flea beetles. We sequenced 2 mitochondrial and 2 nuclear genes previously used for phylogenetic analyses of Aلتicini. We also added numerous Neotropical external feeding alticine genera, because taxon samples from previous studies (Ge et al. 2012; Nie et al. 2017) consisted mainly of Oriental genera. Although deep divergences and phylogenetic positions of several genera were not resolved, the analysis revealed a multiple origin of moss- and leaf litter inhabitation among flea beetles. The morphologically similar Asian genera *Ivalia* and *Cangshanaltica* were revealed as distinct lineages within the *Chabria* generic group. Their species-level phylogenetic analysis indicated that both genera originated in the Sundaland and colonized Eastern Asia, including radiation of *Ivalia* on Taiwan. The Neotropical genera from the *Monoplatys* generic group formed a monophyletic lineage deeply nested inside the generic group, which shows that monoplatines involved this strategy only once. The Palearctic genus *Minota* is revealed as a relative of other mainly Palearctic genera *Mantura* and *Batophila*. Additionally, the study revealed phylogenetic positions of various non-moss-inhabiting flea beetles from the Neotropics. The majority of Neotropical flea beetle genera formed monophyletic clades, which suggests that Neotropical flea beetle fauna is a result of several migration events from the Old World.

References: Ge D. et al. 2012: Suprageneric systematics of flea beetles (Chrysomelidae: Aلتicinae) inferred from multilocus sequence data. *Molecular Phylogenetics and Evolution* 62(3): 793–805. — Nie R.-E. et al. 2017: The phylogeny of Galerucinae (Coleoptera: Chrysomelidae) and the performance of mitochondrial genomes in phylogenetic inference compared to nuclear rRNA genes. *Cladistics* 0: 1–18.



18 Phylogeny of the *Ropalopus ungaricus / insubricus* group (Coleoptera: Cerambycidae: Callidiini) of the West Palaearctic region

LECH KARPIŃSKI (Museum and Institute of Zoology, Polish Academy of Sciences, Warsaw, Poland) — WOJCIECH T. SZCZEPAŃSKI (Department of Zoology, Faculty of Biology and Environmental Protection, University of Silesia, Katowice, Poland)

We revised the phylogeny of *Ropalopus* species belonging to the taxonomically intricate *ungaricus/insubricus* group. The key-characters, including the male terminalia, were examined by means of scanning electron microscopy (SEM). The phylogenetic analyses are based on 34 adult morphological characters. Both the strict and majority consensus trees reveal the monophyly of the revised group. The strict consensus tree strongly indicates that the European populations, consisting of six subspecies of *R. ungaricus*, form a separate clade. The taxa that inhabit the Mediterranean zone are probably evolutionarily older than those that reach the central part of Europe. It seems that the most recent common ancestor of this group was probably present on the territory of the Near East and the Balkan Peninsula. In this region, four separate evolutionary lineages have emerged, which the current species: *R. hanae*, *R. lederi*, *R. nataliyae* and *R. ungaricus* originate from. The ancestor of the last mentioned species most probably inhabited the territory of the Balkan Peninsula, from where its migration process was initiated towards Europe. Likely, it was a thermophilic species that colonized the region of southern Europe. Subsequently, during the Messinian salinity crisis (ca. 5.96–5.33 million years ago), when the land bridge between the Europe and the territory of present North Africa existed, it has extended its range to today's Algeria, and afterwards apparently as far as to mountainous areas of southern Spain. Along with the colonization of the northern areas of Europe, the form adapted to a more moderate climate began to emerge. The differentiation of individual taxa possibly became more intensive during the Pleistocene. The temperature fluctuations (alternate glacials and interglacials) were most probably the main factors responsible for these processes. The thermophilic form could survive in the Apennine, Illyrian and Balkan refugia. The current distribution of the particular subspecies of *Ropalopus ungaricus* results from the recolonization of the populations, which possibly have occurred approx. 11,000 years ago, after the Last Glacial Period. Apart from geographical barriers, the main differentiating factor in this group proved to be the altitude above sea level. Taxa of the discussed group are therefore allopatric or, when parapatric, they are altitudinally isolated.



19 Transcriptome analyses provide an updated phylogeny of the family Cerambycidae and insights into the distribution of plant cell wall degrading enzymes in these beetles

NA RA SHIN (Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany) — **SEUNGGWAN SHIN** (University of Memphis, Department of Biological Sciences, TN, USA) — **ROY KIRSCH** (Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany) — **PETR SVACHA** (Institute of Entomology, Biology Centre, Czech Academy of Sciences, Ceske Budejovice, Czech Republic) — **OLIVIER DENUX** (French National Institute for Agricultural Research, Paris, France) — **SYLVIE AUGUSTIN** (French National Institute for Agricultural Research, Paris, France) — **VINCENT LOMBARD** (AFMB UMR 7257 Case 932, Campus de Luminy, Marseille, France) — **BERNARD HENRISSAT** (AFMB UMR 7257 Case 932, Campus de Luminy, Marseille, France) — **DUANE MCKENNA** (University of Memphis, Department of Biological Sciences, TN, USA) — **YANNICK PAUCHET** (Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany)

The family Cerambycidae represents the most diverse group of xylophagous insects and belongs to the superfamily Chrysomeloidea. Larvae of this beetle family live in a challenging environment as they feed on woody tissues made of large amounts of plant cell wall, notoriously recalcitrant to breakdown. Plant cell walls are predominantly composed of polysaccharides such as cellulose, xylan or xyloglucan. Previous studies have revealed that the genome of beetles of the superfamilies Chrysomeloidea and Curculionoidea harbor gene families encoding so-called plant cell wall degrading enzymes (PCWDEs). The products of these genes enable these beetles to break down most plant cell wall polysaccharides.

To make the most out of their food source, early life stages of cerambycid beetles have to efficiently deconstruct plant cell wall polysaccharides which require them to possess an adequate arsenal of PCWDEs in their digestive tract. The analysis of the complement of PCWDEs harbored by cerambycid beetles has been hampered by the lack of genome/transcriptome data for this family of beetles. Molecular data are to date mostly available for species of the subfamily Lamiinae, due to the fact that the species under study are notorious forest pests. To expand our understanding on the biology, most particularly on the evolutionary history of PCWDEs in cerambycid beetles, we generated larval midgut transcriptomes for 22 species representing six out of the eight recognized subfamilies of the family Cerambycidae. Our sequencing effort provides the most extensive genome/transcriptome dataset for this group of insects. Using these transcriptomes, we first generated a species phylogeny which confirmed previous findings on the phylogenetic relationships of cerambycid beetles at the family and subfamily level. We then annotated all of the carbohydrate active enzymes (CAZymes) present in these 22 transcriptomes, which allowed us to annotate gene families encoding putative PCWDEs. We then analyzed the distribution of PCWDE-encoding gene families in these beetles in a species phylogenetic context. Our data provide new insights into the evolutionary history of PCWDEs in the family Cerambycidae.



20 Integration of molecular and morphological data for species delimitation within *Otiorhynchus tenebricosus* (Herbst, 1784) complex (Coleoptera: Curculionidae)

MAJA PRZYBYCIEŃ (Department of Entomology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland)

Otiorhynchus Germar, 1822 belongs to the subfamily Entiminae. It is the largest group of weevils but its classification into tribes and subtribes remains chaotic (Oberprieler et al. 2007). *Otiorhynchus* includes 1500 species mainly from Palaearctic regions (Magnano 1998) also with doubtful monophyly. Due to high morphological similarity and overlapping geographical ranges, *O. tenebricosus* and *O. lugdunensis* are particularly difficult to recognize and classify. My study on species delimitation within the *Otiorhynchus tenebricosus* complex was based on the analysis of morphological and molecular data (EF1- α and COI markers, karyology). I studied karyotypes of both species. They share the same chromosome number $2n = 22$ and meioformula $n = 10 + Xyp$ at all metaphase I plates of spermatid division. Morphometric analysis did not show any significant differences, but molecular analyzes indicate the distinctness of the examined species while genetic analysis along with available literature data about phenotypic characteristics suggested progressive speciation between *Otiorhynchus tenebricosus* and *Otiorhynchus lugdunensis*.

References: Magnano L. 1998: Notes on the *Otiorhynchus* Germar, 1824 complex (Coleoptera: Curculionidae). In Colonelli E., Low S., Osella G. (eds), Taxonomy, Ecology and Distribution of Curculionoidea. XX I.C.E. (1996, Fizerze, Italy). Mus. Reg. Sci. Nat., Torino, pp. 51–80. — Oberprieler R.G., Marvaldi A.E., Anderson R.S. 2007: Weevils, weevils, weevils everywhere. *Zootaxa* 1668: 491–520.

21 Climate and host plant associations shaped the evolution of ceutorhynch weevils (Coleoptera: Curculionidae: Ceutorhynchinae) throughout the Cenozoic

HARALD LETSCH (Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Vienna, Austria) — **BRIGITTE GOTTSBERGER** (University of Vienna, Austria) — **CHRISTIAN METZL** (University of Vienna, Austria) — **JONAS ASTRIN** (Forschungsmuseum Alexander Koenig, Germany) — **ARIEL FRIEDMAN** (Tel Aviv University, Israel) — **DUANE MCKENNA** (University of Memphis, USA) — **KONRAD FIEDLER** (University of Vienna, Austria)

Using molecular phylogenetic data and methods we inferred divergence times and diversification patterns for the weevil subfamily Ceutorhynchinae in the context of host-plant associations and global climate over evolutionary time. We detected four major diversification shifts that correlate with both host shifts and major climate events. Ceutorhynchinae experienced an increase in diversification rate at ~ 53 Ma, during the Early Eocene Climate Optimum, coincident with a host shift to Lamiaceae. A second major diversification phase occurred at the end of the Eocene (~ 34 Ma). This contrasts with the overall deterioration in climate equability at the Eocene-Oligocene boundary, but tracks the diversification of important host plant clades in temperate (higher) latitudes, leading to increased diversification rates in the weevil clades infesting temperate hosts. A third major phase of diversification is



Abstracts · Poster Presentations

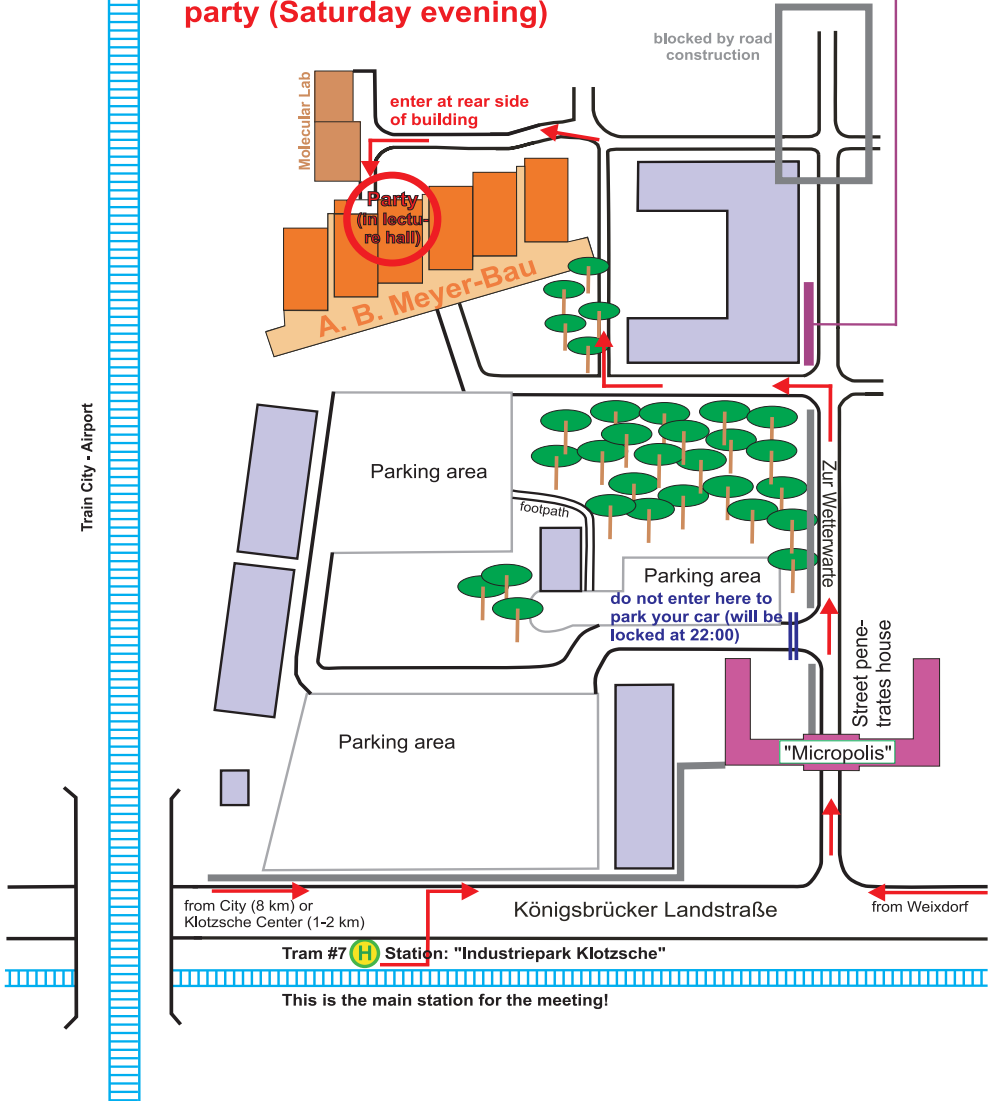
correlated with the rising temperatures of the Late Oligocene Warming Event (~ 26.5 Ma); diversification rates then declined shortly after the Middle Miocene Climate Transition (~ 14.9 Ma). Our results indicate that biotic and abiotic factors together explain the evolution of Ceutorhynchinae better than each of these drivers viewed in isolation.



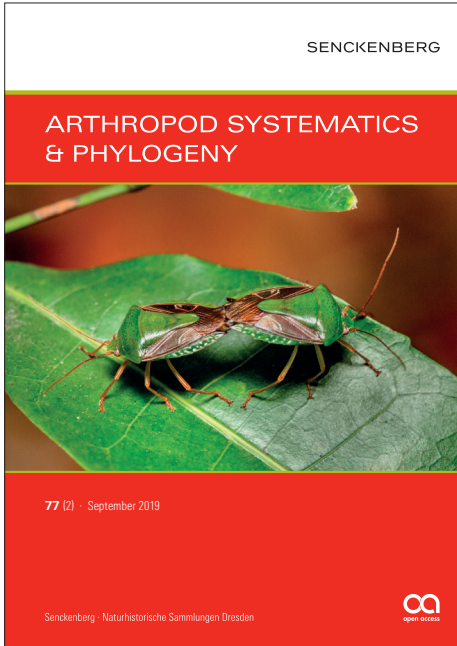
Venue | A.-B.-Meyer-Bau

Wait here for a taxi you have ordered
(address: "Zur Wetterwarte 7" in Klotzsche)
0351 / 8888 8888 or 0351 / 211 211)

How to reach the party (Saturday evening)



Arthropod Systematics & Phylogeny



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.

Research fields covered by Arthropod Systematics & Phylogeny are the taxonomy, morphology/anatomy, phylogeny (molecular or morphology-based), historical biogeography and palaeontology of arthropod taxa.

—
Impact Factor (2018): 1.175

Journal Citation Reports©, Thomson Reuters

—
Indexed in:

BIOSIS Previews, Biology & Environmental Sciences, SCOPUS, Current Contents – Agriculture, Science Citation Index Expanded, Zoological Record

We welcome

the submission of manuscripts to the e-mail-adress » klaus.klass@senckenberg.de

