



# XIX<sup>th</sup> European Congress of Lepidopterology

27 September – 02 October 2015  
Radebeul · Germany

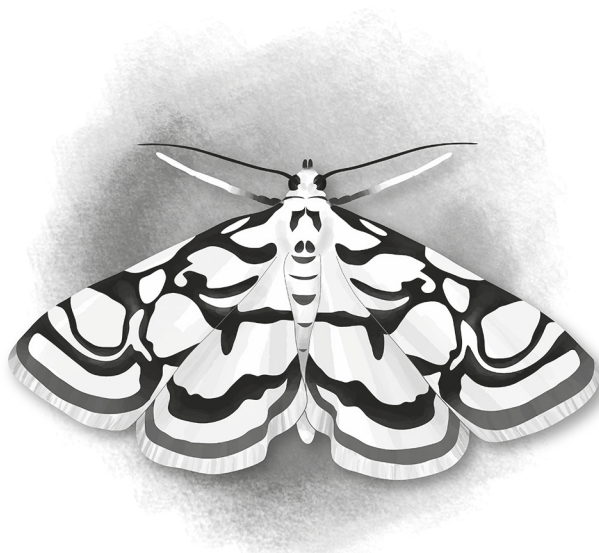


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**Societas Europaea Lepidopterologica**  
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**Senckenberg**  
Museum of Zoology Dresden





## **19<sup>th</sup> European Congress of Lepidopterology**

Sept 27 – Oct 2, 2015

Radebeul, Germany

## **Organizer**

Dr Matthias Nuss  
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## **Team**

Manuela Bartel, Franziska Bauer, Frauke Nielsen, Christian Schmidt,  
Francesca Vegliante, Birgit Walker

## **Cultural programme for accompanying persons**

Manuela Bartel & Frauke Nielsen  
Senckenberg Museum of Zoology Dresden

## **Sponsored by**

Societas Europaea Lepidopterologica  
Senckenberg Museum of Zoology Dresden

## **Venue**

Radisson Blu Hotel Dresden Radebeul, Germany

## **Congress Logo**

Franziska Bauer

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Markward Herbert Fischer

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## **Congress Homepage**

[www.soceurlep.eu](http://www.soceurlep.eu)

## **Title photo**

*Thymelicus lineola*, photo taken in June 2014 near Leipzig (© Bernd Garbe).  
This butterfly species has been described by the Saxon actor Ferdinand Ochsenheimer in 1808. It is native to the entire Palearctic region, and has been introduced to North America by man. From its European congeneric *Thymelicus sylvestris*, with which it often occurs in the same habitat and at the same time, it is best distinguished by the black tips of the antennae in frontal view.



## Dear Lepidopterists – Welcome to Butterfly Saxony!

I would like to welcome you to Saxony, a federal state of Germany with a long and famous tradition in Lepidopterology.

The capital of Saxony, Dresden, is home to the Dresden Museum of Zoology, whose origins date back to the 16<sup>th</sup> century when stuffed bodies of animals were kept as treasures in the Saxon court which was founded by Augustus, Elector of Saxony (reg. 1553 – 1586). The official foundation of the museum itself was in 1728, when the scientific collections moved from the castle to the newly built Zwinger palace.

Unfortunately, the first Lepidoptera collections were entirely destroyed by fire during the revolution in 1849. In the 19<sup>th</sup> century, natural sciences became very popular, and bourgeois societies were founded in Görlitz, Dresden and Leipzig. During that time, Dresden became a true metropolis of Lepidopterology. Here, Dr. Otto Staudinger (1830 – 1900) established his insect trading company in 1859. In 1862, the Entomological Society “Entomologischer Verein Iris zu Dresden” was founded and published the famous journal *Deutsche Entomologische Zeitschrift Iris*. Its membership comprised well-known lepidopterologists from all over the world. As a result of this heyday, many butterfly and moth collections were given to the Museum of Zoology Dresden. Johannes Draeseke (1892 – 1970), who rendered outstanding services as a preparator for many decades in these collections, successfully saved the most important parts of the collection from destruction by World War II. Today, the Lepidoptera collection comprises more than 6,000 drawers, including over 800,000 butterflies and moth specimens of 23,500 species from all over the world. The number of primary types is at about 1,000 species. Some of the most important contributions are those of European and Southeast-Asian Lycaenidae by Carl Ribbe (1860–1934), the Lepidoptera from Tibet by Walter Stötzner (1882–1965) and the Zygaenidae by Manfred Koch (1901–1972). On a regional scale, the Dresden collection is a comprehensive archive of vouchers of the last 150 years, documenting extinctions, fluctuations and first arrivals of Lepidoptera in Saxony. Among its contributions is that of Ernst Möbius (1869 – 1945), who lived in Dresden and Radebeul. Möbius published the fauna of “Macrolepidoptera” from the kingdom of Saxony in 1905 as well as the fauna of “Microlepidoptera” of Dresden and its surroundings in 1936. A vast amount of records for these two works come from the Lössnitz area, where our congress venue is situated.

On behalf of the Senckenberg Society for Nature Research, of which the Museum of Zoology Dresden is an integral part today, and the Societas Europaea Lepidopterologica, it is an honour for me to welcome you in Radebeul as participants



of the XIX<sup>th</sup> European Congress of Lepidopterology. With respect to the lepidopterological history of Saxony, I am very proud to host this congress and welcome participants from so many parts of the world. I am looking forward to a successful and inspiring conference as well as an interesting excursion and hope you will enjoy your stay in Radebeul.

Matthias Nuss

and the organizing team from  
the Senckenberg Museum of Zoology  
Dresden

The A. B. Meyer-Building in Dresden-Klotzsche, home of the Senckenberg Museum of Zoology Dresden.



Monday • 28 September 2015

9:00 – 9:20	<b>Welcome and opening of the congress</b> <b>Niels Peder Kristensen Memorial Symposium</b> <i>Chairs: Jadranka Rota &amp; Thomas Simonsen</i>	
9:20 – 9:30	<b>Introduction</b>	
9:30 – 10:15	Thomas Simonsen	Wing scales and non-ditrysian moths: two key areas in Niels P. Kristensen's and my own research interests
10:15 – 10:45	Malcolm Scoble	Broadening the value of taxonomic studies on Lepidoptera: building on Niels Kristensen's legacy
<b>10:45 – 11:10</b>	<b>Coffee break</b>	
11:10 – 11:35	George Gibbs	Unfinished business: Niels Kristensen's vision for primitive moths of the Southern Hemisphere
11:35 – 11:55	Harald Krenn	Head morphology in adult Lepidoptera – from complexity to simplicity
11:55 – 12:20	Don Davis	A revision of the New World family Adeliidae (Adeloidea)
<b>12:20 – 13:20</b>	<b>Lunch break</b>	
13:20 – 13:45	Joël Minet	Wing venation: its evolution in basal lepidopteran lineages
13:45 – 14:10	Joaquin Baixeras	Functional morphology of the bursa copulatrix wall: a comparative analysis in some groups of Lepidoptera
14:10 – 14:35	Lauri Kaila	Spurious taxonomy and its consequences: a history of wing venation in <i>Elachista</i> (Elachistidae)
14:35 – 15:00	Richard Brown	Structures for attachment of adult appendages: the pretarsi and the fore-wing-metascutal locking mechanism
15:00 – 15:25	April Dinwiddie	Evolutionary patterns of lepidopteran wing scale shapes in a quantitative morphospace
<b>15:25 – 15:45</b>	<b>Coffee break</b>	
15:45 – 16:10	Francesca Vegliante	Musculature and movements of the genitalia of <i>Anania hortulata</i> (Pyraloidea: Crambidae)





# Programme

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Monday · 28 September 2015

16:10 – 16:35	Ole Karsholt	Light trapping Lepidoptera at the top of the Zoological Museum in Copenhagen
16:35 – 17:00	Steen Dupont	The setae of parasitic <i>Liphyra brassolis</i> butterfly larvae form a flexible armour for resisting attack by their ant hosts (Lycaenidae)
17:00 – 17:25	Jadranka Rota	Niels Kristensen from my perspective
17:25 – 17:35		Closure





Tuesday • 29 September 2015

	<b>Fossil Lepidoptera</b> <i>Chairs:</i> Maria Heikkilä & Jae-Cheon Sohn	
9:00 – 9:45	Conrad C. Labandeira	New developments in understanding the biology of Mesozoic Lepidoptera
9:45 – 10:00	Rienk de Jong	Can fossils help us understand the paleobiogeography of the butterflies?
10:00 – 10:15	Zdenek Faltýnek Fric	Coding characters from fossil butterflies for direct inference of times of divergence in Nymphalini
10:15 – 10:30	Maria Heikkilä	Critiques and new hope on divergence time estimation of Lepidoptera
10:30 – 10:45	Wolfram Mey	Notes on Microlepidoptera in Baltic amber and description of an extinct tortricid species (Tortricidae)
<b>10:45 – 11:05</b>	<b>Coffee break</b>	
	<b>Phylogeny Symposium</b> <i>Chair:</i> Akito Kawahara	
11:05 – 11:35	Niklas Wahlberg	Cornucopia or Pandora's Box? Phylogenomics comes of age, data are no longer limiting
11:35 – 12:05	Erik J. van Nieukerken	The oldest lineages of extant Lepidoptera: phylogeny, classification, and life history evolution
12:05 – 12:35	Marko Mutanen	Deep intraspecific barcode splits in Lepidoptera: signs of cryptic diversity or <i>Wolbachia</i> -driven distraction?
<b>12:35 – 13:35</b>	<b>Lunch break</b>	
	<i>Chair:</i> Niklas Wahlberg	
13:35 – 13:55	Kyung Min Lee	The promise of ddRAD-Seq in lepidopteran phylogenetics: a case study using <i>Eupithecia</i> (Geometridae) as a model group
13:55 – 14:15	Maria Heikkilä	Elusive ditrysian phylogeny – from Kristensen & Skalski 1998 to sequence data and systematized morphology
14:15 – 14:30	Richard Mally	The molecular-morphological phylogeny of megadiverse Spilomelinae (Pyraloidea)



Tuesday • 29 September 2015

14:30 – 14:45	Théo Léger	Unravelling the phylogeny of Crambinae, Heliothelinae and Scopariinae (Pyraloidea)
14:45 – 15:00	Franziska Bauer	To hear, or not to hear, that is the question in basal Pyralidae (Pyraloidea)
<b>15:00 – 15:20</b>	<b>Coffee break</b>	
15:20 – 15:35	Vazrick Nazari	Butterflies of ancient Egypt
15:35 – 15:50	Vasilii V. Anikin	Estimating the time of divergence in Coleophoridae based on the analysis of the COI gene
15:50 – 16:05	Mari Kekkonen	DNA Barcoding at the family level: Considering the Gelechioidea
16:05 – 16:20	Katja Rönkä	Putting <i>Parasemia</i> in its phylogenetic place: a molecular analysis of the subtribe Arctiina
	<b>Bombycoidea</b> <i>Chair:</i> Alessandro Giusti	
16:20 – 16:35	Anna K. Hundsdoerfer	Phylogeography of the <i>Hyles euphorbiae</i> complex (Sphingidae) – Diverse patterns of admixture between an African and Eurasian evolutionary lineage
16:35 – 16:50	Gunnar Brehm	The unique sound production of the Death's head Hawkmoth ( <i>Acherontia atropos</i> ) revisited
16:50 – 17:20	Akito Kawahara	Moth tails divert bat attack: Evolution of acoustic deflection
	<b>Final talk of the day</b>	
17:20 – 17:30	Alexander Schintlmeister	Dr. Otto Staudinger in Dresden – a biographical and historical account



Wednesday • 30 September 2015

	<b>Multitrophic interactions: Lepidoptera • plants • parasitoids • microorganisms</b> <i>Chairs:</i> Camiel Dooreenweerd & Carlos Lopez-Vaamonde	
9:00 – 9.40	Lee A. Dyer	Local versus regional networks of phytochemically mediated plant-caterpillar-parasitoid interactions
9.40 – 10:20	Georg Petschenka	How milkweed butterflies (Danaini) tolerate and use plant toxins: evolution of resistance and sequestration
10:20 – 10:45	Carlos Lopez-Vaamonde	Evolution of the tripartite association between leaf-mining moths, <i>Wolbachia</i> , and their host plants
<b>10:45 – 11:05</b>	<b>Coffee break</b>	
11:05 – 11:30	Camiel Dooreenweerd	Adaptive radiations and speciation rates in Holarctic lineages of leafmining Lepidoptera
	<b>Conservation and Ecology</b> <i>Chair:</i> Josef Settele	
11:30 – 12:05	Chris van Swaay	Butterfly Monitoring across Europe
12:05 – 12:30	Irma Wynhoff	LIFE+ Blues in the Marshes – new habitat for <i>Maculinea</i> in The Netherlands
<b>12:30 – 13:30</b>	<b>Lunch break</b>	
13:30 – 13:50	Susanne Kurze	Too much of a good thing: Response of two <i>Lycaena</i> species to fertilised host plants
13:50 – 14:10	Martin Wiemers	LepiDiv – compiling distribution data for more than just distribution atlases
14:10 – 14:30	Martinus E. Huigens	The status of Dutch macro-moths: impact of artificial lighting
14:30 – 14:45	Nils Ryrholm	Maintaining and increasing biodiversity
14:45 – 15:10	Josef Settele	Intergovernmental assessments and the role of Lepidoptera – Insights from IPCC and IPBES
<b>15:10 – 15:30</b>	<b>Coffee break</b>	
<b>15:30</b>	<b>General Meeting</b>	



Thursday • 1 October 2015

	<b>Taxonomy and Phylogeny of Geometroidea</b> <i>Chair: Hossein Rajaei</i>	
9:00 – 9:30	Axel Hausmann	Calibrating the taxonomy of a megadiverse family on BOLD: 2700 geometrid moth types barcoded
9:30 – 10:00	Pasi Sihvonen	Can we speed up the taxonomic process of large-scale revisions? Example from the Geometrid Moths of Europe monograph
10:00 – 10:15	Hossein Rajaei	Phylogeny of the superfamily Geometroidea, with emphasis on the systematic position of <i>Pseudobiston pinratanae</i> Inoue, 1994
10:15 – 10:30	Gunnar Brehm	Towards a phylogeny of Neotropical Geometridae
10:30 – 10:45	Sille Holm	Life span under investigation: a phylogenetic comparative approach
<b>10:45 – 11:05</b>	<b>Coffee break</b>	
11:05 – 11:25	Andro Truuverk	On the Phylogenetic studies of the tribe Larentiini, based on molecular methods
11:25 – 11:40	Robert Trusch	New attainments based on an integrative taxonomic survey of <i>Rhodostrophia</i> Hübner, 1823 of Iran (Sterrhinae)
11:40 – 11:55	Gunnar Brehm	Constant and high: diversity and turnover patterns of geometrid moths along an elevational gradient in the Ecuadorian Andes revisited
	<b>Collections and Digitisation</b> <i>Chair: Matthias Nuss</i>	
11:55 – 12:20	Geoff Martin	iCollections project: the digitisation of the British & Irish Lepidoptera collection at the Natural History Museum, London
12:20 – 12:35	Alessandro Giusti	Re-curation of the slug moths (Limacodidae) collection at the Natural History Museum, London: Challenges, positive outcomes and future value
<b>12:35 – 13:35</b>	<b>Lunch break</b>	
13:35 – 13:55	Claude Sinner	My first steps in citizen science – evaluation and results of the label-butterflies.com project



Thursday • 1 October 2015

	<b>Moths</b> <i>Chair: Axel Steiner</i>	
13:55 – 14:15	Jana Slancarova	Macromoths light trap catches on intensive farmland: Relative effects of crops, land covers and landscape heterogeneity
14:15 – 14:35	Balint Horváth	Which factors influence moth communities in a Hungarian sessile oak-hornbeam forest?
14:35 – 14:50	Mehdi Esfandiari	Genetic diversity and phylogeography of <i>Sesamia nonagrioides</i> (Noctuidae) in Iran inferred from mitochondrial DNA
<b>14:50 – 15:10</b>	<b>Coffee break</b>	
15:10 – 15:25	Sara Farahi Jahromi	A survey of Erebiidae, Nolidae and Euteliidae in southern and northeastern of Iran
15:25 – 15:40	Konstantin A. Efetov	A new sex attractant for the males of Procrinae (Zygaenidae)
15:40 – 15:55	Konstantin A. Efetov	On the way to a world catalogue of the Procrinae (Zygaenidae)
15:55 – 16:10	Łukasz Przybyłowicz	A new genus for an undescribed species of „tufted“ thyretine from Central Africa (Erebiidae: Arctiinae, Syntomini)
16:10 – 16:25	Herbert Beck	Larval characters and molecular phylogenies of Noctuoidea



Thursday • 1 October 2015

	<b>Biogeography</b> <i>Chair: Anna Hundsdoerfer</i>	
9:00 – 9:35	Roger Vila	The closer you look, the more you see. European butterfly diversity through the magnifying glass of phylogeography
9:35 – 9:50	Alena Bartoňová	<i>Proterebia afra</i> – Relic of the glacial steppe in the Balkans?
9:50 – 10:05	Valentina Todisco	The origin of the Sardinian Blue, <i>Pseudophilotes barbagiae</i> (Lycaenidae): Out-of-Europe or Out-of-Africa?
	<b>Butterflies</b> <i>Chair: Roger Vila</i>	
10:05 – 10:25	Blanca Huertas	Hazards of Butterfly Collecting: A tribute to Dr Torben B. Larsen (1944 – 2015)
10:25 – 10:45	Konrad Kalarus	Drivers of colonization of habitat patches by the dryad butterfly ( <i>Minois dryas</i> ) in fragmented grasslands
<b>10:45 – 11:05</b>	<b>Coffee break</b>	
11:05 – 11:30	Andrea Grill	Mate choice in <i>Maniola</i> butterflies: Age beats beauty?
11:30 – 11:50	Judit Bereczki	Preliminary results on <i>Wolbachia</i> infestation in two closely related <i>Melitaea</i> species
11:50 – 12:05	Nikola Micevski	An annotated checklist of the butterflies of the National Park “Mavrovo” (Macedonia)
	<b>Microlepidoptera and Pyraloidea</b> <i>Chair: Joaquín Baixeras</i>	
12:05– 12:20	Pasquale Trematerra	Corks damaged by <i>Nemapogon granellus</i> (L.) in Tuscan wine cellars
12:20 – 12:35	Aihui Yin	Taxonomic status of the genus <i>Cryptolechia</i> Zeller, 1852
<b>12:35 – 13:35</b>	<b>Lunch break</b>	
13:35 – 13:50	Boyan Zlatkov	Lock-and-key mechanisms in some Cochylini (Tortricidae): a morphological study
13:50 – 14:05	Arvind Agrawal	Diversity of Bagworm (Psychidae) species in India



Thursday • 1 October 2015

14:05 – 14:20	Oleksiy V. Bizilya	The study of Microlepidoptera of Ukraine: a part of total inventory of Ukrainian Lepidoptera
14:20 – 14:35	Sergey Yu. Sinev	A revised taxonomy of the bright-legged moths (Gelechioidea: Stathmopodidae)
14:35 – 14:50	M. Alma Solis	<i>Cosmopterosis</i> Amsel and <i>Schacontia</i> Dyar (Crambidae: Glaphyriinae): case studies about pyraloid diversity and biology in the Neotropics
<b>14:50 – 15:10</b>	<b>Coffee break</b>	
15:10 – 15:25	Richard Mally	A report on several long-overlooked species of the <i>Sufetula</i> genus group (Pyraloidea: Crambidae: Lathrotelinae) found in greenhouses and imports into Europe
15:25 – 15:40	Mujie Qi	The fauna of Phycitinae (Pyralidae) in China
15:40 – 16:00	David Agassiz	Lepidoptera on ferns, mostly in Africa
16:00 – 16:25	David C. Lees	DNA barcoding of the microlepidopteran fauna of Madagascar





Friday • 2 October 2015

## The congress excursion

The destination of the congress excursion will be the Elbe Sandstone Mountains. The most popular parts of these mountains are made of cretaceous sediments. Subsequent erosion formed steep slopes and table mountains. The river Elbe breaks through the mountain range in a narrow valley. The mountains range from the German state of Saxony to the North Bohemian region of the Czech Republic. It is declared as National Park in both countries where collecting insects is prohibited. With 723 meters above sea level the Děčínský Sněžník in the Czech Republic is the highest peak of the Elbe Sandstone Mountains. Thus, flora and fauna on top of these mountains are still of lowland type. However, on many steep slopes direct sunlight never arrives which makes the bottom of the slopes shady and humid places and thus a suitable habitat for montane species. That is why some biologist call this mountain range “negative mountains”.



We will leave the congress hotel at 8:45 a.m. and have a 12-minute walk to the railway station Radebeul-Ost. The departure of our train (S1 in the direction Schöna) is at 9:09 a.m. We will arrive at 9:58 a.m. in the small city Wehlen, situated at the river Elbe in the heart of the Elbe Sandstone Mountains.

From there, we will be guiding different hiking tours towards Rathen, because the trails are small and therefore it is advantageous to separate into smaller groups. We will also consider lower trail difficulty levels for those who may not be able to walk up hundreds of steps or have fear of heights. There will be opportunities to have lunch in restaurants.

We will depart from Kurort Rathen at 4:21 p.m. using the S1 train in the direction Meissen Triebischtal. The train stops at Dresden-Hauptbahnhof at 5:00 p.m. and at Dresden-Neustadt at 5:07 p.m. Arrival in Radebeul Ost is at 5:15 p.m.

The bank of the Elbe river and the slopes of the Elbe Sandstone Mountains. Photos: Jan-Michael Lange.



## Niels P. Kristensen,

honorary member and former SEL president, who passed away on December 6<sup>th</sup>, 2014 was one of Europe's foremost and most influential lepidopterists and entomologist for more than four decades.

Throughout his career, Niels was deeply interested in comparative and evolutionary morphology and systematics of the Lepidoptera. Through his early collaborations with Howard E. Hinton (University of Bristol) and Jean Chaudonneret (Université de Dijon), he became highly skilled in the methods of scanning electron microscopy, histology, and semi-thin sectioning. Both methods became cornerstones in his work throughout his career, and in particular the *combination* of scanning electron microscopy and histology in the study of the same structures became a methodological hallmark of his work. Systematically, Niels' main interest were the lower families (the non-ditrysians and the "primitive" ditrysian families), although he also worked on e.g. Sesiidae and butterflies. Morphologically, however, he worked on virtually all aspects of Lepidoptera from larval and adult musculature, head and mouthpart morphology, wing and wing scales morphology, morphology and anatomy of the genitalia, to the nervous system and the histology of digestive and circulatory systems of both larvae and adults.



During the second half of his career, Niels edited the two volumes of The Handbook of Zoology dedicated to Lepidoptera. He wrote very significant parts of both volumes himself, and this work certainly ranks among his most lasting contributions to lepidopterology. Niels supervised several Masters and PhD students as well as postdocs, but his legacy as a mentor goes much beyond that. He was generous with both his knowledge and his time, and advised and supported numerous lepidopterists (professionals and amateurs alike) throughout the years, and influenced many more through his writings.

In this symposium, we honour the memory of Niels P. Kristensen in a series of presentations on a wide range of Lepidoptera morphology and systematics.

Niels Peder Kristensen during the 2013 SEL Congress in Bulgaria.



Monday · 28 September 2015

## Keynote

9:30  
10:15

### Wing scales and non-ditrysian moths: two key areas in Niels P. Kristensen's and my own research interests

**THOMAS J. SIMONSEN**

Natural History Museum Aarhus, Wilhelm Meyers Allé 210, Universitetsparken, DK-8000 Aarhus C, Denmark; [t.simonsen@nathist.dk](mailto:t.simonsen@nathist.dk)

Comparative morphology of lepidopteran wing vestiture, and evolution of the non-ditrysian Lepidoptera were two of Niels P. Kristensen's key research interests throughout his career, and several of his early papers were concerned with the morphology of wing scales. Nevertheless, he felt that many aspects still needed to be addressed (or readdressed), and in particular an overview of the evolution of the wing scales in the non-ditrysians was much needed. When I was looking for a Master's project (in 1997) in systematic entomology, he therefore suggested that I carried out a comparative study of the wing vestiture of the non-ditrysian grade (one of several "long overdue" projects in his cupboard), starting with a detailed study of the European ghost moth, *Hepialus humuli*. This became the start of not only my own journey into systematic and evolutionary entomology, but also a fruitful collaboration and a lasting friendship. Here I present results and anecdotes from my work with Niels in the late 1990s and early 2000s, focusing on three particular studies: sexual dimorphism and regional polymorphism in the European Ghost Moth, *Hepialus humuli*; comparative morphology of wing vestiture in the non-ditrysian grade; and the surprisingly apomorphic wing vestiture in the Kauri Moth, *Agathiphada vitiensis*. I also attempt to reconcile major trends in the comparative morphology of the wing vestiture with the recent changes in our understanding of non-ditrysian evolution brought on by phylogenomic studies.



Monday • 28 September 2015

## Broadening the value of taxonomic studies on Lepidoptera: building on Niels Kristensen's legacy

10:15  
10:45

**MALCOLM J. SCOBLE**

Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK;  
M.Scoble@nhm.ac.uk

Niels Kristensen made exceptional contributions to the systematics of the Lepidoptera, and to insect phylogeny more widely. He also took a great interest in Lepidoptera studies across the world, and in Europe particularly. Today, funding pressures and the trend to support only competitively funded research makes life increasingly difficult for professional researchers – particularly in taxonomy. Restrictions on collecting specimens add a further impediment to all lepidopterists. Fortunately, Lepidoptera have some advantages as a study group. They are used as model organisms in a variety of research projects; they form a conspicuous element of most faunas; and some of them (butterflies especially) are appreciated by the public. We are, moreover, blessed with many lepidopterists, although the number of professionals is declining – at least in Europe. Against this background, how can we honour Niels' legacy? And how can we take it forward? This talk considers some possibilities – focusing on collaboration, networks (human and virtual), wider audiences and social value.



Monday · 28 September 2015

11:10  
11:35

## Unfinished business: Niels Kristensen's vision for primitive moths of the Southern Hemisphere

**GEORGE W. GIBBS**

School of Biological Sciences, Victoria University of Wellington, Wellington 6000, New Zealand;  
[George.Gibbs@vuw.ac.nz](mailto:George.Gibbs@vuw.ac.nz)

A dark cloud passed over the discipline of Lepidopterology in December 2014 with the passing of Niels Peder Kristensen. Ever since my initial request for reprints in 1975 I have admired Niels' unique academic grasp of insect diversity and evolution, especially within the Lepidoptera. I have been privileged to have enjoyed a life-long friendship with him and to have this opportunity to express my appreciation.

NPK's scientific aspirations were revealed in his 1975 reply; a list of topics he was working on and prospects for future study and collaborations. Among the latter were monographic treatments of *Mnesarchaea* and the Southern Hemisphere Micropterigidae. Unfortunately I still hold the incomplete manuscripts for both of these 'retirement' projects. More than most researchers Niels has 'stuck to his knitting' throughout his life, but like most of us, has been distracted for years at a time by the stress of administrative or teaching duties and the demands of more pressing projects, such as in his case, the 'Handbook'. In my view, Niels was the consummate "pure scientist" who sought to work at the heart of the issues of the time – in this case understanding the evolutionary pathway of insects. His time has spanned the very significant crossover from morphological to molecular phylogenetics.

This tribute encompasses NPK's involvement with the Southern Hemisphere, both directly and via its primitive Lepidoptera. It outlines the groups of significance and summarises recent progress with the discovery of new taxa, some of the people involved, and a review of the southern hemisphere micropterigid lineages. A long and productive retirement was part of Niels' vision. Sadly, his untimely death has stolen the opportunity to collaborate on his unfinished business.



Monday • 28 September 2015

## Head morphology in adult Lepidoptera – from complexity to simplicity

11:35

11:55

**HARALD W. KRENN & JULIA A. S. BAUDER**

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The benchmark studies of Niels Peder Kristensen on the basal taxa of the Lepidoptera contributed greatly to our today's understanding of the head morphology and phylogeny of Lepidoptera. In particular, his work filled the gap of knowledge between the ancestral head morphology of the pollen-chewing Micropterigidae and the derived head morphology of the fluid-feeding Macrolepidoptera. Back then, these studies provided major arguments for a nowadays commonly accepted higher level phylogeny of the Lepidoptera. Our collaboration was devoted to the evolution of the head anatomy of Glossata with special focus on the evolution of derived features that are essential for nectar-feeding with a proboscis. The evolution of the Lepidopteran mouthparts from pollen-chewing to nectar-feeding involved a simplification of the mouthparts, such as a reduction of the mandibles and maxillary palps, modifications of the maxilla and labrum as well as the evolution of novel traits, such as a stipital haemolymph pump for proboscis movements, new structures for galeae interlocking, novel proboscis sensilla and intrinsic galeal musculature. These studies provided the framework for recent work on the evolution of the feeding apparatus in butterflies possessing extremely long proboscides that revealed particular morphological adaptations for efficient nectar uptake along a very long proboscis. Surprisingly, these adaptations require low material costs and sometimes even include further simplifications regarding the sensilla equipment of the proboscis.



Monday · 28 September 2015

11:55  
12:20

## A revision of the New World family Adelidae (Adeloidea)

DONALD R. DAVIS & MATHEW MEDEIROS

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The world fauna of the monotrysian family Adelidae currently consists of approximately 5 genera and 294 species (Nieukerken et al 2011), occurring in all major geographical regions except Antarctica and New Zealand. Four of these genera: *Adela* (12 species), *Cauchas* (6 species), *Ceromitia* (15 species), and *Nemophora* (1 species) were known to occur in North and South America, totaling slightly less than 12% of the global diversity of the family. In a project nearing completion, we will be reporting 48 new species, most (37 species) within the large pantropical genus *Ceromitia*.

In the most recent molecular study (Regier et al, 2015), all genera of Adelidae except *Ceromitia* were analyzed using 19 genes. These were grouped together on the basis of morphology and using all 3 nucleotide positions (nt 123), with the nearest outgroup being Heliozelidae. Other families included in this study within the Adeloidea are the Incurvariidae, Prodoxidae, Cecidosidae, and the new North American family Tridentaformidae. A major morphological feature of the Adeloidea is the monotrysian, piercing ovipositor of the females. The basal outgroup of the Adeloidea is the South American Andesianoidea, whose females lack a piercing ovipositor.

Monophyly within the Adelidae, including *Nematopogon*, has been defined by the usually long male antennae, slender cloaca in the female, and the characteristic feeding habits of the case bearing larvae on leaf litter and withering leaves on the ground. Two subfamilies are recognized: Adelinae (maxillary palpi 2-3-segmented, male valvae without pectinifers), including *Adela*, *Cauchas*, and *Nemophora*; and Nematopogoninae (maxillary palpi usually 4-5-segmented; male valvae usually with pectinifers), including *Ceromitia* and *Nematopogon*.

A brief review of the biology, and morphology of the New World Adelidae will be presented.





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## Wing venation: its evolution in basal lepidopteran lineages

**JOËL MINET**

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Since the beginning of the 20<sup>th</sup> century, several authors have attempted to reconstruct a ground plan for the lepidopteran wing venation (cf., e.g., the “archetypes” considered by R. J. Tillyard in 1919 and the “hypothetical ancestral moth” imagined by N. P. Kristensen in 1984). A few details can now be modified in this homoneurous ground plan, notably on account of the discovery of well preserved fossils from the Middle Jurassic (Mesokristenseniidae in particular). At least two wing-venational features can be regarded as lepidopteran autapomorphies clearly absent from the trichopteran ground plan. Although it may be difficult to identify certain veins in groups with highly modified or simplified venations, studying the pupal tracheation often leads to helpful clarification but has been neglected by most contemporary lepidopterists. Such studies once conducted by A. F. Braun and R. J. Tillyard actually show that the long anal vein of the forewing should be termed 1A or, preferably, A1 rather than “1A + 2A” (in the hindwing, nevertheless, the post-CuP venation remains less easy to interpret). Autapomorphies and synapomorphies can be proposed for most of the non-ditrysian lineages recently recognized by molecularists (including the redefined Neopseustoidea). However, these traits often correspond to losses since wing venation tend to be simplified in various clades. For the Ditrysia, the venational ground plan is fairly easy to reassess and somewhat similar to the condition found in certain Eriocottidae.

**13:20**  
13:45



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13:45  
14:10

## Functional morphology of the bursa copulatrix wall: a comparative analysis in some groups of Lepidoptera

**JOAQUÍN BAIXERAS**

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In spite of the extensive use of the genitalia in the taxonomic study of the Lepidoptera, their detailed function and adaptive significance are still poorly understood. The bursa copulatrix is a bottle like structure that receives the spermatophore and other substances from the male during mating. Apart from its interaction with the phallus of the male during mating it is the scenario of quite complex post-copulatory mechanisms. A detailed knowledge of the morphology of the bursa is fundamental, not only to explain the copulatory behaviour, but to understand the selective pressures responsible for the evolutionary origin and diversification of female genital structures and of the male genital traits interacting (and possibly coevolving) with them. The examination under electron microscope of the bursa copulatrix and its associated muscle structure gives some evidences about the function of sclerotized structures and suggests some developmental and physical constraints in the anatomy. In this contribution the present knowledge of the whole bursa wall structure and function, from the luminal side to the external (haemocelic) side, will be reviewed. Although special emphasis will be given to the advances in the Tortricid family, comparative examples from other Ditrysian families will be included in the discussion.



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## Spurious taxonomy and its consequences: a history of wing venation in *Elachista* (Elachistidae)

14:10

14:35

**Lauri Kaila**

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Species taxonomy of Elachistinae (Gelechioidea) is notoriously difficult due to the uniform outer appearance and often slight morphological differentiation in genital morphology of constituted species. A species group in *Elachista*, originally considered to be represented by about ten species, had been found to be more complex, but taxonomic resolution using traditional methods was eluding. This species group (originally artificially divided into two groups) was split to encompass over 60 nominal species late 1980's and early 1990's. Main criterion for the species concept adopted was subtle differences in wing venation details. Soon afterwards, the taxonomic value of this kind of venation pattern was refuted, but the uncertainty on reliable species taxonomy persisted, due to the magnitude of the problem. Virtually no specimens of this group could be associated with a species name with any certainty since the publication of the venation-based taxonomic works. Only now, with integrated taxonomy using morphology and DNA barcodes, including fragments obtained from holotypes, the taxonomy has been more or less settled, involving no less than 45 new synonymies. Thus, the effort required to rectify one spurious work took almost 25 years, with parts of two PhD theses involved. All this could have been avoided, had the nature of variation of venation been even briefly examined using population samples prior any further conclusions. Checking the level of asymmetry would also have been illuminating – it often far exceeds the level originally deemed significant enough to divide specimens into sections of species.



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14:35  
15:00

## Structures for attachment of adult appendages: the pretarsi and the forewing-metascutal locking mechanism

**Richard L. Brown**

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Previous studies of attachment structures of the pretarsus and forewing-thorax are reviewed and additional information is provided based on examinations of species representing 55 families of Lepidoptera. Pretarsal claws have the most detectable differences between taxa, including presence or absence of microtrichia, rugae, serrations, dentitions, and cleft apices. Presence or absence of microtrichia on claws appears to be a defining character for some subfamilies of Geometridae and Tortricidae. Pretarsi of a large number of species carry brochosomes, deposited on plant tissue by the homopterous Cicadellidae. The forewing-metascutal locking mechanism varies in fine structure of microtrichia and density and size of microtrichiate patches. Metascutal patches in some taxa are fused, forming composite microtrichia. The size and form of the metascutum is compared with size of the microtrichiate patches.



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## Evolutionary patterns of lepidopteran wing scale shapes in a quantitative morphospace

15:00  
15:25

**APRIL DINWIDDIE<sup>1,2</sup>, VINCENT BONHOMME<sup>3</sup>, ELISABETH FORRESTEL<sup>1,4</sup> & RICHARD PRUM<sup>1</sup>**

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<sup>4</sup> Arnold Arboretum of Harvard University, Cambridge, MA 02130, USA

We present the first comprehensive morphospace of the shapes of lepidopteran wing scales, and we connect morphological diversity in scale shapes to phylogenetic relationships within the Lepidoptera. The architectural complexity of wing scale shapes and colors arises from variation in the developmental program of just a single cell type. Significant advances have been made in understanding the developmental mechanisms that generate lepidopteran wing pattern diversity, but very little is understood about the causes or correlates of the diversity of scale shapes. The morphospace represents the shapes of 5250 wing scales from 132 species in 39 families that range across the Lepidoptera. It was prepared through Elliptic Fourier analysis on closed outlines. Using a Bayesian phylogeny, we find that, in certain clades, both the morphospace position and volume of convex hulls correlate with the phylogeny. We also assess differences in the amount of morphospace that each species occupies, and identify instances of evolutionary convergence and the appearance of novel shapes. Our morphospace reveals constraints of variation in the shapes of wing scales, and we find that only a few lepidopteran groups have substantially expanded the realized shape space into new territory. Lastly, we connect certain scale shape features (e.g. scale width, scale length, and number of finger-like projections) to processes occurring during scale cell development.



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15:45  
16:10

## Musculature and movements of the genitalia of *Anania hortulata* (Pyraloidea: Crambidae)

**FRANCESCA VEGLIANTE**

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Following investigations on the mechanical fit of the external genitalia in copulating pairs of *Anania hortulata* (Linnaeus, 1758) (Vegliante & Nuss 2013), the musculature of the male and female genitalia was studied in order to gain a better understanding of their movements. No obvious abductor muscles of the valvae were found, although the male must open the valvae in order to grasp the female's abdomen for copulation. Moreover, a rotation of the female's lamella antevaginalis by 165° towards the male is needed for copulation, but the only muscles which could directly operate it are weak and not present in all specimens. Manipulation experiments on anesthetized and dead specimens, together with observations on pre-copulatory genitalia displays by males and on "calling" and oviposition by females, helped in solving these questions. Apparently, a contraction of the elevator muscle of the juxta and a local increase in haemolymph pressure are both needed to produce a sufficient abduction of the valvae for copulation. Moreover, the female could rotate the lamella antevaginalis by contracting the protractor muscles of the anterior apophyses while keeping contracted the muscles connecting the lamella postvaginalis to the dorsal plate of the 8th abdominal segment.

An interesting collateral finding of this study is that the last pair of alary muscles of the female originates on the anterior apophyses. This suggests an at least partially tergal origin of these apodemes.

### Reference

Vegliante, F. & Nuss, M. 2013: Copulatory mechanism of *Anania hortulata* (Pyraloidea: Crambidae). – Pp. 89–90, in XVIII European Congress of Lepidopterology. Programme and Abstracts. 29 July–4 August 2013, Blagoevgrad, Bulgaria. – Pensoft, Sofia.



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## Light trapping Lepidoptera at the top of the Zoological Museum in Copenhagen

16:10  
16:35

**OLE KARSHOLT & NIELS PEDER KRISTENSEN (†)**

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Collecting of night flying insects was carried out with an automatically working light trap at the roof of the Zoological Museum in Copenhagen. The trap was a modified Robinson trap armed with a 250 W mercury vapor bulb, and as a killing agent tetra-chlorethane was used. The trap worked around 4,500 nights from April to November during the years 1992 to 2009. All Lepidoptera was identified to species, counted and written into a data file.

The trap was placed on an east-facing roof at the museum building in an altitude of 17.5 meter above ground level, viz. above most surrounding buildings and trees. The museum is situated c. 3 km from the center of Copenhagen.

During the trapping period 218,161 specimens, representing 1,063 species were caught, which is 42% of Danish lepidopterous fauna. The tree most common species was *Yponomeuta evonymella* with 39,662 specimens, *Agrotis exclamations* with 13,136 specimens and *Yponomeuta padella* with 13,114 specimens. Contrary, a number of species was only found in one specimen.

The species composition indicated that the majority of species in the light trap were attracted from the nearest surroundings in and around Copenhagen, but also included a number of species living in habitats at least 10 km away and most likely further. Thus, the trap caught several species of Lepidoptera whose larvae are monophagous on plants not growing in the near vicinity, e.g. *Monochroa tetragonella* on *Glaux maritima*, *Scrobipalpa stangei* and *Gynnidomorpha vectisana* on *Triglochin maritimum*, *Phiaris metallicana* on *Vaccinium uliginosum* and *Lycophotia porphyrea* on *Calluna vulgaris*. Beside these more or less local migrants the trap also captured several migrating species, which cannot survive the winter in Denmark, and must have arrived from more southern countries. These include *Etiella zinckenella*, *Palpita vitrealis*, *Euchromius ocella*, *Agrius convolvuli* and *Protoschinia scutosa*.

Six species, *Stigmella stettinensis*, *Macrosaccus robinella*, *Diploseustis perieresalis*, *Oegoconia novimundi*, *Gelechia sestertiella* and *Aglossa caprealis* were recorded for the first time in Denmark during this study. Established Danish populations of the three latter have later been confirmed.

The registration of all families of Lepidoptera from a permanent light trap in such a large time span is rather unique, and the present dataset has potential for monitoring fluctuations in single species or larger groups of species, and to compare such changes with e.g. data on climate.





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16:35  
17:00

## The setae of parasitic *Liphyra brassolis* butterfly larvae form a flexible armour for resisting attack by their ant hosts (Lycaenidae)

STEEN. T. DUPONT<sup>1</sup>, DANNY. S. ZEMEITAT<sup>2</sup>, DAVID. J. LOHMAN<sup>3</sup> & NAOMI.E. PIERCE<sup>4</sup>

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This talk is dedicated to the memory of our good friend and mentor, Niels Peder Kristensen, who first suggested that we work together on this fascinating topic.

Caterpillars of the lycaenid butterfly *Liphyra brassolis* live inside the nests of arboreal weaver ants, *Oecophylla smaragdina*, and eat their brood. Observations of mature larvae suggest they are impervious to relentless ant molestation, yet they lack sclerotized cuticular plates. Observations of mature and early instar larvae reveal a novel defensive mechanism along with a number of unique setae, pore structures and antennal morphology. The unique cuticle is covered with lanceolate setae, which act as endocuticular struts, and overlapping scale-like sockets, which form a hard, flexible integument.

The imperfect armour of the early instar larvae suggests that abundant, putatively secretory pores are likely to be homologous to pore cupolae organs (PCOs) found in other lycaenid larvae, and thus may exude semiochemicals to allay ant aggression. The importance of these pores presumably wanes as structural (setal) cuticular defenses are reinforced in later instars, when adult ants have been observed attacking caterpillars to no avail.



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## Niels Kristensen from my perspective

17:00

17:25

**JADRANKA ROTA**

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In addition to Niels Kristensen influencing my development as a lepidopterist through his numerous published works, in the last years of his life, he also directly affected both my professional and personal life. We co-authored only four papers while I was a postdoc in Copenhagen and in the years since then (a short note on thoraco-abdominal articulation of Millieriidae; an extensive publication on the head structure of *Acanthopteroctetes unifascia*; a description of a new family of microlepidopterans – Aenigmatineidae; and a molecular phylogeny of non-ditrysians together with the US LepTree), but several other projects – which will now never be completed – were being planned. In this presentation I will briefly present our co-authored projects and then mainly focus on my personal view of Niels Kristensen.



Tuesday • 29 September 2015

## Keynote

9:00  
9:45

### New developments in understanding the biology of Mesozoic Lepidoptera

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Lepidoptera are a hyperdiverse order of insects with the most deficient taxic fossil record of any other hyperdiverse insect lineage (Hemiptera, Coleoptera, Diptera, Hymenoptera). This depauperate legacy is attributable to their fragile nature and occurrence in environments lacking significant preservational potential. However, during the last five years, paleobiological studies of Mesozoic moths and re-examinations of modern basal moth lineages have provided major insights into early lepidopteran ecology and evolution. For this half-decade, two, new, early-appearing, glossate families have been established, the monotypic Aenigmatineidae and Tridentaformidae, in addition to the new, basal mandibulate families, the Mesokristenseniidae and Ascololepidopterygidae. Together with the earlier described Archaeolepidae and Eolepidopterygidae, these four families consist of 14 genera and 21 species, but more importantly reveal considerable morphological detail. Newly documented features include wing-coupling devices, robust penicillate wing setae socketed on major veins, wing scales, mouthpart specializations such as distinctive mandibular teeth and probable siphonate glossae, and modifications of the genitalia. In addition, fossil leaf-mine data suggest that early moths may have been leaf miners on ferns. These data originate from moth fossils occurring in East Eurasian deposits, from oldest to youngest: the Jiulongshan Formation of northeastern China, of latest Middle Jurassic (late Callovian) age, radioisotopically age-dated to 165 Ma; the Karabastau Formation of southernmost Kazakhstan, of Late Jurassic (probably Kimmeridgian) age, approximating 155 Ma; and Burmese Amber of northern Myanmar, of latest Early Cretaceous (late Albian) age, correlated to ca. 102 Ma. Collectively, these discoveries provide a deep-time perspective into early lepidopteran evolution that document considerable more structural variety than formerly assumed or known.



Tuesday • 29 September 2015

## Can fossils help us understand the paleobiogeography of the butterflies?

9:45  
10:00

**RIENK DE JONG**

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The impact of fossils on understanding the paleobiogeography of fossil-rich groups like Mammalia is well documented. For instance, it is unlikely that we would ever have dreamed of a North American origin of the genus *Equus* based on the distribution of extant species only, which are confined to the Old World. Butterfly fossils are, however, extremely rare. Compared to the *ca* 16.000 extant species of butterflies (three times as many as the entire class of Mammalia), the number of recognizable fossil butterfly species is, with *ca* 43, almost negligible. In this presentation the use of these fossils is examined for elucidating former distributions of butterflies, and with that the possible impact on evolution.

Fossils can help understand paleobiogeography in a direct and an indirect way. In a direct way their presence testifies of the occurrence of the taxon at a particular time in a particular place. In the case of the horses, this can be very surprising. But if the fossil is found in the general area where the extant higher taxon the fossil belongs to occurs, we only learn that the higher taxon has been there at least since the time the fossil was formed. In an indirect way, fossils can be used for calibrating the molecular clock of a phylogenetic tree, i.e. setting dates at splitting points of lineages which, combined with knowledge of the paleocontinental world, can possibly help understand how a particular distribution came about, or why taxa are distributed as they are nowadays.

Finally, the author will express his personal view of the biogeographic evolution in the early part of the butterfly lineage and compare it with paleobiogeography of late Cretaceous and Cenozoic Mammalia.



Tuesday • 29 September 2015

10:00  
10:15

## Coding characters from fossil butterflies for direct inference of times of divergence in Nymphalini

**ZDENEK FALTYNEK FRIC<sup>1</sup> & NIKLAS WAHLBERG<sup>2</sup>**

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Fossil records are indices of permanent changes in the past. They are important for interpretation as well as for verification of present phylogenetic hypotheses. Dating of fossil records is a key to understanding of evolutionary processes leading to current biota. However, fossil records of Lepidoptera and especially butterflies are very fragmentary. Sohn et al. (2012) presented review of fossil Lepidoptera. They showed that only few fossil records of butterflies are currently known, predominantly from the family Nymphalidae. 79 % of butterfly fossils are compression/impression fossils, and about 10 % are from amber or copal. Their ages range between the Late Paleocene and Holocene with one peak in the Late Eocene and another peak around the Oligocene-Miocene boundary.

The fragmented nature of butterfly fossils prevents their use for the inference of detailed phylogeny hypotheses. All known butterfly fossils are too old for DNA to have been preserved. However, as some of the fossils are of high quality, they can be used in a morphological study of extant taxa. In our analyses of Nymphalini, we used two fossil species, *Prodryas persephone* and *Vanessa amerindica*. The position of the first species is unresolved or basal to *Vanessa/Hyparantia/Nymphalis* clade, the second species belongs to *Vanessa cardui* group. The age of the common ancestor of *Vanessa/Hyparantia/Nymphalis* is thus older than 34 mya. The pattern is congruent with previous age estimates without direct inclusion of the fossils.



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## Critiques and new hope on divergence time estimation of Lepidoptera

10:15  
10:30

JAE-CHEON SOHN<sup>1,2,3,4</sup>, **MARIA HEIKKILÄ**<sup>2,3</sup>, CHARLES MITTER<sup>1</sup>, MICHAEL CUMMINGS<sup>5</sup>, DONALD DAVIS<sup>2</sup>, CONRAD LABANDEIRA<sup>3</sup> & CARMEN SORIANO<sup>6</sup>

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Lepidoptera are one of the most diverse phytophagous insect groups. In spite of their importance in terrestrial ecosystems, the evolutionary history of the Lepidoptera remains poorly known. Divergence time estimation over a robust phylogeny is a prerequisite for understanding their evolutionary biology. Recent empirical studies have found that molecular dating analyses are critically affected by the number and temporal distribution of fossil calibration points, the interpretation of relationships between fossil and extant taxa, and how fossil constraints are treated. Confident dating thus requires multiple fossils that are securely identified and of sufficient age. These requirements are often difficult to meet for the depauperate lepidopteran fossil record. There have been only a few attempts to date the molecular phylogeny for the entire Lepidoptera or a few subgroups, notably butterflies. Our aim is to review the fossils and the calibration methods used in previous molecular dating studies of Lepidoptera and evaluate the results under the constraint of reliable dating. We will re-examine several fossils with proposed phylogenetic affinities and look for synapomorphies confirming their identification. We aim to compose a list of lepidopteran fossils potentially useful as calibration points, and use these fossils for dating the current working hypothesis on the phylogeny of Lepidoptera. In our presentation we will show microtomographic images for some lepidopteran fossils we are currently working on.



Tuesday • 29 September 2015

10:30  
10:45

## Notes on Microlepidoptera in Baltic amber and description of an extinct tortricid species (Tortricidae)

**WOLFRAM MEY & HANS BLACKSTEIN**

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In comparison with the other megadiverse insect orders Diptera, Hymenoptera and Coleoptera, the fossil record of Lepidoptera in Baltic amber is extremely poor. One of the reasons is the unfavorable posture of the majority of specimens, which prevent the observation of diagnostic characters. Identification and naming amber species is therefore difficult, and the determination process usually ends up at the family or even at the superfamily level. Moths with outstretched wings and visible genitalia and head structures allow a more precise identification, but they are rarely encountered. The discovery of one of those moths prompted us to get the species identified. The species turned out to belong to the family Tortricidae, which has six named species in Baltic amber. The fossil is described and documented in detail, and its systematic position within the subfamily Chlitanotinae is discussed.





Tuesday • 29 September 2015

## Keynote

### Cornucopia or Pandora's Box? Phylogenomics comes of age, data are no longer limiting

11:05

11:35

**NIKLAS WAHLBERG**<sup>1,2</sup>, **CARLOS PEÑA**<sup>1</sup> & **CHRIS WHEAT**<sup>3</sup>

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In the past couple of years it has become routine to generate transcriptomic or genomic data for various questions, including resolving the relationships of taxa. The term phylogenomics was coined about 10 years ago for studies using a large number of molecular markers in phylogenetics. The definition of “large number” has increased from tens to hundreds or thousands of genes in the last few years. It appears that data is no longer limiting. But still, different phylogenomic datasets produce different phylogenetic hypotheses, despite huge numbers of genes. Phylogenomic datasets have in effect become black boxes where we have no idea what genes are being analyzed. We use almost all published transcriptomes of Lepidoptera (144 species) to search for a panel of protein coding genes that are widely expressed in lepidopteran tissues of any origin and assess their phylogenetic utility. We found 333 genes that are widely expressed and easy to align by eye at the amino acid level. A phylogenetic hypothesis is presented based on these genes and their use in various subclades of Lepidoptera is discussed.



Tuesday • 29 September 2015

11:35  
12:05

## The oldest lineages of extant Lepidoptera: phylogeny, classification, and life history evolution

**ERIK J. VAN NIEUKERKEN<sup>1</sup>**

On behalf of the LepTree consortium: Jerome C. Regier, Charles Mitter, † Niels P. Kristensen, Erik J. van Nieukerken, Donald R. Davis, Jadranka Rota, Thomas J. Simonsen, Kim T. Mitter, Akito Y. Kawahara, Shen-Horn Yen, Michael P. Cummings & Andreas Zwick

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The recently published molecular phylogeny of the so-called non-ditrysian superfamilies in Systematic Entomology is discussed and illustrated with examples. We tested previous hypotheses of non-ditrysian phylogeny against a data set consisting of 61 non-ditrysian species plus 20 representative Ditrysia and eight outgroups (Trichoptera), nearly all sequenced for 19 nuclear genes (up to 14,700 bp total). The major conclusions are as follows: There is very strong support for Lepidoptera minus Micropterigidae and Agathiphagidae, here termed Angiospermivora, but no definitive resolution of the position of Agathiphagidae. There is very strong support for Glossata, which excludes Heterobathmiidae, but weak support for relationships among major homoneurous clades. Eriocraniidae diverge first, corroborating the morphological clade Coelolepida, but the morphological clades Myoglossata and Neolepidoptera are never monophyletic; both are contradicted by strong support for Lophocoronoidea + Hepialoidea, the latter here including Mnesarchaeoidea. The surprising grouping of Acanthopteroctetidae + Neopseustidae (+Aenigmatidae), is consistent with the recent molecular study on Aenigmatidae. Heteroneura is very strongly supported, as is a basal split of this clade into Nepticuloidea + Eulepidoptera. Relationships within Nepticuloidea accord closely with recent studies based on fewer genes but many more taxa. Eulepidoptera are split into a very strongly supported clade consisting of Tischeriidae + Palaephatidae + Ditrysia, termed Euheteroneura, and a moderately supported clade uniting Andesianidae with Adeloidea. Relationships within Adeloidea are strongly resolved and include the new family Tridentaformidae. Within Euheteroneura, the molecular evidence is conflicting with respect to the sister group to Ditrysia, but strongly supports paraphyly of Palaephatidae. Life histories and larval feeding habits are reviewed and the implications for hypotheses about early lepidopteran phytophagy are assessed. We present evidence of the previously unknown life history of Neopseustidae, which suggests that larvae of this family may be parasitoids.



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## Deep intraspecific barcode splits in Lepidoptera: signs of cryptic diversity or *Wolbachia*-driven distraction?

12:05  
12:35

JONNA HÄNNINEN & MARKO MUTANEN

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Many studies of DNA barcodes of Lepidoptera have revealed extraordinary intraspecific variation in mitochondrial DNA in some species. Sometimes this variation is highly clustered so that a species shows a deep intraspecific split in mtDNA with no intermediates. Along with building a complete reference library for ~ 2600 species of Finnish Lepidoptera, about 150 such deep splits were shown up. In order to investigate the presence of cryptic species, we sequenced six taxonomically informative nuclear genes (*EF-1a*, *MDH*, *CAD*, *IDH*, *RpS5* and *wingless*) in 29 lepidopteran species, each having a deep (> 2 %) sympatric intraspecific split in the DNA barcode region. The results suggest that some, but only a minority of splits are due to the presence of a previously undetected morphologically cryptic species. *Wolbachia* infection was detected in most species and many splits may be explained by *Wolbachia*-driven spread of an alien mitochondrial haplotype in the population followed by mitochondrial introgression. Overall, our results support the previous findings that DNA barcodes have great potential in revealing new species even among well-investigated groups and areas, but also reveal the high importance of *Wolbachia* screening in such cases.



Tuesday • 29 September 2015

13:35  
13:55

## The promise of ddRAD-Seq in lepidopteran phylogenetics: a case study using *Eupithecia* (Geometridae) as a model group

KYUNG MIN LEE<sup>1</sup>, AXEL HAUSMANN<sup>2</sup>, NIKLAS WAHLBERG<sup>3</sup>, VLADISLAV IVANOV<sup>1</sup> & MARKO MUTANEN<sup>1</sup>

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The order Lepidoptera (butterflies and moths) is one of the most species-rich groups of organisms, containing 500K species estimated world-wide. Phylogenetic affinities of many major lepidopteran groups have been intensively studied with molecular tools during the last decade. *Eupithecia*, with hundreds of described species, is one of the most species-rich genera of the looper moths (Geometridae), but the phylogenetic relationships within this genus have not been studied yet using molecular data. Here, we used next-generation sequencing based double digest Restriction site Associated DNA (ddRAD) methods and separately a set of eight genes by traditional Sanger sequencing of both nuclear (CAD, EF1 $\alpha$ , GAPDH, IDH, MDH, RpS5, wingless) and mitochondrial (COI) markers to construct phylogenetic trees of 35 species of the genus *Eupithecia*. The ddRAD provided a data of 726,658 base pairs data against the 6,172 base pairs by Sanger sequencing. In this case study, we demonstrated the high potential of RAD-Seq in Lepidoptera phylogenetics which enables the collection of huge amounts of data. Thus, RAD-Seq appears to hold promise for taxonomic studies even in genus level. By comparing the phylogenies of RAD-Seq and concatenated nrDNA+mtDNA, we showed some incongruence: these observations may suggest that processes that can cause gene tree heterogeneity, such as incomplete lineage sorting and horizontal gene transfer, may be involved.



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## Elusive ditrysian phylogeny – from Kristensen & Skalski 1998 to sequence data and systematized morphology

13:55

14:15

MARIA HEIKKILÄ<sup>1</sup>, MARKO MUTANEN<sup>2</sup>, NIKLAS WAHLBERG<sup>3</sup>, PASI SIHVONEN<sup>4</sup> & LAURI KAILA<sup>5</sup>

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The morphology of ditrysian Lepidoptera (ca. 99% of all moths and butterflies) has been claimed to be homogenous and offer little clues about the superfamilial affinities within this group. However, previous inferences were based on a limited amount of morphological characters, were not systematically examined across all ditrysian superfamilies and families, and were not analyzed using phylogenetic methods. To test the claimed lack of informative morphological characters, validity of previously proposed characters, and hypotheses based on sequence data, we constructed and analyzed the most comprehensive morphological dataset on Ditrysia to date. The dataset includes over 500 characters examined from larvae, pupae and adult males and females representing most ditrysian families and subfamilies. These data are analyzed alone and combined with sequence data from eight gene regions. Data from 473 taxa makes our dataset one of the largest taxon samplings in phylogenetic studies on Ditrysia to date.

Our results indicate that morphological characters are informative at the family and subfamily level, and that characters indicating affinities between larger assemblages of superfamilies are indeed scarce. Previously proposed characters for the subclades Apoditrysia and Obtectomera are supported with some provision. By systematically examining characters across Ditrysia we were able to obtain a better picture of the distribution of characters, assess the uniqueness of certain structures, and find new diagnostic characters for some clades. The phylogenetic positions suggested by morphological characters for certain taxa seem to be more stable than those based on molecular data. The multiple uses of the morphological dataset are also discussed.



Tuesday • 29 September 2015

14:15  
14:30

## The molecular-morphological phylogeny of megadiverse Spilomelinae (Pyraloidea: Crambidae)

**RICHARD MALLY<sup>1</sup>**, CHRISTOPH NEINHUIS<sup>2</sup> & MATTHIAS NUSS<sup>3</sup>

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



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## Unravelling the phylogeny of Crambinae, Heliothelinae and Scopariinae (Pyraloidea)

14:30  
14:45

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A molecular analysis on the phylogeny of the megadiverse snout moths (Pyraloidea) by Regier et al. (2012) largely resolved the relationships among the two pyraloid families and 15 of its subfamilies. Crambinae and Scopariinae have been discovered as sister groups. Since that finding was based on only five terminal taxa from these two groups, it raises a number of questions, especially whether the two groups remain monophyletic under the analysis of a larger taxon sample and whether the current generic and tribal classifications reflect natural relationships. The monophyly of the Heliothelinae has been debated; some authors placed it in Scopariinae, but it has never been included in a molecular analysis. Larvae of Crambinae are generally known to feed on grasses and some species are pests of economic importance. Also, the larvae of some species of Scopariinae and Crambinae are known to feed on mosses, which is a very rare habit in the animal kingdom. Currently, we are analysing the phylogeny of the three groups using a molecular dataset of the four nuclear genes GAPDH, IDH, MDH and rps5. At present the results confirm the monophyly of Crambinae and Scopariinae as well as their sister-group relationship. In contrast, Heliothelinae are poly- or paraphyletic depending on different analysis methods. The evolution of the moss-feeding habit will be discussed. Further, the current classification will be compared with the results of our analysis and possible nomenclatural changes debated.

### Reference

Regier, J. C., C. Mitter, M. A. Solis, J. E. Hayden, B. Landry, M. Nuss, T. J. Simonsen, S.-H. Yen, A. Zwick & M. P. Cummings 2012: A molecular phylogeny for the pyraloid moths (Lepidoptera: Pyraloidea) and its implications for higher-level classification. – *Systematic Entomology*, London **37** (4): 635 – 656.



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14:45  
15:00

## To hear, or not to hear, that is the question in basal Pyralidae (Pyraloidea)

FRANZISKA BAUER & MATTHIAS NUSS

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The abdominal tympanal organ is regarded as an autapomorphy of Pyraloidea. It detects the ultrasounds of mating partners as well as of echolocating insectivorous bats. Distinct character states in this organ are used to argue for a basal dichotomy in Pyraloidea, leading to the current classification into Pyralidae and Crambidae. The lack of the tympanal organ has been recorded for very few pyraloid species only, namely in *Lathroteles* from Rapa Island (1 species), *Helenoscoparia* (5 sp.) and *Zovax* (1 sp.) from St. Helena, *Exsilirarcha* from Campbell I., New Zealand (1 sp.), *Protyparcha* from Auckland I., New Zealand (1 sp., female only) and *Michaelshaffera* (2 sp.) from tropical South America. In species of *Lathroteles*, *Helenoscoparia* and *Zovax*, the tympanal organ is reduced. This is explained by the absence of insectivorous bats on the oceanic islands where these moths occur, rendering their tympanal organs unnecessary. *Exsilirarcha* and *Protyparcha* have reduced wings, which is correlated with tympanal organ reduction. Neither of these scenarios can be applied to *Michaelshaffera*, whose lack of the tympanal organ has so far been regarded as a secondary absence as well. We conducted a phylogenetic analysis based on one dried specimen of *M. maidoa* from Bolivia, for which seven gene regions were sequenced and combined with a previously published dataset for a broad sampling across major lepidopteran lineages. Our results confirm *M. maidoa*'s affiliation to Pyraloidea, but reveal it to be sister to all remaining pyralids. This phylogentic position implies that the lack of a tympanal organ in *Michaelshaffera* is ambiguous. Considering the morphological differences of tympanal organs in Crambidae and Pyralidae, it could even be primary. Moreover, a reduction of a moth ear in the Amazon rain forest, where insectivorous bats are present, is barely plausible. Our findings should be tested with a much broader gene sampling in order to receive more robust evidence for the basal relationships within Pyraloidea and to test another possible scenario of *Michaelshaffera* being sister to all other pyraloids.





Tuesday • 29 September 2015

## Butterflies of ancient Egypt

**VAZRICK NAZARI<sup>1</sup> & LINDA EVANS<sup>2</sup>**

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A review of butterflies depicted in ancient Egyptian tomb scenes and other artefacts dating from the predynastic period (c. 3000 BCE) until the end of the pharaonic era (c. 100 BCE) reveals a wide spectrum of stylistic changes over time. A cladistic analysis shows relative consistency of style during the Old Kingdom period, copying of old styles during the Middle Kingdom period, and a deviation from tradition during the New Kingdom period. The utility of a cladistic approach in assigning dates and localities to ancient Egyptian artefacts with unknown origins is demonstrated. We discuss lepidopteran symbolism in ancient Egypt, and investigate how some of these depictions may highlight historical shifts in species ranges since pharaonic times.

**15:20**  
15:35



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15:35  
15:50

## Estimating the time of divergence in Coleophoridae based on the analysis of the COI gene

**VASILII V. ANIKIN<sup>1</sup>, A. G. DEMIN<sup>2</sup> & M. A. KNUSHEVITSKAYA<sup>1</sup>**

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Reconstruction of divergence time for the major taxa of Coleophoridae conducted by the authors demonstrated that casebearer moths are evolutionarily young, which may be due to an early evolution in a specific environment of grassland ecosystems during Eocene – Oligocene. Analysis of the evolutionary divergence of species indicates that the ancestors of modern taxa of Coleophorinae lived in the early Oligocene and probably were associated to herbaceous plants of Amaranthaceae, Fabaceae and Asteraceae. In general, the most active processes of speciation among casebearer moths took place in the second half of the Miocene, which may be due to the increasing diversity of habitats and active change of woody and herbaceous plant formations on the territory of the ancient Mediterranean in this historical period.



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## DNA Barcoding at the family level: Considering the Gelechioidea

15:50  
16:05

**MARI KEKKONEN**

Biodiversity Institute of Ontario, University of Guelph, 50 Stone Road East, Guelph, ON, Canada N1G 2W1; [kekkonen@uoguelph.ca](mailto:kekkonen@uoguelph.ca)

Although DNA barcoding is mainly a tool for specimen identification, it has increasingly been employed for species discovery and delineation. Several ongoing bio-assessment programs are now producing very large numbers of barcodes that have been assigned to putative species through the Barcode Index Number (BIN) system on BOLD. Many of these BINs are currently only assigned to an order, but the capacity to automatically generate a family-level assignment for these taxa would greatly aid subsequent taxonomic work on them. For this reason, studies are needed to ascertain the ability of DNA barcodes to provide family-level assignments.

The Gelechioidea is one of the most diverse lepidopteran groups; it includes over 18,000 described species. However, it is also one of the least studied superfamilies. Even family-level assignment of gelechioids can be challenging due to their diversity, small size and the lack of diagnostic external characters. My presentation will consider the cohesiveness of the 16 gelechioid families *sensu* Heikkilä *et al.* (2014) on DNA barcode gene trees. In addition, I will discuss the opportunities and challenges of family-level barcoding from a wider perspective.



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16:05  
16:20

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

KATJA RÖNKÄ<sup>1</sup>, JOHANNA MAPPES<sup>1</sup> & NIKLAS WAHLBERG<sup>2,3</sup>

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In order to study the evolutionary history of phenotypic features observed in current organisms, such as the spectacular warning signal coloration of arctiine moths, complete phylogenies on multiple levels are inevitably needed. 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* (Lepidoptera: Noctuoidea: Erebiidae: Arctiinae). To this end we sampled 100 species in 52 genera that were considered to be closely related to *Parasemia*. The phylogeny is based on eight gene regions including one mitochondrial (COI barcode region) and seven nuclear protein-coding gene fragments: elongation factor 1- $\alpha$  protein, wingless, ribosomal protein subunit S5, carbamoylphosphate synthase domain regions, glyceraldehyde-3-phosphate dehydrogenase, isocitrate dehydrogenase and cytosolic malate dehydrogenase. We analyzed the DNA sequence data using both maximum likelihood (ML) and Bayesian inference (BI). The phylogeny is then further used to study the evolutionary history of polymorphic warning signal coloration in *P. plantaginis*.



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## Phylogeography of the *Hyles euphorbiae* complex (Lepidoptera: Sphingidae) – Diverse patterns of admixture between an African and Eurasian evolutionary lineage

16:20  
16:35

MICHAEL B. MENDE, HEIKO STUCKAS, MANUELA BARTEL & ANNA K. HUNSDOERFER

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Widespread species complexes offer unique opportunities to gain insights into the formation of phylogeographic patterns and thus the very origin of species. Based on colour pattern morphotypes, it has been hypothesised that the Western Palaearctic spurge hawkmoths are divided into two main evolutionary entities, the Eurasian *H. euphorbiae* and Afro-Macaronesian *H. tithymali*, which merged into several hybrid swarm populations. However, a mitochondrial phylogeography (about 2300bp of COI/II) suggested more local differentiation. We strongly augmented this previous dataset to about 900 specimens and assessed nuclear population structure by means of 12 microsatellite loci. Nuclear genetic analyses corroborate the superordinate division into two entities but also revealed an overall weak differentiation and/or indications for range-wide gene flow. A mitochondrial polymorphism retained in *H. euphorbiae* indicates incomplete mitochondrial lineage sorting and pervasive historic admixture of the entities. Large areas in the Mediterranean and the Middle East show diverse patterns of probably more recent admixture in one or both markers and/or mito-nuclear discordance. The latter indicates massive introgressions of *tithymali*-related mtDNA into the Italian and Aegean *H. euphorbiae* populations which possibly even gained a distinct evolutionary identity due to a parallel minor introgression of nuclear alleles. This complex patchwork of divergence and reintegration is assumed to have been mainly influenced by permeable barriers to gene flow, such as the Mediterranean Sea and environmental variables.



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16:35  
16:50

## The unique sound production of the Death's head Hawkmoth (*Acherontia atropos* (Linnaeus, 1758)) revisited

**GUNNAR BREHM**<sup>1</sup>, MARTIN FISCHER<sup>2</sup>, STANISLAV GORB<sup>3</sup>, THOMAS KLEINTEICH<sup>3</sup>,  
BERNHARD KÜHN<sup>2</sup>, DAVID NEUBERT<sup>1</sup>, HANS POHL<sup>1</sup>, BENJAMIN WIPFLER<sup>1</sup> &  
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<sup>2</sup> Ernst-Abbe-Hochschule Jena, Germany

<sup>3</sup> Functional Morphology and Biomechanics, Kiel University, Germany

<sup>4</sup> Universitätsklinikum Jena, Germany

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\* List of coauthors in alphabetical order

When disturbed, adults of the Death's-head Hawkmoth (Sphingidae: *Acherontia atropos*) produce short squeaks by drawing in and deflating air into and out of the pharynx as a defence mechanism. We took a new look at Prell's hypothesis of a two phase mechanism by providing new insights into the functional morphology behind the pharyngeal sound production of this species. First, we compared the head anatomy of *A. atropos* with another sphingid species, *Manduca sexta*, by using micro computed tomography (CT) and 3D reconstruction methods. Despite differences in feeding behaviour and capability of sound production in the two species, the musculature in the head is surprisingly similar. However, *A. atropos* has a much shorter proboscis and a modified epipharynx with a distinct sclerotised lobe projecting into the opening of the pharynx. Second, we observed the sound production in vivo with X-ray videography, mammography CT, and high speed videography. Third, we analysed acoustic pressure over time and spectral frequency composition of six *A. atropos* specimens, both intact and with a removed proboscis. Single squeaks of *A. atropos* last for ca. 200 ms and consist of an inflation phase, a short pause and a deflation phase. The inflation phase is characterised by a burst of ca. 50 pulses with decreasing pulse frequency and a major frequency peak at ca. 8 kHz, followed by harmonics ranging up to more than 60 kHz. The deflation phase is characterised by a less clear acoustic pattern, a lower amplitude and more pronounced peaks in the same frequency range. The removal of the proboscis resulted in a significantly shortened squeak, a lower acoustic pressure level, and a slightly more limited frequency spectrum. We hypothesize that the uptake of viscous honey facilitated the evolution of an efficient valve at the opening of the pharynx (i.e. a modified epipharynx), and that sound production could relatively easily have evolved based on this morphological pre-adaptation.



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## Moth tails divert bat attack: Evolution of acoustic deflection

16:50  
17:20

**AKITO KAWAHARA**, BRIAN C. LEAVELL<sup>2</sup>, ADAM L. KEENER<sup>2</sup>, JESSE W. BREINHOLT<sup>1</sup>,  
BRAD A. CHADWELL<sup>2</sup>, CHRISTOPHER MCCLURE<sup>2</sup>, GEENA M. HILL<sup>1</sup> & JESSE BARBER<sup>2</sup>

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Adaptations to divert the attacks of visually guided predators have evolved repeatedly in animals. Using high-speed infrared videography, we show that luna moths (*Actias luna*) generate an acoustic diversion with spinning hindwing tails to deflect echolocating bat attacks away from their body and toward these non-essential appendages. We pit luna moths against big brown bats (*Eptesicus fuscus*) and demonstrate a survival advantage of ~47% for moths with tails versus those that had their tails removed. The benefit of hindwing tails is equivalent to the advantage conferred to moths by bat-detecting ears. Moth tails lured bat attacks to these wing regions during 55% of interactions between bats and intact luna moths. We analyzed flight kinematics of moths with and without hindwing tails and suggest that tails have a minimal role in flight performance. Using a robust phylogeny, we find that long spatulate tails have independently evolved four times in saturniid moths, further supporting the selective advantage of this anti-bat strategy. Diversionary tactics are perhaps more common than appreciated in predator-prey interactions. Our finding suggests that focusing on the sensory ecologies of key predators will reveal such countermeasures in prey.



Wednesday · 30 September 2015

## Keynote

9:00  
9:40

### Local versus regional networks of phytochemically mediated plant-caterpillar-parasitoid interactions

**LEE A. DYER**, NICK PARDIKES, WILL LUMPKIN, LORA A. RICHARDS, ANGELA M. SMILANICH & MATT FORISTER

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The devaluation of natural history and taxonomy has added to the failure of ecologists to document biodiversity and subsequently to understand the consequences of the growing extinctions caused by global change. Natural history is especially important for understanding networks of interactions between organisms. Phytochemical interaction diversity is one metric derived from well characterized networks; it is the number and relative abundance of chemically mediated interactions linking species together into communities. This interaction diversity is affected by taxonomic diversity as well as ecological specialization and it is very dependent on the scale at which it is measured. Using results from models, observational data, and experiments, we demonstrate that interaction diversity measured at the large scales that are utilized for most food webs are misleading and not relevant to local community processes. We also examine some mechanisms by which factors such as phytochemistry, parasites, and pathogens affect interaction and species diversity at different scales.





Wednesday · 30 September 2015

## Keynote

### How milkweed butterflies (Danaini) tolerate and use plant toxins: evolution of resistance and sequestration

9:40  
10:20

**GEORG PETSCHENKA**

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In the course of evolution plants developed a huge array of plant toxins to defend themselves against phytophagous insects. In turn, insects evolved counterstrategies to cope with plant defensive compounds. Remarkably, many insects can not only cope with plant toxins but also absorb and retain them in the body (sequestration) for their own benefit. Sequestration was first described in the monarch butterfly (*Danaus plexippus*) whose caterpillars store toxic milkweed cardenolides protecting the resulting butterfly from bird attacks. Cardenolides are specific inhibitors of  $\text{Na}^+/\text{K}^+$ -ATPase, an enzyme which is present in every animal cell. It is known that monarch butterflies have a modified  $\text{Na}^+/\text{K}^+$ -ATPase which has a high resistance against these toxins. We have shown that in the milkweed butterflies (Lepidoptera, Danaini) cardenolide resistance of  $\text{Na}^+/\text{K}^+$ -ATPase evolved in a step-wise manner. Basal genera of Danaini have an ancestral form of  $\text{Na}^+/\text{K}^+$ -ATPase which is highly susceptible to cardenolides. The sister genera *Danaus* and *Tirumala* share a derived form of  $\text{Na}^+/\text{K}^+$ -ATPase with an increased resistance to cardenolides and only the monarch butterfly and its closest relatives have a third form of  $\text{Na}^+/\text{K}^+$ -ATPase which is highly resistant to cardenolides. Recently, we have tested which selective pressures caused evolution of cardenolide resistant  $\text{Na}^+/\text{K}^+$ -ATPases and found that this adaptation is not necessary to cope with cardenolides in the diet. In contrast, our data indicate that modified  $\text{Na}^+/\text{K}^+$ -ATPase is essential to sequester cardenolides. Our findings thus suggest that not only the first trophic level (plants) but also the third trophic level (predators) can drive specific adaptations to host plant toxins which has implications for our understanding of how insect-host plant associations evolve.



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10:20  
10:45

## Evolution of the tripartite association between leaf-mining moths, *Wolbachia*, and their host plants

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Internally feeding herbivorous insects such as leaf-mining moths have developed the ability to manipulate the physiology of their host plants in a way to best meet their metabolic needs. For instance, some leaf-miners can induce green-islands on yellow leaves in autumn, which are characterized by photosynthetically active green patches in otherwise senescing leaves. It has been shown that endosymbionts, and most likely bacteria of the genus *Wolbachia*, play an important role in green-island induction in the apple leaf-mining moth *Phyllonorycter blancardella*. However it is currently not known how widespread is this moth-*Wolbachia*-plant interaction. Here we studied the co-occurrence between *Wolbachia* and the green-island phenotype in 74 species of Lepidoptera. Using a combination of molecular phylogenies and ecological data we show that the acquisitions of the green-island phenotype and *Wolbachia* infections have been associated through the evolutionary diversification of Gracillariidae. We also found intraspecific variability in both green-island formation and *Wolbachia* infection, with some species being able to form green islands without being infected by *Wolbachia*. In addition, *Wolbachia* variants belonging to both A and B supergroups were found to be associated with green-island phenotype suggesting several independent origins of green-island induction. We also reconstructed a multiple gene phylogeny for a complex of four closely related leaf-mining species feeding on apple. We found a strong correlation between the divergence of the four apple feeding species and the status of infection by *Wolbachia*.



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## Adaptive radiations and speciation rates in Holarctic lineages of leafmining Lepidoptera

11:05  
11:30

**CAMIEL DOORENWEERD, ERIK J. VAN NIEUKERKEN & CARLOS LOPEZ-VAAMONDE**

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Many Holarctic lineages of leafmining Lepidoptera have diversified on similar host plant families, most often including ecologically dominant families such as Fagaceae, Rosaceae and Salicaceae. It has been proposed that co-evolutionary dynamics with the hosts or increased speciation rates following a shift to a different host family have driven speciation in Holarctic groups of leafminers. To test this, we inferred species-level phylogenies for Tischeriidae, the graciariid subfamily Lithocolletinae, and the nepticulid subgenus *Ectoedemia*, using eight genetic markers, and subsequently used fossil and secondary calibration points to estimate the timing of diversification. We used maximum likelihood approximations to estimate the ancestral shifts to a different host family, and tested for changes in the rate of speciation throughout the phylogenies. We found that shifts to particular families appear to be favoured within a certain time-frame, roughly coinciding with the emerging ecological dominance of those families. The large number of species feeding on certain plant families can best be explained by adaptive radiations, but we found no evidence for changing rates of speciation. Nonetheless, the speciation dynamics in the different groups of leafminers are strongly divergent, suggesting that there are likely important intrinsic (i.e. genetic) factors that also shape the evolution of these groups.



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## Keynote

11:30  
12:05

### Butterfly Monitoring across Europe

**CHRIS VAN SWAAY**

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Monitoring butterflies is one of the oldest examples of citizen science. The success of these schemes is due to many factors, not least that the techniques are easy to learn and the field work fun to do. The results of such schemes have proven invaluable in providing robust data on changes in butterfly populations in nature reserves, local areas, countries and even whole regions such as Europe.

Butterfly monitoring enjoys a growing popularity in Europe. Long time-series are now available for 22 countries: Armenia, Andorra, Belgium, Estonia, Finland, France, Germany, Ireland, Jersey, Lithuania, Luxembourg, Norway, Portugal, Romania, Russia (Bryansk region), Slovenia, Spain, Sweden, Switzerland, The Netherlands, Ukraine (Transcarpathia) and the United Kingdom. Butterfly monitoring is based on the fieldwork of thousands of trained professional and volunteer recorders, counting butterflies on more than 3700 transects scattered widely across Europe. These counts are made under standardised conditions.

Well-designed butterfly monitoring programs make it possible to assess the trends of butterfly populations across time and space. This allows us to track population changes on a local scale as well as nationally, regionally, or globally. These trends can be used as indicators of biodiversity and environmental change.

#### Some examples of the use of Butterfly Monitoring:

- The European Grassland Butterfly Indicator, one of the EU biodiversity indicators of the European Environment Agency, is based on the trends of 17 characteristic grassland butterflies. The indicator shows that since 1990, grassland butterfly abundance has declined by 30%. The main driver behind the decline of grassland butterflies is the change in rural land use: agricultural intensification where the land is relatively flat and easy to cultivate; and abandonment in mountains and wet areas, mainly in Eastern and Southern Europe. It should be noted that the biggest loss of butterflies in the intensified grasslands of Western Europe occurred before the 1990s and therefore don't show up in the indicator.



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- The Climate Change Indicator uses the principle of the Climate Temperature Index (CTI): the average of each individual's temperature preference present in the butterfly assemblage. A high CTI would thus reflect a large proportion of species with a high STI, i.e. of more high-temperature dwelling species. This way, the CTI can be used to measure local changes in species composition. If climate warming favours species with a high STI, then the CTI should increase locally. Butterfly communities have shifted northwards by an equivalent of 114 km in 20 years, whereas the temporal trend in temperature has shifted north by 249 km, showing that butterflies are lagging significantly behind climate change.
- Relationships between butterflies and environmental indicators and the use of such relationships for environmental indicators. This will be illustrated with a nitrogen and moisture indicator.

At the moment we are in the process of expanding the guidelines for butterfly monitoring to tropical regions, e.g. by adding different protocols as fruit baiting. We hope to be able to produce a Global Butterfly Index in future, comparable with the Wild Bird Indicator.



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12:05  
12:30

## LIFE+ Blues in the Marshes – new habitat for *Maculinea* in The Netherlands

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In the Netherlands, the single population of the obligate myrmecophilic butterfly *Maculinea (Phengaris) teleius* occurs on only 3 ha of habitat, however at least 40 ha of habitat are required for a sustainable metapopulation. Therefore, 170 ha of farmland will be converted within a LIFE+ project. This involves top soil removal and hay inoculation, aiming not only on the establishment of wet meadow vegetation, but also on restoration of the ecosystem including the host ant, *Myrmica scabrinodis*, and its food source, springtails (Collembola). A field experiment has been conducted in formerly restored areas to investigate the colonization potential of ants and springtails after soil removal. Preliminary results indicate that *Myrmica* and Collembolan density, biomass and species richness have not been restored 8 years after removal. It is likely that food availability rather than dispersal ability is the main cause for slow Collembolan community recovery. However, hay inoculation, originally initiated to speed up the vegetation restoration process, improved microclimatical conditions and food resources, resulting in a richer community of springtails and *Myrmica* ants. *Myrmica scabrinodis* needs a minimum vegetation cover before being able to successfully colonize restored areas. Our approach enables further facilitation of the establishment of the key species for *Maculinea teleius* butterflies.



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## Too much of a good thing: Response of two *Lycaena* species to fertilised host plants

13:30  
15:50

SUSANNE KURZE<sup>1</sup>, THILO HEINKEN<sup>1</sup> & THOMAS FARTMANN<sup>2</sup>

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Nutrient enrichment from agricultural and atmospheric sources affects many habitats in the northern hemisphere. In general, the fertilisation of permanent grasslands, which often means a nitrogen input of more than 100 kg N/ha y, it goes along with a higher land-use intensity. The resulting shifts in the plant species composition and vegetation structure influence butterflies indirectly due to alterations in the abundance of their host plants. In addition, fertilisation causes a higher nitrogen content in the plants themselves, which mainly affects the larvae of butterflies. According to the “nitrogen limitation hypothesis” nitrogen is a limited factor for herbivorous insects and a positive relationship between the nitrogen content of the host plant and the insect performance exists. But few empirical studies undermine this hypothesis by presenting negative effects for herbivorous insects due to a higher nitrogen content in their host plants.

This study investigates the larval survival rate of the two common *Lycaena* species, *L. phlaeas* and *L. tityrus*, with the host plant *Rumex acetosella* under three treatments: one control treatment and two fertilisation treatments with an input of 150 kg N/ha y and 300 kg N/ha y respectively. In both species the larval survival rate decreases significantly in the fertilisation treatments. In particular under the fertilisation treatment with 300 kg N/ha y less than half of the larvae of *L. tityrus* survive. These results suggest that the high nitrogen input in permanent grasslands contributes to the recent decline of both *Lycaena* species. Further research is needed to assess whether these effects also occur in other butterfly species.



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13:50  
14:10

## LepiDiv – compiling distribution data for more than just distribution atlases

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LepiDiv can be regarded as a successor of MEB (Mapping European Butterflies) which produced distribution Atlases of Butterflies in Europe in printed form (Kudrna et al. 2011). The underlying database was already used for further research, e.g. on the effects of climate change (Settele et al. 2008) and the calculation of climatic niche characteristics of European butterflies (CLIMBER, see separate poster; Schweiger et al. 2014).

LepiDiv intends to further develop and extend this database as an invaluable community resource for ecological research on butterflies of Europe and adjacent areas. As a first step, online distribution maps are provided for Europe and Asian Turkey (<http://www.ufz.de/european-butterflies/index.php?de=22477>). By inclusion or linkage to further National or regional mapping schemes and interaction with recorders it is intended to update these maps and improve their resolution in space and time, which will help to enhance the quality of dependent data such as the climatic niche characteristics.

Apart from distribution data and their derivatives, we have also started to collect and integrate further data on ecological characteristics of European butterflies. In addition, a molecular phylogenetic tree, based on mitochondrial and nuclear sequences, is almost complete and has already been used for ecological analyses.

We hope for your support to further improve this online resource and greatly appreciate your feedback.

### References

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## The status of Dutch macro-moths: impact of artificial lighting

14:10  
14:30

**MARTINUS E. HUIGENS**<sup>1</sup>, WILLEM N. ELLIS<sup>2</sup>, KOERT G. VAN GEFFEN<sup>3</sup>, ROY H. A. VAN GRUNSVEN<sup>3</sup>, DICK GROENENDIJK<sup>1</sup>, MATHILDE M. GROENENDIJK<sup>1</sup>, MAURICE G. M. JANSSEN<sup>2,4</sup>, JIPPE VAN DER MEULEN<sup>1</sup>, ERIK J. VAN NIEUKERKEN<sup>2,5</sup>, ROB DE VOS<sup>2,5</sup>, FRANK BERENDSE<sup>3</sup>, MARCEL E. VISSER<sup>6</sup>, KAMIEL SPOELSTRA<sup>6</sup>, PHILIPP GIENAPP<sup>6</sup>, MAURICE DONNERS<sup>7</sup>, ROY SLATERUS<sup>8</sup> & ELMAR M. VEENENDAAL<sup>5</sup>

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Moths are a highly abundant and species-rich group of insects that play an important role in natural ecosystems as herbivores, as food for other animals such as birds, bats and arthropods, and as pollinators of plants. Research has, however, indicated a general decline of moths in Europe. In this study, we more specifically investigated trends in abundance and distribution of macro-moths in the Netherlands over the past 30 years. The results show that 7% of originally 741 resident species has disappeared and 60% is more or less endangered. Eight % of the species are even critically endangered. One potential reason for moth declines is the increase in artificial lighting over the past decades. Here, we present data on the impact of artificial lighting on moths, not only on adult attraction to light but also on reproduction. This research project is part of a large-scale experimental field study on the long-term effects of artificial lighting on plants and nocturnal animals, including moths.



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14:45

## Maintaining and increasing biodiversity

**NILS RYRHOLM**

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I will give examples of some practical projects for maintaining and increasing biodiversity that I have been part in initiating in recent years. I have co-operated with Swedish defense forces, Swedish Motorcycle Association, local communities and NordensArk. I have also discussed biodiversity issues with the leadership of FIM (Fédération Internationale de Motocyclisme) Europe so hopefully more European motor tracks in the near future can be maintained in such a way that they support the local and regional biodiversity. I also would like to discuss this with my fellow European conservationist colleagues during the conference.



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## Intergovernmental assessments and the role of Lepidoptera – Insights from IPCC and IPBES

14:45  
15:10

**JOSEF SETTELE**<sup>1,2</sup>

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The IPCC (Intergovernmental Panel on Climate Change) and the IPBES (Intergovernmental science-policy Platform on Biodiversity and Ecosystem Services) are both processes in which assessments play a crucial role. In its last Assessment Report (AR5), as in the ones before, IPCC assessed “The Physical Science Basis” (Working Group I), “Impacts, Adaptation and Vulnerability” (WG II), and “Mitigation of Climate Change” (WG III). The IPBES (Diaz et al. 2015) has started with thematic assessments - one on scenarios and one on pollination, which will be finished in early 2016. Several regional assessments have started as well, e.g. for a) Europe and Central Asia, b) Asia - Pacific, c) Americas, and d) Africa.

In the presentation experiences from some of these assessments will be presented, based on the IPCC involvement (Settele et al. 2014) and on the involvement in the ongoing pollination work as well as the regional assessment for Asia and the Pacific and some cases will be shown where information on Lepidoptera was used.

### References

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## Keynote

9:00  
9:30

### Calibrating the taxonomy of a megadiverse family on BOLD: 2700 geometrid moth types barcoded (Geometridae)

**AXEL HAUSMANN<sup>1</sup>**, SCOTT MILLER & SEAN PROSSER

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One of the major challenges in creating a global database like BOLD is warranting the correct identification of the voucher specimens. The strict BOLD-policy to require images, indication of specimen deposition and accurate geo-referencing for all submitted datasets is extremely helpful to control doubtful data and potential misidentifications. Nevertheless there are still many incomplete identifications (to genus or subfamily level), interim names or even misidentifications on BOLD, mainly for species from tropical regions. Unfortunately experts are lacking for many problematic groups and regions and even if there are experts they usually do not have the time to correct the taxonomy of large amounts of datasets. The only way to achieve an unambiguous calibration of the system is to barcode the original type specimens. In the last years, the challenge of sequencing up to 250 years old museum specimens has been overcome by improved techniques and protocols developed by the CCDB. These innovations allowed for the generation of barcode sequences for approximately 2,700 geometrid type specimens, which represent 2,150 species corresponding to about 9% of the 23,000 described species worldwide. Here we present case studies to show the efficiency, reliability and sustainability of this approach as well as promising strategies to complete the calibration of the reference library within a reasonable amount of time.



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## Keynote

### Can we speed up the taxonomic process of large-scale revisions? Example from the Geometrid Moths of Europe monograph

9:30  
10:00

**PASI SIHVONEN<sup>1</sup> & PEDER SKOU<sup>2</sup>**

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The preparation of a large-scale taxonomic revision may take years, even more than ten years. The investments of time and resources are justifiable if the end-result is a high quality, user-friendly product that provides solid base for various aspects such as nomenclature, alphataxonomy, biology and distribution. We use the Geometrid Moths of Europe monograph on the subfamily Ennominae as an example to discuss if the taxonomic process of large-scale revisions could be speeded up. In addition, we present several cases where further taxonomic research is needed, including (but not restricted to) *Isturgia spodiaria*, *Crocallis elinguaris*, *Neognopharmia stevenaria* and genus *Aspitates*.



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10:00  
10:15

## Phylogeny of the superfamily Geometroidea, with emphasis on the systematic position of *Pseudobiston pinratana* Inoue, 1994

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The systematic position, at family level, of the enigmatic *Pseudobiston pinratana* Inoue, 1994 (originally described in Geometridae), has been questioned by several entomologists. A complete lack of abdominal tympanal organs was seemingly incompatible with a position among the Geometridae, while the other morphological characters of *P. pinratana* were a priori considered poorly informative phylogenetically. Then, in order to elucidate this systematic position, we used a large molecular dataset (sequences of eight genes, viz. the mitochondrial gene COI and seven nuclear genes: EF-1 $\alpha$ , Wingless, RpS5, MDH, GAPDH, CAD and IDH) taking into account *P. pinratana* and 111 other species, mostly members of various macroheteroceran families. All phylogenetic analyses (Maximum likelihood, Parsimony and Bayesian inference) revealed a fairly well supported sister-group relationship between *Pseudobiston* and the Epicopeiidae, and the former was assigned to a new, monotypic family (Pseudobistonidae Minet, Rajaei & Stüning, 2015). In the shadow of this study, the phylogenetic relationship between the families of Geometroidea were discussed and new morphological synapomorphies were proposed.



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## Towards a phylogeny of Neotropical Geometridae

**GUNNAR BREHM**<sup>1</sup>, **PASI SIHVONEN**<sup>2</sup> & **NIKLAS WAHLBERG**<sup>3</sup>

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The Neotropical region comprises the most species rich geometrid moth assemblages on earth with a large fraction of undescribed species and many unresolved systematic problems. A reliable assignment of species to genus or tribal or higher level is often impeded because many higher level taxa are not well defined, paraphyletic, or simply not existing. Our project aims to resolve some of the most urgent taxonomic problems with a phylogenetic analysis of ca. 200 of the ca. 500 Neotropical geometrid genera. We will present results for the first ca. 100 genera analysed. We apply a standard eight-genes approach (6365 base pairs) and Maximum-Likelihood and Bayesian methods.

First results are shedding light on the systematic position of many taxa, and suggest many new combinations at tribal level, and some at subfamily level. A clade of three genera (*Ergavia*, *Ametris*, *Macrotis*) currently assigned to the Oenochrominae form a clade within the Sterrhinae. The Oenochrominae genera *Racasta* and *Nearcha* do not group together with *Oenochroma* but with members of the Desmobathrinae. All subfamilies, except the Sterrhinae, comprise larger exclusively Neotropical clades, suggesting that these clades have longer been biogeographically isolated. Results confirm that Neotropical members of the genera *Idaea* and *Hydriomena* are congeneric with their Holarctic relatives. Within the largest subfamily Ennominae, a major clade includes many genera currently assigned to the Ennomini, Nephodiini, Ourapterygini, the *Cratoptera*-group as well as many unassigned genera. In particular, the Neotropical Nephodiini form a clade, but results clearly suggest that the very species-rich genus *Nephodia* is paraphyletic.

10:15  
10:30



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10:30  
10:45

## Life span under investigation: a phylogenetic comparative approach

**SILLE HOLM<sup>1</sup>**, ROBERT B. DAVIS<sup>1</sup>, JUHAN JAVOIŠ<sup>1</sup>, ERKI ÕUNAP<sup>1,2</sup>,  
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Life span has unarguably a central part in species life history. Although thoroughly studied in vertebrates, life span studies in insects have received not even closely that much attention. Until recently the vast potential of using phylogenetic comparative analysis has remained poorly exploited, partly due to scarcity of reliable phylogenetic reconstructions: a problem which is now gradually disappearing. Insect studies can significantly contribute to comparative life span studies: the huge species-richness of the order provides great opportunities, lifespan can be feasibly measured in a high number of species, and selective forces having shaped the life span can be expected to vary largely between species.

We recorded adult lifespan in 90 species of geometrid moths (Geometridae) and applied phylogenetically explicit comparative analyses to study variation of life span and its ecological and life history correlates. As the primary result, among species and between-gender differences in life span turned out surprisingly small. Also, there was no evidence of phylogenetic signal, neither could the species-specific longevity values be explained by various ecological traits of the species. However, larger moth species, as well as the more income breeding species had longer life spans. It seems, that uniform extrinsic mortality rate is the reason for weak patterns of life spans of geometrid moths.





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## On the Phylogenetic studies of the tribe Larentiini (Geometridae), based on molecular methods

11:05  
11:25

**ANDRO TRUUVERK<sup>1</sup> & ERKI ÕUNAP<sup>1,2</sup>**

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During recent years, phylogenetic studies on the family Geometridae have been intensified, mainly due to significant advances in methods of sequencing and phylogenetic analysis of genetic data. To date, subfamily-scale classification of geometrid moths is rather well established, as similar phylogenies have been independently recovered by different authors.

However, phylogenetic studies on tribe and genus level of Geometridae have been largely out of focus and the monophyly of many groups has therefore never been tested analytically. Hereby we concentrated on resolving the phylogeny of the tribe Larentiini and its relationships with other tribes from the subfamily Larentiinae. DNA sequences of more than 60 species from 22 tribes were included into the analysis. 16 species from 11 genera belonged to the tribe Larentiini according to the recent classification. Sequence data from one mitochondrial and eight nuclear genes were used. Data were analysed by Bayesian phylogenetic method using program BEAST and by maximum likelihood using RAXML. Our results demonstrate that the tribe Larentiini within its current limits is not monophyletic. Majority of the studied larentiine genera formed a well-supported monophyletic lineage together with *Larentia*, the type genus of the tribe. However, some of the genera were placed into different sub-lineages of the subfamily Larentiinae. Analyses with additional taxa are needed to verify the placement of Larentiini genera placed into clades other than „*Larentia* lineage“.



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11:25  
11:40

## New attainments based on an integrative taxonomic survey of *Rhodostrophia* Hübner, 1823 of Iran (Sterrhinae)

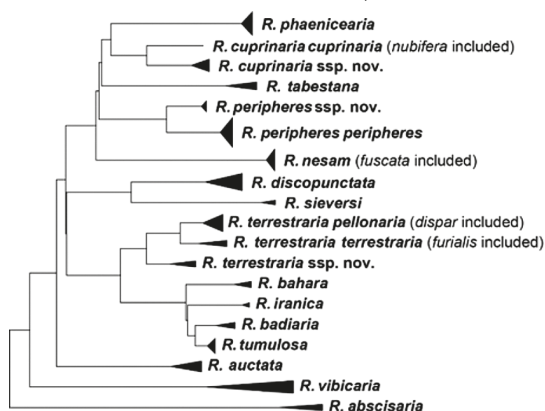
ROBERT TRUSCH<sup>1</sup>, HOSSEIN RAJAEI<sup>2</sup> & AXEL HAUSMANN<sup>3</sup>

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An integrative taxonomic survey of the species of the geometrid genus *Rhodostrophia* Hübner, 1823 of Iran is presented. At the SEL congress 2007, a new interpretation of its taxonomy was presented, but only based on morphological data. However, especially the results within the terrestraria-species-group, e.g. synonymisation of well-known species like *R. dispar* Chr., *R. pellonearia* Stgr. vs. the establishment of a new subspecies of *R. terrestraria* for south Iran, was not convincing to all of us. After integrating the results of DNA-Barcoding for multiple specimens from all studied morphospecies, surprisingly all morphological interpretations of 2007 were confirmed. Furthermore within the terrestraria-species-group another well-known species, the apparent extremely rare high-mountain-“species” *R. furi-alis* is now considered conspecific with *R. terrestraria*. And three new subspecies (of *R. terrestraria*, *R. peripheres* and of *R. terrestraria*) were confirmed. Our DNA information, however, show an inconsistency with respect to the badiaria-species group. The morphologically well-defined *R. badiaria* (not occurring in Iran) is clustered within *R. tumulosa*. This is open for discussion at the congress.



**Fig. 1.** Un-rooted neighbour-joining tree based on individuals of all studied *Rhodostrophia* morpho-species distributed in Iran and adjacent countries.



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## Constant and high: diversity and turnover patterns of geometrid moths along an elevational gradient in the Ecuadorian Andes revisited

11:40  
11:55

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We re-sampled and analysed diversity patterns of geometrid moths along a forested elevational gradient in northern Podocarpus National Park and adjacent areas in southern Ecuador, sampled with standard manual light trapping methods. Previous studies (1020–2677 m a.s.l., 22 sites, in 1999–2000) found unique elevational diversity patterns of geometrid moths and a constant species turnover. Using a completely new dataset of comparable size, we sampled moths with the same methods along a slightly extended gradient (1020–3021 m a.s.l., 28 sites, in 2008–2013). For the new study, we used a combination of COI barcoding as a key tool for species delineation compared to sorting to morphospecies as standard in the previous studies.

We counted a total of 14,603 specimens from 1,857 species, an increase of species diversity by 80%. Although local diversity was higher, we confirm the unique diversity patterns found in previous studies, i.e. a constant high diversity almost over the entire gradient. Only diversity at the highest elevation sites (> 2,800 m) decreases slightly. Species turnover was higher than previously shown, but similarly constant along the elevational gradient, still indicating no discrete faunal zones. Our results confirm previous key findings and show that even substantial changes in sampling scheme and species delineation techniques can provide overall stable and well interpretable results.



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11:55  
12:20

## iCollections project: the digitisation of the British & Irish Lepidoptera collection at the Natural History Museum, London

**GEOFF MARTIN**

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G.Martin@nhm.ac.uk

The Natural History Museum, London is committed to digitising 20 million specimens by 2019. The British and Irish collection of Lepidoptera contains around 1,000,000 specimens spanning 200 years of collecting. This collection was chosen as a pilot project for the digitisation of the museum's collections. The project started in January 2013 and is expected to take three years to complete. The talk will go through the digitisation process highlighting the many issues and show the results so far including research and curation benefits. The unlocking of these data will be of enormous benefit to those interested in the British and Irish Lepidoptera, will be accessible to all on the museum's data portal and will set the standard for future museum digitisation projects.



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## Re-curation of the slug moths (Limacodidae) collection at the Natural History Museum, London: Challenges, positive outcomes and future value

12:20  
12:35

**ALESSANDRO GIUSTI**

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Even though we know that well organized museum collections are crucial for assisting and simplifying works of taxonomic revisions, historically, many of the least appealing groups of organisms have been both taxonomically and curatorially neglected in museum's collections.

This often creates a vicious cycle of prolonged negligence.

The family Limacodidae is one of these long-term forgotten groups; but not for long, at least in our collection, as I have just finished re-curating the collection of this family in the museum.

In this talk I will give a brief overview of the process of re-curating the entire collection of Limacodidae, describing the various challenges, positive outcomes, and the potential usage of a better organized collection for the future.



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13:55

## My first steps in Citizen Science – evaluation and results of the label-butterflies.com project

**CLAUDE SINNER**

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Several efforts are currently undertaken to digitize the vast amount of collections found in museums throughout the world. Large global databases of data labels will transform the availability and accessibility of biogeographical information. While digitizing and photographing labels can be automated by machines, the transcription of the labels is not straight forward as most OCR software fails with the peculiar layout of data labels. One promising method to reach this goal despite these problems are 'Citizen Science' projects, a new scientific method, which includes the general public in scientific research. They convert tasks too complicated for current software, into simple and fun tasks that can even be performed by children or high schoolers without much former training.

In August 2013 I launched the project [label-butterflies.com](http://label-butterflies.com) to transcribe my collection of digital data labels, which focuses on the family Lycaenidae, Leach 1815. Contrary to competing projects, this website tries to keep users focused by an interactive game. Through the transcription of data labels users can unlock a range of butterfly pictures of varying difficulty. The server, self-written using the programming language python, has been run with a test set of 7,410 different labels from two major museums. I will introduce the system and discuss the implementation of different strategies to prevent users from exploiting the system. Finally, I will give insights into user effectiveness and discuss the credibility and exactitude of the obtained data.



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## Macromoths light trap catches on intensive farmland: Relative effects of crops, land covers and landscape heterogeneity

13:55  
14:15

JANA SLANCAROVA, D. NOVOTNY, J. BENES, M. ZAPLETAL & MARTIN KONVICKA

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Moths are a highly diverse group forming a bulk of herbivorous insect biomass in European ecosystems. Because many insect species can harm crop production, monitoring systems recording selected pest species have been established in many countries. Czech State Phytosanitary Administration operates a system of ca 20 light traps, all situated on intensive farmlands and evenly distributed across the country, regularly recording seven pest species. For three years, we processed entire catches from the light traps to investigate determinants of moth community composition.

The processed material contained 91,726 individuals and 564 species in 2008 (18 traps); 93,515 individuals and 620 species in 2009 (19 traps); 89,222 individuals and 625 species in 2010 (21 traps). Consistently for all three years, as well as in combined analysis with year effect as covariable (attributable variation: 8%), crop composition around traps had no effect on the species composition of the catches. In contrast, geographical position of the traps and surrounding plant species composition always affected the catches (attributable variation: 10-20%). Finally, predictors describing land covers and land cover heterogeneity around the traps explained ca 10% of moths species composition, retaining their effects even after control for covariates; the most important predictors were woodland cover and woodland edge density within a radius of 1,000 meters around the traps.

We conclude that farmland pests inhabiting cropland and forming the bulk of moth catches (2008: 36% of all individuals; 2009: 27%; 2010: 21%) were unaffected by momentary crop composition. The community composition was mainly affected by relative representation of woodland species, whose catches on the farmland depended on woodland proximity.



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14:35

## Which factors influence moth communities in a Hungarian sessile oak-hornbeam forest?

**BALINT HORVÁTH<sup>1</sup>, V. TÓTH<sup>1</sup>, CS. SZABÓKY<sup>2</sup> & F. LAKATOS<sup>1</sup>**

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A question posed by many community ecologists is: which factors influence biodiversity? The answer is: multiple factors, but specialists have agreed that plants have an important role. Thus, one of the key components in maintaining the biodiversity of temperate forests is the vegetation that has a strong influence on herbivores.

A considerable mass of herbivores is represented by Lepidoptera, numerous of them have adapted to special environmental conditions, and thus are suitable as indicators of biodiversity. Tree species composition in forested ecosystems is determined by environmental conditions, natural processes and human impacts.

In forests where thinning occurs the changing micro-environmental conditions (e.g. light regime, humidity and climate) are relevant variables for plant abundance, species composition, species diversity, and growth of seedlings. Through these variables, thinning plays a decisive role for Lepidoptera communities as well.

Despite the numerous papers on the relation between Lepidoptera communities and forest management practice we have not always enough information how to maintain the existing biodiversity. The lack of information is caused by the high variability of forests even in the temperate zone.

In the last few years we have investigated Lepidoptera communities in sessile oak-hornbeam forests in north-western Hungary (Sopron Mountains). Several variables were chosen for the analyses, such as cover and species richness of each vegetation layer, extension of forest stand, forest stand age, trunk quantity and thinning parameters. Each variable *per se* may have no influence on the Lepidoptera communities, but condensed parameters (PCA) may have a significant effect on moth assemblages.

Based on our results the vegetation layers have substantial influence on Lepidoptera communities, but the complex vegetation structure play a more significant role. The mixture rate of trees is important, but low abundance of mixture tree species is not favourable for moth species richness and abundance. We studied the effect of thinning on moth assemblages in short time scale (last 10 years). Lepidoptera abundance increased after thinning, that explained by the increasing number of microhabitats. However, the micro- and macrolepidoptera communities responded differently to thinning.





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## Genetic diversity and phylogeography of *Sesamia nonagrioides* (Noctuidae) in Iran inferred from mitochondrial DNA

14:35  
14:50

NEDA MEHRAVAR, **MEHDI ESFANDIARI**<sup>2</sup>, HOSSEIN MOTAMED<sup>1</sup>, HAMID RAJABI MEMARI<sup>3</sup> & HOSSEIN RAJAEI<sup>4</sup>

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Although the stem borer *Sesamia nonagrioides* (Lefèbvre, 1827) is one of the most destructive agricultural pests in South and Southwest Iran, the structure of these populations is not yet well understood. In this study, we sequenced two mitochondrial genes (CO1 and Cyt-*b*) of populations collected in cultivated sugarcane and rice in South and Southwest Iran. We compared the genetic data of Iranian populations with those of already published from West Palaearctic (Africa and Europe). To testing the intra- and inter-population variations, different population analysis (e.g. haplotype network, haplotype and nucleotide diversity) were executed. Our results indicate a considerable genetic variation in Iranian populations of *S. nonagrioides* compare to those of previously published from African and European populations. This result may support the idea that *S. nonagrioides* populations established longer time in Iran than recent invasion, leads to generating of multiple haplotypes. Close genetic relationship of Iranian population of *S. nonagrioides* to a population of Central Ethiopia, supports the scenario of the origin of this species from Africa to Palearctic and western Asia through the Trans-Arabian bridge. Our results help to explain the variation in pest status of *S. nonagrioides* observed across its distribution range in Iran.



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15:25

## A survey of Erebidae, Nolidae and Euteliidae in southern and northeastern of Iran

**SARA FARAH JAHROMI**<sup>1</sup>, **MOHAMMAD MAHDI RABIEH**<sup>2</sup> & **MEHDI ESFANDIARI**<sup>1</sup>

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Noctuoidea are the largest superfamily of Lepidoptera which have not yet fully investigated in Iran. In order to inventories such important group, faunistic studies on the families Erebidae, Nolidae and Euteliidae were made by light traps mainly in the three Iranian provinces of Fars, Khuzestan and Khorasan-e-Razavi during 2009–2011. Here we report part of the results including 42 taxa belonging to 26 genera and 7 subfamilies. Among these, one species is newly reported for the Iranian fauna, together with 23 new provincial records. Taxonomy of the species and their distribution pattern are discussed.



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## A new sex attractant for the males of Procridinae (Zygaenidae)

15:25  
15:40

KONSTANTIN A. EFETOV<sup>1</sup>, ELENA E. KUCHERENKO<sup>1</sup>, EKATERINA V. PARSHKOVA<sup>1</sup> & GERHARD M. TARMANN<sup>2</sup>

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2-butyl 2-dodecenoate was synthesized and its property as a sex attractant for the males of some Procridinae species has been proved in field observations undertaken in the Crimea, Austria and Italy.

The baits were tested in Delta traps containing removable sticky layers and hung on bushes or trees at a height of 1.0–1.5 m above the ground. In all sites that were prospected we also placed control traps containing rubber caps that were not impregnated with the attractant. The distance between traps was not less than 10 m). Sometimes we merely placed the lure in the habitat. In this case we collected attracted specimens by netting them near the lure.

An application of 2-butyl 2-dodecenoate demonstrated its attractiveness for the males of *Theresimima ampellophaga*, *Rhagades (Rhagades) pruni*, *Adscita (Adscita) alpina*, *A. (A.) italica*, *A. (A.) geryon*, *A. (A.) dujardini*, *A. (Tarmannita) mannii*, *Jordanita (Roccia) volgensis*, *J. (Tremewania) notata*, *J. (Jordanita) graeca*, *J. (J.) tenuicornis*, *J. (J.) globulariae*, and *J. (Solaniterna) subsolana*. We found two different types of attraction.

1. *Th. ampellophaga*, *Rh. pruni*, *J. notata*, *J. globulariae*, and *J. subsolana* were found mainly as glued specimens on the sticky layers.

2. The other species were coming to the lures that were placed in the habitat. Most probably the males that came to the lure but did not adhere to the sticky layers realized at a close distance that 2-butyl 2-dodecenoate is not their natural pheromone.

Thus, 2-butyl 2-dodecenoate can be used for identifying the presence of Procridinae species in different regions and for seasonal monitoring of these moths.



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## On the way to a world catalogue of the Procridinae (Zygaenidae)

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A new and revised world catalogue of the Procridinae is urgently needed because a number of new and significant characters of the Procridinae have been discovered; moreover, major revisions have been published and, as a consequence, our views on the phylogeny of the group have changed. Many new taxa were described during the last thirty years. Moreover, the status of some groups has also changed. As an additional tool to our morphological, biological, karyological and other data, we have obtained information on sequences of the 658-bp region of the cytochrome c oxidase I (COI) gene of many species. A list of the taxa newly described during the last three decades (1985–2015) is provided below.

**One tribe:** Artonini Tarmann, 1994.

**Ten genera:** *Fuscartona* Efetov & Tarmann, 2012; *Striartona* Efetov & Tarmann, 2012; *Thibetana* Efetov & Tarmann, 1995; *Pseudoinope* Efetov & Tarmann, 1999; *Myrtartona* Tarmann, 2004; *Australartona* Tarmann, 2004; *Pseudoamuria* Tarmann, 2004; *Palmartona* Tarmann, 2004; *Pseudoilliberis* Efetov & Tarmann, 2012; *Erythroclelea* Efetov & Tarmann, 1995.

**Twelve subgenera:** *Chyrtremewana* Efetov, 2006; *Chyrtarmanna* Efetov, 2006; *Nikilliberis* Efetov & Tarmann, 2012; *Wiegelia* Efetov & Tarmann, 1995; *Molletia* Efetov, 2001; *Keilia* Efetov, 2001; *Efetovia* Mollet, 2001; *Procriterna* Efetov & Tarmann, 2004; *Tarmannita* Efetov, 2000; *Tremewania* Efetov & Tarmann, 1999; *Rjabovia* Efetov & Tarmann, 1995; *Solaniterna* Efetov, 2004.

**Sixty valid species:** *Fuscartona martini* Efetov, 1997; *F. parilis* Efetov, 1997; *Balataea kimurai* Owada & Inada, 2005; *Thibetana witti* Efetov, 1997; *Chrysartona efetovi* Parshkova, 2007; *Ch. hausmanni* Efetov, 2006; *Ch. stueningi* Efetov, 2006; *Ch. tremewani* Efetov, 2006; *Ch. sinevi* Efetov, 2006; *Ch. birmiana* Efetov, 2006; *Ch. honeyi* Efetov, 2006; *Ch. sikkima* Efetov, 2006; *Ch. margarita* Efetov, 2006; *Ch. mineti* Efetov & Tarmann, 2013; *Ch. meyi* Efetov, 2006; *Pollanisus nielseni* Tarmann, 2004; *P. modestus* Tarmann, 2004; *P. marriotti* Kallies & Mollet, 2011; *P. edwardsi* Tarmann, 2004; *P. contrastus* Tarmann, 2004; *P. eungellae* Tarmann, 2004; *P. commoni*



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Tarmann, 2004; *P. incertus* Tarmann, 2004; *P. angustifrons* Tarmann, 2004; *P. isolatus* Tarmann, 2004; *Onceroptyga pulchra* Tarmann, 2004; *Hestiochora continentalis* Tarmann, 2004; *H. furcata* Tarmann, 2004; *H. queenslandensis* Tarmann, 2004; *H. occidentalis* Tarmann, 2004; *H. intermixta* Tarmann, 2004; *Myrtartona marianae* Tarmann, 2004; *Australartona mirabilis* Tarmann, 2004; *Homophylotis pseudothyridota* Tarmann, 2004; *H. artonoides* Tarmann, 2004; *Pseudoamuria uptoni* Tarmann, 2004; *P. neglecta* Tarmann, 2004; *Pseudoilliberis kuprijanovi* Efetov, 1995; *Illiberis yeni* Efetov, 1997; *I. cernyi* Efetov & Tarmann, 2013; *I. banmauka* Efetov & Tarmann, 2014; *Hedina louisi* Efetov, 2010; *H. taiwana* Efetov, 1997; *H. vietnama* Efetov, 1997; *Goe tarmanni* Efetov, 1998; *G. dentata* Efetov, 1998; *Rhagades tarmanni* Keil, 1999; *Zygaenoprocris efetovi* Mollet & Tarmann, 2007; *Z. hofmanni* Mollet & Tarmann, 2007; *Z. minna* Efetov, 1991; *Z. albertii* Efetov, 1991; *Z. naumanni* Efetov, 1994; *Adscita pligori* Efetov, 2012; *A. krymensis* Efetov, 1994; *A. dujardini* Efetov & Tarmann, 2014; *Jordanita tianshanica* Efetov, 1990; *J. almatiensis* Mollet, 2008; *J. kurdica* Tarmann, 1987; *J. benderi* Tarmann, 1985; *J. fazekasi* Efetov, 1998.



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15:55  
16:10

## A new genus for an undescribed species of “tufted” thyretine from Central Africa (Erebidae: Arctiinae, Syntomini)

ŁUKASZ PRZYBYŁOWICZ<sup>1</sup> & MICHAEL OCHSE<sup>2</sup>

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Tiger moths (Erebidae: Arctiinae) are despite their attractive coloration and the diurnal activity of many species taxonomically still underexplored. This is especially the case with respect to the African fauna. Recent taxonomic studies clearly indicate how superficial our knowledge is not only on species level diversity but also in the higher categories. Even more incomplete is the biological information in most cases. Detailed lifecycle descriptions of virtually all species are lacking, and the defense strategies of the many presumably mimetic or aposematic species within the groups are yet to be described.

Based on the extensive morphological analysis of all African representatives of the subtribe Thyretina a new genus is designated and its single species is described from western and central Africa (Cameroon, Gaboon, Ivory Coast). The description is based on the male sex only but the unique combination of characters justifies this decision. The genus is separable from closely related genera by the occurrence of pectinate antenna and a tuft of elongate scales on the tip of the abdomen in males. The systematic position of the new genus within the tribe Syntomini is discussed on the basis of morphological characters and molecular data. The short review of the “tufted” genera of African Arctiinae is also provided with emphasis on the diagnostic differences. Wing pattern and male genitalia of the new species are depicted and notes on the habitat are presented. The possible function of the elongate tuft of hair present on the tip of male abdomen is briefly discussed.



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## Larval characters and molecular phylogenies of Noctuoidea

16:10  
16:25

**HERBERT BECK**

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If a morphology-based system is well founded (e.g. Hasenfuss 1963), it should be expected that a molecular analysis will be in congruence with the morphological results (Wägele 2014). In Noctuoidea, this is often not the case. This mismatch might be due to a wrong (imaginal-)morphological system or the choose of genes which do not display the evolutionary scenario. In case of different concepts of the phylogeny and classification of a group based on morphological arguments, it should be expected that a molecular analysis do not confirm a wrong morphology-based system. But what is if a wrong morphological system becomes confirmed by a molecular study? I think this is currently the case with Nolidae s. l. The group is morphologically characterized by the synapomorphy of a boat-shaped cocoon with a vertical exit slit. A larval characterization is omitted because this does not, can not exist for the concept of Nolidae s.l. s. Kitching: The concerning larval characterization of the Nolidae s. str. (s. Hampson, s. Beck) is omitted (is not taken in consideration by Zahir & al.) because this concept does not fit into the concept of Nolidae s.l., s. Kitching & Rawlins).



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## Keynote

9:00  
9:35

### The closer you look, the more you see. European butterfly diversity through the magnifying glass of phylogeography

**ROGER VILA**

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Our work as biologists, as well as our passion as lepidopterists, is describing biodiversity at all levels, understanding how it is generated and maintained, and, of course, finding ways to protect it. Technical advances, especially recent molecular techniques, but also morphometric and chemical analyses, are unfolding a previously invisible layer of complexity: genotypically and phenotypically differentiated lineages, evolutionary significant units, and even cryptic species.

This new viewpoint brings a wealth of knowledge, but also of challenges and questions. How to methodologically approach the enormous descriptive task at the fine phylogeographic scale? How much should we invest on deeply studying each taxon in the quest for cryptic diversity? Can we develop methods for comparative phylogeography? Grey zones in the classical systematic classification become now enhanced, but eventually novel results have to be harmoniously integrated into the previous evidence and taxonomic corpus. Does recognising cryptic diversity represent a rather meaningless burden for monitoring and conservation, or does it have fundamental implications for biogeography, ecology and the preservation of existing diversity? Even if butterflies are an exceptionally well-studied group of invertebrates, a good number of cryptic species are still being discovered or confirmed. But most importantly, novel data give us some clues to answer the previous questions.





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## ***Proterebia afra* – Relic of the glacial steppe in the Balkans?**

**9:35**  
9:50

**ALENA BARTOŇOVÁ<sup>1,2</sup>, ZDENĚK FALTÝNEK FRIC<sup>1,2</sup>, PAVEL SUCHÁČEK<sup>3</sup>,  
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Steppe biome, highly associated with large herbivores, expanded several times during the Quarternary under the dry glacial climate and covered major parts of Eurasia. In present, natural steppes in Europe retreated and only few isolated parts persist. *Proterebia afra* is a representative of a steppe butterfly fauna, inhabiting only separated regions in Europe (Askion Mts. in Greece, Dalmatia in Croatia and Crimean peninsula), but distributed rather continuously in Ural and Kazakhstan steppes and Caspian Sea surroundings. We surveyed the biotopes of *P. afra* in Askion Mts and in Dalmatia, focusing on co-occurring biota inventory and microhabitat preferences of the species in the two regions. Numerous steppe specialists from various taxa co-occurred locally with *P. afra*. In addition, samples of *P. afra* from most of its total range were obtained for phylogeographical and population genetic study. We reconstructed the species historical expansion events and dating using COI gene, via haplotype network and Bayesian analysis with molecular clock. The understanding of steppe species ecology in its relic biotopes is important for conservation, as they are highly dependent on a combination of specific mesoclimates and traditional pastoral land use.

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The study was supported by Faculty of Science (054/2015/P), University of South Bohemia (04-168/2013/P), The Explorers Club Exploration Fund and FAN (B).



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9:50  
10:05

## The origin of the Sardinian Blue, *Pseudophilotes barbaggiae* (Lycaenidae): Out-of-Europe or Out-of-Africa?

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The island of Sardinia is characterized by an extraordinary richness of endemic species, evolved as a result of its geographic position and geological history. Here, we try to reconstruct the evolutionary history of the endemic Sardinian blue butterfly, *P. barbaggiae* de Prins and van der Poorten 1982, using the DNA barcoding region of the COI mitochondrial gene. The species is restricted to a few slopes in the mountainous areas of the island, and has been described as distinct from the continental and Corsican *P. baton* by characteristics of the male genitalia and wing markings.

We analyzed 11 individuals of *P. barbaggiae* and compared them with all European and north African congeneric species: a group of 77 sequences including *P. baton* (Corsica, Italy, France, Spain), *P. vicrama* (Romania, Turkey, Kazakhstan, Russia) and *P. panoptes* (Spain), as well as several BINs containing 20 sequences of *P. abencerragus* (Spain, Morocco, Tunisia, Portugal), 10 sequences of *P. bavius* (Romania, Russia) and 4 sequences of *P. fatma* (Morocco). The Bayesian phylogenetic tree showed that the group with *P. baton*, *P. vicrama* and *P. panoptes* forms a well-supported clade, but DNA barcodes do not distinguish these three species. The largest interspecific distance (4.8%) was found between *P. fatma* and *P. baton* - *P. vicrama* - *P. panoptes* group, while the smallest (1.2%) was between *P. abencerragus* and *P. barbaggiae*. The latter also forms a well-supported monophyletic group and has closer affinity to *P. abencerragus* (1.2%) than to *P. baton* - *P. vicrama* - *P. panoptes* group (1.8%).

Two hypotheses on a European versus an African origin of *P. barbaggiae* will be presented in the light of genetic and biogeographic data. This study will contribute to the emerging picture of butterfly diversification in the Palearctic region, and contribute to our understanding of the evolution of endemism in the European butterfly fauna.



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## ***Hazards of Butterfly Collecting: A tribute to Dr Torben B. Larsen (1944 – 2015)***

**10:05**  
10:25

**BLANCA HUERTAS**

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Dr Torben Larsen was a remarkable figure in butterfly research, not only in African butterflies's systematics, but also in studies in biodiversity, biogeography, ecology and the conservation of butterflies and their use as indicator species in environmental impact assessments. Torben wrote an amazing collection of books and monographic treatments on the butterflies of Lebanon, Jordan, Oman, Yemen, the Arabian Peninsula, Egypt, southern India (Nilgiris), Bangladesh, Kenya and Botswana. Many of these remain as the only books covering the relevant country or region's butterflies. During almost 10 years, he worked on the landmark publication *Butterflies of West Africa*, whilst continuing parallel research in other faunas and travelling widely. This book was the first published in this important region and to date the only one of its kind. His impressive publication list stands at more than four hundred items, including scientific and popular articles, books and monographs in different topics. Twelve genera and more than 150 species or subspecies of butterflies new to science were named in these papers. Aside from his professional achievements, it is worth reflecting on Torben's person and sense of humour. Torben is also well evoked among entomologists because his *Hazards of Butterfly Collecting* book, a collection of anecdotes when studying butterflies. Torben was elected President of the Association for Tropical Lepidoptera in Florida in 1996 and held a Research Associate status with the McGuire Centre for Butterflies and Biodiversity (University of Florida) and the Carnegie Museum (Pittsburgh), and was appointed as Scientific Associate at the Natural History Museum (London). Torben is survived by his wife Nancy, but also by his extensive butterfly collections donated to various museums, including type material at the Lebanese University (Beirut), the African Butterfly Research Institute (Nairobi), the Zoological Museum, University of Copenhagen and the Natural History Museum, London. Torben died last May at the age of 71, leaving not only an immeasurable legacy in our knowledge of African butterflies, but also, tantalisingly, many butterflies in his incomplete monographs awaiting formal description, including the long awaited HesperIIDae of Africa. His kindness, sharp sense of humour and insurmountable knowledge will be sorely missed.



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10:45

## Drivers of colonization of habitat patches by the dryad butterfly (*Minois dryas*) in fragmented grasslands

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Most studies dealing with the patterns of species distribution focus on the characteristics of habitat patches influencing local occurrence and abundance, but they tend to neglect the drivers of species colonization of previously unoccupied patches. We combined classic approaches deriving from metapopulation theory and landscape ecology to investigate factors driving colonization process from recent refugium in the dryad butterfly. The presence and numbers of adult individuals were assessed through three consecutive transect surveys conducted in 27 patches of xerothermic grasslands and 26 ones of wet meadows. Among the predictors affecting the occurrence and the abundance of the dryad we considered environmental variables reflecting (i) quality of habitat patches i.e. goldenrod cover, shrub density, vegetation height, (ii) factors associated with spatial structure of habitats e.g. patch sizes, their isolation and fragmentation (iii) characteristics of patch surroundings constituting potential barriers or corridors. The surrounding was recorded in 100-m buffers around patches. The colonization of patches by the dryad was strongly limited by the patch distance from the species refugium in the region. We also detected a slight positive effect of shrub density in this respect. In turn, the butterfly abundance increased at smaller and more fragmented habitat patches; in addition, it was negatively impacted by invasive goldenrod cover as well as positively influenced by the density of watercourses in patch surroundings. Nectar plant availability was positively related to the species abundance in xerothermic grasslands, while in wet meadows an opposite effect was detected. We conclude that colonization of our study area by the species is very recent, and the dryad is a habitat quality-based species.



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## Mate choice in *Maniola* butterflies: Age beats beauty?

11:05  
11:30

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Male mating success is higher in older than in younger males in a number of insect species. This can be explained by two hypotheses. First, older males court more often or more intensely than younger ones, and second, females might genuinely prefer older males. Both hypotheses would indicate that, although the males have a more active role, female choice plays an important role in mating behaviour. Anyway, the existence of age-dependent mating preferences requires that butterflies can detect each others' age, for example based on chemical cues such as pheromones. We conducted a study on the mate choice of *Maniola* butterflies, by experimentally staging encounters in which individuals of different ages could choose to mate or not to mate. The butterflies used in the experiment were laboratory reared. This ensured that their hatching date was exactly known and that they did not have prior experience in mating or interacting with the opposite sex. For each trial ( $n=23$ ), 4 males and 2 females (all individually marked) were simultaneously placed together in a cage ( $70 \times 60 \times 50$  cm) and left there until mating occurred or for a maximum of 240 minutes. We found that the age difference between mating partners was important for mating success. Preferred median age difference for successful mating was  $-4$  days for males chosen by females, and  $+3$  days for females accepted by males. Therefore, in this unusually long-lived butterfly species mate choice appears to go both ways, viz. females as well as males have their share in choosing. Older males were consistently preferred upon younger males, and younger females upon older females, even if the age difference was just one single day. Whether this is caused by increased eagerness of older males to mate, or other fitness-indicating cues like pheromones, needs to be explored in future work.



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## Preliminary results on *Wolbachia* infestation in two closely related *Melitaea* species

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*Wolbachia* is a genus of intracellular bacteria found in arthropods and filarial nematodes. It has various effects on hosts, which range from reproductive manipulation to mutualism. The bacterium is mainly inherited maternally, but it also could transmit horizontally between host species via parasitoid-host interaction or prey-predator relations. In our project, we investigated *Wolbachia* infestation level and pattern in two closely related *Melitaea* species (*M. phoebe* and *M. ornata*). *M. phoebe* was infected in 94% in the Carpathian Basin (50 individuals from 53) and in 76% at Palaearctic level (16 individuals from 21). At the same time, we found only one infected *M. ornata* individual from Macedonia. We also carried out *Wolbachia* strain identification by the sequencing of *Wolbachia* surface protein (WSP) and identified three different strains in our samples. Besides, we screened the progeny of five different *M. phoebe* females out of which the offspring of four females were infected in 100% and the descendants of the remained one female were uninfected. We could detect the infestation in all developmental stages. On the basis of this infestation pattern it seems that *Wolbachia* show perfect maternal transmission in *M. phoebe*: the transmission rate is 100% and specimens do not lose the infection during the lifecycle. In addition, *Wolbachia* infection from the few tested individuals of parasitoid wasps and flies which hatched from *M. phoebe* pre-imago stages during laboratory rearing was also reported.



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## An annotated checklist of the butterflies of the National Park “Mavrovo” (Macedonia)

11:50  
12:05

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A faunistic study on the Lepidoptera in the NP Mavrovo (Western Macedonia) was conducted in 2010 – 2013. An updated checklist of 144 species is presented based on literature data and my own records from the conducted surveys. Twenty-five species were recorded for the first time in the park and one species – *Erebia triaria* (de Prunner, 1798) – is new for the butterfly fauna of Macedonia (Micevski 2013). Furthermore, new data on the distribution of some species are given, particularly for the southern part of the park, Mt Bistra, including 31 new species for this mountain. Moreover, interesting records of some rare and localized species are discussed.



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## Corks damaged by *Nemapogon granellus* (L.) in Tuscan wine cellars

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European grain moth, *Nemapogon granellus* (L.), is cosmopolitan in the temperate regions of the world and includes indoor and outdoor populations. Larvae feed on cereals, soybeans, almonds, hazelnuts, walnuts, peanuts, bran, grass seeds, clovers, flax, ergot, dry fruits, chocolate, mushrooms, seeds, moldy cheese, prunes, chestnuts, garlic, decayed wood, lichens, tobacco and pharmaceutical products. Some authors have stressed the importance of *N. granellus* as a pest in wine cellars where larvae feed on, and tunnel into, the corks of wine bottles. This causes aesthetic damage to the corks, which must be replaced before delivery to consumers. When tunnels ultimately connect both ends of the cork, the wine itself is affected and bottles rejected due to alteration in the organoleptic properties of the wine. During 2011, heavy infestations of European grain moth occurred in some Italian wine cellars in Tuscany (Italy), causing serious damage on exposed wine-bottle corks. The infestation occurred on red wine bottles (approximately 9,000) stored for aging for over 20 years. Integrated Pest Management (IPM) strategy was adopted, monitoring *N. granellus* adults with pheromone traps, accompanied by careful cleaning of the rooms, shelves and machinery, alternated to localized treatments using fogs with pyrethrum, and by the replacement of the infested corks. In addition, application of cellar sanitation procedures reduced the sources of pests as well as the possibility of insect reproduction, particularly in the areas of corks storage.





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## Taxonomic status of the genus *Cryptolechia* Zeller, 1852

12:20  
12:35

AIHUI YIN & SHUXIA WANG

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The genus *Cryptolechia* was erected by Zeller in 1852, with *C. straminella* Zeller, 1852 from India as the type species. Subsequently, its systematic position changed frequently. Meyrick (1883, Proc. Linnean Soc. New South Wales 8), mainly based on the wing venation, placed *Cryptolechia* in Cryptolechiidae. Toll (1964, Polish Ent. Soc. 27), based on the labial palpi, antennae, wing venation and genitalia, placed *Cryptolechia* in Depressariinae (Oecophoridae). Lvovsky (1974, Ent. Obozr. 53) placed it in Orophini (Elachistidae: Depressariinae). Minet (1990, Alexanor 16), after a phylogenetic analysis of the Gelechioidea based on morphology and behavior, placed *Cryptolechia* in Cryptolechiinae (Elachistidae). The phylogenetic analysis of the Gelechioidea by Hodges (1998, in Kristensen, Handbook of Zoology 4 (35), De Gruyter, Berlin), based on preimaginal and adult morphology, largely supported Minet's system, but he treated Cryptolechiinae as a synonym of Depressariinae. Lvovsky (2012, Ent. Rev. 92) regarded Cryptolechiidae as a family on its own under Elachistoidea. The genus *Cryptolechia* includes approximately 161 species, of which 104 are distributed in the East Palaearctic and Oriental Region, 28 in the Neotropical Region, 4 in the African Region, 5 in the Nearctic Region, and several in the Australian Region. The taxonomic status of many species needs further study. The type species of the genus, *C. straminella*, is characterized by a spiny gnathos and by the sacculus not being separated from the rest of the valva. However, most *Cryptolechia* species lack a gnathos. Based on our investigations, species without a gnathos and with a free sacculus may represent a subfamily of Oecophoridae including more than one genus. *Cryptolechia* comprises 63 described species in China (Wang 2006, Oecophoridae of China, Science Press, Beijing), and many more remain to be described. All Chinese species lack a distinct gnathos; their forewing patterns and male genitalia are diverse. We tentatively divide them into 6 species groups based on morphology: the *concolora*-group, the *lunifurcata*-group, the *infundibularis*-group, the *falsivespertina*-group, the *torophanes*-group, and the *malacobrysa*-group.



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## Lock-and-key mechanisms in some Cochylini (Tortricidae): a morphological study

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The genitalia (both external and internal) of some Cochylini are the most elaborate within the Tortricidae and provide plenty of morphological characters. Convincing anatomical evidence for presence of lock-and-key mechanisms was found in several Cochylini species. Various genital structures of males are involved in the locking process: sacculus of valvae, transtilla, juxta (external genitalia); the posterior portion of phallus; and vesica including large cornuti (internal genitalia). These structures find their counterparts in the females: modified areas of the abdominal sterna VII and VIII and their derivatives (external); ductus bursae, posterior portion of corpus bursae (internal). In general, the more complex internal genitalia, the less complex external genitalia. In most studied *Aethes* spp. was found a specialised area of corpus bursae corresponding to an outpocketing of vesica. In *Eugnosta* were found thick-walled processes of corpus bursae fitting the large cornuti of the male. In *Agapeta* the external genitalia are more complex in comparison to the internal. An evidence for probable mechanisms for mechanical isolation was found in some groups of closely related species, but in other groups no differences in the internal genitalia were found.



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## Diversity of Bagworm (Psychidae) species in India

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14:05

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India is endowed with rich biological diversity. In this paper, we have reviewed diversity of bagworm species (Psychidae) based on available information and our own study. Bagworms – case bearers – are known for their distinctive features. Some of them are known as aggressive defoliators and have been established as pests with potentiality to inflict large scale ecological and economical damages. Brahmachari (1938) was the first author who reported the presence of the bagworm *Kophene cuprea* on *Musa paradisiaca*. Thereafter, many workers described new species of bagworms collected from diverse hosts. A majority of the works on bagworm species in India emanated from Kerala. Some of the Indian states that were surveyed include Tamil Nadu, Uttar Pradesh, Chhattisgarh, Goa, Karnataka, Andhra Pradesh, and West Bengal. We have prepared a list of Indian bagworm species with their preferred host plants. According to Rhainds et al. (2009) there are about 1,000 bagworm species distributed worldwide. India is expected to harbor a large number of bagworm species. Our current endeavor of mapping bagworm diversity is restricted only to the Chhattisgarh State of the vast Indian subcontinent. We possibly discovered four new species that await confirmation and taxonomic description. There is an urgent need to scale up research on biology and biodiversity of bagworm species occurring in India.

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## The study of Microlepidoptera of Ukraine: a part of total inventory of Ukrainian Lepidoptera

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During the last ten years we have been focusing on the study of Microlepidoptera of Ukraine as a step towards a total inventory of Lepidoptera of our country. Special emphasis was given to the families Elachistidae, Scythrididae, Coleophoridae, Gelechiidae and Tortricidae, which were revised based on all available material. As a result of this study one new species of Gracillariidae, one new species of Coleophoridae, two new species of Gelechiidae and three new species of Tortricidae were described and the descriptions of thirty-one additional species and subspecies from the families Tineidae (4), Bucculatricidae (1), Gracillariidae (1), Elachistidae (1), Scythrididae (3), Coleophoridae (15), Gelechiidae (5), Tortricidae (1) were prepared. 242 species of Micropterigidae, Adelidae, Tineidae, Bucculatricidae, Gracillariidae, Yponomeutidae, Argyresthiidae, Ypsolophidae, Plutellidae, Lyonetiidae, Ethmiidae, Depressariidae, Elachistidae, Scythrididae, Oecophoridae, Coleophoridae, Momphidae, Blastobasidae, Autostichidae, Gelechiidae, Cosmopterigidae, Brachodidae, Tortricidae, Pterophoridae, Alucitidae, Pyralidae and Crambidae were recorded from Ukraine for the first time, among them fourteen – *Argyresthia juniperivorella*, *Elachista purella*, *Zagulajevia hemerobiola*, *Casignettella majuscula*, *Chrysoesthia falkovitshi*, *Scrobipalpa chetitica*, *Turkopalpa glaseri*, *Vladimirea glebicorella*, *Anarsia stepposella*, *Doloploca praeviella*, *Alucita araxella*, *Conobathra celticola*, *Syrianaripa mendicalis*, *Parapoxyn affinalis*, “*Aporodes dentifascialis*” were recorded in Europe for the first time.

The distribution in 23 administrative regions of about 3,800 species of Lepidoptera recorded in Ukraine is summarized in an Excel data-base. Kiev, Lviv, Luhansk, Donetsk and Zaporozhie regions as well as the Crimea are studied most satisfactory, whereas Kirovograd, Rivne, Volyn’ and Zakarpatie regions request further investigation. Among main landscape areas of Ukraine the highest level of taxonomic diversity of Lepidoptera is characterized for the southern, eastern and the mountain parts of the Crimea, eastern steppes in Luhansk and Donetsk regions and the Yuzhnyi Bug river valley. The Carpathian Mountains have also a high level of Lepidoptera diversity, although there is a number of alpine and sub-alpine species, which occur in the higher mountains of adjacent countries, but has not



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been yet found in the Ukrainian Carpathians. Not very rich, but a characteristic Lepidoptera fauna occurs in the sand areas along the lower Dnipro river, in saline habitats along the Azov Sea coast and in eastern Crimea, from where most of the endemic and sub-endemic species are known.

It is expected that after revisions of such still insufficiently studied families as Nepticulidae, Tineidae, Gracillariidae, Pyralidae and Crambidae the total number of Lepidoptera species of Ukraine will increase at least to 3,900 species.



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## A revised taxonomy of the bright-legged moths (Gelechioidea: Stathmopodidae)

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The bright-legged moths have nearly world-wide distribution and number 21 genera and 350 described species. A monophyly of the group is well supported by the following apomorphic traits: extremely narrow, linear or linear-lanceolate wings with very long fringes; modified (ciliate, long-scaled or flattened) antennae in males; hind legs with bundles of long and stout motley bristles; abdominal tergites with transversal rows of modified scales; desclerotized phallus in male and divaricated bursa copulatrix in female; peculiar hobbling gait and resting posture with hind legs raised considerably over the body; predominantly carpophagy or predation at larval stage. Its sister-group relationship remains debatable. It was treated as a separate family or as a subfamily and even tribe within Oecophoridae. A number of autapomorphies and clear distinctness from other gelechioids by the complex of characters weigh for the family rank of Stathmopodidae which became generally accepted only very recently. Sister-group of the family is Blastobasidae or Momphidae, according to the morphological data, and Scythrididae according to the molecular data. The known genera of Stathmopodidae are classified into three groups. Those with rounded head, ciliate antennae in males, fasciated or spotted forewings and trophic associations mainly with various angiosperms form the nominate Stathmopodinae (*Stathmopoda*, *Aeoloscelis*, *Hieromantis*, *Tortilia*, *Oxycrates*, *Atrijuglans*). Those with wide head, prominently scaled antennae, rich but rather uniform coloration of forewings, patterned hindwings and predation on small sucking insects form a group not yet assigned to a family name (*Oedematopoda*, *Atkinsonia*, *Bonia*, *Snellenia*, *Cyanarmostis*, *Magorhabda*, *Adamantoscelsis*, *Phytophlops*). Those with more or less anteriorly protruded or dorsoventrally compressed head, non-ciliate and slightly flattened antennae in males, rather poorly patterned forewings and trophic association with ferns form another group not yet assigned to a family name (*Cuprina*, *Calicotis*, *Thylacosceles*, *Pachyrhabda*, *Actinoscelis*, *Lissocnemitis*, *Thylacosceloides*). A revised taxonomy of the bright-legged moths is published by the author in the World Catalogue of the family Stathmopodidae.



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## ***Cosmopterosis* Amsel and *Schacontia* Dyar (Glaphyriinae: Crambidae): case studies about pyraloid diversity and biology in the Neotropics**

**M. ALMA SOLIS**

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Pyraloids are especially plagued by adults that exhibit obvious gaps in the external morphology, but lack divergence in internal morphology such as in genitalia, or the reverse where adults do not exhibit obvious gaps externally, but divergence in internal morphology can be great among species, and finally the most difficult state is where neither the external or internal morphology exhibit much divergence. For these morphological reasons alone, it has been commonly found that genera upon further study result in more new species than have been previously included under a name. But the actual size of the organism has presented various different challenges in the study of previously unexplored pyraloid groups in the Neotropics. Subfamilies or genera with large-winged adults have been found to have more synonyms and fewer new species. Glaphyriine species with smaller-winged taxa have fewer or no synonyms, but have had more new species discovered. In Costa Rica more than 27% of the Glaphyriinae are new species in comparison to pyraloids, such as spilomeline genera, that have wings 4 times as long. Two glaphyriine genera distributed throughout the Western Hemisphere, *Cosmopterosis* and *Schacontia*, exemplify common issues in the study of pyraloids small in size (< 9mm wing length). The Glaphyriinae *sensu stricto* has 33 genera and 174 species that occur mostly in the Western Hemisphere, with the exception of a few species in *Hellula*. It is a biologically diverse group with many plant feeders on Brassicales, but some species feed on *Opuntia* and lichens, and still others do not feed on plants and are parasites in *Polistes* wasp nests. Collaboration with Janzen & Hallwachs on Costa Rican pyraloids has added larval and molecular data to propel discovery about diversity in pyraloids despite the morphological or biological challenges.

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15:25

## A report on several long-overlooked species of the *Sufetula* genus group (Pyraloidea: Crambidae: Lathrotelinae) found in greenhouses and imports into Europe

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We report the encounter of several species of the recently reinstated subfamily Lathrotelinae found in greenhouses and imports into Europe. The presence of these small, inconspicuous, dull-coloured moths has long been overlooked, and some might have been established in greenhouses for up to 15 years. As known larvae of this group feed on the roots of monocotyledons, our findings are of concern to nurseries of ornamental plants such as palms and cultivated grasses. We intend to identify the collected material based on DNA barcoding as well as external and genital morphology of the adults, and here we present first results of these efforts. We find the genera *Sufetula* and *Diplopseustis* in need of revision as several studied species seem to be misplaced. Furthermore we detected cryptic diversity of hitherto undescribed species.





Thursday · 1 October 2015

## The fauna of Phycitinae (Pyralidae) in China

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Phycitinae are one of the largest subfamilies in the family Pyralidae. The larvae of Phycitinae feed on various host-plants, dried products, and some species are harmful to stored products in warehouses or parasites in galls or nests of Hymenoptera. Given the phycitines' economic and ecological significance, it is of great importance to study the Chinese Phycitinae systematically. Dr. H. Höne was the first researcher to collect Lepidoptera in China during 1930s, followed by Caradja (1926–1939), Shibuya (1928) and Caradja & Meyrick (1933–1938). Roesler (1965–1993) did research on Palearctic Phycitinae with many taxa of the Chinese fauna. The first Chinese entomologist studying Phycitinae was Wu (1938), who listed 19 genera and 36 species in his Catalogues, followed by Luh & Kuan (1953), who recorded 56 genera and 170 species. Yang (1977) recorded 11 genera and 15 species from northern China. Wang (1980) recorded 13 genera and 18 economic species, and after that a few articles about Chinese Phycitinae have been published. With the support from the National Natural Science Foundation, the systematic study of Phycitinae in China was intensified at the beginning of the 21th century, and more than 20 papers have been published, such as, Du, Li & Wang (2002a, b), Ren & Li (2006a, b), Kuang & Li (2009), Liu & Li (2010, 2011, 2012, 2013), Qi *et al.* (2014a, b), Liu & Li (2014a, b, c), Ren & Li (2015), etc. To date, we know 372 species in 106 genera from China. Among them, more than 100 species are described as new to science, about 150 species in 44 genera are reported for the first time in China, but several species still await investigation. In addition, a monograph on Chinese Phycitinae is in preparation.

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16:00

## Lepidoptera on ferns, mostly in Africa

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Africa is a predominantly dry continent, so ferns are scarce except in rainforests and at high altitude. The Hosts data base (NHM) lists 6+ species on ferns from Africa and the Afromoths website only 5 species.

Musotiminae is a subfamily whose larvae are said to feed chiefly on ferns, a number of species occur on Mt Kenya so we decided to look for larvae.

Larvae were found by searching on several species of fern, sometimes feeding externally – usually on the underside of the fronds. Some were within spinings and a few Noctuid larvae were noted.

Although nine different species of Musotiminae had been taken as adults at this locality we only succeeded in rearing two species, one of which had not been taken as an adult on Mt Kenya. In addition we bred one Spilomelinae species (*Pilocrocis patagialis*) and one Noctuid (*Nyodes* sp.).

In England a Musotimine species has occurred since 2009, originating from Australia or New Zealand. Searches of ferns yielded larvae of this species enabling its life history to be documented.



Thursday · 1 October 2015

## DNA barcoding of the microlepidopteran fauna of Madagascar

16:00  
16:25

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Recent checklists have inventoried ~ 29 superfamilies, ~ 74 families and ~ 4,589 species for the Lepidoptera of Madagascar, but sequencing effort was modest until 2015. Expeditions in 2011 – 2014 focused on freshly sampled microlepidopterans in both degraded areas and primary rainforest biotopes (0 – 2,000 m). 1,674 specimens, prioritising singletons, were identified as far as feasible morphologically at MNHN. DNA barcoding had a success rate of 98.7%, for profiling this tropical fauna. Species-level matches from batch identification requests were improved by individual queries. Among 21 superfamilies and ~ 45 different families, Blastobasidae and Peleopodidae are newly reported, while Micropterigidae and Opistegidae have no described Malagasy species. 1,403 non-macroheteroceran individuals yielded 968 BIN clusters, most new. ~ 13% of individuals remain unassigned to family/superfamily, either using morphology or DNA barcode trees. Interestingly, 20% of species from degraded habitats were also found outside the island, but only 3% from primary forests. We reveal anthropogenic influences (12/30 broadly distributed BINs are known invasives) and faunal connections (11.7% of BIN overlaps were exclusively Afrotropical). We also highlight the vast taxonomic effort needed to document the disappearing diversity of Madagascan microlepidopterans.



1

## Morphology of basistipal fimbriate pockets of *Cactoblastis cactorum*

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Unique structures with an apparent glandular function have been found on the ventral surfaces of the larval heads of the cactus moths, *Cactoblastis cactorum* and *Melitara prodenialis*. In *C. cactorum* the two invaginated pockets on the basistipal region contain 66-75 fimbria that are wide basally base and tapered apically. In cross-section the fimbria are hollow and are filled with an electron-opaque material. The fimbria arise from the apex of a projecting sac within each pocket. The sac includes a reservoir filled with an electron-opaque material and is lined at the bottom with a single layer of large cells. The cellular structures include extensive rough endoplasmic reticula, numerous mitochondria, and large nucleus and are indicative of a secretory function.



## Relating colour and toxicity in the burnet moths (Zygaenidae)

2

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Species in the burnet moth family possess chemical defences, toxic cyanogenic glycosides which they can both sequester from their host plants and synthesise *de novo*. This toxicity is advertised with conspicuous wing patterns, known as aposematic signals, which warn predators of the prey's unprofitability, so as to deter them from attacking. While the theory of warning colouration is well-established, there is still much controversy over whether these visual displays can function as quantitative signals of defence potency. The variation in wing colour and pattern seen in the Zygaenidae, both subtle within the Zygaeninae and more dramatic between sub-families, provides an ideal system in which to test the idea of honesty in aposematic signalling. Accurate measures of several colour and pattern metrics, such as luminance, saturation and chromatic contrast, are obtained by photographing the wings of each individual; these images are then mapped to avian visual models, to investigate how these signals are perceived by their intended receivers, the potential predators of burnet moths. Biologically-relevant measures of signal form can thus be related to the individual's toxin levels, determined by liquid chromatography - mass spectrometry, in collaboration with Dr Mika Zagrobelny at the University of Copenhagen. Testing for correlations between display and defence will suggest whether wing colour can be used as a reliable cue for toxicity, both within and between species, as well as between sexes. Based on a range of species found in France and the United Kingdom, with a special focus on *Zygaena filipendulae*, this project will make a significant contribution to the current debate over honesty in aposematic signalling.



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## The prominent moths (Notodontidae) from the Middle and Eastern Anatolia, Mediterranean and Black Sea Regions of Turkey

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We report the recent distribution and systematic classification of the Notodontidae family in eighteen provinces located in the Middle and Eastern Anatolia, Mediterranean and Black Sea Regions of Turkey. External morphology and the genitalia characters of adults with photographs were given. Totally, 29 species, *Cerura vinula vinula* (Linnaeus, 1758), *C. intermedia* (Teich, 1896), *Furcula furcula turcica* Schintlmeister, 1998, *F. bifida bifida* (Brahm, 1787), *F. interrupta interrupta* (Christoph, 1867) and *F. interrupta syra* (Grum-Grshiamilo, 1899), *Dicranura ulmi* (Denis & Schiffermüller, 1775), *Harpyia milhauseri* (Fabricius, 1775), *Stauropus fagi fagi* (Linnaeus, 1758), *Drymonia dodonaea wagneri* de Freina, 1981, *D. melagonea esmera* de Freina, 1981, *D. querna djezina* Bang-Haas, 1937, *D. velitaris pontica* (Rebel, 1908), *Notodonta dromedarius pontica* Witt, 1980, *N. derbendica* Daniel, 1965, *N. tritopha irfana* de Freina, 1983, *Peridea anceps* (Goeze, 1781), *P. korbi korbi* (Rebel, 1918) and *Pheosia tremula* Clerck, 1759, *Pterosoma palpina palpina* Clerck, 1759, *Ptilodon saerdabensis* (Daniel, 1938), *Ptilophora plumigera* (Denis & Schiffermüller, 1775), *Phalera bucephala becephala* (Linnaeus, 1758), *P. bucephaloides* (Ochsenheimer, 1810), *Spatalia argentina* (Denis & Schiffermüller, 1775), *Rhegmaphila alpina osmana* Friedel, 1967, *Clostera curtula curtula* (Linnaeus, 1758), *C. pigra staudingeri* Koçak, 1980 and *C. anastomosis* (Linnaeus, 1758) were determined, belonging to six subfamilies of the Notodontidae which are Cerurinae Butler, 1881, Dicranurinae Duponchel, 1845, Notodontinae Stephens, 1829, Ptilodontinae Packard, 1864, Phalerinae Butler, 1886 and Pygaerinae Duponchel, 1845, respectively.

Turkey, extending from Asia to Europe, is one of the species-richest countries in the western Palaearctic. Determination of moth species, their biology and areals is crucial for Turkey's faunistic studies. Like many other species, many notodontid species are facing extinction due to global climate change and human activities. A detailed study of specimens of the Notodontidae family from four different regions of Turkey shows that *Stauropus fagi* (Linnaeus, 1758) is a new record for the Mediterranean region in Turkey.



## The need to re-assess the taxonomy of the genus *Colias* Fabricius, 1807 (Pieridae) in Central Europe

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Taxonomy is a scientific discipline, which involves a study of several other disciplines. Accurate taxonomic knowledge and ability of correct identification are key requisites for the higher classification of organisms. A variety of complications making species classification extremely difficult are found within the genus *Colias*. In Central Europe, four species cause special problems even for experienced specialists since generally applied behavioural, ecological, morphological differences are often unavailable or insufficient for reliably telling species apart. In case of *C. alfacariensis* and *C. hyale*, the only credible distinguishing morphological feature is the coloration of caterpillars. Alleged diagnostic features based on external morphology, such as shape of wings, eyespots or colour of wings are often causing more obstructions than leading to the correct identification of specimens. We examined the reliability of these characters and also studied whether DNA barcoding could shed more light on the identification issues. The second pair of similar species include *C. croceus* and *C. erate*. Identification of these species is mostly based on wing colour and absence of scent-producing organ in *C. erate*. On the other hand, occurrence of yellow form of *C. croceus*, and possibly also hybridization, is complicating safe identification of these two species. This pair is also known for the barcode sharing. To verify the alleged differences in morphology of male ectodermal genitalia, geometric morphometrics tools were used. This method is generally recognized as one of the most powerful morphological method to study morphological variability. Morphological study was followed by DNA barcoding and after confirmation of barcode sharing between *C. croceus* and *C. erate*, by the study of seven nuclear genes.

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## 5 “*Diaphania*” *costata* (F.), a pest of Apocynaceae in the south-eastern United States

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“*Diaphania*” *costata* (F.) (Crambidae: Spilomelinae) is endemic to Central America and the Caribbean, where it is a leaf-folder on Apocynaceae. Although it has been recorded in Texas, USA for decades, in fact it has become widespread across the southeastern US, usually misidentified as *Palpita* spp. We recently discovered it defoliating *Vinca major* L. and other ornamental Apocynaceae in Georgia and North Carolina. Collection records indicate that the population has expanded from Texas since at least 1979. It is related to *Cydalima perspectalis* (Walker), and like the box tree moth, it has been historically placed in many genera. Analysis of an expanded dataset from Mally & Nuss (2010) indicates that *D. costata* and related Neotropical Spilomelinae should be transferred to the Palaeotropical genus *Parotis* Hübner. With many exceptions, the trend of host associations in the *Glyphodes-Diaphania* group is feeding on laticiferous plants.





## Preliminary results of the pine processionary moth (*Thaumetopoea pityocampa* (Denis & Schiffermüller, 1775)) monitoring in Albania

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The pine processionary moth (PPM, *Thaumetopoea pityocampa*) is one of the main defoliating pests of pines (*Pinus* spp.) in the Mediterranean. The urticating hairs of the caterpillars can cause serious human health problems too. The species has been studied in many contexts in several European countries recently. Despite the numerous papers in Europe, Albania is one of the less studied areas of PPM. In Albania the larvae feed mainly on black pine (*Pinus nigra*), that covers approximately 110,000 hectares in the country. We have compared PPM abundance in the northern (Pukë) and southern (Korcë) range of *P. nigra* to evaluate the relative infection. The study was carried out from early July until middle of August in 2014, using long life PPM pheromone lures and sticky plates for the trapping. During the survey 207 traps were setup in the South and 208 traps in the North. Altogether 21,692 specimen were collected, 11,347 in the North (Pukë) and 9,537 in the South (Korcë). Average number of caught individual/trap ( $\pm$  SE) was 47.69 ( $\pm$  13.29). We found significant difference in PPM abundance between the northern and southern range. Caterpillar nests also were counted in a 10-m radius around each trap. We found altogether 8104 nests and the number nests was also significant higher in North than in South Albania. We found a weak positive correlation between the number of trapped moths and the counted caterpillar nests. The influence of elevation on the moth and caterpillar nets abundance was also studied, but we have not found any correlation between them. To evaluate the exact PPM abundance, distribution and economical importance in Albania further investigation is required.



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## First results of long-term monitoring of moths in the middle of the Mediterranean Basin with a Rothamsted light trap

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Long term monitoring projects of moths are very scarce in Europe, and generally concentrated in northern countries. This occurs despite the importance of such kind of data to identify ecosystem changes due to long term ecological dynamics as climate and land-use changes. Few Rothamsted light traps works in the Mediterranean Basin, insufficient to depict changes in an early-warning area especially for climate driven changes in animal communities.

A contribute to increase the Mediterranean network of Rothamsted light traps was done last year by the Sila National Park, MaB UNESCO Area, and the Unità di Ricerca per la Selvicoltura in Ambiente Mediterraneo. One trap was located in the locality Vivaio Sbanditi, Sila Massif, Calabria, southern Italy. The study area is located at 1345 meters of altitude, and its forest cover is dominated by *Pinus laricio* and other planted conifers (*Picea abies*, *Larix decidua*). Few deciduous trees are present.

The trap was installed the 17<sup>th</sup> July 2014 and weekly activated as long as the temperature was above 0° Celsius. Then it was re-activated in springtime 2015 at the snowmelt. 34 trap nights were carried out until now allowing us to collect 185 identified species for a total of 2,740 specimens. Further 286 additional specimens are still unidentified at species level.

Among others, the most interesting species was *Eupithecia conterminata*, surely known in Italy only for this site (identification confirmed by Vladimir Mironov, Russia). Its larvae feed on *Picea abies*, a tree present in Peninsular Italy only in artificial plantations.



## Effectiveness of UV LED light traps for macro-moth communities sampling

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In order to sample moths communities in Mediterranean forests, high brightness (400-315 nm, light angle 120°) UV-LED strips-based light traps have been used. UV LED light strips, for a total of 150 LEDs, enveloped a tube placed above the collecting funnel. Traps were powered by a 12V battery. Traps were positioned at approximately 1.30 meters above the ground level. UV LEDs have the following advantages: (1) to be low energy demanding (4.8W/m); (2) to have a longer life than conventional lights (about 50K hours); (3) to have a high and constant luminous intensity throughout the course of their life (about 1200 lumens/m equivalent to a 60W mixed light lamp); and (4) to be resistant to hits and sudden changes in voltage.

Traps equipped with UV-LED strips are now used in four areas representative of the main Calabrian forest types (Southern Italy). One trap/stand was placed within 9 forest stands representing different maturation stages of forests. Samplings have been carried out monthly since May 2015. It was possible to evaluate the performance of UV-LED light traps placed in the pine forests of the Sila Massif comparing collected data with those collected by a Rothamsted light trap (200W incandescent lamp), in a similar forested habitat of the same mountainous massif.

The Rothamsted trap captured 272 individuals belonging to 67 species in three nights of sampling. During the same nights, UV-LED light traps collected a median of 770 individuals (1744 max; 166 min) and 86 species (97 max; 43 min). 7 out of 9 UV-LED traps collected more species and individuals than the Rothamsted trap. Therefore, UV-LEDs showed a high effectiveness in attracting moths in comparison to a well known light source.



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### A survey of Erebidae, Nolidae and Euteliidae in southern and northeastern of Iran

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Noctuoidea are the largest superfamily of Lepidoptera which has not yet been fully investigated in Iran. In order to inventory such an important group, faunistic studies on the families Erebidae, Nolidae and Euteliidae were made by light traps mainly in the three Iranian provinces of Fars, Khuzestan and Khorasan-e-Razavi during 2009-2011. Here we report part of the results including 42 taxa belonging to 26 genera and 7 subfamilies. Among these, one species is newly reported for the Iranian fauna, together with 23 new provincial records. Taxonomy of the species and their distribution pattern are discussed.



## DNA-barcoding campaign of Lepidopteran leaf miners in Siberia

10

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DNA-barcoding campaigns significantly facilitate inventory of the regional insect faunas and help to reveal cryptic and overlooked species. Lepidopteran leaf miners are highly diverse taxonomic group of insects with number of important pests of orchard crops, ornamental woody plants and forest plantations. In Northern Asia, particularly in Siberia this insect group is still very poorly studied. We carry DNA-barcoding campaign of leaf-mining moths collected on woody plants in botanical gardens, urban and wild plantations in Siberia. We sampled both immature stages (larvae and pupae) and reared adults. We obtained DNA-barcodes of 296 specimens and identified 44 species feeding on 55 plant species from Adoxaceae, Betulaceae, Fagaceae, Malvaceae, Oleaceae, Rosaceae, Salicaceae and Ulmaceae. The two families best represented are: Gracillariidae (23 species) and Nepticulidae (11). Eight species were first records for Siberia and twenty one species were new regional records. Three putative new species of Gracillariidae were discovered feeding on *Caragana* and *Tilia* in Northern Asia. This ongoing barcoding campaign will greatly contribute to the biodiversity exploration, molecular taxonomy, phylogeography and invasive ecology of leaf mining moths. The work was supported by LE STUDIUM (France) and RFBR (grant # 15-29-02645 **офи\_м**).



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

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*Aenigmatinea glatzella* Kristensen & Edwards, 2015, a recently discovered species of microlepidoptera on the Kangaroo Island off southern Australia, is a fascinating moth. Immediately upon its discovery it was clear that *A. glatzella* belonged to one of the earliest lineages of Lepidoptera, but based on its morphology, it could not be placed in an existing family, and therefore a new family – Aenigmatineidae – was erected to accommodate it. We analyzed 25 genetic loci to try to determine its relationships to other old lineages of lepidopterans and found that it is related to Neopseustidae and Acanthopterocetidae. In addition to presenting the phylogenetic results, we provide an overview of the interesting morphological features present in *A. glatzella*, which are reshaping our understanding of the evolution of the earliest lepidopteran lineages.



## Impact of changes in the fauna of Polish Tortricidae on agriculture and horticulture

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Tortricidae (Tortricidae) are the most species rich family of Polish moths with about 460 species reported so far. Global climate change increases the potential establishment and spread capability of many species which can cause considerable economic damage. In the last twenty years several dozen species have been recorded in Poland for the first time or significantly increased their reach and abundance in the country. Among them there are species of economic importance. In horticulture potentially harmful species are *Ditula angustiorana* (HAWORTH, 1811), *Cacoecimorpha pronubana* (HÜBNER, 1799) and *Grapholita lobarzewskii* (NOWICKI, 1860) but so far there are no reports on damage caused by these species in Poland. The new threat in agriculture are species from genus *Cnephasia*. In several localities in the west part of the country larvae of these leafrollers were found in numbers on cereals. Most of them belong to two species – *Cnephasia longana* (HAWORTH, 1811) and *C. pumicana* (ZELLER, 1847). The first significantly expanded its range eastward and is locally abundant. The second one is a new element in Polish fauna. This species is a serious pest of grain in many countries of Western and Southern Europe and could pose a serious threat to our crops.



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## Phylogeography of two butterfly species with similar distribution – *Boloria eunomia* and *B. selene* (Nymphalidae)

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*Boloria eunomia* and *B. selene* occur over large areas of the Holarctic region. We studied the phylogeographic patterns of both species using one mitochondrial (COI) and two nuclear genes (Wingless, Arginine Kinase). Although both butterflies have a similar distribution pattern, they do not show the same phylogeographic history. We found strong phylogeographic structure in *B. eunomia*, characterised by eight geographically distinct haplotype groups. *B. eunomia* (re)colonised northern Europe from the east and not from the south as is the case of many other species. Polish populations are probably derived from Bulgarian population and Poland might be the contact zone for different lineages of this species. Populations from Czech Republic, Germany and Austria are closely related and also derived from Bulgarian population. Populations from Spain, France and Belgium form a cluster distinct from other European populations. In contrast to this highly structured phylogeographic pattern *B. selene* is characterised by a single widespread haplotype occurring in high frequency. This pattern suggests a rapid expansion scenario. The single congruent pattern found for both species is a considerable strong genetic split between Nearctic and Palearctic populations.





## Syntomini (Erebidae: Arctiinae) of Korea

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Lepidoptera fauna of the Korean Peninsula has been intensively investigated during the last decades. Several books devoted mostly to the so called Macro moths have been published. Among elaborated groups there are also tiger moths (Erebidae: Arctiinae). Surprisingly in all these publications the information about the tribe Syntomini is completely lacking, and only representatives of the two remaining ones e.g. Lithosiini and Arctiini are included.

We would like to fulfill this gap and provide the information on all species of Syntomini recorded from the Korea. The main reason for this summary is the fact that in the collection of the Institute of Systematics and Evolution of Animals Polish Academy of Sciences there is a large sample of *Amata sperbius* (Fabricius, 1787). These specimens were collected during one of the several expeditions undertaken to North Korea by the staff of the Institute in the second half of XX century.

Except this newly recorded species the tribe is also represented in Korea by two other, already known syntomines: *Amata fortunei* (De L'Orza, 1869) and *Amata germana* (Felder, 1862). Illustrations of habitus as well as the male and female genitalia are provided for all three species. We also propose the keys for determination of species based on all three types of characters.

We also discuss the problem of occurrence of *A. sperbius* in Korea, as the species was recorded until now mostly from the tropical and subtropical regions of SE Asia. The literature data corroborate however that it is not restricted to this climate zone and the records from north India and east China come from much colder and higher elevated localities. These evidences together with the relatively poorly investigated SE Asian lepidopterofauna make the occurrence of *A. sperbius* in Korea very probable.



## 15 Flowering meadows for Saxony's butterflies

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Urbane areas have a large proportion of grass land, which is usually frequently mowed using rotating mowing machines. As a result of this practice, such areas are no longer inhabited by butterflies and people are forgetting about butterfly diversity. In May 2015, a new public project started in Saxony explaining the metamorphosis of butterflies and calling for attention of their entire life cycle during all over the year. People are asked to take action, changing the mowing system to a low frequency, partial mowing of a certain area and using cutting instead of rotating mowing machines.

In order to publicize the project across the Federal State, all relevant information is available via a freely available brochure as well as on the website [www.schmetterlingswiesen.de](http://www.schmetterlingswiesen.de). Thirty local collaborators across Saxony take care of at least one meadow and organize public events in order to demonstrate the alternative mowing system and identify butterflies and their food-plants. Press releases are used to get public awareness. A smartphone app for interactive identification and recording of butterflies is in preparation.

After the first few months of the project, we recognize a big interest in this topic, but frequently observe a slow change when it comes to practice. Obstructive are especially multi-year maintenance agreements and the cost-intensive, but necessary change of mowing equipment in horticulture companies. On the other hand, there are already positive observations. Where the mowing system changed, e.g. from 6-times last year to so far zero this year, some common species like *Polyommatus icarus*, *Ochlodes sylvanus* and *Maniola jurtina* already returned in couples, raising hope for newly established populations.

The project is a collaboration of the Sächsische Landesstiftung Natur und Umwelt, the Senckenberg Museum of Zoology Dresden, the Naturschutzbund Deutschland (NABU) Landesverband Sachsen e. V., the Deutscher Verband für Landschaftspflege e. V. (DVL), the Landschaftspflegeverband Torgau-Oschatz e. V. and is funded by the Lotterie Glücksspirale.



## Molecular insight into *Erebia euryale* (Nymphalidae) phylogeography in a less studied region of Carpathian Mountains

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Global climate has changed and fluctuated repeatedly during the Quarternary (Pleistocene) and it have led into recent glacial periods. Influences of last glaciation within the family Nymphalidae in Western Carpathians is not well studied. Oscillations in temperature conditions likely caused important changes in distributions and genetic structures of species. These changes can be traced by studying extant patterns of genetic diversity and allele distribution using molecular methods. Rapidly evolving mitochondrial DNA markers are expected to be informative to address these questions. We also tested the usefulness of nuclear DNA markers in clarifying phylogeographic patterns of species. We furthermore tested the validity of present species limits of the butterfly genus *Erebia* (Lepidoptera: Nymphalidae: Satyrinae) and elucidated their phylogeographic and phylogenetic histories using cytochrome oxidase subunit I (COI), control region (mtDNA D-loop, CR) of mitochondrial genome and three nuclear markers. We observed distribution of different haplotypes being associated with southern and carpathian populations. The geographical extension of haplotypes in Carpathians elucidated phylogeography of *E. euryale* in Western Carpathians. We conclude that 1.) important refugial area has been located in southeastern Europe; 2.) important refugial areas also existed in parts of the Western Carpathians; 3.) genetic pattern shown by the species of the Southern Carpathians populations revealed their probable re-colonisation routes from the Balkan Peninsula to the northern parts of Europe in postglacial period. According to several previous studies, certain regions in southern Europe and Balkans were a main origin of re-colonisation for most species currently occurring in the northeastern and western Europe.

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## New informative characters in the female genitalia in assessing the phylogeny of Palearctic Satyrina

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Female genitalia of many taxa of butterflies have not been studied so far. This also concerns the genera of the Palearctic group of Satyrinae, the subtribe Satyrina, surprisingly, including some well-known and widely researched genera such as *Minois*, *Satyrus* or *Oeneis*. From among 15 genera associated with Satyrina female genitalia were studied previously only for *Hipparchia* and *Pseudochazara*, and some information was published for *Neominois*. Our study shows that the female genitalia of these 15 genera are widely divergent and present a number of characters that do not occur in other genera of Satyrinae. Molecular phylogenies of Satyrinae referred to only a few genera of Satyrina, such as *Hipparchia*, *Brintesia*, *Chazara*, *Pseudochazara* and *Neominois*. A more comprehensive phylogenetical proposition is available on Tree of Life ([tolweb.org](http://tolweb.org)), and it is the most recent source of information on the infrasubtribal relationships. It does not resolve however the position of several genera such as *Minois*, *Paraoeneis*, *Kanetisa*, *Aulocera* and *Davidina*. Here, we examine the female genitalia of 14 genera of Satyrina (except *Davidina* unavailable for studies). We identify several undescribed characters, for which we propose new terms, especially in the pregenital and postgenital lamellae area which present extreme divergence within the examined clade. Homologous characters are identified. We confront a preliminary phylogeny based on female genitalia with previously proposed trees, based on molecular and partly, morphological data. We propose to synonymize the genus *Pseudochazara* as a subjective junior synonym of *Chazara* based on a salient synapomorphy, a well-developed appendix bursae. A rudimentary appendix bursae is also found in *Minois* however the latter genus presents a very wide ventral tray. Such a tray exists also in *Brintesia* but is massive, covering the entire ventral side of genital plates. The genus *Aulocera* although externally, especially as far as its colour pattern is concerned, is closely similar to *Brintesia* has completely divergent female genitalia, and hardly any synapomorphies can be identified, thus it confirms its separate generic status. We also suggest a synonymy between *Oeneis* and *Paraoeneis* based on far reaching genital similarities.



## The historical biogeography of the hawkmoth genus *Ambulyx* (Sphingidae) in Indonesia based on mitochondrial DNA genes

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The family Sphingidae currently comprises more than 1450 species placed in around 200 genera. Of these, *Ambulyx* (Westwood, 1847) is the largest genus of the tribe Ambulicini in subfamily Smerinthinae. It contains around 60 species with a wide distribution across the Indo-Pacific Region, from North Pakistan and India (including Sri Lanka) to Japan and North Australia. In general, we can assume that fauna of SE Asia started to disperse during late Pliocene and continued during Pleistocene using the re-emergences of a bridge between the mainland and islands. Our results show that the dispersion of the hawkmoths in this region followed the general trend. Firstly evolved a complex of species in western part of Asia and then started their dispersal to Australia together with dispersal to eastern parts of the Palaearctic Region (China, Japan and Korea). The group of species colonised Australia form together with their neighbours from New Guinea isolated group of haplotypes. On the other hand, islands of Indonesia (including Sulawesi and Moluccas) were in this case colonised repeatedly during the late Pleistocene following the dispersal routes from the west. Some species of the genus *Ambulyx* colonized for example the northern Borneo or the Lesser Sunda Islands following the dispersal routes via Philippines. Our analyses also show the monophyly of this genus.

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## The importance of long-distance dispersal and establishment events in small insects: historical biogeography of metalmark moths (Choreutidae)

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In this study we examined the importance of long-distance dispersal and establishment (LDDE) for the current distribution of metalmark moths (Choreutidae), a small microlepidopteran family with global distribution, using a dated molecular tree. By using different models in a likelihood framework we estimated the probability of LDDEs. Our sampling included 104 species of metalmark moths with representatives from all six major biogeographical regions of the world (Afrotropical, Australasian, Neotropical, Nearctic, Oriental, and Palaearctic). The resulting phylogeny is well supported and very similar to earlier works. The ancestral range for metalmark moths is estimated as being in Australasia and the Neotropics, and the historical biogeographical model that has the highest likelihood for explaining our data is the one that includes the so-called founder-event parameter, suggesting that LDDEs have played an important role in shaping the current distribution of metalmark moths. We provide an overview of the different biogeographical events estimated for the evolutionary history of metalmark moths and briefly discuss possible LDDE events in a few other groups of microlepidoptera.



## Dr. Otto Staudinger in Dresden – a biographical and historical account

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Otto Carl Heinrich Richard Staudinger (2 May 1830 in Gross-Wüstenfelde – 13 October 1900 in Luzern) belongs to the most important lepidopterists in history. He came to Dresden in 1859 and established an own insect trading company, which became the largest in its kind world wide. Besides his own collecting activities in the Mediterranean region, Staudinger employed many collectors, which were residents in interesting regions and also sent collectors to interesting places to collect Lepidoptera. About 300,000 insect specimens from around the world arrived every year at Dresden-Blasewitz. Thus the collection of Staudinger has rapidly become one of the largest private collections of butterflies and moths in the world. A staff up to 7 employees sorted and spread the material. In 1880, he was able to win the Dane Andreas Bang-Haas for his company. Bang-Haas married Staudinger's daughter, Carmen Dolores and joined as a partner the company Staudinger & Bang-Haas. Bang-Haas attended primarily by the operational business.

In this way, Staudinger had his back free to spend on scientific activity. He published 137 papers and described about 3,932 taxa as new to science, in almost all families of Lepidoptera. Among them are 518 species group taxa belonging to the European fauna and currently treated as valid. Staudinger was in contact with almost all the major lepidopterists of his time and much of his material (in particular from the tropics) became the base of descriptions by other specialists. 115 species names in Lepidoptera are devoted to Staudinger (patronyms).

From a handwritten essay of his grand daughter („Aus dem Leben meines Großvaters Entomolog Dr. Otto Staudinger † 1900“) we know some facts of the life of Staudinger and his many famous visitors.

The „exotic“ collection of Staudinger with all types he described and including several collections he purchased such as the Atkinson collection, the collection of Möschler or parts of the Herrich-Schäffer collection, was sold after his death in 1907 to the Museum für Naturkunde in Berlin. The Palaearctic collection of microlepidoptera and caterpillars followed in 1937 as well as that of macrolepidoptera, including the types described by A. and O. Bang-Haas, after the death of Otto Bang-Haas in 1948. A second collection, for commercial use only, was purchased after World War II by the company Wernicke & Kotzsch and eventually came to the Museum für Tierkunde Dresden in 1961.



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## The preliminary results of the biology of *Alucita grammodactyla* ZELLER, 1841 (Alucitidae) on *Scabiosa ochroleuca* L. in the Kraków – Częstochowa Upland (Poland)

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There are five species belonging to the Alucitidae family (Many-plumed moths) and rated to the Alucitoidea superfamily known in Poland. One of them, *Alucita grammodactyla* Zeller, 1841, was the object of studies that have been undertaken because of lack of data on the biology of this species.

These studies were carried out from 2010 to 2013. The area of the studies included mainly the Kraków – Częstochowa Upland. During the field research observations of the host plant (*Scabiosa ochroleuca* L.) and the developmental stages of the moth were carried out. The laboratory research consisted mainly in breeding, observation of the developmental stages (eggs, caterpillars, pupae, imago).

The studies discovered details concerning the place of oviposition and development of eggs; moth life cycle; the number of larval stages; the behavior of larvae, pupae and imago.

This information can be used to develop the conservation strategy of this species and its natural habitat.

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These studies were carried out within the project “Bionomics and Morphology of Developmental Stages of Some Species of *Alucita* genus (Lepidoptera: Alucitidae)” under the guidance of Prof. Tomasz Baran; The project was funded by the Faculty of Biology and Agriculture, University of Rzeszów.





## Recent distribution and status of *Zeuzera pyrina* L. (Cossidae) in Turkey

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As a xylophagous and invasive pest, the leopard moth, *Zeuzera pyrina* L. (Cossidae) became an important pest on several cultivated plants. It causes serious economic losses in the world which are reported on a wide range of host plants from a total of over 150 plant species belonging to twenty families. *Z. pyrina* has a wide range of distribution in the world. It is recorded from almost entire Europe, certain states of the U.S.A. and Canada, northern and southern Africa and Asia.

During the last decade, the Leopard moth has continued to spread in the Mediterranean region. It has been determined that *Z. pyrina* L. occurs in all the seven geographical regions of Turkey. It is common in most of these regions, except for the Aegean and Eastern Anatolian region. The latest information of the distribution area and status of *Z. pyrina* L. in Turkey is given in this research.

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## Interesting moths (Noctuidae, Erebidae, Nolidae) identified in the Rzezińskie Peatbog (Natura 2000 area)

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The insects inhabiting peatbogs are of particular importance to biodiversity in Europe. Wetlands of all kinds are often a refuge for many Boreal relict species. In Poland such areas are unfortunately among the most seriously threatened ecosystems. Moreover, because of their specific microclimates and inaccessibility, they are rarely the objects of entomological research. Moths from the families Noctuidae, Erebidae and Nolidae in and around the Rzezińskie Peatbog (Natura 2000 area) (UTM: WU84) were investigated from 2006 to 2011.

The Rzezińskie Peatbog PLB300019 is situated in western Poland (52°45' N, 16°19' E). The research was carried out from early April to late October. The research material – adult moths – were attracted to light and bait. In the outer part of the peatbog, moths were attracted to a screen illuminated by a portable generator-powered mercury vapour lamp; accumulator-powered fluorescent tube traps were used in the inner part.

The Rzezińskie Peatbog lies in a broad depression among the dunes of the Noteć Forest, which in turn is situated between the valleys of the Rivers Noteć and Warta, some 60 km to the north-west of the city of Poznań.

The protected area (236 ha) includes Lake Rzezińskie together with the adjacent, extensive transitional bog, meadows, reedbeds and willow scrub. The area is a rich mosaic of different natural habitats (7 types covering ca 80% of the surface area) defined in Annex I. This locality is of great significance for the conservation of transitional bogs, which in western Poland are rare and threatened ecosystems.

The fieldwork yielded a total of 228 species from the three families: Nolidae (6), Erebidae (22) and Noctuidae (198). Species characteristic of peatbogs and wetlands are particularly deserving of attention: *Hypenodes humidalis* Doubleday, 1850, *Mac-rochilo cribrumalis* (Hübner, 1793), *Plusia putnami* (Grote, 1873), *Acronicta menyanthidis* (Esper, 1789), *Chilodes maritima* (Tauscher, 1806), *Athetis palustris* (Hübner, 1808), *Apamea unanimis* (Hübner, 1813), *Amphipoea lucens* (Freyer, 1845), *Nonagria typhae* (Thunberg, 1784), *Celaena haworthii* (Curtis, 1829), *Phragmitiphila nexa* (Hübner, 1808), *Archanara geminipuncta* (Haworth, 1809), *Archanara dissoluta* (Treitschke, 1825), *Archanara sparganii* (Esper, 1790), *Sedina buettneri* (Hering, 1858), *Arenostola phragmitidis* (Hübner, 1803), *Lacanobia splendens* (Hübner, 1808), *Papestra biren* (Goeze, 1781), *Mythimna straminea* (Treitschke, 1825), *Leucania obsoleta* (Hübner, 1803) and *Diarsia florida* (Schmidt, 1859).



## Climatic niche characteristics of the butterflies in Europe (CLIMBER) – a new database for measuring the response of butterflies to climatic changes

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CLIMBER is a database providing information on the position and breadth of major climatic niche characteristics for almost all European butterfly species (Schweiger et al. 2014). It includes the mean annual temperature which forms (as ‘species temperature index’ = STI) the basis to calculate the ‘community temperature index’ (CTI). This index already proved to be a powerful indicator in the context of climate warming. In addition to temperature-based climatic indices, the database also includes several indices for water availability.

Here, we present new applications of this dataset, which help to assess how butterfly communities react to climatic change. The results demonstrate that butterfly communities across Europe have already been responding to climate warming by shifting their composition towards warm-adapted species. Butterfly species assemblages are fast indicators of climate change and respond to temperature fluctuations with a time lag of only 1–2 generations, supporting the assumption that CTI increases are not merely caused by land-use changes.

However, responses are smaller than anticipated from climate warming and differ among regions and according to species traits. Communities at lower latitudes and higher altitudes are changing less, and the same applies to warm-adapted specialists and forest species.

A phylogenetic analysis of the CLIMBER dataset revealed that adaptations to cold thermal limits are phylogenetically conserved while adaptations to the warm limits are not. We assume that the phylogenetic signal for cold-adaptation is a legacy of the ice ages. The lack of evidence for phylogenetic conservatism of warm-adaptations may indicate different evolutionary or ecological processes at cold and warm range margins probably caused by increased importance of biotic interactions under warmer conditions. A potential quicker adaptation to warmer conditions or a lack of range-filling at the warm ends due to biotic interactions together with anthropogenic landscape barriers to dispersal might lead to the observed climatic debts of butterflies.

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## How differences in behaviour among Macroheterocera may contribute to sampling bias in interception traps

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Quantitative community-wide moth surveys usually employ flight-interception traps equipped with UV-light emitting tubes as attractants. It has long been known that moth species differ in their responsiveness to light traps. We here studied how aspects of flight behaviour of different moth taxa may contribute to sampling bias of such traps. We directly observed the behaviour of 1420 moth individuals at a light tower (consisting of a gauze cuboid, 1.80 m high, top edge length 0.40 m, 500 W bulb) at 7 sampling sites in Pineta san Vitale, Italy. Moths were classified as either settling down immediately upon arrival, or continually flying at the gauze for extended periods of time. The latter moths are more likely to be captured by an interception trap, whereas the former may well not end up in the sampling container and therefore be under-represented in trap samples relative to their true proportions in the community. Our analyses confirmed highly significant differences between moth groups. Representatives of three taxa (Nolidae, Geometridae-Eupitheciini, Erebidae-Lithosiini) usually settled down immediately, whereas most other moth groups remained in active flight at the trap for some time. Moth behaviour was also modulated by ambient temperature. Representatives of most moth groups were less likely to settle down immediately at higher temperatures, but the opposite was observed with Eupitheciini. These results contribute to estimating the extent of sampling bias that is to be expected when analysing and interpreting automatic light-trap samples.



## A phylogeny with a larger sampling of genera reveals hidden Neotropical clades and confirms previous evolutionary hypothesis for the Arctiinae moths: preliminary results

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The most recent phylogeny of Arctiinae (Noctuoidea: Erebidae, Zaspel et al. 2014: PlosONE 9:e101975) sampled all major lineages worldwide, but the number of genera sampled was relatively small (i.e. 68) and the highly speciose Neotropical region was underrepresented. We added a large number of Neotropical genera to Zaspel et al.'s phylogeny with a comparable set of genes to assess possibly neglected Neotropical lineages. A total of eight genes and 278 taxa were used to reconstruct the phylogeny of the Arctiinae, representing all four tribes, i.e. Arctiini, Lithosiini, Syntomini and Amerilini. Maximum likelihood analysis recovered the monophyly of Arctiinae and its four tribes, as in Zaspel et al. The tribe Lithosiini was monophyletic and similarly to Zaspel's phylogeny was the sister group of the Amerilini. A total of five Lithosiini groups were recovered monophyletic and our results suggest the presence of an endemic Neotropical clade composed by genera never sampled before. Our results for the tribe Arctiini, the largest within the arctiines, differed substantially from those of Zaspel et al. Similarly to Zaspel et al.'s phylogeny the subtribe Callimorphina was recovered non-monophyletic and was the sister group of the Arctiina, which was confirmed to be monophyletic, but differently the tribe Pericopina was recovered non-monophyletic. Although Phaegopterina was recovered monophyletic in Zaspel et al. it was poorly supported; our results showed two large well supported sister clades, one of them composed exclusively of Neotropical species. The tribes Euchromiina and Ctenuchina were found to be sister groups and monophyletic, in contrast to Zaspel et al. The results described here suggest that Arctiinae classification needs to be updated and taxa from other underrepresented tropical regions should be included to a better understanding of the evolution of the Arctiinae.



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