



**20TH EUROPEAN CONGRESS
OF LEPIDOPTEROLOGY**

**April 24th — April 30th, 2017
Podgora, Croatia**

BOOK OF ABSTRACTS

Editors: Martina Šašić, Jadranka Rota, Iva Mihoci

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Programme committee: Martina Šašić, Jadranka Rota, Iva Mihoci

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PROGRAMME

Venues:

HOTEL MEDORA AURI

– Large Room

– Small Room

MOVIE THEATRE PODGORA

Monday, 24th April 2017

14:00 – 17:00	Registration Desk – Registration of participants	Hotel Medora Auri
17:00 – 18:30	Congress opening	Movie theatre
17:00 – 17:15	Welcoming words by organizers	
17:15 – 17:30	Welcoming words by the SEL President	
17:30 – 18:00	Ksenija Protrka/Biokovo Nature Park	
18:30	<i>A welcome drink</i>	<i>Hotel Medora Auri</i>
19:00	<i>Dinner</i>	

Tuesday, 25th April 2017

Movie Theatre

8:45 – 9:30 **Keynote speaker: Vlad Dincă:** Genetic map of European butterflies: what DNA tells us about European butterfly diversity

Cataloguing, preserving, describing, and studying Lepidoptera

9:30 – 9:45 **Session opening: Erik van Nieuwerkerken,** Ian J. Kitching: Towards a global Lepidoptera catalogue

9:45 – 10:00 **Geoff Martin:** The Lepidoptera collections at the Natural History Museum, London, UK

10:00 – 10:15 **Natalia Kirichenko,** Paolo Triberti, Carlos Lopez Vaamonde: Using herbarium data to understand the invasion history of the lime leaf miner *Phyllonorycter issikii* (Gracillariidae) in the Palearctic

10:15 – 10:30 **Vazrick Nazari:** A dead animal is not necessary to establish a new taxon

10:30 – 11:00 Coffee break

11:00 – 11:15 **Alberto Zilli:** In quest of identity

11:15 – 11:30 **Elsa Call:** Ancient DNA extraction from museum collection: What do Lepidoptera species tell us?

11:30 – 11:45 Luc Willemse, **Max Caspers:** Butterflies in bags: saving time, space and money

11:45 – 12:00 **Claude Sinner:** Lycaenidae of the World – a web-based catalogue

12:00 – 12:15 **Toomas Tammaru,** Robert Davis, Sille Holm, Juhan Javoiš, Erki Õunap: Phylogenetic comparative studies on Lepidoptera

12:15 – 12:30 **Sergey Yu. Sinev:** Fauna Lepidopterologica Rossica: towards a new edition of the national catalogue

12:30 – 14:00 Lunch break

Hotel Medora Auri Parallel Sessions

Small room

Gelechioidea

- 14:00 – 14:30 **Session opening: Lauri Kaila:** Recent development in gelechioid systematics and progress in understanding their life history evolution (Skype presentation)
- 14:30 – 14:45 **Bernard Landry:** Diversity of the Gelechioidea of the Galápagos Islands, Ecuador
- 14:45 – 15:00 **David Adamski:** Status on constructing a "natural" phylogenetic classification for the world Blastobasidae (Gelechioidea) based on macromorphological features of the adult
- 15:00 – 15:15 **Ole Karsholt, Peter Huemer:** Some considerations toward preparing a review of Gelechiidae from Crete Island
- 15:15 – 15:30 **Mari Kekkonen, Marko Nieminen, Paul D. N. Hebert:** Distance matters – the use of the BIN system for identifying gelechioids

15:30 – 16:00 Coffee break

Small room

Gelechioidea – continuation

- 16:00 – 16:15 **Daniel Rubinoff, William Haines:** Remarkable evolution in the carnivorous clades of Hawaiian Fancy Case caterpillars (Hyposmocoma: Cosmopteridgidae)
- 16:15 – 16:30 **Vazrick Nazari, Jean-Francois Landry:** The Nearctic Gnorimoschemini: An overview
- 16:30 – 16:45 **Sergey Yu. Sinev:** Some unexpected recent findings of the rarest gelechioid moths in Eurasia

Large room

Lepidopteran diversity of the Balkans

- 14:00 – 14:30 **Session opening: Gerhard M. Tarmann**, Predrag Jakšić, Ana Nahirnić: Zygaenids of the Balkan Peninsula and the Greek Islands – diversity and possible origin
- 14:30 – 14:45 **Martina Šašić**: Butterflies of Croatia: the state of knowledge
- 14:45 – 15:00 Leona Lovrenčić, Martina Podnar, Višnja Besendorfer, Martina Šašić, Valentina Toth, Toni Koren, **Nikola Tvrtković**: The Balkan Green-veined White (*Pieris napi balcana*): did the barcoding approach resolve its taxonomic status?
- 15:00 – 15:15 **Alena Bartonova**, Martin Konvicka, Stanislav Korb, Katja Kramp, Thomas Schmitt, Zdeněk Faltýnek Fric: Twice to Europe and then north-eastwards: Phylogeography of *Proterebia afra* (= *phegea*)
- 15:15 – 15:30 **Barbara Zakšek**, Nika Kogovšek, Franc Rebeušek, Mojmir Lasan, Marijan Govedič: Macromoth diversity in three different types of floodplain forests along the Mura River in Slovenia

15:30 – 16:00 Coffee break

Large room

Lepidopteran diversity of the Balkans – continuation

- 16:00 – 16:15 **Stanislav Gomboc**: Biodiversity of Lepidoptera fauna in the Sečovlje Salina nature park (SW Slovenia) and its conservation
- 16:15 – 16:30 **Ferdije Etemi**, Pajtim Bytyqi, Milaim Musliu, Rushan Ceka: Composition of the butterfly fauna (Papilionoidea) in the protected area "Mirusha Waterfalls" in Kosovo
- 16:30 – 16:45 **Feza Can Cengiz**, Konstantin A. Efetov, Kamuran Kaya, Elena E. Kucherenko, Zühal Okyar, Gerhard M. Tarmann: Zygaenidae in Thrace Region of Turkey
- 16:45 – 17:00 Blerina Vrenozhi, Eyjolf Aistleitner, **Gerhard M. Tarmann**: An overview on the Zygaenidae of Albania

19:00 Dinner

Wednesday 26th April 2017

Biokovo – *fieldtrip*

Large Room

Three-minute talks and poster session

17:00 – 17:15 Three-minute talks. Presenters and talk abstracts can be found on pages 80–83.

17:15 – 18:00 Poster flashtalks

Hotel lobby - poster mingle

18:00 – 18:30 Poster authors standing next to their posters.

18:30 – 19:00 Poster mingle

19:00 **Dinner**

Thursday 27th April 2017

Movie Theatre

8:45 – 9:30 **Keynote speaker: David L. Wagner:** Harnessing the larval stage in the biosystematics of Lepidoptera

Evolution of Lepidoptera: mimicry, biogeography, fossils, and more

9:30 – 10:00 **Session opening: Marianne Elias:** The far-reaching implications of mimicry in butterflies

10:00 – 10:15 **Katja Rönkä:** Could multiple-model mimicry explain local warning signal polymorphism in the wood tiger moth?

10:15 – 10:30 **Carlos Lopez Vaamonde,** Antoine Guiguet, Françoise Laurans, Issei Ohshima, David Giron: Molecular basis and evolution of gall-inducing in *Caloptilia* (Gracillariidae)

10:30 – 11:00 Coffee break

11:00 – 11:15 **Nicolas Chazot:** Timing of diversification in butterflies

11:15 – 11:30 **Martin Wiemers:** The butterflies of the Canary Islands and Madeira – aspects of colonization, differentiation, ecology, and conservation

11:30 – 11:45 **Jadranka Rota:** Metalmark moths (Choreutidae) crossing oceans: perspectives from historical biogeography

11:45 – 12:00 **Valentina Todisco,** Vazrick Nazari, Paul D. N. Hebert: Preliminary molecular phylogeny and biogeography of the monobasic subfamily Calinaginae (Nymphalidae)

12:00 – 12:15 **Maria Heikkilä:** A collaborative, community effort: re-examining the lepidopteran fossil record

12:15 – 12:30 **Wolfram Mey,** Wilfried Wichard: Report on the establishment of a new order of insects from Burmese amber (Insecta, Amphimesenoptera)

12:30 – 14:00 Lunch break

Hotel Medora Auri Parallel Sessions

Large room

Geometroidea

11:45 – 12:15 **Session opening: Axel Hausmann:** Non-destructive Micro-CT technology and DNA barcodes from old type specimens help to realize difficult XXL-revisions (Geometridae, Geometrinae: *Prasinocyma*)

12:15 – 12:30 **Pritha Dey**, V. P. Uniyal, Kailash Chandra, Axel Hausmann: Diversity patterns and integrative analysis (morphology, DNA barcoding) of geometrid moths of western Himalaya

12:30 – 14:00 Lunch break

Small room

Geometroidea – continuation

- 14:00 – 14:15 **Iva Mihoci**, Mladen Kućinić, Axel Hausmann: Diversity of geometrids (Geometridae) in the mountains of Dinaric karst and ecological patterns of their vertical stratification
- 14:15 – 14:30 **Andro Truuverk**, Erki Õunap, Gunnar Brehm: Preliminary insight into the phylogeny of South American Larentiinae (Geometridae)
- 14:30 – 14:45 **David Plotkin**, Akito Kawahara: Phylogenomic analysis of the emerald moths (Geometridae: Geometrinae)
- 14:45 – 15:00 **Hamid Reza Ghanavi**: Diversification dynamics of Geometridae moths

15:00 – 15:30 Coffee break

Large room

General Biology

- 14:00 – 14:15 **Sarah Saadain**: The curious incident of the moth at light-time: a study testing different street lamps for Lepidoptera attraction
- 14:15 – 14:30 **David Agassiz**: Do *Yponomeuta* species sing? A study of some hindwing structures.
- 14:30 – 14:45 Konstantin A. Efetov, **Gerhard M. Tarmann**, Elena E. Kucherenko: Catches of Procridinae (Zygaenidae) by new synthetic sex attractants in Italy, Austria and Greece
- 14:45 – 15:00 **Dubi Benyamini**: Swarm explosion build-up of millions of *Vanessa cardui* in the Araba & Negev Deserts in Israel, winter – spring 2015–2016.

15:00 – 15:30 Coffee break

Large room

15:30 **General Meeting**
19:00 Dinner

Friday 28th April 2017

Movie Theatre

8:45 – 9:30 **Keynote speaker: Chris van Swaay:** Red Lists, indicators and butterfly conservation

Ecology and Conservation

9:30 – 10:00 **Session opening: Irma Wynhoff,** M. P. Berg, F. van Langevelde: LIFE+ Blues in the Marshes – using habitat islands for ants to restore habitat for *Maculinea* butterflies in The Netherlands

10:00 – 10:15 **Martin Warren:** Conserving butterflies at a landscape scale: lessons from the UK

10:15 – 10:30 **Marcin Sielezniew,** Agata Kostro-Ambroziak, Przemysław Klimczuk, Krzysztof Deoniziak, Piotr Nowicki: Comparison of population demography in two ecotypes of the Bog Fritillary *Boloria eunomia*

10:30 – 11:00 Coffee break

11:00 – 11:15 **Sille Holm,** Juhan Javoš, Erki Ōunap, Robert B. Davis, Ants Kaasik, Toomas Tammaru: Latency to oviposition as a measure of ecological specificity: a cross-region phylogenetic comparative study

11:15 – 11:30 **Cristina Craioveanu,** Laszlo Rakosy: Butterfly communities in semi-natural grasslands: short- and long-term effects of management practices in Transylvania, Romania

11:30 – 11:45 **Bálint Horváth, István Szentirmai, Ferenc Lakatos:** Traditionally-mowed fruit orchards and their butterfly fauna in Órség National Park (Hungary)

11:45 – 12:00 **Martin Konvicka,** Zdeněk Faltýnek Fric, Thomas Schmitt, Alena Bartonova, Jana Slancarova, Michaela Kopeckova, Michal Zapletal: Does targeted management for the habitat directive butterfly *Euphydryas aurinia* protect non-target species? Lesson from the Czech Republic

12:00 – 12:15 **Miloš Popović,** Martina Šašić, Rudi Verovnik: Using limited data to create a preliminary Red List of Serbian butterflies

12:15 – 12:30 **Pasquale Trematerra,** Marco Colacci: Management of *Thaumetopoea pityocampa* in urban and recreational areas

12:30 – 14:00 Lunch break

Large room

Evolutionary history hidden in the genome

- 14:00 – 14:30 **Session opening: Marko Mutanen**, Kyung Min Lee, Axel Hausmann, Paul D. N. Hebert, Peter Huemer, Carlos Lopez Vaamonde, Rodolphe Rougerie, Andreas Seegerer: A genomic perspective on deep DNA barcode splits in European Lepidoptera
- 14:30 – 14:45 **Kyung Min Lee**, Camiel Doorenweerd, Erik J. van Nieukerken, Marko Mutanen: Clarifying species boundaries with ddRAD sequencing in two species complexes of pygmy leaf-mining *Ectoedemia* moths
- 14:45 – 15:00 **Zdeněk Faltýnek Fric**, Jana Maresova, Tomas Kadlec, Robert Tropek, Martin Wiemers: The world travellers – Phylogeny and phylogeography of the butterfly genus *Leptotes* (Lycaenidae)
- 15:00 – 15:15 **Jana Maresova**, Michal Rindoš, Roger Vila, Zdeněk Faltýnek Fric: Phylogeny of the African members of the butterfly genus *Azanus* (Lycaenidae)
- 15:15 – 15:30 **Nicholas Homziak**: Anchored hybrid enrichment recovers a robust phylogeny of erebine moths (Erebidae)

15:30 – 16:00 Coffee break

- 16:00 – 16:15 **Marianne Espeland**, Jesse Breinholt, Akito Kawahara: A backbone for the butterflies: Tribal-level phylogeny of Papilionoidea based on 352 loci
- 16:15 – 16:30 **Łukasz Przybyłowicz**, Sebastian Tarcz: Genus *Amerila* Walker, 1855 in Africa (Noctuoidea: Erebidae: Arctiinae) – is it still terra incognita?
- 16:30 – 16:45 **Mikhail Kozlov**: The fairy moth genus *Nemophora* (Adelidae): taxonomic composition, diversity and distribution
- 16:45 – 17:00 **David C. Lees**, Klaus Sattler: *Antispila treitschkiella* (Heliozelidae), highly invasive but overlooked on *Cornus mas* in Britain

Hotel Restaurant - congress closing

19:00 Gala dinner

Student award announcements and closing words

Saturday 29th April 2017

Neretva – *fieldtrip*

ABSTRACTS

ORAL PRESENTATIONS

Genetic map of European butterflies: what DNA tells us about European butterfly diversity

Vlad Eugen Dincă

Institut de Biologia Evolutiva (CSIC-UPF), Barcelona, Spain

vlad.e.dinca@gmail.com

Accurate knowledge of species composition and distribution, as well as their genetic features, has numerous theoretical and practical implications. Genetic data can provide valuable information regarding species formation, their dynamics and biogeography, and can also help prioritize conservation measures. Since time and material resources are limited, wide-scale previews (such as those provided by DNA barcoding) are particularly useful because they highlight cases of particular interest that can be later investigated in a more detailed manner. The European butterflies are arguably the most intensively studied invertebrate group in the world and they represent a key resource in providing models for research and nature conservation. Within the framework of the EUGENMAP project, we assembled a comprehensive, continental-scale, DNA barcode library for European butterflies, which comprises 20,000 DNA barcodes representative for 99% of the continent's butterfly fauna. This high resolution preview of genetic diversity revealed a series of patterns highlighting potential gaps in knowledge and the need for further research. We present examples of such patterns and, for some of the cases, show what can be learned when performing deeper studies using multiple data sources. Europe is the first continent to benefit from a comprehensive DNA barcode library for its butterfly fauna, and this will likely foster research in butterfly taxonomy, ecology and evolution, as well as practical applications in specimen identification and conservation.

Towards a global Lepidoptera catalogue

Erik J. van Nieukerken¹, Ian J. Kitching²

¹Naturalis Biodiversity Center, Leiden, The Netherlands; ²Department of Life Sciences, Natural History Museum, London, U.K.

nieukerken@naturalis.nl

More than ever there is a need of one global catalogue of all biota, so that major biodiversity projects and websites such as GBIF, Encyclopedia of Life, Biodiversity Heritage Library and Barcode of Life Data Systems all share a single source for names and taxa. The Catalogue of Life (CoL) was set up to be such a list, but until now has not been able to deliver a complete catalogue, and furthermore is hampered by old technology. GBIF and Species2000 have recently begun an initiative to build a single, sustainable taxonomic backbone, named Catalogue of Life + (CoL+). For Lepidoptera, the databases LepIndex (The Global Lepidoptera Names Index) and Generic Names (Butterflies and Moths of the World), hosted by the NHM London, provide a historic nomenclature, rich in information, but are not yet maintained and updated by the lepidopterist community. Currently, the content of these databases is in the process of being migrated to the TaxonWorks platform, the successor of Species File, with the aim of becoming a global platform for Lepidoptera taxonomy, maintained by specialist editors. Existing active global databases, such as those for butterflies (GloBIS), Pyraloidea (GloBiZ), Tortricidae (Tortricid.net) and Gracillariidae could either serve as sources for the new LepIndex or be integrated, and the whole database could then serve as a source database for CoL+. As an example, we will describe how the global catalogue for Nepticuloidea was built and currently serves as basis for CoL.

The Lepidoptera collections at the Natural History Museum, London, UK

Geoff Martin

Natural History Museum, London, United Kingdom

g.martin@nhm.ac.uk

The collections at the Natural History Museum, London, are amongst the largest in the world (10,000,000+ specimens) and certainly the most type rich (125,000 primary Types). Whilst familiar to many, the collections have undergone considerable changes in the last few years prompted by the move into a new building in 2009, which allowed a complete reorganisation of the collections. I will be presenting an update of the collections including an overview of the collection organisation, current staff working on the collections and their research and projects. In particular, I will outline how digitisation is making the collection much more accessible to the research community.

Using herbarium data to understand the invasion history of the lime leaf miner *Phyllonorycter issikii* (Gracillariidae) in the Palaearctic

Natalia Kirichenko¹, Paolo Triberti², Carlos Lopez Vaamonde³

¹Sukachev Institute of Forest SB RAS, Krasnoyarsk, Russia; ²Museo Civico di Storia Naturale, Verona, Italy; ³INRA, Orléans, France

nkirichenko@yahoo.com

Historical herbaria are a relevant source of information for investigating origin and past distribution of invasive insect species. The lime leaf miner *Phyllonorycter issikii* (Kumata, 1963) is a pest of *Tilia* from East Asia presently recorded in most of Europe and Russia. We studied *Tilia* herbarium data to understand this leaf miner's invasion history. In total, 2850 herbarium sheets carrying about 40,000 leaves of *Tilia* spp., collected between 1808–2014 in the Palaearctic, have been carefully examined in the Botanical Institute of the Russian Academy of Sciences (Saint Petersburg) for the presence of mines. The two thirds of the herbarium sheets originated from Europe (30 countries), Western Russia and Siberia, one third from East Asia. In Europe and Western Russia, about 70% of *Tilia* herbaria (ca 1400 herbarium sheets) were collected in 1880–1960s but no single *Phyllonorycter*-like mine was found on this extensive material. On the contrary, the mines (often in mass) were regularly recorded in Western Russia in the last two decades, despite the low number of herbarium sheets (17). In East Asia, *Phyllonorycter*-like mines were found starting from 1859. Single mines were recorded in Japan and Korea in 1885–1900. The mines were regularly present on *Tilia* in the Russian Far East and Northeast China, and in 1914, 1936, 1951 they were numerous in the Russian region Primorye. Our findings support the hypothesis about recent occurrence of *Tilia*-feeding *Phyllonorycter* in the west and its long-term occurrence in the east.

The study is supported by the Russian foundation for basic research (grant No15-29-02645)

A dead animal is not necessary to establish a new taxon

Vazrick Nazari

Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa, Ontario, Canada

nvazrick@yahoo.com

Much proverbial ink has been spilled over the absolute necessity of a dead specimen to bear the weight of a taxonomic name and how any deviation from this antiquated notion will cause chaos and end humanity as we know it. The International Commission for Zoological Nomenclature (ICZN) rightfully allows for a taxonomic name to be established in the absence of a physical type specimen, albeit with many recommendations. Knowledge of the history of this debate and a broader taxonomic perspective across the entire Animal Kingdom, which I hope to provide in this talk, helps in understanding why this provision was put in the place and why it needs to be maintained. Since the late 1980s, this provision has allowed a handful of ethically responsible taxonomists to forego killing of individuals of newly discovered and vulnerable species of birds, mammals or reptiles, where instead they presented photos, and sometimes blood or tissue samples as supporting evidence for establishing new binomial names. Although this would be difficult to achieve with insects, with increasing restrictions on collecting across the world and with advances in modern photography it is possible to envision a future when a combination of photographic evidence and non-invasive tissue sampling (=DNA sequences) will eventually completely replace the need for preservation of a dead type specimen.

In quest of identity

Alberto Zilli

Department of Life Sciences, Natural History Museum, London, United Kingdom

A.Zilli@nhm.ac.uk

Information preserved in natural history museums, both in the form of physical specimens, particularly primary types, and the data and metadata associated with them, is essential to determine unequivocally the identity of named taxa. During the recuration of the Lepidoptera collection at the Natural History Museum (London), it was found that the activity of matching available information with commonly accepted concepts of various taxa is far from routine. As a matter of fact, several idiosyncrasies of collectors of the past may be revealed that can hamper present-day assessments of identities, e.g. when historical types are found to be “chimaerae” consisting of parts of different animals glued together. This was the case for *Gonitis combinans*, which was invasively restored to reconstruct its integrity, but the same situation applies to many specimens in the Felder collection, including some of Cramer’s types, which had been incorporated into it. Another frequent outcome is when the current accepted concept for a well-known species is discovered not to fit the original, as in *Hypopyra feniseca*, with unexpected taxonomic consequences. Even the first species ever described by Cramer, *Papilio dedalus*, today known by the replacement name given to it by Fabricius (*Papilio cyparissias*), resides in the middle of an extraordinarily complex nomenclatural stalemate. Luckily, there are some happy endings, as the solution to one of the most long-standing mysteries of lepidopterology will reveal, that of the so far unrecognised species *Hesperia busiris*.

Ancient DNA extraction from museum collection: What do Lepidoptera species tell us?

Elsa Call

Lund University, Lund, Sweden

elsa.call.fr@gmail.com

Natural history museums around the world hold vast amounts of biological material collected over hundreds of years that have almost exclusively been used for morphological studies of species. During the past decades, it was thought that the DNA in these specimens was too degraded to be of use for molecular work, e.g. looking at the relationships of taxa based on comparisons of DNA sequences. The recent advent of so-called next generation sequencing techniques has opened up new possibilities, as these techniques are based on sequencing short fragments of DNA. Such techniques have been used successfully to sequence genomic material from fossilized taxa, such as Neanderthals, mammoths and cave bears. However, the techniques have rarely been applied to museum specimens so far, although the term “museomics” has already appeared in the literature. The main aim of this thesis work will be to investigate the level of DNA degradation in museum specimens of various ages, to develop protocols to sequence genomic DNA from museum specimens, and to target various rare, difficult to collect lineages of Lepidoptera to complement the transcriptomic data which is becoming available for phylogenetic work. The thesis will advance the field of “museomics”, as well as further our understanding of relationships of major lineages in Lepidoptera.

Butterflies in bags: saving time, space and money

Luc Willemse, **Max Caspers**

Entomology Department, Naturalis Biodiversity Center, Leiden, Netherlands

max.caspers@naturalis.nl

In terms of amateurs and professionals studying and collecting insects, Lepidoptera represent one of the most popular groups. It is their popularity, in combination with wings being routinely spread during mounting that results in Lepidoptera often taking up the largest number of boxes and amount of space in entomological collections. As space, time and money are commodities museums want to use as efficiently as possible, any process that results in saving either one forms a welcome and timely addition to collection management. Here we propose a means to permanently store unmounted air-dried Lepidoptera in glassine envelopes. The described workflow entails registration and graphic documentation of the specimens to ensure accessibility of the data, and limits mounting to those specimens for which mounting is considered essential. The entire workflow can be carried out by non-specialist volunteers. Additionally, by disclosing data and images via internet, specialists worldwide may assist with identifications. Although so far only tested for Papilionidae, results suggest that the workflow and permanent storage in glassine envelopes described here can be applied to most groups of Lepidoptera.

Lycaenidae of the World – a Web-Based Catalogue

Claude Sinner

Linkenheim, Germany

euxoa@yahoo.de

Lycaenidae LEACH, 1815 are one of the most species-rich families of Papilionoidea and currently comprise over 5000 species. In this talk, I will introduce the current status of the "Lycaenidae of the World" project, a web-based database of Lycaenidae. The scope of the work is to illustrate every species of the family and collect additional information of biological significance. I will introduce valuable tools to the interested listener to deal with this massive amount of data and display it in a user friendly and publication-worthy way.

Phylogenetic comparative studies on Lepidoptera

Toomas Tammaru, Robert Davis, Sille Holm, Juhan Javoiš, Erki Õunap

University of Tartu, Tartu, Estonia

toomas.tammaru@ut.ee

The availability of reliable phylogenies has opened the road for the application of phylogenetic comparative analyses. With appropriate analytical methods having been developed, evolutionary ecologists can now use among-species variation in trait values to explicitly test for adaptive hypotheses. However, the vast potential of insects as objects of phylogenetic comparative studies has still received surprisingly limited attention. First, I am going to present a short overview of comparative studies recently performed on Lepidoptera. Second, I will present our original research which uses phylogenetic and ecological data on the family Geometridae. In particular, phylogenetically explicit analyses have confirmed the long-suspected link between body size and the degree of polyphagy. Egg size was found to strongly depend on adult size, with little evidence of the effect of ecological selective pressures. The same applies to adult longevity measured in laboratory conditions. The gradation from income to capital breeding (= the importance of adult feeding in egg production) was confirmed to serve as an axis usable for ordinating lepidopteran life histories, with anatomical proxies available to assess the position of each species in this ordination scheme. There is also some evidence that capital breeding rather than income breeding species have more variable and more regularly changing population densities.

Fauna Lepidopterologica Rossica: towards a new edition of the national catalogue

Sergey Yu. Sinev

Zoological Institute of the Russian Academy of Sciences, Saint Petersburg, Russia

sergey.sinev@zin.ru

The first catalogue of Russian Lepidoptera published in 2008 fixed the state of knowledge on the taxonomic pattern of the whole fauna and more or less revealed the species composition of the regional faunas and the geographical distribution of species. It made it possible to compare the regional faunas, to reveal the less lepidopterologically studied territories and to introduce the modern taxonomy and nomenclature in the national practice of entomological investigations. The Catalogue quite expectedly stimulated further both taxonomical and faunistic studies. For the last decade, about 90 new species from different families were described from Russia and more than 400 species were found on its territory for the first time. The species lists for some regions whose faunas remained very poorly known (north-east of European Russia, Northern Siberia, Yakutia, Kamchatka, etc.) were compiled. Some cryptic species shared with the fauna of North America were found using DNA barcoding. Several cases of recent invasions were revealed, and a few unexpected findings of enigmatic species happened during very last years. The great volume of new information requires generalization in a new edition of the Catalogue of Russian Lepidoptera, which is planned to be published within three years. This time, it will be supplied with a list of the main taxonomic and faunistic literature. The improved data on the geographical pattern of the lepidopteran diversity in Russia will considerably contribute to a better knowledge of the composition and distribution of the Palaearctic fauna as a whole.

Recent development in gelechioid systematics and progress in understanding their life history evolution

Lauri Kaila

Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland

lauri.kaila@helsinki.fi

The phylogeny of Gelechioidea has been extraordinarily difficult to unveil. Further issues are the instability in their family level classifications which rarely show full agreement between any two larger works. Since 1990s these issues have increasingly drawn attention, and systematized approaches on their morphological and molecular characters have been implemented in several projects. At present a more robust phylogenetic hypothesis supported by independent studies is taking shape, yet with large gaps and partly weak support. A revised family classification has been suggested, though refinements to it are constantly appearing. A stable and well-supported phylogeny is the prerequisite for understanding the evolution of gelechioid traits, larval feeding biology in particular. A special trait in Gelechioidea is an adaptation to feed on dead material; the superfamily also contains external and internal feeders of plant tissues, including leaf-miners. Patterns of evolution of these traits are reviewed.

Diversity of the Gelechioidea of the Galápagos Islands, Ecuador

Bernard Landry

Muséum d'histoire naturelle, Switzerland

bernard.landry@ville-ge.ch

Following five expeditions to the Galápagos Islands starting in 1989, including eight months of field work, to investigate the Lepidoptera, the Gelechioidea were treated in 11 publications. There were six species known before our field work started, while our list now includes 51 species excluding the Scythrididae, still under investigation. The families present on the Galápagos are Autostichidae (14 species), Blastobasidae (3 spp.), Coleophoridae (1 sp.), Cosmopterigidae (9 spp.), Elachistidae (2 spp.), Gelechiidae (22 spp.), and Scythrididae (9 spp.). Twenty-nine species have been described as new thus far, all except one purportedly endemic. Including the Scythrididae, the percentage of endemism stands at 67%. The adaptive radiation of the autostichid genus *Galagete* Landry, containing 12 species, will be discussed in some details.

Status on constructing a "natural" phylogenetic-classification for the world Blastobasidae (Gelechioidea) based on macromorphological features of the adult

David Adamski

Department of Entomology, Smithsonian Institution, Washington, USA

adamskid@si.edu

Previous intuitive classifications of world Blastobasidae have contributed in generating a computer phylogenetic-classification for the family. Three analyses were conducted. All characters and character states were coded into Mesquite matrices, converted into TNT format files, and uploaded into TNT for tree analysis. All trees obtained, including a consensus tree were retained. If necessary, a Maximum Likelihood Analysis was conducted using CIPRES. The first two analyses are similar as coded data were taken solely from the type-species of each genus. While, in the last analysis, coded data were taken from all primary types and/or authoritatively identified specimens representing species in the analysis. For this study 395 species of Blastobasidae worldwide were used. (499 minus 64 species that were described only from females, minus 35 species whose data were not included at this time). Using an "all-inclusive study" for phylogenetic analysis indicates that the exemplar approach relies heavily on intuitive decisions for placement of species within the in-group. This type of decision making underestimates diversity within the in-group, and overlooks new combinations at the generic and species levels. An "all-inclusive" approach also finds unrecognized genera represented from type specimens not previously dissected. While analyses 1 and 2 show a strong signal for well-defined tree topology at the family, subfamily, and generic levels, the character state frequencies of analysis 3 present a more accurate and more complicated tree topology. Once stability is achieved in the later analysis the evolution of hosts preferences of world Blastobasidae and zoogeographical hypotheses can be attempted.

Some considerations toward preparing a review of Gelechiidae from Crete Island

Ole Karsholt¹, Peter Huemer²

¹Zoological Museum, Natural History of Denmark, Denmark; ²Tiroler Landesmuseen, Innsbruck, Austria

okarsholt@snm.ku.dk

Our study is mainly based on material kept in our museums (TLMF and ZMUC), but includes also additional material from museums and private collections. We have until now confirmed the presence of 113 species of Gelechiidae on Crete, nine of which have been identified only to genus. Three previously published species records should be removed from the list due to misidentification. Crete is known for its many endemic species. About 10% of vascular plants are considered endemic, and so are 6.5% of geometrid moths (Ruckdeschel, 2007). But only one species of Gelechiidae (*Teleiodes albiluculella* Huemer & Karsholt, 2001) - or less than 1% - is known only from Crete. There are, however, candidates for further Cretan endemic Gelechiidae, partly among the species only identified to genus, and partly among species identified on basis of morphological characters, but showing differences in the DNA barcode towards specimens from mainland Europe referred to the same species. We plan to further investigate such cryptic diversity, but descriptions of new species should preferably be made in taxonomic revisions. The Gelechiidae fauna of Crete is far from being thoroughly investigated. Most of the specimens studied by us originated from localities in West Crete, and mostly from localities below 1200 m (with material from only one locality at 1550 m). Almost all specimens were collected by light (especially automatic light traps), and not a single specimen was bred from larva!

Distance matters – the use of the BIN system for identifying gelechioids

Mari Kekkonen, Marko Nieminen, Paul D. N. Hebert

Centre for Biodiversity Genomics, Biodiversity Institute of Ontario,
University of Guelph, Canada

kekkonen@uoguelph.ca

Incredible diversity among lepidopterans is both joyful and painful. Especially species-rich groups with few external diagnostic characters, such as the Gelechioidea, pose a challenge for species identification. DNA barcodes have been helpful in many cases, but the quality of these identifications depends on several factors. One such feature is the distance between BINs. Barcode Index Number (BIN) system provides putative species based on DNA barcode sequence similarity and is publicly available on the BOLD website. Each BIN has its nearest neighbour (NN) BIN identified on the BIN page along with the molecular distance (p-distance) between the two. Taxonomic information associated with the NN can be used for identification purposes, but its reliability depends on the distance. Hence, it is important to know which distances can be considered safe for making reliable identifications. This study examines the distances between all public gelechioid BINs and their NNs in three geographical areas (Australia, Europe and North America). All distances are further divided into three categories: SAME FAMILY where the focal BIN and its NN belong to the same family, DIFFERENT FAMILY where the BIN belongs to a different gelechioid family from its NN, and NON-GELECHIOID where the NN is not a gelechioid. Our aims are to study the differences i) between geographical areas and ii) between 16 gelechioid families, as well as iii) the ranges of distances in the three categories. Preliminary results suggest 5% as a general upper limit for correct family level identifications, but there are differences between the gelechioid families.

Remarkable evolution in the carnivorous clades of Hawaiian Fancy Case caterpillars (*Hyposmocoma*: Cosmopteridgidae)

Daniel Rubinoff, William Haines

The University of Hawaii, Honolulu, USA

Rubinoff@hawaii.edu

Hyposmocoma is a remarkable genus of endemic Hawaiian moths with over 500 species. The caterpillars represent a variety of remarkable and globally rare life histories, including carnivory. Only the unique tree-snail feeding species have been previously reported. We now add to that record by reporting additional, surprising, diversity of carnivorous life histories in the genus. New discoveries are placed in the broader phylogenetic context of the group.

The Nearctic Gnorimoschemini: An overview

Vazrick Nazari, Jean-Francois Landry

Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa
Research and Development Centre, Agriculture and Agri-Food Canada,
Ottawa, Canada

nvazrick@yahoo.com

According to the latest checklist of North American Gelechiidae (Lee et al. 2010), the Nearctic Gnorimoschemini fauna comprises 175 species in 17 genera. Globally, the group includes some of the most serious and best-studied pests of Solanaceae (e.g. *Tuta absoluta*, *Symmetrischema tangolias*, *Phthorimaea operculella* etc.), yet taxonomically they remain poorly studied. In this talk I summarize results of some of the taxonomic work carried out in the Canadian National Collection on Gnorimoschemini fauna of North America over the past six years and provide some examples of new faunal records and surprising discoveries.

Some unexpected recent findings of the rarest gelechioid moths in Eurasia

Sergey Yu. Sinev

Zoological Institute of the Russian Academy of Sciences, Saint Petersburg,
Russia

sergey.sinev@zin.ru

Our study of recently obtained material of Microlepidoptera from different regions of Europe and Asia reveals several rarest species of gelechioid moths which were not collected since their description over a hundred years ago, or were found in the regions situated far away from their main distribution areas. One of the most striking Palaeartic micros, *Pantelamprus staudingeri* (Christoph, 1882), previously known from Russia from a single type specimen, was rediscovered more than 130 years later in the mixed coniferous forests of southern Sikhote-Alin Mts. at a surprisingly high elevation. The second known species of the most enigmatic European genus, *Xenopathia nivea* Rebel, 1902, described from a single specimen and never collected again, was rediscovered in Turkmenia and appears to be a smallest representative of the family Ethmiidae. The peculiar species of fern-feeding Stathmopodidae, *Cuprina fuscella* Sinev, 1988, previously known from a rather limited area of the Russian Far East, was suddenly found in the middle of Eastern Europe. The Holarctic boreo-montane species *Mompha sexstrigella* Braun, 1921, which is rather widespread in Siberia and during last decades constantly collected in Northern Europe, was suddenly found far to the south, in Lipetsk area of European Russia. New methods of light-trapping and new methods of species identification (DNA barcoding) can reveal much more interesting additions to the regional faunas and shed light on the real distribution ranges of many Palaeartic species of Microlepidoptera.

Zygaenids of the Balkan Peninsula and the Greek Islands – diversity and possible origin

Gerhard M. Tarmann¹, Predrag Jakšić², Ana Nahirnić³

¹Tiroler Landesmuseen, Ferdinandeum, Naturwissenschaftliche Abteilung, Innsbruck, Austria; ²Čingrija 14/25, 11000 Belgrade, Serbia; ³National Museum of Natural History, Sofia, Bulgaria

g.tarmann@tiroler-landesmuseen.at

Zygaenids of the Balkan Peninsula have been studied for a long time and rich material is deposited in European collections. When we compare the zygaenid fauna of the three great peninsulas of southern Europe (Iberian, Apennine and Balkan Peninsula) we notice significant differences in the number of endemic species. On the Iberian Peninsula we find six endemic zygaenid species (*Rhagades predotae*, *Adscita schmidtii*, *A. jordani*, *A. bolivari*, *Jordanita vartianae*, *Zygaena ignifera*), on the Apennine Peninsula four endemic species (*Adscita italica*, *Jordanita tenuicornis*, *Zygaena rubicundus*, *Z. oxytropis*) but on the Balkan Peninsula there is not a single species endemic. In geological and tectonic history the Balkan Peninsula was several times connected with Asia. A large number of Asian species could have invaded south-eastern Europe. However, we find only a small number of them, e.g. *Rhagades amasina*, *Adscita capitalis*, *Zygaena sedi*, all of Ponto Mediterranean origin. None of them were able to settle in the central and northern parts of the Balkans. It is obvious that the orographic and climatic conditions are responsible for that situation. The Balkan was always open to the cold continental winds from the Northeast whereas the Iberian and Apennine Peninsulas were protected by high mountain systems. Although there are no endemic species on the Balkan Peninsula, it is characterised by a significant number of well-separated subspecies. The postglacial re-invasion of populations from various sides and interbreeding with existing relic populations in the Balkan refugia has caused a complicated mixture of forms that makes biogeographic analyses difficult today.

Butterflies of Croatia

Martina Šašić

Department of Zoology, Croatian Natural History Museum, Zagreb, Croatia

martina.sasic@hpm.hr

In the last decade, our goal has been to create a national database of distributional records in Croatia and publish a national checklist of butterflies. At this point the records include published papers, collection data, as well as unpublished records (e.g. Lorković diaries, fieldwork data) from three centuries. Even though sampling has been sporadic and uneven, with some areas receiving more attention than others, we managed to assess the threat status of the butterfly fauna and this was published in the Red Book of threatened butterflies of Croatia. About 25% of Croatia's butterfly fauna is of conservation concern. The main causes of the decline are thought to be changes in rural land use, especially land abandonment and agricultural intensification because of demographic changes and economic transition. The main objective of the Lepidoptera working group (formed as part of the EU Natura 2000 Integration Project – NIP) has been to gather new distributional data and use this information for establishing of future species monitoring schemes. The progress that the group has recently made resulted in much new insight. The level of knowledge has been increased considerably but information on trends in population dynamics of many species is still lacking. Future monitoring plans will help us to understand impact of the environmental change, particularly how climate change and habitat loss are affecting our wildlife.

The Balkan Green-veined White *Pieris (napi) balcana*: did the barcoding approach resolve its taxonomic status?

Leona Lovrenčić¹, Martina Podnar¹, Višnja Besendorfer², Martina Šašić^{1,3},
Valentina Toth³, Toni Koren⁴, **Nikola Tvrtković³**

¹Croatian Natural History Museum, Zagreb, Croatia; ²University of Zagreb, Zagreb, Croatia; ³Association Natura, Zagreb, Croatia; ⁴Association Hyla, Zagreb, Croatia

nikolatvrtkovic71@gmail.com

To resolve taxonomic status and distribution of the enigmatic *Pieris (napi) balcana* Lorković, 1970 specimens from a *P. napi* aggregate were collected in the karst habitats of the western part of the Croatian Dinaric Alps. Wing pattern characters were studied on a large sample (n=323). Egg laying of *balcana* females on the larval host-plant *Arabis turrita* was observed in spring at three localities, and butterflies have been reared on the same plant. DNA barcodes of 58 individuals (39 localities) were obtained and complemented by sequences of a fragment of the nuclear wingless (*wg*) gene. Tissue from fresh adult males was used for karyotyping (n=21). '*Balcana*' shares the DNA barcode with the subalpine *P. (napi) bryoniae*, while *balcana/bryoniae* and *napi* haplotypes segregated into two distinct mitochondrial clusters. Barcoding results agree with the absence of reproductive isolation between *balcana* and *bryoniae* in former hybridisation studies, and both taxa have the same polymorphic karyotype, different from the *napi* karyotype. '*Balcana*' and *napi* could not be distinguished by *wg* sequence data. At 26 localities, we found only *bryoniae/balcana* DNA barcodes, and *P. (napi) napi* was detected only in probably parapatric area. On Žumberak Mt. we discovered F1 hybrids with *napi* barcode and hybrid wing pattern.

Twice to Europe and then north-eastwards: Phylogeography of *Proterebia afra* (= *phegea*)

Alena Bartonova^{1,2}, Martin Konvicka^{1,2}, Stanislav Korb³, Katja Kramp⁴, Thomas Schmitt⁴, Zdeněk Faltýnek Fric²

¹University of South Bohemia, Ceske Budejovice, Czech Republic; ²Biology Centre CAS, Ceske Budejovice, Czech Republic; ³Ural Division of the Russian Academy of Sciences, Syktyvkar, Russian Federation; ⁴Senckenberg Deutsches Entomologisches Institut Munchenberg, Germany

al.bartonova@gmail.com

Proterebia afra (Nymphalidae: Satyrinae) is a remarkable dry grassland butterfly with limited distribution within Europe, an iconic species for the Dalmatia Region in Croatia. The species' overall distribution consists of a southern part, the Irano-Turanian region (Turkey, Caucasus, N Iran), and a northern part, Eurasian steppes (Crimea, Volga, S Ural, Kazakh steppes to Altai). In the Balkans, apart from Dalmatia, the species is known from Askion Mountains and a small locality in Thrace (both Greece). Dalmatia thus represents the westernmost projection of the species distribution. We sequenced mtDNA (cytochrome oxidase 1 and 2; 1700 bp) and AFLP markers from 184 specimens originating from the whole distribution area. The data were processed both on population and phylogeographic level, using a wide range of methods. Analyses show that the first separation of populations is between NE Iran and the rest of the region. The whole northern part (Crimea to E Kazakhstan) shares haplotypes and the haplotype diversity is high, showing a rather continuous, well-established population in recent history. On the other hand, the southern populations are highly differentiated. The Dalmatian population is closely related to the Turkish and they must have been connected along the coast, whereas the Greek population is related to the northern clade and the species must have been distributed continuously in the Pontic Region. This shows two independent expansions to Europe during the species' history. *P. afra* probably expanded several times both along the longitude and latitude.

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Macromoth diversity in three different types of floodplain forests along the Mura River in Slovenia

Barbara Zakšek, Nika Kogovšek, Franc Rebeušek, Mojmir Lasan, Marijan Govedič

Centre for Cartography of Fauna and Flora, Miklavž na Dravskem polju, Slovenia

barbara.zaksek@ckff.si

Communities of nocturnal macromoth species along the Mura River (NE Slovenia) were surveyed in three most typical and most abundant forest types in the region. Field work was carried out in years 2013 and 2014 from April to October. In every forest type (Physis typology), three portable UV-light traps were used. Most of the moths were identified on the site, while some species were identified later in the laboratory. For identification of some species a detailed examination of genitalia was necessary. A total of 293 species and 6,844 specimens were recorded. Shannon and Fisher alpha diversity indexes were used as measures of diversity. The highest number of species (234) was recorded in the Illyrian ash-oak-alder forest (FFH 91F0) and 231 species in Ponto-Pannonic tall herb ash-alder wood (FFH 91E0*), while the minimum number of species (141) was found in Eastern European poplar-willow forest (FFH 91E0*). As expected, both diversity indices were the highest in Illyrian ash-oak-alder forest and Ponto-Pannonic tall herb ash-alder wood. Moreover, also the number of unique species was the highest in these two forest types (36 and 30 unique species, respectively). The highest number of endangered species (7; listed on Slovenian Red list) was found in Eastern European poplar-willow forest, compared to 6 in the other two forest types.

Biodiversity of Lepidoptera fauna in the Sečovlje Salina Nature Park (SW Slovenia) and its conservation

Stanislav Gomboc

Šiškovno naselje 19 4000 Kranj, Slovenia

stanislav.gomboc@siol.net

In Sečovlje Salina Nature Park, a total of 843 Lepidoptera species were recorded until 2016, including 54 protected species, 65 red list species and two Natura 2000 species, all together 69 species of high conservation value (7.7% of the known fauna). The number of observed Lepidoptera species represents 23% of the known Lepidoptera fauna of Slovenia. More than 20 species were observed for the first time for Slovenia. All of these numbers indicate the importance of Sečovlje salt pans for the conservation of high biodiversity and protection of rare and protected species, although their scope is relatively small – protected area of only 650 ha. Although the terrestrial habitats cover only 15% of the total area, they are of the utmost importance for the conservation of biodiversity of insects. Even Shannon Biodiversity Index for Lepidoptera (5.3) is well above average and indicates a very large diversity of fauna in such a small and ecologically extreme area. This is linked with the great diversity of habitats in a small area and surrounding habitats around the Sečovlje salt pans that actually provide a flow of genetic material between these habitats. Very important here are also halophytic Lepidoptera species, which occur in Slovenia only in a small endangered coastal area, which are under high pressure from urbanization as the Slovenian coastline is very short. We also recognized the pressure of non-native invasive plants that threaten native flora and fauna. Since 2011, three non-native Lepidoptera species were also observed in the salt pans.

Composition of the butterfly fauna (Papilionoidea) in the protected area "Mirusha Waterfalls" in Kosovo

Ferdije Etemi, Pajtim Bytyqi, Milaim Musliu, Rushan Ceka

University of Priština, Priština, Kosovo

ferdijezhushi2010@gmail.com

In this paper the results of a study on composition of butterfly fauna in the protected area "Mirusha Waterfalls" in Kosovo, conducted in the period April to the end of September 2016 are presented. "Mirusha Waterfalls" is a Natural Monument (III category according to IUCN) with a surface of 598.4 ha, located in the central part of Kosovo. No studies on butterfly fauna in this area were realized prior to this one. The survey was organized in 13 sites with different types of habitats, mostly dominated by grassland, combined with rocks and shrubs. During our study 83 species of butterflies were recorded. The highest diversity (Shannon –Wiener diversity index H) was registered at the site 12 where 68 out of 83 recorded species were present. In regard to biogeography, the highest number of the species are Circum–Palaeartic (CP), followed by North and Pontic–Mediterranean (NPM), West–Palaeartic (WP) and Holarctic species (HO). Our results confirm a rich diversity of butterfly fauna influenced by climate characteristics and geology.

Zygaenidae in Thrace Region of Turkey

Feza Can Cengiz¹, Konstantin A. Efetov², Kamuran Kaya¹, Elena E. Kucherenko¹, Zühal Okyar¹, Gerhard M. Tarmann³

¹Mustafa Kemal University, Antakya, Turkey; ²Crimean Federal University, Crimea; ³Tiroler Landesmuseum, Ferdinandeum, Naturwissenschaftliche Abteilung, Innsbruck, Austria
cezafan_onurcan@hotmail.com

The fauna of Zygaenidae of the Thrace Region (European Turkey) was studied in 2016 by attractant traps as well as by netting of specimens in biotopes. The sex attractants had been produced in the Crimean Federal University and were esters of 2-dodecenoic acid and isomers of 2-butanol: EFETOV-2 (racemic mixture of R- and S-enantiomers) and EFETOV-S-2 (R-enantiomer). Some specimens collected by netting in previous years were determined and included too.

The list of Zygaenidae of European Turkey is presented below:

Theresimima ampellophaga (Bayle-Barelle, 1808)
Rhagades (Wiegelia) amasina (Herrich-Schäffer, 1851)
Rhagades (Rhagades) pruni ([Denis & Schiffermüller], 1775)
Adscita (Adscita) statices drenowskii (Alberti, 1939)
Adscita (Adscita) obscura (Zeller, 1847)
Adscita (Tarmannita) mannii (Lederer, 1853)
Jordanita (Tremewania) notata (Zeller, 1847)
Jordanita (Jordanita) graeca (Jordan, 1907)
Jordanita (Jordanita) globulariae (Hübner, 1793)
Jordanita (Solaniterna) subsolana (Staudinger, 1862)
Zygaena (Mesembrynus) punctum Ochsenheimer, 1808
Zygaena (Mesembrynus) purpuralis (Brünnich, 1763)
Zygaena (Agrumenia) carnialica (Scopoli, 1763)
Zygaena (Agrumenia) loti ([Denis & Schiffermüller], 1775)
Zygaena (Zygaena) filipendulae (Linnaeus, 1758)

Among the 15 Zygaenidae species recorded for the Thrace Region, *Rh. pruni* and *J. globulariae* were found for the first time in Turkey. Moreover, the vicariant species *Rh. pruni* and *Rh. amasina* were registered in the same province Tekirdağ (*Rh. pruni* – in Çorlu, *Rh. amasina* – in Malkara).

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An overview on the Zygaenidae of Albania

Blerina Vrenozi¹, Eyjolf Aistleitner¹, Gerhard Tarmann²

¹Tirana University, Albania; ²Tiroler Landesmuseen, Ferdinandeum, Naturwissenschaftliche Abteilung, Innsbruck, Austria

bvrenozi@gmail.com

Zygaenidae Latreille, 1809 are day-flying moths including the red and black burnets (Zygaeninae) and the shiny metallic green foresters (Procridinae). Albanian Lepidoptera are not sufficiently studied. If we consider the richness of habitats and the known plant biodiversity in this country many more species must be here than recorded so far. The study presented here is part of the project "Zygaenidae of the Balkan Peninsula". Our results are based on historical data and on field work since 2011 on the territory of Albania. At the moment, 26 species of Zygaenidae from 101 localities from Albania are included in our project database (14 Zygaeninae, 12 Procridinae). The distribution maps show their occurrence all over the Albanian territory. Some species can still be expected in Albania but have not been found so far. *Theresimima ampellophaga* (Bayle-Barelle, 1808) has been mentioned from Albania in literature. *Adscita (Adscita) capitalis* (Staudinger, 1879), *Zygaena (Mesembrynus) laeta* (Hübner, 1790) and *Zygaena (Zygaena) nevadensis* Rambur, 1858, which are known from Macedonia and Greece, may also occur in Albania. *Adscita (Adscita) albanica* (Naufock, 1926) was described from Albania in 1918 and since then it has never been found again. *Adscita (Adscita) obscura* (Zeller, 1847) is only known from one female specimen and has to be confirmed. *Adscita statices statices* (Linnaeus 1758) is present only in northern and *Adscita statices drenowskii* (Alberti, 1939) in central and southern Albania, but no hybrids of these two taxa have been found, although they are known in the adjacent countries.

Harnessing the larval stage in the biosystematics of Lepidoptera

David L. Wagner

University of Connecticut, Storrs, USA

david.wagner@uconn.edu

I briefly review advantages and disadvantages of using larval data in alpha systematics and phylogenetic inference, and then examine two classic examples where larvae played a valuable role in systematic efforts. In addition to larval morphology, the utility of larval behaviour and host-plant associations will be addressed. Most examples draw from my studies on acronictine Noctuidae and Notodontidae (both Noctuoidea), Geometrinae, and Zygaenoidea. The use of larvae and life history data to get evolutionary units (species-level taxa) accurately delimited in the face of equivocal (CO1) barcode data will be another emphasis of the presentation. I will conclude with examples where larval life history data has been used to answer big questions in ecology and evolutionary biology.

The far-reaching implications of mimicry in butterflies

Marianne Elias

Institute of Systematics, Evolution, Biodiversity, CNRS, MNHN, Paris, France
elias@mnhn.fr

Prey have evolved multiple strategies to escape predation. Camouflage is a strategy of avoiding detection by potential predators while resting, whereas aposematism relies on advertising chemical defences with conspicuous warning signals. While the efficacy of camouflage decreases with the abundance of prey using the same cryptic pattern, the efficacy of a warning signal increases with its own local abundance. Because of this “strength-in-number” effect, multiple chemically-defended species exposed to the same suite of predators gain a selective advantage from converging on the same warning signal. Convergence in warning signals is called Müllerian mimicry. Here, I review the results of recent genetic and ecological research on two well-studied groups of neotropical Müllerian mimetic butterflies, the genus *Heliconius* and the tribe Ithomiini, which advertise their unpalatability through conspicuous wing colour patterns. Mimicry represents a major adaptation in these groups, where the effects of selection extend well beyond mere phenotypic resemblance. Selection acts on other traits used as mating cues, on the genes underlying wing colour patterns and even on the ecological niche of species. The origin of mimicry itself and the coexistence of multiple mimicry patterns are well understood, but the ultimate drivers of mimicry diversity remain unclear.

Could multiple-model mimicry explain local warning signal polymorphism in the wood tiger moth?

Katja Rönkä

University of Jyväskylä, Centre of Excellence in Biological Interactions,
Jyväskylä, Finland

katja.h.ronka@jyu.fi

The wood tiger moth (*Arctia plantaginis*) is chemically defended and known for its great local and geographic diversity in wing patterning. One possible explanation for the maintenance of local variation is multiple-model mimicry. If each colour morph shares the cost of predator education with another defended species showing similar warning coloration, selection could favour local polymorphism instead of warning signal monomorphism. We studied whether mimetic relationships could exist between the wood tiger moth and several potentially aposematic, sympatric moth species in Finland. First, we tested the relative palatability of *Lomaspilis marginata*, *Rheumaptera hastata*, *Arichanna melanaria*, *Pseudopanthera macularia*, *Autographa gamma* and *Zygaena* sp. compared to the palatability of white and yellow morphs of *Arctia plantaginis*, in assays with great tits (*Parus major*). We offered the birds specimens without visual cues. Second, different morphs of *A. plantaginis* and one of the possible co-mimics were sequentially offered to great and blue tits (*Cyanistes caeruleus*) to test if previous experience with a co-mimic influences predator's willingness to attack other species. We found that all the moths tested are relatively unpalatable to birds and thus potential co-mimics/models for *A. plantaginis*. Our results show that previous encounters with one species can alter bird reactions towards the other species, indicating that the co-existence of even vaguely similar species may protect co-mimics from predator attacks. We conclude that multi-model mimicry rings may provide an explanation for the paradoxical existence of local warning signal polymorphism.

Molecular basis and evolution of gall-inducing in *Caloptilia* (Gracillariidae)

Carlos Lopez Vaamonde¹, Antoine Guiguet², Françoise Laurans³, Issei Ohshima⁴, David Giron²

¹INRA Orléans & IRBI, France; ²IRBI CNRS/Université François-Rabelais de Tours, France; ³INRA Orléans, France; ⁴Kyoto Prefectural University, Kyoto, Japan

carlos.lopez-vaamonde@orleans.inra.fr

Galls induced by arthropods constitute one of the most spectacular examples of hijacking of plant physiology by a parasite. During evolution, this ability to manipulate plant development seemed to evolve several times in diverse insect orders. Price (1987) proposed an evolution of the galligenous lifestyle from the leaf-miner lifestyle. This assertion is questioned by the fossil record which suggests that gall inducers evolved before leafminers. In addition, recent work on leafminers shows that their ability to reconfigure plant physiology is in fact comparable to gall-inducing insects. Little is known about the molecular basis of gall-inducing, and the chemical effectors involved. Our work aims to answer these two questions by studying a Japanese gall-inducing moth, *Caloptilia cecidophora* (Gracillariidae). The *Caloptilia* genus includes almost only leafminers. *C. cecidophora* is an exception with its larvae that induce a foliar gall after digging a mine. This mixed feeding strategy allows us to develop a transcriptomic approach of salivary secretions at two levels: intra-species (by comparing galling and leaf-mining instars) and inter-species (by comparing with closely related leaf-mining *Caloptilia*). We first developed a rearing protocol and studied the gall histology of *C. cecidophora*. Preliminary results confirm the feasibility of the transcriptomic approach and provides hypotheses about the larval mode of action. In parallel, examination of old literature revealed the existence of numerous other gallers potentially closely related to *C. cecidophora*.

Timing of diversification in butterflies

Nicolas Chazot

Lund University, Lund, Sweden

chazotn@gmail.com

Understanding when and where clades diversified is at the core of macroevolutionary investigations and it requires both phylogenetic trees and powerful tools to trace back this past history. Recently, there has been a large number of tools developed to assess lineage speciation and extinction rates and ancestral geographic distributions. The power and reliability of these methods strongly rely on the robustness of the phylogenetic information. Hence, it is necessary to build phylogenetic trees that sample a large fraction of lineages and are reliably time-calibrated. The amount of molecular resources has massively increased allowing us to build large phylogenies containing more lineages and spanning longer periods of time. Focusing on the butterflies (Papilionoidea) we have assembled a large molecular dataset, sampling up to 11 genes from hundreds of lineages. A recent revision of the Papilionoidea fossil record suggested 14 calibration points that can be used at the scale of all Papilionoidea. We combined this fossil information with calibration points set by host-plant ages. The results provide a robust time-calibrated tree that can be used for further analyses of diversification and biogeography but also as a valuable source of information for future phylogenetic work at smaller time-scales.

The butterflies of the Canary Islands and Madeira – aspects of colonization, differentiation, ecology, and conservation

Martin Wiemers

Helmholtz Centre for Environmental Research – UFZ, Halle, Germany

martin.wiemers@ufz.de

The Canary Islands and Madeira are a hotspot for rare endemic butterfly species in Europe. Twenty of the 35 native species are endemic to these archipelagos, and for some of them there is conservation concern, with one species (*Pieris wallastoni*) already extinct, representing the only European butterfly species now thought to be globally extinct. On the other hand, at least 8 additional species have colonized the islands in historic times, with potential effect on endemic species, and some endemic species have lately been (re-)introduced to some of the islands. In recent years, molecular data have been accumulated which shed new light on the colonization history and inter-island differentiation. This talk presents an up-to-date overview on the current knowledge of the islands' butterfly fauna, their biogeographic history of colonization and cryptic diversity, including still unpublished molecular data. According to the molecular analyses, most of the endemics colonized the islands during the Pliocene and quickly spread within an archipelago after initial establishment. Many of them show substantial interisland differentiation, which is only partially reflected in morphological differences. Conservation efforts should take this differentiation into account in order to preserve the species' adaptive and evolutionary potential.

Metalmark moths (Choreutidae) crossing oceans: perspectives from historical biogeography

Jadranka Rota

Lund University, Lund, Sweden

jadranka.rota@biol.lu.se

In the past, highly disjunct distributions of many groups of organisms were usually attributed to vicariance events, i.e. range separation through an appearance of a geological barrier to dispersal such as a large body of water, mountain chain or something similar. In recent years it has become possible to statistically test whether vicariance occurred by using time-calibrated molecular phylogenies together with likelihood models of ancestral range evolution. Using these methods, we demonstrated that vicariance played only a small role in shaping the current distribution of metalmark moths, and that long-distance dispersal and establishment happened many times, even over oceanic distances. We propose a mechanism for how small moths such as metalmark moths could cross oceans.

Preliminary molecular phylogeny and biogeography of the monobasic subfamily Calinaginae (Nymphalidae)

Valentina Todisco¹, Vazrick Nazari², Paul D. N. Hebert³

¹University of Vienna, Vienna, Austria; ²Canadian National Collection of Insects, Arachnids and Nematodes, Ottawa, Canada; Centre for Biodiversity Genomics, Biodiversity Institute of Ontario, University of Guelph, Canada

valentina.todisco@gmail.com

Calinaga (Moore, 1857) is a rare and enigmatic Asian butterfly genus whose phylogenetic placement within Nymphalidae has only recently been established. The evolutionary history of *Calinaga* species, however, remains unknown. Here we explore the evolutionary history of *Calinaga* using 1310 base pairs of sequence data from two molecular (mtDNA barcode and ribosomal protein S5 nuclear gene) and two morphological traits (genitalia and wing pattern). Within the proposed phylogenetic framework, we estimate the ages of divergence within the genus and reconstruct the historical biogeography. We found strong support for monophyly of *Calinaga* and support for the most recent accepted species in the genus. Our results indicate that the common ancestor of *Calinaga* first split in the Eocene (~43 million years ago) in southern China, probably as a consequence of geological and environmental impacts of the collision of the Indian and Asian subcontinents. In the Oligocene/Miocene, the extrusion of Indochina from the continent prompted further dramatic orogenetic changes that promoted isolation and speciation events within the genus while Pleistocene climatic changes also influenced the distribution and further speciation. A dispersal–vicariance analysis suggests that vicariance events have played a far more important role than dispersal in the distribution of extant species.

A collaborative, community effort: re-examining the lepidopteran fossil record

Maria Heikkilä

Smithsonian Institution National Museum of Natural History, Washington, USA and Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland

a.a.maria.heikkila@gmail.com

Lepidopterans are poorly represented in the fossil record and the known fossils have been only minimally studied and lack convincing, synapomorphy-based assignments of systematic position. However, this is now changing thanks to an international effort to re-examine the identification of known fossil Lepidoptera. Teams consisting of experts in different lepidopteran superfamilies have critically reviewed the identification of these fossils. I will be presenting results of several of the working groups and talking about the problems they have been tackling. More reliable identifications will improve our understanding of the nature of the lepidopteran fossil record and of the possibilities of its application. Using securely identified fossils in divergence time analyses will also allow us to obtain a better time frame for the diversification of moths and butterflies.

Report on the establishment of a new order of insects from Burmese amber (Insecta, Amphiesmenoptera)

Wolfram Mey¹, Wilfried Wichard²

¹Museum für Naturkunde, Leibniz Institute of Evolution and Biodiversity Research at the Humboldt University, Berlin, Germany; ²University of Koeln, Institute of Biology, Koeln, Germany

wolfram.mey@mfn-berlin.de

Based on a total of 13 inclusions from Burmese amber the new insect order Tarachoptera was established. The previously described family Tarachocelidae from Burmese amber, which was at the time placed in Amphiesmenoptera *incertae sedis*, is now assigned to this new order. The family contains two genera, *Tarachocelis* and *Kinitocelis*. The latter genus differs from *Tarachocelis* by the absence of androconial scales on the male wings and the loss of Cu₂ in the forewings. Both males and females were described. The species can be distinguished by traits in the wing venation. The new order Tarachoptera is placed in the superorder Amphiesmenoptera based on the presence of seven amphiesmenopteran apomorphies and nine tarachopteran apomorphies. Apomorphic characters of Trichoptera and Lepidoptera could not be found, which suggests an independent origin and evolution from an amphiesmenopteran ancestor which was not the ancestor of the Trichoptera + Lepidoptera. The species of Tarachoptera are tiny insects with wing span of 2.3–4.5 mm but highly specialised according to their aberrant morphology. Aspects of the presumed life-history of the adults were deduced from some of the derived morphological traits that could be interpreted as adaptations to a highly structured micro-environment.

Non-destructive Micro-CT technology and DNA barcodes from old type specimens help to realize difficult XXL-revisions (Geometridae, Geometrinae: *Prasinocyma*)

Axel Hausmann

SNSB - Bavarian State Collection of Zoology, Munich, Germany

axel.hausmann@zsm.mwn.de

The genus *Prasinocyma* Warren, 1897 (Geometridae) is one of the most difficult genera creating problems in identification and taxonomy; therefore, in most collections the species are not identified to species level. The world catalogue of geometrid moth names (Scoble 1999) lists 94 valid species for the Afrotropical region. Since many new and undescribed species were expected in this genus, the aims of the present study were to test how new approaches and modern techniques can foster integrative revisions in particularly large and difficult cases. For our study, we used conventional morphological approaches as well as three-dimensional μ CT-scanning and molecular methods, including DNA barcoding of old type specimens using the Sanger approach and Next Generation Sequencing (NGS) protocols. The identification of the known biodiversity (described species and synonyms) was based on type photographs and genitalia dissection of type specimens as well as on DNA barcodes from type specimens, using a single leg, with tissue recovery after DNA extraction. More than 800 African *Prasinocyma* (Bavarian State Collection of Zoology, Munich; ZSM) were submitted to DNA barcoding and resulted in more than 230 genetic clusters ('BINS'), apparently including many undescribed species. Genitalia dissections confirmed this diagnosis. Moreover, we could show that μ CT-scans can provide similar information as 'conventional' genitalia dissections in a non-destructive way. Based on this example, we show how integrative taxonomic revisions can profit from using minimally invasive methods like three-dimensional μ CT-scanning and molecular methods, including DNA barcoding of old type specimens.

Diversity patterns and integrative analysis (morphology, DNA barcoding) of geometrid moths of Western Himalaya

Pritha Dey¹, V. P. Uniyal¹, Kailash Chandra¹ and Axel Hausmann²

¹Wildlife institute of India, Zoological Survey of India; ²SNSB - Bavarian State Collection of Zoology, Munich, Germany

dey.pritha126@gmail.com

In many countries, a comprehensive inventory, particularly in threatened and fragmented landscapes, such as the Western Himalaya, is lacking. This scanty information prevents effective geographical mapping and the understanding of ecology and finally conservation in the present situation of habitat degradation brought about by resource extraction. Integrative analysis of diversity allows exploration to a scale that is not currently feasible using morphology alone. We collected moths at Nanda Devi Biosphere Reserve, with an area of 6403 km² and elevation range 1800–7817 m. Collection was done along two different mountain slopes across 96 plots between 2000 and 3800 m every 200 m. Moths were collected for 3–4 hours at randomly selected sites starting from dusk. Hourly variation of temperature, relative humidity and wind speed was recorded. Presence of disturbance signs were noted along 50 m transects around the site of collection. Vegetation sampling was done in a nested method in circular plots within a 50 m radius of the site. DNA barcoding of the Geometridae moth specimens collected during fieldwork has been started at the Zoologische Staatssammlung München. The subfamily Ennominae represents most of the species and the subfamily Larentiinae was found to be restricted to higher elevations. Western Mixed Coniferous forest held the maximum number of species. The species diversity showed a differential response to vegetation structure at the two locations. There was a mid-elevation peak (2300–3000m) at both locations. A negative impact of resource extraction on moth populations was observed. Interestingly, the forest types have more prominent effects in disturbed mountain slopes.

Diversity of geometrids (Geometridae) in the mountains of Dinaric karst and ecological patterns of their vertical stratification

Iva Mihoci¹, Mladen Kučinić², Axel Hausmann³

¹Croatian Natural History Museum, Zagreb, Croatia; ²Faculty of Science, Division of Biology, Zagreb, Croatia; ³SNSB - Bavarian State Collection of Zoology, Munich, Germany

iva.mihoci@hpm.hr

Diversity and ecological patterns of vertical stratification of one of the largest Palaearctic moth families (Geometridae) were researched on two Dinaric karst mountains. Out of a total of 464 geometrid species in Croatia, 232 species were found in the study areas, 164 on Mt. Biokovo and 132 on Mt. Lička Plješivica. There are two peaks in the vertical stratification observed on both mountains. These are at the transition zones (ecotones) of mid altitudes towards both lower and higher elevations. All diversity indices are inversely correlated with altitude. Mt. Lička Plješivica and Mt. Biokovo are distinct in diversity with low levels of similarity. There is a significant separation of zones corresponding to low, mid and high altitudes in both areas. The impact of variables significantly changes with seasons but is almost unaffected with respect to elevation. Single, most important variable affecting altitudinal distribution on both mountains is the dewpoint temperature. Species inhabiting mid-altitudes showed a wide altitudinal range in contrast to the narrow ranges observed for representatives of the low and high altitudes, which is not in accordance with Rapoport's rule. Future activities should focus on addressing the question whether the fairly broad elevation ranges in the middle elevations on both mountains can be explained by the mid-domain effect.

Preliminary insight into the phylogeny of South American Larentiinae (Geometridae)

Andro Truuverk¹, Erki Õunap¹, Gunnar Brehm²

¹University of Tartu, Tartu, Estonia; ²University of Jena, Jena, Germany

andro.truuverk@ut.ee

Modern advances in molecular phylogenetics have significantly improved the understanding of the tribe-level classification of the subfamily Larentiinae. Despite the few relatively comprehensive studies having been published during recent years, the immense diversity of South American larentiines has unfortunately been largely overlooked. Specifically, only very few species from this large continent have been included in earlier studies. Hereby we demonstrate preliminary results of possible tribal-group placements of more than 30 South American larentiine species. Altogether, DNA sequences of more than 100 species were included into the analysis, covering all known tribes. Sequence data from one mitochondrial and eight nuclear genes were used. Data were analysed by Bayesian phylogenetic method using program MRBAYES and by maximum likelihood using RAXML. According to earlier expectations, many of the analysed South American larentiines clustered into tribes considered valid in most recent treatments of Larentiinae. Nevertheless, phylogenetic placement of several species does not allow association with known tribes comfortably.

Phylogenomic analysis of the emerald moths (Geometridae: Geometrinae)

David Plotkin, Akito Kawahara

University of Florida, Gainesville, FL, USA

dplotkin@ufl.edu, kawahara@fmInh.ufl.edu

The emerald moths (Geometridae: Geometrinae) are a cosmopolitan subfamily with over 225 genera and 2,500 species. The majority of these moths are characterized by a green ground colour, although the precise shade of green varies across the subfamily. The monophyly of Geometrinae has been confirmed by multiple recent phylogenetic analyses. However, the relative placement of many of the geometrine tribes is poorly supported, and it has been speculated that some tribes are paraphyletic. Anchored hybrid enrichment was used to obtain phylogenomic data for the major lineages of emerald moths, and to subsequently perform a maximum likelihood analysis and determine the inter-tribal relationships of Geometrinae. These estimated relationships are compared with previously proposed tribal-level hypotheses, and putative synapomorphies for some well-supported clades are discussed.

Diversification dynamics of Geometridae moths

Hamid Reza Ghanavi

Lund University, Lund, Sweden

hamid.ghanavi@biol.lu.se

The moth family Geometridae Leach, 1815 with over 23,000 species and 2000 genera is one of the most diverse families within Lepidoptera. Species of this family have a global distribution and some of them are important pests having a big impact on human societies. In recent years, some studies approached the evolutionary relationship of Geometroidea species using molecular markers, focusing especially on the relationship between different families and superfamilies which gives us a relatively clear image of the evolutionary history at higher levels but in many cases our knowledge of the phylogenies or evolutionary processes within families is still very limited. In this study, we focused on the phylogenetic relationship and diversification processes within the family Geometridae. In order to investigate questions on the evolutionary processes shaping the diversity of this family we used 13 genetic markers, one mitochondrial and the rest nuclear protein coding genes, first to obtain a robust phylogeny of the family. Then, based on the available fossil information of the family, we calibrated the phylogenetic tree to infer the times of divergence for the major lineages. Results of the study will be presented.

The curious incident of the moths at light-time: a study testing different street lamps for Lepidoptera attraction

Sarah Saadain

University of Vienna, Vienna, Austria

sarah.saadain@univie.ac.at

The term “light pollution” describes the excessive or misdirected use of artificial light. It can have a serious impact on wildlife, especially on orientation of nocturnal species. Over the last decades, light pollution has increased because of urbanization. During a period of several weeks, different types of modern commercial street lights were tested in relation to insect attraction. The lamps were incorporated in special light traps and placed along a street in a montane region in Vorarlberg, Austria. While all insects were counted and categorized in different orders, special emphasis was placed on the nocturnal Lepidoptera. With more than 20,000 specimens from 13 different orders and at least 60 different species of Lepidoptera, the study shows a high difference between LED and gas discharge lamps. The metal halide lamp had the highest attraction with an average number of 41 Lepidoptera per night, while a LED lamp gave an output of only 2 individuals on average per night. These results point out the enormous influence of streetlights on Lepidoptera activity and show that the negative impact of light pollution can be minimized by using the appropriate lamp type.

Do *Yponomeuta* species sing? A study of some hindwing structures

David Agassiz

Natural History Museum, London, United Kingdom

david.agassiz@gmail.com

Yponomeuta spp. contain a hyaline (scaleless) patch near the base of the hindwing, in these are some ridges, which have not previously been described. It is suggested they may be used for stridulation. Production of sound and a facility for "hearing" is common in Lepidoptera, especially in Noctuoidea, Geometroidea and Pyraloidea; however, it has never been reported in Yponomeutoidea. Several questions ensue: if sound is produced presumably there is a capacity for hearing. Is it likely that the hyaline wing membrane is used also for this purpose? It seems plausible that a membrane without scales makes a better "eardrum". If sound is produced what is its purpose? The same structures occur in both males and females of the same species, but they do differ between species. The commonly surmised purpose is defence against bats. Without experiments with live specimens it is difficult to verify this. The times when stridulation occurs should indicate whether its purpose is defensive or romantic. One use of this structure for systematists is that it is a morphological character which is likely to indicate an evolutionary relationship and help us classify the species and genera correctly; this will need to be confirmed by examination of the DNA. More profound examination of the phenomenon is left to others with the resources and time to investigate the issues thoroughly.

Catches of Procridinae (Zygaenidae) by new synthetic sex attractants in Italy, Austria and Greece

Konstantin A. Efetov¹, Gerhard M. Tarmann², Elena E. Kucherenko¹

¹Crimean Federal University, Crimea; ²Tiroler Landesmuseen, Ferdinandeum, Naturwissenschaftliche Abteilung, Innsbruck, Austria

efetov.konst@gmail.com, g.tarmann@tiroler-landesmuseen.at

The esters of 2-dodecenoic acid and 2-butanol were synthesized recently in the Crimean Federal University in the laboratory of the first author. These substances have properties of sex attractants for the males of Procridinae. We applied three attractants: EFETOV-S-S-2 (S-enantiomer), EFETOV-S-2 (R-enantiomer) and EFETOV-2 (racemic mixture). Field tests were carried out by the second author at several sites in Italy, Austria and Greece in 2015–2016. The lures were hung on twigs of plants or fixed on a hat of the researcher during investigation of the biotopes.

The numbers of attracted males are listed below:

Rhagades pruni: 18 males (Italy, 2016);

Adscita alpina: 20 males (Italy, 2015), 20 males (Italy, 2016);

A. statices: 3 males (Italy, 2016);

A. alpina X *A. statices* (hybrids): 5 males (Italy, 2016);

A. geryon: 4 males (Italy, 2015);

A. manni: 20 males (Italy, 2015), 4 males (Italy, 2016);

Jordanita notata: 8 males (Italy, 2015), 1 male (Italy, 2016);

J. globulariae: 4 males (Italy, 2015);

J. subsolana: 107 males (Italy, 2015), 101 males (Italy, 2016), 4 males (Austria, 2015), 9 males (Austria, 2016), 37 males (Greece, 2016).

It should be noted that the males of *J. subsolana* and *J. globulariae* were mainly attracted by EFETOV-S-2, while the males of *Rh. pruni* – by EFETOV-S-S-2.

Rh. pruni was recorded for the first time since more than 100 years in Piemonte and northwestern Italy and for the first time ever in the Ligurian Alps.

Swarm explosion build-up of millions of *Vanessa cardui* in the Araba & Negev Deserts in Israel, winter – spring 2015–2016

Dubi Benyamini

4 D Micro Robotics, Beit Arye, Israel

dubi_ben@netvision.net.il

The Middle East was strongly suspected for many years to be a source and start point for *Vanessa cardui* spring migrations to south-eastern Europe and Turkey. Since the mid-1950s the author has studied and documented butterfly migrations in Israel, Sinai and Jordan. Accumulating a vast number of records, he analyzed this phenomenon and finally succeeded in documenting the complete process of a progressive huge build-up in the autumn of 2015 – spring 2016, in the Araba and the Negev Deserts in southern Israel. It all started with heavy rainfall in late October 2015 resulting in floods in all the valleys and depressions in the Araba and Southern Negev, up to about 100 km north of Eilat. Prolific germination of annuals, many of them host-plants of *Vanessa cardui*, encouraged egg-laying for the first local brood in November – December 2015. Adults of the first brood split; the majority remained to lay eggs for the second brood, while fewer adults migrated about 200 km to the northern Negev to lay eggs for the second brood there in January – February. In mid-late February, second brood adults laid millions of eggs in the Northern Negev to start building up the huge swarm migration of the third brood northwards to Europe. We will follow this five months process of population explosion along three generations – from a few hundred females to the migrating millions.

Red Lists, indicators and butterfly conservation

Chris van Swaay

Dutch Butterfly Conservation & Butterfly Conservation Europe, Wageningen,
The Netherlands

chris.vanswaay@vlinderstichting.nl

Effective butterfly conservation needs high quality data on distribution and trend. Open distribution data is available via the GBIF portal. However, there are still large gaps in Europe, and ways to fill these gaps will be discussed. Butterflies offer the possibility to be used as a structural headline indicator, not only for grasslands, but also for other habitats, and help evaluate agriculture policy and track the impacts of other pressures such as climate change. To facilitate this, Butterfly Conservation Europe (BCE) started a new initiative with the Centre for Ecology & Hydrology (CEH) to develop a European Butterfly Monitoring Scheme (eBMS) and a single database containing all European monitoring data from which we could produce a range of indicators.

LIFE+ Blues in the Marshes – using habitat islands for ants to restore habitat for *Maculinea* butterflies in The Netherlands

Irma Wynhoff, M. P. Berg, F. van Langevelde

Dutch Butterfly Conservation, Wageningen, The Netherlands

irma.wynhoff@vlinderstichting.nl

In the Netherlands, the single population of the obligate myrmecophilic butterfly *Maculinea (Phengaris) teleius* occurs on only 3 ha of habitat, whereas at least 40 ha of habitat are needed for a sustainable metapopulation. Therefore, 170 ha of farmland is being restored within a LIFE+ project by large scale soil excavation and inoculation of clippings of the target vegetation. For successful restoration, the habitat requirements of the butterfly, with *Sanguisorba officinalis* as host-plant and its particular life cycle as parasite of the ant species *Myrmica scabrinodis*, have to be taken into account. We tested whether colonization of nests of this ant species in the restoration areas is facilitated by translocation of sods collected from fen meadows. We divided 54 sods, each sized one m², randomly over six patches and measured vegetation development and ant presence in the sods and surrounding control plots for two years. In the first summer, significantly more *Myrmica* ants were found in the transplanted sods in comparison to the surrounding area. Herb cover had a significant positive effect on *Myrmica* ant presence while it did not affect the presence of the pioneer ant species *Lasius niger*. In the second year, *Myrmica* ants were found in the surrounding control plots as well. This study contributes to the knowledge-base required for the design of restoration projects aimed at expanding the habitat of the critically endangered butterfly *Maculinea (Phengaris) teleius*.

Conserving butterflies at a landscape scale: lessons from the UK

Martin Warren

Butterfly Conservation Europe, Wageningen, The Netherlands

martin.warren@bc-europe.eu

Habitat fragmentation is one of the biggest threats facing butterflies across Europe. In the UK, over 90% of semi-natural grasslands have been lost and remaining fragments are very small (typically <10ha) and isolated. Conserving threatened species in such habitat fragments is a huge challenge but in this paper, I show that it is possible. Using examples of successful conservation projects run by Butterfly Conservation (UK), I will explain the role of agri-environment schemes to restore and reconnect habitats and the lessons learnt that are relevant across Europe. A report on some of the projects is available on the BC website <http://butterfly-conservation.org/4463/conservation-projects.html>

Comparison of population demography in two ecotypes of the Bog Fritillary *Boloria eunomia*

Marcin Sielezniew¹, Agata Kostro-Ambroziak¹, Przemysław Klimczuk¹, Krzysztof Deoniziak², Piotr Nowicki³

¹University of Białystok, Białystok, Poland; ²Adam Mickiewicz University, Poznań, Poland; ³Jagiellonian University, Kraków, Poland

marcins@uwb.edu.pl

The rare and regionally endangered butterfly *Boloria eunomia* (Nymphalidae) is generally considered a habitat specialist, but it occurs in very distinct biotope types across its boreal-mountain distribution range. East-central Europe is particularly interesting in this respect due to the co-occurrence of two different eco- and morphotypes classified often into different subspecies. Some populations inhabit damp, sunny, flower-rich meadows and use *Bistorta major* as their only host-plant, while others are restricted to raised peat bogs and pine bogs, where caterpillars probably feed mainly on *Vaccinium oxycoccus*. In June 2015, we carried out simultaneous studies of both ecotypes by mark-recapture sampling of two large populations in the Knyszyn Forest (NE Poland) separated by a distance of about 30 km. The flight period of *B. eunomia* at the bog site was a few days shorter and delayed by a few days in comparison with the meadow site. The emergence of imagoes was highly synchronized and protandry was very conspicuous. A total number of 1097 and 642 individuals was marked at the bog and meadow sites respectively, and 51% and 33% of them were recaptured at least once. The estimated number of males was insignificantly higher than that of females in both localities. Interestingly, the estimated life span of males was considerably shorter than that of females at each site. Additionally, both sexes of the 'meadow' ecotype lived significantly longer than those from the raised bog.

Latency to oviposition as a measure of ecological specificity: a cross-region phylogenetic comparative study

Sille Holm, Juhan Javoiš, Erki Õunap, Robert B. Davis, Ants Kaasik, Toomas Tammaru

University of Tartu, Tartu, Estonia

sille.holm@ut.ee

Ecological specialization is a central concept applied to organise our understanding of living nature in most diverse contexts. A particularly important question is whether the increase of herbivore species richness towards the tropics is a direct consequence of the species richness of their hosts, or it can be explained by the increase in ecological specialisation towards the equator. Defining and measuring specialisation (host specificity) is not, however, an easy task. Here we propose oviposition latency as a novel and simple measure of host specificity in herbivorous insects. The latency to accepting offered suboptimal substrate for oviposition (= 'waiting' time before laying first eggs) should reflect the natural diet breadth (host specificity) of the species: polyphagous insects should be less reluctant to lay eggs in the absence of a suitable host-plant. We measured oviposition latency for about 1000 field-collected females from 165 geometrid moth species representing a temperate (Estonia) and an equatorial region (Uganda). We applied the novel index to answer the following questions: 1) does oviposition latency correlate with host specificity across species; and 2) does oviposition latency differ between the regions. An original phylogeny for 366 taxa of geometrid moth from temperate and tropical region was used as a basis for modern phylogenetic comparative methods. We found significant correlation between oviposition latency and host specificity, whereas no differences in oviposition latency between the temperate Estonia and equatorial Uganda were found. Our results are thus inconsistent with the idea that tropical moths are more specialised than temperate ones.

Butterfly communities in semi-natural grasslands: short- and long-term effects of management practices in Transylvania, Romania

Cristina Craioveanu, Laszlo Rakosy

Babes-Bolyai University, Cluj-Napoca, Romania

cristinacraioveanu@gmail.com

The profitability of agricultural land is a major driver for the dynamics of land use practices and patterns. In Romania centuries of extensive traditional land-use practices have favoured a high biodiversity in grassland communities, indicated very often by a high butterfly diversity. The present socio-economic context, however, is driving agriculture towards intensification or abandonment of grasslands, reflected rapidly by changes in butterfly communities. Even unique grassland habitats, which are emblematic for Transylvania, are at risk. Our study investigated butterfly communities of older and younger age from representative mesophilous grasslands from Transylvania, in and around the area of a Natura 2000 site (“Dealurile Clujului Est”). We selected a set of grasslands managed through modern and traditional practices, in order to see which practice would be most beneficial in terms of preserving grassland biodiversity, while not lowering too much the productivity or economic benefit for the local communities. We have found that long-term extensive traditional practices favoured butterfly-rich communities, with specific profiles. On the other hand, short-term changes in most practices have not altered significantly the original communities, except intensification of sheep grazing, which seems to be particularly detrimental to butterflies. Short term changes affect mostly sensitive species (e.g. Large blues), which become less abundant. Another important aspect was the fact that using light mechanical mowers is a more profitable alternative that could replace hand mowing without compromising meadow biodiversity.

Traditionally-mowed fruit orchards and their butterfly fauna in Órség National Park (Hungary)

Bálint Horváth^{1,3}, István Szentirmai², Ferenc Lakatos³

¹Green Woodpecker Foundation, Hungary; ²Órség National Park Directorate, Hungary; ³University of Sopron, Hungary

macrolepidoptera@gmail.com

Órség National Park in western Hungary contains a variety of habitats. Many of these have been affected by stockbreeding activities during the last century. Back then, farmers extensively mowed the meadows and fruit plantations creating a unique habitat type in the region known as a “traditionally-mowed fruit orchards” (henceforward TMFO). Due to altered economic and social conditions, many TMFOs have transformed or have vanished in the last couple of decades, which is unfortunate as these habitats most likely support a high diversity of butterflies. In 2012–2013, we surveyed the national park’s TMFO localities for butterfly fauna. Our goals: collect exact information about butterfly fauna, assess threat factors, examine potential reasons of species disappearance, and gauge maintenance potential. We found a total of 83 TMFOs and detected 53 butterfly species, including 14 protected species. The fruit trees in TMFOs do not maintain a high butterfly species diversity, but the undergrowth vegetation does. Many habitats have been abandoned, some are threatened by *Solidago gigantea*, and the native under-layer vegetation has changed. A further threat is intensive land use as the under-layer is ploughed or is cut using a lawnmower. To reverse the decline of these habitats, the National Agri-Environmental Scheme (AES) offers a compensation program for farmers. Although the program’s prescriptions support the maintenance of biodiversity, it does not focus on butterflies. In TMFOs, the herb-layer provides higher butterfly diversity, but the AES mainly supports avifauna. We framed additional prescriptions for AES to prevent the loss of butterfly diversity in traditional fruit plantations.

Does targeted management for the habitat directive butterfly *Euphydryas aurinia* protect non-target species? Lesson from the Czech Republic

Martin Konvicka^{1,2}, Zdeněk Faltýnek Fric², Thomas Schmitt³, Alena Bartonova^{1,2}, Jana Slancarova², Michaela Kopeckova⁴, Michal Zapletal²

¹University of South Bohemia, Ceske Budejovice, Czech Republic; ²Biology Centre CAS, Czech Republic; ³Senckenberg Deutsches Entomologisches Institut Munchenberg, Germany; ⁴Ametyst, o.s., Czech Republic
konva333@gmail.com

The distribution of *Euphydryas aurinia* in the Czech Republic is limited to westernmost fringe of the country, Karlovy Vary region, where it forms a metapopulation system inhabiting remnants of seminatural grasslands in a submountainous landscape. Annual monitoring, mark-recapture counts, behavioural studies, population genetic analyses and site management proposals occupied the authors for large parts of the last decade, resulting in several papers and much unpublished results. In 2015, we revisited the system, asking whether the targeted conservation of *E. aurinia* sites contributes to preserving species richness of non-targeted butterflies. We compared butterfly assemblages inhabiting *E. aurinia* sites, seminatural grasslands without *E. aurinia*, and intensively used grasslands. The answer was positive, indicating, first, that sites hosting *E. aurinia* are the best grassland patches in the whole landscape, and second, that management aimed at preserving *E. aurinia* contributes to preserving other butterflies as well.

Using limited data to create a preliminary Red List of Serbian butterflies

Miloš Popović¹, Martina Šašić², Rudi Verovnik³

¹University of Niš, Niš, Serbia; ²Croatian Natural History Museum, Zagreb, Croatia; ³University of Ljubljana, Ljubljana, Slovenia

milos@habiprot.org.rs

For the great majority of insect species population data are limited and Red Lists usually meet only the IUCN criterion B related to changes in distribution. Using this criterion with field records from Alciphron database and R statistical software, we assessed the National Red List status for 191 butterfly species of Serbia. 70,031 field records from 2005–2016 were available for the analysis. EOO was calculated using Delaunay triangulation. AOO value was calculated by counting occupied 2×2 km squares and it was corrected since only 13% of these squares were surveyed (AOCor). To obtain more precise estimates for species with limited data the Maxent ecological niche modelling procedure was also used (AOMax). A total of 55 species (29%) have a threshold value of AOO/EOO under the B criterion, but only 24 species (12%) also meet additional criteria and could be classified as threatened (CR = 2, EN = 13, VU = 9). The remaining 28 species were Near Threatened and additional 3 were Data Deficient and one was not assessed. In comparison, the Red Data Book of Serbian Butterflies from 2003 lists 71 species (37%) as Endangered or Vulnerable (old IUCN categories) and includes 34 species (18%) in the final Red List, disregarding the assessed IUCN threat categories. A procedure for Red List assessment when only limited distributional data is available will be discussed. This could help to create more objective Red Lists and optimally allocate conservation efforts.

The study was supported by Grants No. 173025 and 1613051 of the Ministry of Education, Science and Technological Development of Republic of Serbia

Management of *Thaumetopoea pityocampa* in urban and recreational areas

Pasquale Trematerra, Marco Colacci

University of Molise, Campobasso, Italy

trema@unimol.it

The research activities are aimed at the development of innovative technologies for pest management of *T. pityocampa*.

A) Trunk barrier traps. Eight devices were placed on equal number of trees in a public park located in Campobasso with 50 infested trees of *Pinus nigra*. After larval trapping, significantly fewer male adults were captured during summer 2016 in comparison with 2015. Similarly, significantly fewer nests were formed on the experimental trees in winter 2016 and 2017 compared with 2015. The results show the potential of the trunk barrier trap devices as a control method for the management of *T. pityocampa* infestations after long-term application.

B) Activity of pheromone trap devices. Six different devices were tested during the 2015 flight period of *T. pityocampa* (between July and September). Most of the adults were captured in August. From the trap devices tested, G-trap was found superior to the other devices.

C) Mating Disruption method (MD). In a tourist recreational area, two plots composed of one hectare each were identified during 2015 and 2016. One plot was a control, while in the other MD pheromones were applied. In both plots about 600 infested trees of *Pinus halepensis* were present. MD showed a high effectiveness. Both in 2015 and 2016 the number of males monitored by pheromone traps and the number of nests present in the plot with MD were lower than males and nests recorded in the plot without pheromones. MD can be also applied in private gardens, public parks, in urban and semi-urban areas.

A genomic perspective on deep DNA barcode splits in European Lepidoptera

Marko Mutanen¹, Kyung Min Lee¹, Axel Hausmann², Paul D. N. Hebert³, Peter Huemer⁴, Carlos Lopez Vaamonde⁵, Rodolphe Rougerie⁶, Andreas Segerer⁷

¹University of Oulu, Oulu, Finland; ²SNSB - Bavarian State Collection of Zoology, Munich, Germany; ³Biodiversity Institute of Ontario, University of Guelph, Canada; ⁴Tiroler Landesmuseen, Innsbruck, Austria; ⁵INRA, Orléans, France; ⁶Muséum national d'Histoire naturelle, Paris, France; ⁷Zoologische Staatssammlung München, Munich, Germany

marko.mutanen@oulu.fi

Many large-scale investigations in a plethora of animal taxa have revealed that deep intraspecific splits in DNA barcodes are a pervasive phenomenon, although the frequency of such splits may vary among groups. In Lepidoptera, splits over 2% have been used to flag possible cryptic diversity, and often led to the description of new species through an integrative approach. European Lepidoptera have been barcoded comprehensively in several national campaigns, and investigations of barcodes of thousands of species have revealed hundreds of deep intraspecific splits. While many of those splits were shown to represent overlooked cryptic species, preliminary investigations have failed to provide further support of cryptic diversity in most cases. We adopted a genome-wide ddRAD approach to obtain in-depth understanding of mitochondrial splits in 46 species (belonging to 18 families) of European Lepidoptera with one or more deep intraspecific splits. Some technical challenges were encountered during the construction of the RAD library, resulting in SNPs being generally less numerous than expected; nevertheless, typically hundreds or thousands of SNPs per species were recovered. In some cases, the analysis of RAD markers strongly supports the presence of cryptic diversity (e.g. in *Perizoma incultaria*, *Neofaculta infernella* and *Hoplodrina octogenaria*), while in most cases such evidence was not found. In many cases, it is likely that deep intraspecific splits are due to mitochondrial introgression or other biological processes that are not reflected in the nuclear genome.

Clarifying species boundaries with ddRAD sequencing in two species complexes of pygmy leaf-mining *Ectoedemia* moths

Kyung Min Lee¹, Camiel Doorenweerd^{2,3}, Erik J. van Nieuwerkerken³, Marko Mutanen¹

¹University of Oulu, Oulu, Finland; ²University of Hawaii, Honolulu, USA;

³Naturalis Biodiversity Center, Leiden, The Netherlands

algaekmlee@gmail.com

The phylogeny and taxonomy of the pygmy leafmining moth genus *Ectoedemia* (Nepticulidae) has previously been studied with the mtDNA barcoding marker COI and the nuclear EF1-alpha as well as on the basis of morphology. Two species complexes, viz. the *E. rubivora* complex and *E. subbimaculella* complex, remained with unclear species boundaries. These complexes were sampled in greater intensity from different host-plants and a wide geographic range: 33 samples for the three species in the *E. rubivora* complex and 60 samples for the four species in the *E. subbimaculella* complex. We used next-generation sequencing based double digest Restriction-site Associated DNA (ddRAD) to clarify species boundaries. The ddRAD provided 409,246 SNPs in 4,852,467 base pairs for the *E. rubivora* complex and 570,943 SNPs in 4,618,495 base pairs for the *E. subbimaculella* complex. In the *E. rubivora* complex, contrary to morphological and COI data, a clear genetic differentiation between species was observed. The pairwise divergences range between 3.9-4.7% among the three species (*E. rubivora*, *E. arcuatella* and *E. atricollis*) that feed on different host-plants. We found no indication of host race formation in the oligophagous *E. atricollis*. In the *E. subbimaculella* complex, ddRAD data failed to distinguish between the two widespread species *E. subbimaculella* and *E. heringi*, whereas *E. liechtensteini* and *E. phyllotomella* formed distinct monophyletic groups within a larger paraphyletic group of *E. subbimaculella* and *E. heringi*. Morphological characters, leafmine morphology and food plant separation are at present inconclusive to distinguish them.

The world travellers – Phylogeny and phylogeography of the butterfly genus *Leptotes* (Lycaenidae)

Zdeněk Faltýnek Fric¹, Jana Maresova¹, Tomas Kadlec², Robert Tropek³, Martin Wiemers

¹Biology Centre, Czech Academy of Science, Czech Republic; ²Czech University of Life Sciences Prague, Prague, Czech Republic; ³Charles University in Prague, Prague, Czech Republic; ⁴Helmholtz Centre for Environmental Research – UFZ, Halle, Germany

fric@entu.cas.cz

The butterflies of the subtribe Leptotina occur in tropical and subtropical areas around the globe. We investigated phylogenetic and biogeographical relationships of most members, using both likelihood and Bayesian approaches. We also estimated diversification times within the subtribe. Lastly, we investigated phylogeographic patterns of the most widespread Old World species, *Leptotes pirithous*. DNA sequences from two mitochondrial (COI, COII) and two nuclear genes (Wingless, Ef1 α) were analysed for 13 species of the genus *Leptotes* and one species of the genus *Cyclyrius*. Both genera together form a monophyletic clade, *Cyclyrius* is placed deep inside the genus *Leptotes*. Therefore, we confirmed that the name *Cyclyrius* is a junior synonym of *Leptotes*, thus the subtribe Leptotina consists only of a single genus, *Leptotes*. The genus *Leptotes* originated in the Oriental Region between late Eocene and early Oligocene (35–31 Mya) and later during Miocene it dispersed to the rest of the Southern Hemisphere. *L. pirithous*, the species with the largest distribution in the Old World, originated in Madagascar and invaded all of Africa and Europe including numerous surrounding islands.

The study was supported by the Czech Science Foundation (14-36098G) and the University of South Bohemia (168/2013/P).

Phylogeny of the African members of the butterfly genus *Azanus* (Lycaenidae)

Jana Maresova^{1,2}, Michal Rindoš^{1,2}, Roger Vila³, Zdeněk Faltýnek Fric²

¹University of South Bohemia, Ceske Budejovice, Czech Republic; ²Biology Centre, Czech Academy of Sciences, Czech Republic; ³Institut de Biologia Evolutiva (CSIC-UPF), Barcelona, Spain

maresovajana2@gmail.com

The butterfly genus *Azanus* Moore, (1881) is known from Old World tropics and subtropics. It consists of four species distributed in Asia, six species distributed in continental Africa (two species, *A. jesous* and *A. ubaldus* are shared between the continents and reach also the Mediterranean) and two species from Madagascar. Although the species are generally widespread, they differ in habitat utilization (from savannah, forests, agricultural landscapes to desert oases). We analysed phylogenetic patterns of the genus based on two mitochondrial (COI, COII) and two nuclear (Wingless, Ef1 α) markers. Congruent phylogenetic trees were reconstructed using both likelihood and Bayesian approaches. Our data indicate that African members of the genus *Azanus* form a monophyletic group. We recognize two main clades within African *Azanus*, with *A. ubaldus* forming the first one and the rest of the species the second one. Within the second clade *A. jesous* was a sister species to *A. isis* and *A. natalensis*. However, according to molecular data, the relationships within morphologically different *A. isis* and *A. natalensis* were not well resolved. Both Madagascan species form a single clade sister to *A. moriqua* (ML) or sister to *A. moriqua* + *A. mirza* (BI).

The study is supported by the Czech Science Foundation (14-36098G) and the University of South Bohemia (168/2013/P).

Anchored hybrid enrichment recovers a robust phylogeny of erebine moths (Erebidae)

Nicholas Homziak

University of Florida, Gainesville, FL, USA

nhomziak@ufl.edu

The Erebinæ is one of the most taxonomically diverse subfamilies of the superfamily Noctuoidea, containing roughly 10,000 species. Erebinæ utilize a diverse range of plants as larval hosts, and the subfamily includes several pest species. Erebinæ also possess a number of adaptations for predator defence, including highly sensitive hearing organs, and striking wing colouration which is revealed when some species are disturbed from rest. Despite the relevance of erebine moths to both applied and basic research, studies of their evolution are hindered by the lack of a robust phylogenetic hypothesis for the subfamily. The present study utilized anchored hybrid enrichment sequencing to obtain large numbers of unlinked genes for phylogenetic analysis through maximum likelihood, parsimony, and gene tree–species tree approaches. Taxon sampling included type genera for 19 of the 23 tribes of Erebinæ, resulting in the first robust support for backbone relationships within the subfamily. The relationships recovered here are compared to earlier hypotheses of tribal composition and inter-tribal relationships. Additionally, our results support several novel relationships within the Erebinæ.

A backbone for the butterflies: Tribal-level phylogeny of Papilionoidea based on 352 loci

Marianne Espeland^{1,2}, Jesse Breinholt², Akito Kawahara²

¹Zoological Research Museum Alexander Koenig, Bonn, Germany;

²University of Florida, Gainesville, FL, USA

m.espeland@zfmk.de

Higher-level butterfly phylogenetics has so far been dominated by studies using 4–10 genes using Sanger sequencing. These studies have given us great insight into classification of butterflies, but many relationships remain poorly supported. Using a target enrichment approach and Illumina sequencing we enriched 352 loci (exons) for about 160 specimens, and combined these with available transcriptome and genome data, for a total of 208 specimens including outgroups. This probe kit contains COI and all commonly used nuclear loci (Ef1-a, wg, GAPDH, Rps5, Rps2, IDH, MDH, CAD, ArgK, DDC), and can readily be combined with available sequence data. Using the full dataset and various subsets to study effects of locus length, GC content, pairwise identity and missing data, we infer a generally well supported phylogeny covering all families and subfamilies within Papilionoidea, as well as all tribes except three, and many currently unplaced taxa. Papilionidae is sister to the remaining butterflies followed by Hedyliidae+ Hesperiiidae, Pieridae, Riodinidae+Lycaenidae and Nymphalidae. Within Lycaenidae we find Polyommatae well supported as nested within Theclinae in all main datasets, and many tribes, especially within Theclinae are polyphyletic. Two seemingly rapid radiations in the tree are still largely unsupported – the Riodininae (Riodinidae) and the Satyrinae (Nymphalidae). Additionally, in Nymphalidae the longstanding question about the placement of Libytheinae as either sister to Danaeinae or to the rest of Nymphalidae still cannot be resolved.

Genus *Amerila* Walker, 1855 in Africa (Noctuoidea: Erebidae: Arctiinae) – is it still terra incognita?

Łukasz Przybyłowicz, Sebastian Tarcz

Polish Academy of Sciences, Kraków, Poland

lukasz@isez.pan.krakow.pl

Genus *Amerila*, traditionally placed within the tribe Arctiini, is a diverse group of tiger moths with more than 60 described species distributed across tropical parts of the Old World. However, modern taxonomic studies based on molecular data provided evidence that *Amerila* actually constitutes the sister group of the Syntomini+Arctiini clade. Despite its large size and attractive colouration, the genus has received little interest from both collectors and scientists. The milestone in the taxonomy and distribution of the African species is the monograph by Häuser & Boppré (1997). The reproductive organs of both *Amerila* sexes are highly unevenly studied as male genitalia are much better known. No sufficient description of any African *Amerila* female reproductive organs has been published yet. The relationships within the genus remain completely unknown. The pretext to our study is the ongoing Czech grant “Changes in biodiversity of Lepidoptera along an altitudinal gradient of Mt. Cameroon”. Initially, the faunistic study aimed to be a simple list of Cameroonian *Amerila* moths, but then it quickly turned into a taxonomic and revisionary work with the description of a new cryptic species, descriptions and illustrations of unknown female reproductive organs and a preliminary study of *Amerila* systematics based on DNA barcoding (fragment of the mtDNA cytochrome oxidase gene). Even the limited material from this very restricted area showed that the group which, due to the monograph of Häuser & Boppré, seemed to be one of the best studied African arctiine genera, is becoming a terra incognita with a number of intriguing problems deserved to be studied.

The fairy moth genus *Nemophora* (Adelidae): taxonomic composition, diversity and distribution

Mikhail Kozlov

University of Turku, Turku, Finland

mikoz@utu.fi

The genus *Nemophora* Hoffmannsegg, 1798 includes 154 described and ca. 140 undescribed species. The highest diversity of *Nemophora* is observed in the Oriental and Oceanian Regions. The genus is taxonomically complicated, due to geographical variation in diagnostic characters and sexual dimorphism recorded in some species; at the same time, the majority of species are known from few specimens only. The closely related species are often distinguished by wing pattern better than by characters of male genitalia. This particularly concerns two currently described European species, which differ from *Nemophora degeerella* in wing pattern and some other external characters, but not in male genitalia. Despite considerable progress in investigation of fairy moths achieved during the past decade, phylogeny of the family remains obscure. The current DNA analysis clearly demonstrated that the genus *Cauchas* Zeller, 1839 is paraphyletic; this finding changes our understanding of the taxonomic composition of the genus *Nemophora*. I did not identify even a single morphological synapomorphy of this genus yet; the best character (simple inwardly directed antennal pegs) was repeatedly lost in about 10% of species. The genus *Nemophora* is split into a number of species groups, but the relationships between these groups remain obscure, in particular due to numerous parallelisms in taxonomically important characters.

***Antispila treitschkiella* (Heliozelidae), highly invasive but overlooked on *Cornus mas* in Britain**

David C. Lees, Klaus Sattler

Natural History Museum, London, United Kingdom

davil@nhm.ac.uk

On 23 August 2016, an adult *Antispila* came to light in the Natural History Museum Wildlife Garden, a late date for the two native feeders on *Cornus sanguinea*. This moth was suspected and confirmed to be *A. treitschkiella*, a species long on the British list due merely to its incorrect synonymy with *A. petryi*, despite prior indications to the contrary, including host-plant and differences in a potential stridulatory organ on dorsal A8 of the larva. A survey to confirm the presence of the true *A. treitschkiella* was commenced in the UK on *Cornus mas* in parks and herbaria. All trees examined in Greater London and Cambridge had moderate to high densities of *A. treitschkiella* mines and parasitism levels were high. DNA barcodes confirm the deep separation of *A. treitschkiella* and *A. petryi* and those of the species new to UK match the most highly represented haplotype in the Netherlands on BOLD. High mine densities suggest a reasonably long presence at least in southern Britain. However, no herbarium specimen or historical photo of specimens of *C. mas* from Britain has been detected bearing a mine. *A. treitschkiella* was detected in one nursery. Botanic garden surveys of the planted *Cornus* species reveal near monophagy on *C. mas*.

THREE-MINUTE TALKS

Long-term changes in distribution and occurrence of *Leptidea sinapis* and *L. juvernica* in Germany

Oliver Schmitz

Dallgow-Doeberitz, Germany

schmitz.o@arcor.de

Leptidea sinapis and *L. juvernica* are distributed across Germany. However, the frequency of occurrence of the two species differs considerably on a regional level. Moreover, the presence of both species during the past 50 years shifted distinctly depending on the geographical scale within Germany and beyond. Results will be presented based on > 4,000 specimen collected during the past 150 years. Lepidopterologists are invited to provide the author with additional material of interest for further investigations.

***Arctia plantaginis* (L.) (Erebidae, Arctiinae) in Newfoundland, Canada:
Autochthonous or recently introduced from Europe?**

Bernard Landry¹, Christian Schmidt²

¹Muséum d'histoire naturelle, Genève; ²Agriculture and Agri-Food Canada, Ottawa

bernard.landry@ville-ge.ch

Arctia plantaginis (L.) is holarctic in distribution. In North America it occurs widely in the Rocky Mountains east into the Canadian provinces of Saskatchewan, Manitoba, Ontario, and Québec, where it reaches the easternmost point of its distribution in the west of the province, in the clay belt south of James Bay. However, in the summer of 2016, a population was found about 1800 km to the east, in Newfoundland, the easternmost province of Canada. The COI DNA barcode of one specimen from this population and that of several other specimens from Canada were obtained to investigate the relatedness of the Newfoundland population. The question of whether this population has been overlooked, or recently introduced will hopefully be answered.

The European *Charissa* and *Psodos* – a call for cooperation (Geometridae)

Sven Erlacher

Museum of Natural History Chemnitz, Germany

erlacher@naturkunde-chemnitz.de

Charissa Curtis, 1826 (nomen protectum) and *Psodos* Treitschke, 1825 (= *Glacies* Millière, [1874] 1869) are species-rich genera within the Ennominae. Apart from one species, they all occur in the Palaearctic region and the Arabian Peninsula, respectively. Due to their adaptation to rocks, both genera are generally considered to be hard to determine. Until now, 24 species of *Charissa* and 13 species of *Psodos*, as well as about twice as many subspecies of each genus, are known from Europe. Concerning the preparation of the relevant chapters in “The Geometrid Moths of Europe, Vol. 6”, any kind of references would be useful, e.g. records of rare species, notes on biology, photos of living moths or caterpillars, and opinions on the status of species or subspecies. The manuscript must be finished by the end of September 2017. Therefore, receiving interesting findings before the end of August would be highly appreciated.

***Peribatodes perversaria* (Boisduval, 1840) species complex, call for cooperation**

Hossein Rajaei

State Museum of Natural History, Stuttgart, Germany

hossein.rajaei@smns-bw.de

Genus *Peribatodes* Wehrli, 1943 with 14 known species is distributed mainly in western Palaearctic and has 11 species in Europe. Some European species of this genus are not easily delimited using diagnostic characters. The *perversaria* species-complex is one of the most complicated groups in this genus. This species complex includes the following: *Peribatodes perversaria* Boisduval, 1840 (from Valais); *P. abstersaria* 1840 (from Pyrenees); *P. subflavaria* Millière, 1876 (from Maritime Alps) and *P. buxicolaria* Mabilie, 1873 (from Central France). Except slightly different wing colour, there are no clear-cut diagnostic characters in internal or external morphology. DNA-barcoding of few screened examples of these taxa shows low genetic distance (less than 1%). Some authors regard these taxa as synonyms, but others as subspecies of *perversaria*; however, nobody ran a comprehensive multidisciplinary taxonomic project on this group. I will carry out an integrative taxonomy project (using biological data, mitochondrial and nuclear genetic data, morphological data and biochemical data) to study the species concept in this species complex.

POSTERS

1. Butterfly Conservation Europe (BCE): European Butterfly Recovery Strategy

Sue Collins

Butterfly Conservation Europe

sue.collins@bc-europe.eu

Butterflies have declined in abundance across Europe. Causes include habitat loss and quality declines, particularly of semi-natural grassland, often driven by agricultural intensification or abandonment. BCE has a Strategy for helping to halt losses and declines and support recovery. Progress is slow given the need for policy reform and more financial support. BCE has Partners in 36 countries across Europe. Many volunteers carry out standardised transect butterfly monitoring each year. BCE Partners validate and report their results, enabling BCE to publish and update a European Grassland Butterfly Indicator. It is a priority of BCE's to help extend such butterfly monitoring schemes to more countries, including Bulgaria, Greece, Hungary, Italy, Portugal and Romania. Some Partners own or manage land to support butterfly recovery in local areas. They also carry out research on Lepidoptera. BCE works with NGO colleagues in the European Habitats Forum (EHF) in Brussels to influence EU policies and their implementation so they impact more positively on wildlife and support the recovery of ecosystem functionality and resilience and underpin the recovery of ecosystem services, including pollination. BCE promotes knowledge and understanding about butterflies and moths and raises the profile of the urgent need for more concerted action to stop declines and support recovery. Some Partners work with children and BCE is active on social media, tweeting @europebutterfly and with an active Facebook page and website, www.bc-europe.eu.

2. Conservation of the Lepidoptera species in Croatia following the obligations from the Habitats Directive

Luka Katušić¹, Martina Šašić²

¹Croatian Agency for the Environment and Nature; ²Croatian Natural History Museum, Zagreb, Croatia

luka.katusic@dzzp.hr, martina.sasic@hpm.hr

Within the European Union, the principal legal instrument for ensuring favourable conservation status of species and habitats are Council Directive 92/43/EEC of 21 May 1992 on the conservation of natural habitats and of wild fauna and flora (“Habitats Directive”) and Directive 2009/147/EC of the European Parliament and of the Council of 30 November 2009 on the conservation of wild birds (“Birds Directive”). Every member country of the EU is obligated to transpose the Directives into national laws, among others, by designating areas important for the conservation of species and habitats listed in Annex II of the Habitats Directive and Annex I of the Birds Directive as a part of EU Natura2000 ecological network. Altogether, 36.73% of land territory and 15.42% of coastal sea of Croatia is included in the NATURA2000 ecological network. Among that, 87 Sites of Community Importance are designated as important for the conservation of 11 Lepidoptera species: *Euphydryas aurinia*, *Hypodryas maturna*, *Lycaena dispar*, *Phengaris (Maculinea) nausithous*, *P. teleius*, *Leptidea morsei*, *Nymphalis vaualbum*, *Coenonympha oedippus*, *Callimorpha quadripunctaria*, *Eriogaster catax*. Also, following the obligation from the Article 17 of the Habitats Directive, system for monitoring of conservation status is being established for these 11 species listed on the Annex II of the Habitats Directive and additional eight species from the Annex IV, present in Croatia: *Apatura metis*, *Lopinga achine*, *Papilio alexanor*, *Parnassius apollo*, *Parnassius mnemosyne*, *Maculinea arion*, *Proserpinus proserpina* and *Zerynthia polyxena*.

3. Development of an EU Pollinator initiative that delivers for moths and butterflies as well as bees

Ravikash Prasad

University of Cambridge, Cambridge, United Kingdom

rrp25@cam.ac.uk

Early in 2016, the European Parliament expressed considerable concern about the poor state of nature including calling on the “EU Commission and EU Member States to launch a European initiative on pollinators without delay.” EU Nature Directors and the EU Commission’s DG Environment recently approved a Road Map for strengthening the implementation of the EU Biodiversity Strategy and this includes an expectation that an EU Pollinator initiative will be developed. The project to design this pollinator initiative will begin in May as part of the authors professional placement for the MPhil in Conservation Leadership program at the University of Cambridge, UK. The project aims to review the 1) status of the conservation and management of pollinators in Europe and 2) the understanding of the political, economic and social drivers of biodiversity loss affecting its status. This poster will outline the protocol of the review and its supporting appraisals. The goal is to create an evidence-base of European pollinators that will inform the design and implementation of the Pollinator initiative and how its benefits could be maximised for pollinators and its implementation made more successful through best engagement with landowners and farmers. Eventually, the project will strive to test the approach to engage landowners and stakeholders.

4. Systematics and biogeography of East Asian Yponomeutoidea: new records from Korea and revised systematic status of two odd groups

Jae-Cheon Sohn¹, Shigeki Kobayashi², Sei-Woong Choi¹

¹Mokpo National University, Korea; ²Osaka Prefecture University, Japan
jay.c.sohn@gmail.com, crossroad1994@hotmail.co.jp, choisw@mokpo.ac.kr

Yponomeutoidea represent one of the major radiations in the basal ditrysian Lepidoptera. A recent phylogenetic study established the monophyly of Yponomeutoidea in which eleven family-groups are included. However, the monophyly of each included family has been poorly explored. Inevitably, this gap resulted in taxonomic problems, leaving many taxa defined provisionally and often unnaturally. It is also responsible for substantial underestimation of yponomeutoid biodiversity in many parts of the world. The species diversity of Yponomeutoidea is highest in East Asia due to rigorous taxonomic works by the Japanese and Chinese researchers. Nonetheless, new findings for the East Asian yponomeutoid fauna are continuously being added. We report four species of Yponomeutoidea new to Korea and discuss their interesting distribution in East Asia. In addition, we scrutinise two interesting yponomeutoid genera, *Tonza* and *Diathryptica*, that exhibit a signature of Gondwanan distribution. Their systematic positions remain unsatisfactorily defined. We discuss their affinities with yponomeutoid families based on morphological and molecular evidences.

5. Overview of the butterfly (Papilionoidea) fauna of Hrvatsko Zagorje, Croatia

Toni Koren¹, Boris Lauš¹, Martina Šašić², Iva Mihoci², Ana Štih¹, Petra Šemnički³, Stanislav Gomboc⁴

¹Association Hyla, Zagreb, Croatia, ²Croatian Natural History Museum, Zagreb, Croatia, Public ³Institutions for the Management of Protected Areas in the Krapina-Zagorje County, Radoboj, Croatia; ⁴EGEA, Institution for Nature, Ljubljana, Slovenia

koren.toni1@gmail.com

Hrvatsko Zagorje is a region located in the north-eastern part of Croatia just north from the capital Zagreb. Due to its vicinity to Zagreb, where many lepidopterists were working, a rather low number of historical records is very surprising. The first comprehensive butterfly survey started in 2008. Until today a total of 112 butterfly species have been recorded, with an additional six species known from the literature. This adds up to 118 species or 60% the Croatian butterfly fauna. The highest butterfly diversity was registered in the mountains Ivanščica and Strahinjščica, as well as in the significant landscape Zelenjak–Risvica and Cesar Hill. Several rare and endangered species were recorded in the region, i.e. *Zerynthia polyxena*, *Parnassius mnemosyne*, *Phengaris arion*, *P. alcon*, *P. teleius*, *Polyommatus thersites*, *Lycaena dispar* and *Lopinga achine*. Most of the butterflies in the region are grassland specialists, which are in rapid decline due to the abandonment or intensification of meadows, spreading of the invasive alien plant species, and urbanisation of wetland areas or changes in land use. To preserve the key species of butterflies in the area extensive maintenance of mainly dry and wet meadows and flowering forest edges is needed.

6. Historical biogeography of the hawkmoth genus *Theretra* Hübner, 1819 (Sphingidae) based on mitochondrial genes

Michal Rindoš, Tomáš Melichar, Zdeněk F. Fric

Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic

michal.rindos@gmail.com

The family Sphingidae includes more than 1600 species. With more than 70 already described species, *Theretra* Hübner, 1819 is among the three most diverse genera in the subfamily Macroglossinae. It occurs throughout the Old World, from Africa across Asia and Australia up to New Caledonia and Melanesia. The main aim of the study was to find the centre of radiation and to reconstruct the dispersal routes of these hawkmoths. Our results confirmed that the genus originated in Eastern Africa approximately 12 Mya and then due to the ability to disperse, they were able to colonise Asia and adjacent areas including Indonesia. We hypothesise that *Theretra* started to disperse from Africa in late Miocene using re-emergent bridges between East Africa and Middle East and also between SE Asia and Indonesia. In Pleistocene, they colonised Australia and, together with species from Papua, formed a unique group of haplotypes. In Pliocene different parts of Melanesia and New Caledonia were colonised repeatedly following various dispersal routes. The results showed also multiple re-colonisation of Africa and Indonesia.

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7. An integrated molecular and ecological trait dataset for the Tuscan Archipelago butterflies: a resource to understand the evolution and extinction of island biodiversity

Raluca Voda¹, Leondaro Dapporto², Alessandro Cini², Mattia Menchetti², Simona Bonelli¹, Luca P. Casacci¹, Vlad Dincă³, Stefano Scalercio⁴, Joan C. Hinojosa³, Heinrich Biermann⁵, Leonardo Forbicioni⁶, Umberto Mazzantini⁷, Lucia Venturi⁸, Franca Zanichelli⁹, Emilio Balletto¹, Tim Shreeve¹⁰, Roger L. H. Dennis¹¹, Roger Vila³

¹Università degli Studi di Torino, Italy; ²Università degli Studi di Firenze, Italy; ³Institut de Biologia Evolutiva (CSIC-Universitat Pompeu Fabra), Spain; ⁴Unità di Ricerca per la Selvicoltura in Ambiente Mediterraneo, Italy; ⁵Independent researcher, Germany; ⁶Independent researcher, Italy; ⁷Legambiente Arcipelago Toscano, Italy; ⁸Parco Regionale della Maremma, Italy; ⁹Parco Nazionale Arcipelago Toscano, Italy; ¹⁰Oxford Brookes University, UK; ¹¹Staffordshire University, UK

raluvoda@gmail.com

Island biogeography postulates the importance of integrating the study of molecular data with species traits in explaining the evolution of endemic taxa, the persistence of relicts and the extinction of populations, but so far very few empirical tests have used species-rich animal groups over entire archipelagos. We assembled a dataset of DNA barcodes for the 52 butterfly species reported from the Tuscan Archipelago, including comparative material from neighbouring areas (Sardinia, Corsica and Tuscany). We also compiled data on 10 species traits and on the apparent disappearance of some of the butterfly species from the main islands of this archipelago in the last 115 years. We assessed: i) the phylogeographic structure of each species across the Ligurian-Tyrrhenian area, as well as ii) the overall phylogeographic pattern in the same region, and iii) we identified the traits associated with population diversification, uniqueness, or recent extinction from specific islands. There was a considerable degree of population diversification in many species, which confirms that the Tuscan Archipelago hosts highly diverse butterfly communities. Phylogenetic regressions showed that smaller-sized and more specialized species, with a preference for drier regions, display greater genetic structure and/or uniqueness. Moreover, species adapted to colder and wetter areas and with shorter flight periods are more likely to become extinct. The methodology used here can be applied to reveal fine-scale diversity patterns, their origins and the vulnerability of taxa to current and future environmental changes, thus providing a valuable tool for evidence-based conservation prioritization.

8. Multi-scale assessment of moth diversity in Mediterranean mountain forests

Stefano Scalercio, Giuseppe Luzzi, Silvia Greco, Marco Infusino

Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Ente Parco Nazionale della Sila, Italy

stefano.scalercio@crea.gov.it, silvia.greco@crea.gov.it,
marco.infusino@crea.gov.it, direttore@parcosila.it

Distribution of diversity in mountainous areas is of particular interest in the Mediterranean Basin, where consequences of climate change could be a serious threat to its conservation in the coming decades. Furthermore, a large assessment of diversity could be a basis for evaluation of the impact of forest management and for planning of forest restoration. We surveyed moth communities using UV-LEDs light traps, from 2015 to 2016, along successional stages of four different forest types: beech, Calabrian black pine, silver fir and chestnut. Study areas were located in Calabria, the southernmost region of peninsular Italy. We sampled 48 sites, 15 per forest type, monthly from May to November. Three sites per forest type were sampled for two years obtaining a total of 72-year samples. We collected 77,504 individuals belonging to 589 species, which is 66% of the whole regional fauna with nocturnal habits. Among them, we found: 1 species new to science, recently described; 5 spp. new to southern Italy; 18 spp. new to Calabria. This study significantly increased the knowledge on the fauna of southern Italy. Communities of the four forest types were clearly distinguished by multivariate analyses (non-metric multidimensional scaling and clustering). Sites belonging to the same forest type and sampled in different years always grouped together, but in some cases differences among years were detectable. Differences in the community composition of surveyed successional stages of forests depend on forest type. Early successional stages were clearly distinguishable only when grasslands of natural origin naturally occur in the surrounding of forests.

9. Late spring frost in a Mediterranean beech forest: short-term effects on moth communities

Stefano Scalercio, Carlo De Donato, Marco Infusino, Silvia Greco

Consiglio per la ricerca in agricoltura e l'analisi dell'economia agrarian,
Rende, Italy

stefano.scalercio@crea.gov.it, silvia.greco@crea.gov.it,
marco.infusino@crea.gov.it, carlodedonato@alice.it

Extreme climatic events, which occasionally occur, can cause dramatic consequences to biodiversity, and they are predicted to become more frequent in the future as result of the current climate change. Lepidoptera are quite sensitive to climate change, in particular they suffer from effects of extremely cold temperature. No data about short-term effects after extreme events are available in literature. In this work we studied moth communities inhabiting a Mediterranean forest of *Fagus sylvatica* affected by a late spring frost. The study was carried out on the Pollino Mountains, Calabria (the southernmost region of peninsular Italy), using UV-Led light traps for sampling moth communities. One trap was positioned in each stand and activated one night per month from May 2015 to November 2016. Nine stands were selected, three of which were located at highest altitudes where the frost occurred during spring 2016. The stands affected by the frost collected 8,556 moths belonging to 248 species in total. Species richness was not significantly different the second year, but the loss of abundance was evident. The frost event affected mostly the species trophically related to beech. The most negatively affected species were *Operophtera fagata* and *Epirrita christyi*, which had drastically reduced their abundances (-83.56% and -80.66% of individuals, respectively) and their dominances (-64.97% and -59.52%, respectively). Extremely cold temperatures and larval starvation in springtime due to the loss of trophic resources probably caused a high mortality of young larvae. At lower altitudes, where frost and starvation didn't occur, abundance patterns were much more comparable among years.

11. Combined phylogeny of Geometridae from Estonia and Uganda: an essential tool for comparative studies

Sille Holm, Erki Õunap, Toomas Tammaru

University of Tartu, Tartu, Estonia

sille.holm@ut.ee

Phylogenetically explicit comparative analyses are still scarce due to difficulties in obtaining comparable data, but also the scarcity of phylogenetic information available has been an obstacle. To employ the vast potential of phylogenetic comparative methods to study evolution of several life history traits such as longevity, host-plant specialisation, and egg laying strategy, we have inferred a phylogeny of 366 taxa of geometrid moths (Geometridae) mainly from the temperate region Estonia and equatorial Uganda. The phylogenetic tree of temperate and tropical region species was constructed on the basis of original sequences for tropical region and data submitted to GenBank by earlier researchers for temperate region. The tree to be presented is based on 6522 base pairs from eight markers that have repeatedly been used for phylogenetic inference in geometrid moths: cytochrome oxidase subunit 1 (COI), elongation factor 1 alpha (EF-1a), wingless (wgl), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), ribosomal protein S5 (RpS5), isocitrate dehydrogenase (IDH), malate dehydrogenase (MDH) and carbamoyl phosphate dehydrogenase (CAD). ML tree was constructed using RAxML 7.7.1 via the RAxML online platform. Identifications of tropical species, based on wing pattern and/or genitalia dissection, were cross-checked with their DNA barcodes in the Barcode of Life Data Systems (http://www.boldsystems.org/index.php/IDS_OpenIdEngine). Despite extensive use of DNA barcodes, numerous African moths could not be reliably associated with any known species.

12. Putting *Parasemia* in its phylogenetic place: a molecular analysis of the subtribe Arctiina

Katja Rönkä

University of Jyväskylä, Centre of Excellence in Biological Interactions,
Jyväskylä, Finland

katja.h.ronka@jyu.fi

The phylogenetic relationships of tiger moths and woolly bears (Noctuoidea: Erebidae: Arctiinae) are surprisingly poorly resolved, despite being subjected to ample ecological and evolutionary research and popularity among amateur and professional lepidopterologists. We present a species level phylogeny for the subtribe Arctiina with the aim to infer the phylogenetic placement of the monotypic wood tiger moth *Parasemia plantaginis*. To this end we sampled 89 species in 52 genera considered to be closely related to *Parasemia*, 11 species of *Callimorphina* and two outgroups. From these we sequenced up to eight gene regions including one mitochondrial (COI barcode region) and seven nuclear protein-coding gene fragments (CAD, GAPDH, IDH, MDH, Ef1 α , RpS5 & Wingless), totaling 5915 base pairs. We analyzed the DNA sequence data using both maximum likelihood and Bayesian inference. Based on our results, we present a new classification, where we consider *Arctia*, *Micrarctia*, *Apantesis*, *Chelis* and *Diacrisia* as valid genera within Arctiina s.s. and sink 33 genera as synonyms of one or other of these. The wood tiger moth *Arctia plantaginis* comb.n. is placed as sister to the hebe tiger moth *Arctia festiva* comb.n..

13. The Moths of Shirui Hills, Manipur, NE India

Jatishwor Irungbam

Faculty of Science, University of South Bohemia; Institute of Entomology,
Biology Centre, Czech Academy of Science, Ceske Budejovice

Czech Republic

jatishwor.irungbam@gmail.com

Manipur lies in north-eastern India on the border between Chinese subdivision of the Palaearctic Region and Malayan subdivision of the Oriental Region and is hence considered very rich in terms of biodiversity. The state has been neglected for a long time in terms of study on moths. Some of the records on the moth fauna of Manipur have been reflected in the "Fauna of British India, Moths" and studies conducted by Zoological Survey of India in Manipur. Thus, a complete checklist of the moths is lacking. Hence, I decided to study the moths of Manipur focusing particularly on the different altitudinal gradients in the Shirui National Park (SNP)(24°N - 25.41°N; 94°E - 94.47°E), Ukhrul district of Manipur state, north-eastern India. The park covers 100 km² in area and altitude varies from 1,715 m to 2,567 m (the peak). East Himalayan wet temperate forests with high altitude grasslands and rainforest dominate in the park. Light trapping at different elevations using a set of 12V battery fitted with LED+UV lights was conducted for a week during July 2016. The moths were collected manually, killed, dried by silica gel and specimens were transported to the Czech Republic. 497 individuals (441 identified + 56 unidentified) of moths belonging to 167 species in 14 families were collected. The preliminary investigation reveals that 25.5% (n=42) species are recorded for the first time from the territory of Manipur, India and that 6% (n=9) species are undescribed."

14. Mark-recapture study on *Phengaris teleius* in the Gödörház Meadow (Őrség National Park, Hungary)

Bálint Horváth^{1,3}, Zoltán Scherer¹, István Szentirmai², Ferenc Lakatos³

¹Green Woodpecker Foundation, ²Őrség National Park Directorate,

³University of Sopron, Hungary

macrolepidoptera@gmail.com

The scarce large blue (*Phengaris teleius*) is a threatened butterfly species in the whole of Europe. Due to altered management practices, it suffered a serious loss of habitat in the last century. *P. teleius* have narrow habitat requirements and need special habitat management. *P. teleius* is a flagship species for nature conservation and is even regarded as an umbrella species in Őrség National Park (ŐNP). It responds quickly to environmental changes, so it is important to follow its demographic patterns and habitat use, at least in meadows with high biodiversity values. Due to decreased stockbreeding, numerous meadows, such as the Gödörházi Meadow in ŐNP, were neglected during the past couple of decades. Increased shrub cover and invasive plants have transformed the meadow's vegetation; many protected species have disappeared. A few years ago, ŐNP Directorate employees and volunteers rehabilitated the meadow and have maintained it since by mowing. To follow the rehabilitation process, a mark-recapture (MR) study on *P. teleius* was initiated. The first survey was completed during a 12-day period in 2016. Jolly-Seber model was fitted to the dataset to estimate the demographic pattern. In total, 142 specimens were marked and the recapture rate was 41.5%. We estimated the superpopulation of males, which we calculated to be 107 males (CI: 85–135) and 158 females (CI: 124–201). We calculated the daily population size as well. Our goals are to continue the MR study on the Gödörházi Meadow and extend the survey to other *Phengaris* species as well.

15. Mark-recapture study on two forest-defoliating moth species: *Erannis aurantiaria* and *E. defoliaria* (Geometridae)

Bálint Horváth^{1,2}, András Ambrus³, Kristóf Kálmán²

¹Green Woodpecker Foundation, ²University of Sopron, ³Fertő-Hanság National Park Directorate, Hungary

macrolepidoptera@gmail.com

The mottled umber (*Erannis defoliaria*) and scarce umber (*Erannis aurantiaria*) are among well-known pest species in European deciduous forests. The male imagoes fly in the late autumn; the females, however, have vestigial wings. *E. defoliaria* and *E. aurantiaria* exhibit cyclic outbreaks at approximately 10 year intervals. Together with some other geometrid species, they can cause extensive defoliation. In 2016 an overall study to assess the demographic and movement patterns of forest-defoliating moths using the mark-recapture (MR) method was started in north-western Hungary. Male imagoes were attracted by portable light-traps that did not include a killing agent. Moths were trapped in five different points; the average distance between the traps was 205.5 m (± 68.4 m). Three traps worked simultaneously. In total, we marked 764 *E. defoliaria* and 433 *E. aurantiaria* specimens, and the recapture rate was around 5%. Jolly-Seber models were fitted to each dataset to estimate demographic patterns. The estimated superpopulation size of *E. defoliaria* was higher, but confidence intervals were very broad (*E. defoliaria*: 12452 [CI: 3283–47435]); *E. aurantiaria*: 9410 [CI: 145–608585]). We recorded the average movement of marked specimens between the traps; this also differed: *E. defoliaria*: 160m (± 83 m); *E. aurantiaria*: 110m (± 49 m).

16. Mark-recapture study on the Woodland Brown Butterfly (*Lopinga achine*) in Hungary (Nymphalidae)

Zoltán Scherer¹, Bálint Horváth¹, István Szentirmai², Ádám Kőrösi³

¹Green Woodpecker Foundation, ²Őrség National Park Directorate, ³MTA-ELTE-MTM Ecology Research Group, Hungary

macrolepidoptera@gmail.com

The Woodland Brown (*Lopinga achine*) is an endangered butterfly species in Europe. It has disappeared from many locations due to habitat loss and degradation. In 2009, *L. achine* populations were discovered in Órség National Park in western Hungary, occurring in Alder gallery forests located in narrow stream valleys. We surveyed two Woodland Brown populations in nearby valleys using the mark-recapture (MR) method to assess demography, habitat use, and dispersal. The sampling period covered 19 days and each site was visited every other day. Cormack-Jolly-Seber and Jolly-Seber models were fitted to each dataset separately to estimate demographic parameters. Altogether, we marked 315 specimens of *L. achine* (199 males and 116 females); 33.4% of them were recaptured. The apparent daily survival rate was similar in the two populations and in males and females (~0.93–0.97). Mean residency time was ~15–30 days. The estimated population size of males was higher in both populations, but confidence intervals were large, especially for females (males: 180 [CI: 150–230], 130 [CI: 105–180]; females: 140 [CI: 95–220], 118 [CI: 79–213]). The longest detected movements were 1250 m (male) and 857 m (female); most individuals flew within a relatively small area. Butterflies seemed to prefer to stay within the food plant patches. Dispersal between the valleys was observed for four male specimens (~1.2 km in bee-line).

17. Management of Scottish lowland peatland habitats for Lepidoptera

David Hill, Paul Kirkland

Butterfly Conservation Scotland, Stirling, Scotland

pkirkland@butterfly-conservation.org

The lowland peatlands or ‘Mosses’ of central Scotland are waterlogged, acidic, nutrient-poor environments dominated by *Sphagnum* mosses. They began to develop in post-glacial times and have since become characterised by deep peat deposits. The habitat is host for a wealth of fauna and flora specially adapted to living in the harsh conditions including many species of Lepidoptera. In particular, *Coenonympha tullia*, which declined in distribution by 58% across the UK between 1976 and 2014, is endemic to peatland habitats where its larval foodplant *Eriophorum vaginatum* is found. Historical attempts at drainage aimed at improving grazing or implementing forestry have resulted in a large majority of lowland peatland habitats being in poor condition with *Calluna vulgaris* and *Molinia caerulea* becoming overly dominant in the drier conditions. Additionally, mosses have become increasingly isolated and fragmented in a landscape dominated by intensive agriculture. These factors can be strongly linked to the decline of *Coenonympha tullia* across the lowlands. Secondary woodland has developed on the fringes of many lowland peatland sites and has become a refuge for a variety of Lepidoptera species including *Boloria selene*, another butterfly that has undergone a dramatic decline across the UK. Butterfly Conservation Scotland has been working with volunteers to carry out measures that help restore and protect these fragile habitats. Damaged peatlands have been restored by implementing measures designed to improve the hydrological integrity of the bog such as ditch-blocking and clearance of invasive scrub.

18. Scotland's Urban Butterfly Project

Paul Kirkland, Anthony Mccluskey

Butterfly Conservation Scotland, Stirling, Scotland

pkirkland@butterfly-conservation.org

The Urban Butterfly Project is working in central Scotland to engage with the people who live in towns and cities. Volunteers are being trained to identify and record the butterflies they see in urban greenspaces. The project is also working with volunteers to improve these greenspaces for butterflies. Already the results are providing useful information about the species found in urban spaces, as well as the habitat preferences of these. Semi-natural grassland and vegetation along rivers and coasts appear to have the greatest diversity of butterfly species. Some species often regarded as widespread such as *Polyommatus icarus* were almost entirely absent in the urban sites visits by recorders, possibly reflecting the lack of caterpillar food plant availability. Through the project, *Lotus corniculatus* is now being grown by volunteers at a new wildflower nursery managed by Glasgow City Council. These plants will be planted out around Glasgow. The results have also revealed that rare or declining species can sometimes be found living very close to dense urban areas. For example, *Boloria selene* is found in the heart of Cumbernauld, a town with over 50,000 residents. The project is also developing novel ways to provide habitat for butterflies in crowded urban spaces. In Edinburgh, several buildings (including the Scottish Parliament) with green roofs and roof gardens are having butterfly caterpillar foodplants places on them. Users of these buildings will be trained to identify butterflies, and asked to send in their records.

19. Ennominae (Geometridae) in central Spain: new data on distribution, biology and the early stages

Gareth Edward King, José Luis Viejo Montesinos

Universidad Autónoma de Madrid, Madrid, Spain

joseluis.viejo@uam.es

Data are provided on three ennomine taxa:

- *Synopsis sociaria* (Hübner, [1799]) was taken as L5 larvae with further details given on its food-plants and its larval behaviour.
- *Dasypterothauma thaumasia* (Staudinger, 1892): Original data are given on its L5 larval morphology and larval food-plants.
- *Euchrognophos mucidarius* (Hübner, 1799): A detailed description is provided of the L5 larva, as well as an introduction to its chaetotaxy with original data on its assumed trophic preferences in the wild state.

20. Sterrhinae (Geometridae) in Central Spain: new data on distribution, biology and early stages

Gareth Edward King, José Luis Viejo Montesinos

Universidad Autónoma de Madrid, Madrid, Spain

joseluis.viejo@uam.es

Data are provided on three sterrhine taxa:

- *Cleta ramosaria* (Villers, 1789): New distributional data in Madrid, as well as original data on food-plants and larvae; it is detritivorous.
- *Idaeia figuraria* (Bang-Haas, 1907) was taken in two anthropogenically-disturbed localities in Madrid, even though it is known to be rare and local.
- *Idaeia calunetaria* (Staudinger, 1859) was also taken in disturbed habitats and original data are given on the larva, as well as morphological details, which includes chaetotaxy; in addition, observations as to its development under captive conditions are given.

21. Tortricidae from Pelion Mountains Greece

Pasquale Trematerra, Marco Colacci

University of Molise, Campobasso, Italy

trema@unimol.it, marco.colacci@unimol.it

The Pelion Mountain range closes off the Pagasetic Gulf. The highest peak is Pourianos Stavros (1,624 m). Pelion's diverse ecosystem is made up of coastal, plain and mountain zones. The area consists of thick forestal vegetation of deciduous forests and developed maquis shrubs. It has three vegetation zones supporting rich species communities. The typical Mediterranean shrubland (*Quercetalia ilicis*) covers the low altitudes and includes most of the self-sown aromatic and pharmaceutical taxa, such as *Salvia fruticosa*, *Thymus* spp., *Sideritis* spp. The para-Mediterranean broad-leaved deciduous trees zone (*Quercetalia pubescentis*) covers the middle altitude of the area and includes oak (*Quercus frainetto*) and chestnut forests (*Castanea sativa*). The beech forest zone (*Fagetalia*) covers the areas above the para-Mediterranean zone up to the tree-limit zone. The Tortricidae reported here were collected by net and by attraction to light at night-time. The localities visited were: Portaria, at 750 and at 1000 m a.s.l.; Drakia, at 980 m a.s.l.; Chania, at 1150 m a.s.l. and at 1350 m a.s.l. The material was primarily identified morphologically, supplemented by molecular data of the COI barcode region. There were 50 species collected, of which 11 were recorded for the first time in Greece: *Aethes margaritana*, *Eana incanana*, *Paramesia diffusana*, *Tosirips magyarus*, *Eudemis profundana*, *Ancylis badiana*, *Pelochrista modicana*, *Grapholita lathyra*, *Grapholita tenebrosana*, *Dichrorampha alpigana* and *Dichrorampha inconspiqua*. *Ceratoxanthus giansalottii*, *Endothenia apotomisana*, *Cydia pelionae* and *Cydia magnesia* are endemic to Greece. The latter three taxa were described as new. *Dichrorampha inconspiqua* is reported as new to Europe.

22. Butterfly (Papilionoidea) diversity in Paklenica National Park

Jadranka Rota¹, Martina Šašić²

¹Lund University, Lund, Sweden; ²Croatian Natural History Museum, Zagreb, Croatia

jadranka.rota@biol.lu.se, Martina.Sasic@hpm.hr

Paklenica National Park is located on the coast of the Croatian Adriatic, in the southern part of the Velebit Mountain. Because of the geological and biological distinctiveness of this area, the national park was established in 1949. The park has an area of 95 square kilometres and it stretches from the bottom of the Velebit Mountain, almost reaching the shore, to the highest peaks Sv. Brdo (1753 m) and Vaganski Vrh (1752 m). The steep ascent from the sea to the Alpine zone, combined with the deep canyons of Mala and Velika Paklenica, results in a variety of habitats in a relatively small area. A survey of butterflies (Papilionoidea) was carried out in the park area from 1997 to 1999 at 14 localities. We present the results of this survey and discuss some of the interesting findings.

23. Contribution to the fauna of Sphingidae in the Republic of Macedonia

Vladimir Krpach

Institute of Ecology and Tehnology DUT - Tetovo

vkrpach@gmail.com

Sphingidae are commonly represented among the night-active macro-moths. According to literature, hawkmoths, sphinx moths or hornworms – Sphingidae Latreille, [1802] – in Macedonia have been partially investigated by many foreign scientists who briefly stayed in our country. Although numerous species from this family (shown by literature data) have been recorded, we are still missing data on their distribution in Macedonia. Sphingidae are a relatively large family, present on all continents. The family belongs to the superfamily Bombycoidea and is represented in Europe by 40 species arranged in 20 genera of 3 subfamilies. The subfamily Macroglossinae has 11 genera with 26 species. The subfamily Smarintinae is represented by 6 genera and 9 species. The subfamily Sphinginae has 3 genera with 5 species. According to available literature, 22 species belonging to 17 genera and three subfamilies are known from Macedonia. The Macedonian Museum of Natural History has a modest collection of sphingids. Analyzing entomological material from the collection and literature data we found 25 species which are found in Macedonia.

A

Nini Cecilie Roll Aarvik
Nyborgvn 19A NO-1430 Ås
Norway
nini.aarvik@gmail.com

Leif Aarvik
Nyborgvn 19A NO-1430 Ås
Norway
leif.aarvik@nhm.uio.no

Xhezair Abdija
DUT - Drzaven Univerzitet Tetovo
Ilindenska bb 1200 Tetovo
Macedonia
xhezair_abdija@hotmail.com

David Adamski
Department of Entomology
1616 East Capitol Street 20003
Washington, DC
USA
adamskid@si.edu

Dot Agassiz
Garden house, Stafford Place
BS23 2QZ Weston-super-Mare
Great Britain
dotagassiz@gmail.com

David Agassiz
Garden House, Stafford Place
BS23 2QZ Weston-super-Mare
Great Britain
david.agassiz@gmail.com

B

Thomas Baron
87 Sok. No.2, Turunc 80600
Marmaris / Mugla
Turkey
thomas.r.baron@gmail.com

Alena Bartonova
University of South Bohemia in
Ceske Budejovice, Faculty of
Science
Branisovska 31 37005 Ceske
Budejovice
Czech Republic
al.bartonova@gmail.com

Daniel Bartsch
Staatliches Museum für
Naturkunde Stuttgart
Rosenstein 1 70191 Stuttgart
Germany
daniel.bartsch@smns-bw.de

Franziska Bauer
Senckenberg
Königsbrücker Landstraße 159
01109 Dresden
Germany
franziska.bauer.dd@gmx.de

Stella Beavan
The Hayes EX17 6DF Zeal
Monachorum
Great Britain
stellabeavan@outlook.com

Marianne Beck
Elchweg 27 73434 Aalen
Germany
beck.mary@web.de

Andreas Beck
Hochschule Aalen
Elchweg 27 73434 Aalen
Germany
aaa.beck@web.de

Leah Benyamini
4D MicroRobotics
91 Levona Str. 7194700 Beit Arye
Israel
leah@mr4d.com

Dubi Benyamini
4D MicroRobotics
91 Levona Str. 7194700 Beit Arye
Israel
dubi_ben@netvision.net.il

Maryam Boroomandi
Ihmlingstr. 52, 70374 Stuttgart
Germany

John Brown
US National Museum of Natural
History
5829 Cove Landing Rd. #102
22015 Burke
USA
tortricidae@gmail.com

Poody Brown
5829 Cove Landing Rd. #102
22015 Burke
USA
pbinva@aol.com

Rudolf Bryner
Bergluftweg 19 CH - 2505 Biel /
Bienne
Switzerland
rbryner@bluewin.ch

Pajtim Bytyçi
Street Tring Smajli 54/6 10000
Prishtinë
Kosovo
pajtim.bytyqi@hotmail.com

C

Elsa Call
Lund University
Sölvegatan 37 22362 Lund
Sweden
elsa.call.fr@gmail.com

Feza Can Cengiz
Mustafa Kemal University,
Faculty of Agriculture,
Department of Plant Protection
31034 Hatay
Turkey
cezafan_onurcan@hotmail.com

Max Caspers
Naturalis Biodiversity Centre
Vondellaan 55 2332AA Leiden
Netherlands
max.caspers@naturalis.nl

Rushan Ceka
Kaqanik 10000 Prishtine
Kosovo
rushanceka@hotmail.com

Nicolas Chazot
Lund University
Sölvegatan 37 22362 Lund
Sweden
chazotn@gmail.com

Marco Colacci
University of Molise de Sanctis
street 86100 Campobasso
Italy
marco.colacci@unimol.it

Sue Collins
Butterfly Conservation Europe
27 Madingley road CB3 0EG
Cambridge
Great Britain
sue.collins@bc-europe.eu

Cumplido Consuelo Sánchez
28049 Madrid
Spain

Cristina Craioveanu
Babes-Bolyai University
Clinicilor 5-7 400006 Cluj-Napoca
Romania
cristinacraioveanu@gmail.com

D

Martin Davies
5 Winfield, Great Gransden
SG19 3AN Sandy, Beds
Great Britain
mdavies854@btinternet.com

Mignon M. Davis
United States National Museum,
Smithsonian Institution National
Museum of Natural History
PO Box 37012, 20013-7012
Washington, D.C.
USA
hallj@si.edu

Donald R. Davis
National Museum of Natural
History, Smithsonian Institution
Dept of Entomology
PO Box 37012, 20013-7012
Washington, D.C.
USA
davisd@si.edu

Jurate De Prins
Dorpstraat 401B 3061 Leefdaal
Belgium
jurate.deprins@gmail.com

Willy De Prins
Dorpstraat 401B 3061 Leefdaal
Belgium
willy.deprins@gmail.com

Pritha Dey
Zoologische Staatssammlung
München
Münchhausenstraße 21, 81247
München
Germany
dey.pritha126@gmail.com

Vlad Eugen Dincă
Institut de Biologia Evolutiva
(CSIC-UPF)
Passeig Maritim de la
Barceloneta 08003 Barcelona
Spain
vlad.e.dinca@gmail.com

Annick Drouet
86 b route de la Luye 05000 Gap
France
annickgap56@gmail.com

Eric Drouet
86b route de la Luye 05000 GAP
France
edrouet.zyg@wanadoo.fr

E

Wolfgang Eckweiler
Gronauer Str. 40 60385 Frankfurt
am Main
Germany
ems@wolfgang-eckweiler.de

Ulf Eitschberger
Humboldtstrasse 13 A D-95168
Marktleuthen
Germany
ulfei@t-online.de

Marianne Elias
CNRS ISYEB, MNHN,
45 rue Buffon CP50 75005 Paris
France
elias@mnhn.fr

Josepha Erlacher
Further Str. 18 D-09113
Chemnitz
Germany
josepha.erlacher@gmail.com

Sven Erlacher
Museum of Natural History
Chemnitz
Moritzstr. 20 D-09111 Chemnitz
Germany
erlacher@naturkunde-chemnitz.de

Marianne Espeland
Zoological Research Museum
Alexander Koenig
Adenauer Allee 160 53113 Bonn
Germany
m.espeland@zfmk.de

Ferdije Etemi
University Hasan Prishtina
Lagjja Marigona,nr.1; rruges per
Ajvali 10000 Prishtina
Kosovo
ferdijezhushi2010@gmail.com

F

Michael Falkenberg
Staatliches Museum für
Naturkunde
Erbprinzenstr. 13 76133
Karlsruhe
Germany
m.falkenberg@smnk.de

Markus Fluri
Rötistrasse 545 4716
Welschenrohr
Switzerland
markus.fluri@bluewin.ch

Zdeněk Faltýnek Fric
Biology Centre CAS, Institute of
Entomology
Branišovská 31 37005 České
Budějovice
Czech Republic
fric@entu.cas.cz

Dieter Fritsch
Josef-Pfeffer-Weg 9 79540
Lörrach
Germany
dfritsch@vfritsch.de

G

Theo Garrevoet
Kampioenstraat 14 2020
Antwerpen
Belgium
theo.garrevoet@gmail.com

Hamid Reza Ghanavi
Lund University
Sölvegatan 37 22362 Lund
Sweden
hamid.ghanavi@biol.lu.se

Stanislav Gomboc
Šiškovo naselje 19 4000 Kranj
Slovenia
stanislav.gomboc@siol.net

Carmela Rosalba Guglielmino
Via Cascina Margarina 6 27048
Sommo (Pavia)
Italy
c.r.guglielmino@gmail.com

H

Axel Hausmann
Münchhausenstr. 21 81247
Munich
Germany
axel.hausmann@zsm.mwn.de

Silvia Guaragna Hausmann
Münchhausenstr. 21 81247
Munich
Germany
axel.silvia@onlinehome.de

Robert Heckford
67 Newnham Road, Plympton
PL7 4AW Plymouth
Great Britain
bob.heckford@btinternet.com

Maria Heikkilä
Otsolahdentie 7 A 7 02110 Espoo
Finland
a.a.maria.heikkila@gmail.com

Joan Carles Hinojosa
IBE (Institut de Biologia
Evolutiva) c/Poeta N'Assam
25300 Tàrrrega
Spain
sirsphingidae2@gmail.com

Sille Holm
University of Tartu
Vanemuise 46-303 51014 Tartu
Estonia
sille.holm@ut.ee

Nicholas Homziak
University of Florida
3465 NW 1st Ct 32607
Gainesville, Florida
USA
nhomziak@ufl.edu

Bálint Horváth
Green Woodpecker Foundation
(Zöld Harkály Alapítvány)
Dózsa György u. 117/D H-8800
Nagykanizsa Hungary
macrolepidoptera@gmail.com

I

Jatishwor Irungbam
University of South Bohemia
Branišovská 1760 370 05 Ceske
Budejovice
Czech Republic
jatishwor.irungbam@gmail.com

K

Lauri Kaila
Finnish Museum of Natural
History, University of Helsinki
FI-00014 Helsinki
Finland
lauri.kaila@helsinki.fi

Jari Kaitila
Acleris
Kannuskuja 8 D 37 01200 Vantaa
Finland
jari@perhostutkijainseura.fi

Ole Karsholt
Natural History Museum of
Denmark
Universitetsparken 15 DK-2100
Copenhagen Ø
Denmark
okarsholt@snm.ku.dk

Luka Katusić
Croatian Agency for the
Environment and Nature
Radnička cesta 80 10000 Zagreb
Croatia
luka.katusic@dzzp.hr

Akito Kawahara
University of Florida McGuire
Center for Lepidoptera and
Biodiversity, Florida Museum of
Natural History
32611 Gainesville
USA
kawahara@flmnh.ufl.edu

Mari Kekkonen
Centre for Biodiversity Genomics,
University of Guelph, 50 Stone
Road East N1G 2W1 Guelph
Canada
kekkonen@uoguelph.ca

Natalia Kirichenko
Sukachev Institute of Forest,
Siberian Branch of the Russian
Academy of Sciences
Akademgorodok 50/28 660036
Krasnoyarsk
Russia
nkirichenko@yahoo.com

Paul Kirkland
Butterfly Conservation
24 Allan Park FK8 2QG Stirling,
Scotland
Great Britain
pkirkland@butterfly-conservation.org

Martin Konvicka
University of South Bohemia in
České Budejovice, Faculty of
Science
Branisovska 31 37005 České
Budejovice
Czech Republic
konva333@gmail.com

Andreas Kopp
Wilerstrasse 9 8370 Sirmach
Switzerland
koppandy@bluewin.ch

Toni Koren
Association Hyla
Jezerška 70a 10000 Zagreb
Croatia
koren.toni1@gmail.com

Mikhail Kozlov
University of Turku Section of
Ecology, University of Turku
20014 Turku
Finland
mikoz@utu.fi

Vladimir Krpach
Institute of Ecology and
Technology DUT - Tetovo
Fjodor Dostoevski 40b 1000
Skopje
Macedonia
vkrpach@gmail.com

L

Bernard Landry
Muséum d'histoire naturelle
Route de Malagnou 1 1208
Genève
Switzerland
bernard.landry@ville-ge.ch

Ton van Langen
van Abkoudeplantsoen 6708 ST
Wageningen
Netherlands
tonvanlangen@planet.nl

Kyung Min Lee
University of Oulu
Pentti Kaiteran katu 1 90014
Oulu
Finland
algaekmlee@gmail.com

David Lees
Natural History Museum
Cromwell Road SW7 5BD London
Great Britain
davil@nhm.ac.uk

Theo Leger
Senckenberg Museum für
Tierkunde Dresden
Helgolandstrasse 19 01097
Dresden
Germany
theo.leger@outlook.com

Hans Löbel
Wilhelm Külz Straße 11 99706
Sondershausen
Germany
gertraud.loebel@googlemail.com

Carlos Lopez Vaamonde
INRA Orléans - Unité de
Recherche en Zoologie Forestière
2163 Avenue de la Pomme de
Pin, CS 40001 ARDON 45075
ORLEANS Cedex 2
France
[carlos.lopez-
vaamonde@orleans.inra.fr](mailto:carlos.lopez-vaamonde@orleans.inra.fr)

M

Richard Mally
University of Bergen
Realfagbygget, Allégaten 41 5007
Bergen
Norway
richard.mally@uib.no

Jana Maresova
University of South Bohemia,
Faculty of Science
Branisovka 1760 37005 Ceske
Budejovice Czech Republic
maresovajana2@gmail.com

Geoff Martin
Natural History Museum
Cromwell Road SW7 5BD London
Great Britain
g.martin@nhm.ac.uk

Carlo Matessi
Via Cascina Margarina 6 27048
Sommo (Pavia)
Italy
matessi.carlo@gmail.com

Wolfram Mey
Museum für Naturkunde
Invalidenstr. 43 10115 Berlin
Germany
wolfram.mey@mf-n-berlin.de

Rolf Mörtter
Dürerstr. 12 76709 Kronau
Germany
rolf.moertter@t-online.de

Margit Müller
Weissdornallee 13 13158 Berlin
Germany
margitskitchen@gmx.de

Bernd Müller
Weissdornallee 13 13158 Berlin
Germany
geobernd@gmx.de

Marko Mutanen
Unniversity of Oulu
Vehmaansuontie 202 90900
Kiiminki
Finland
marko.mutanen@oulu.fi

N

Wolfgang A. Nässig
Senckenberg
Senckenberganlage 25 60325
Frankfurt am Main
Germany
wnaessig@senckenberg.de

Vazrick Nazari
Agriculture and Agri-Food
Canada
960 Carling Ave K1A 0C6 Ottawa
Canada
nvazrick@yahoo.com

Erik van Nieukerken
Naturalis Biodiversity Center
PO Box 9517 2300 RA Leiden
Netherlands
nieukerken@naturalis.nl

Romualda Nowacka
Dworcowa 69 62-007 Biskupice
Poland
r.nowacka@interia.eu

Janusz Nowacki
Poznań University of Life
Sciences Department of
Entomology and Environment
Protection
ul. Wojska Polskiego 28 60-637
Poznań
Poland
noctuajn@gmail.com

P

David Plotkin
University of Florida
3150 Hull Road, 32611-2710
Gainesville
USA
dplotkin@ufl.edu

Miloš Popović
Department of Biology and
Ecology, Faculty of Sciences and
Mathematics, University of Niš
Višegradska 33 18000 Niš
Serbia
mpopovic@pmf.ni.ac.rs

Ravikash Prasad
University of Cambridge
Downing College CB2 1DQ
Cambridge
Great Britain
rrp25@cam.ac.uk

Mike Prentice
Starveall Barn, Quarry Road,
Hornton OX15 6DF Banbury
Great Britain
mike.prentice@cbre.com

Łukasz Przybyłowicz
Institute of Systematics And
Evolution of Animals, Polish
Academy of Sciences
Sławkowska 17 31-016 Kraków
Poland
lukasz@isez.pan.krakow.pl

R

Hossein Rajaei
Staatliches Museum für
Naturkunde Stuttgart
Stuttgart
Germany
hossein.rajaei@smns-bw.de

Laszlo Rakosy
Babes-Bolyai University
Clinicilor 5-7 400006 Cluj-Napoca
Romania
laszlorakosy@ubbcluj.ro

Silvia Richter
Gerard Brandtstraat 109 2332 AK
Leiden
Netherlands
s.richter109@gmail.com

Michal Rindoš
Faculty of Science, University of
South Bohemia
Branišovská 31, 37005 České
Budějovice
Czech Republic
michal.rindos@gmail.com

Katja Rönkä
University of Jyväskylä
Suuruspääntie 18 A 5 40520
Jyväskylä
Finland
katja.h.ronka@jyu.fi

Ivanka Rota
Ulica Sv. Roka 3b 10010 Zagreb
Croatia
ivanka.rota@gmail.com

Jadranka Rota
Lund University
Sölvegatan 37 22362 Lund
Sweden
jadranka.rota@biol.lu.se

Daniel Rubinoff
The University of Hawaii
310 Gilmore Hall, 3050 Maile
Way 96822 Honolulu
USA
rubinoff@hawaii.edu

Nils Ryrholm
University of Gavle
SE-801 76 Gavle
Sweden
nils.ryrholm@hig.se

S

Sarah Saadain
Department of Intergrative
Zoology, University of Vienna
Althanstraße 14 1090 Vienna
Austria
sarah.saadain@univie.ac.at

Stefano Scalerio
Consiglio per la ricerca in
agricoltura e l'analisi
dell'economia agraria (CREA)
c.da Li Rocchi 87036 Rende
Italy
stefano.scalericio@crea.gov.it

Cornelia Schintlmeister
Calberlastr. 3 01326 Dresden
Germany
corneliawosnitza@aol.com

Alexander Schintlmeister
Calberlastr. 3 01326 Dresden
Germany
schintlm@aol.com

Barbara Schmitz
Johannes-Brahms-Str. 16 14624
Dallgow-Döberitz
Germany
schmitzb@uni-potsdam.de

Oliver Schmitz
Johannes-Brahms-Str. 16 14624
Dallgow-Döberitz
Germany
schmitz.o@arcor.de

Harald Schreiber
Delattinia Naturforschende
Gesellschaft d.
Saarlandes Am Mittelberg 1
66583 Spiesen-Elversberg
Germany
h.schreiber39@delattinia.de

Marcin Sielezniew
University of Bialystok
M. Skłodowskiej-Curie 14 15-097
Bialystok
Poland
marcins@uwb.edu.pl

Sergey Sinev
Zoological Institute of the
Russian Academy of Sciences
Universitetskaya emb. 1 199034
St.Petersburg
Russia
sergey.sinev@zin.ru

Claude Sinner
Eggensteiner Weg 8 76351
Linkenheim
Germany
euxoa@yahoo.de

Jana Slancarova
University of South Bohemia in
Ceske Budejovice
Branisovska 1645/31a, Ceske
Budejovice 2 37005 Ceske
Budejovice
Czech Republic
slancar@gmail.com

Jae-Cheon Sohn
Mokpo National University
1666, Yeongsan-ro, Cheonggye-
myeon 58554 Muan
South Korea
jay.c.sohn@gmail.com

Axel Steiner
Staatliches Museum für
Naturkunde Karlsruhe
Erbprinzenstr. 13 D-76133
Karlsruhe
Germany
a-steiner@web.de

Marja van der Straten
NVWA
van Abkoudeplantsoen 35 6708
ST Wageningen
Netherlands
m.j.vanderstraten@nvwa.nl

Chris van Swaay
Dutch Butterfly Conservation
PO Box 506 NL 6700 AM
Wageningen
Netherlands
chris.vanswaay@vlinderstichting.nl

Š

Jan Šumpich
National Museum Prague
Cirkusová 1470 19300 Praha 9 -
Horní Počernice
Czech Republic
jansumpich@seznam.cz

T

Toomas Tammaru
University of Tartu
Vanemuise 46 EE-51014 Tartu
Estonia
toomas.tammaru@ut.ee

Gerhard Tarmann
Tiroler Landesmuseen
Feldstrasse 11a A-6020
Innsbruck
Austria
g.tarmann@tiroler-landesmuseen.at

Christiane Theimer
Belsstr. 30a 12277 Berlin
Germany
Franz Theimer
Belsstr. 30a 12277 Berlin
Germany
franz4theimer@gmx.de

Valentina Todisco
Via Costa Caselle lotto 7 int.1
00047 Marino
Italy
valentina.todisco@gmail.com

Pasquale Trematerra
University of Molise
Via De Sanctis, 1 86100
Campobasso
Italy
trema@animol.it

Robert Trusch
Staatliches Museum für
Naturkunde Karlsruhe
Erbprinznstr. 13 D-76133
Karlsruhe
Germany
trusch@smnk.de

Andro Truuverk
University of Tartu
Vanemuise 46-216 51014 Tartu
Estonia
andro.truuverk@ut.ee

Nikola Tvrtković
Natura
Alagovićeva 21 10000 Zagreb
Croatia
nikolatvrtkovic71@gmail.com

V

Karine Vandermeiren
Belgium
andre.karine.verboven@telenet.be

Andre Verboven
Groeneweg 60 B-3001 Heverlee
Belgium
verboven.pc@outlook.be

José Luis Viejo Montesinos
Universidad Autónoma de
Madrid C/.
Darwin, 2 28049 Madrid
Spain
joseluis.viejo@uam.es

Roger Vila
Institut de Biologia Evolutiva
(CSIC-UPF)
Passeig Marítim de la
Barceloneta 37 08003 Barcelona
Spain
roger.vila@csic.es

Raluca Voda
University of Turin
Via Accademia Albertina 13
10123 Torino
Italy
raluvoda@gmail.com

Blerina Vrenozhi
Museum of Natural Sciences
Faculty of Natural Sciences
Boulevard "Zog I" 1001 Tirana
Albania
bvrenozhi@gmail.com

W

David L. Wagner
University of Connecticut Dept of
Ecology and Evolutionary Biology
75 North Eagleville Rd. 06269-
3043 Storrs
USA
david.wagner@uconn.edu

Niklas Wahlberg
Lund University Department of
Biology, Section of Biodiversity
22362 Lund
Sweden
niklas.wahlberg@biol.lu.se

Martin Warren
Butterfly Conservation Europe
2 Fairside, Higher Ansty DT2 7PS
Dorchester
Great Britain
martin.warren@bc-europe.eu

Martin Wiemers
Helmholtz Centre for
Environmental Research - UFZ
Theodor-Lieser-Str. 4 06120
Halle
Germany
martin.wiemers@ufz.de

Wolfgang Wittland
Mozartstr. 19 41844 Wegberg
Germany
wolfgang@wittland.org

Irma Wynhoff
Dutch Butterfly Conservation
PO Box 506 NL 6700 AM
Wageningen
Netherlands
irma.wynhoff@vlinderstichting.nl

Z

Norbert Zahm
Delattinia Naturforschende
Gesellschaft d.
Saarlandes Ludwig-Uhland-
Strasse 34 66839 Schmelz
Germany
NZahm@t-online.de

Barbara Zakšek
Centre for Cartography of Fauna
and Flora
Antoličičeva 1 2204 Miklavž na
Dravskem polju
Slovenia
barbara.zaksek@ckff.si

Hans Christof Zeller
Forsthubfeld 14 5303 Thalgau
Austria
christof.zeller@gmx.net

Alberto Zilli
Natural History Museum
Cromwell Road SW7 5BD London
Great Britain
A.Zilli@nhm.ac.uk

Petra Zub
Lange Str. 13 36381 Schluechtern
Germany
zub@arge-helep.de

Hrvatski
prirodoslovni
muzej



Croatian
Natural History
Museum



Societas
Europaea
Lepidopterologica
(SEL)