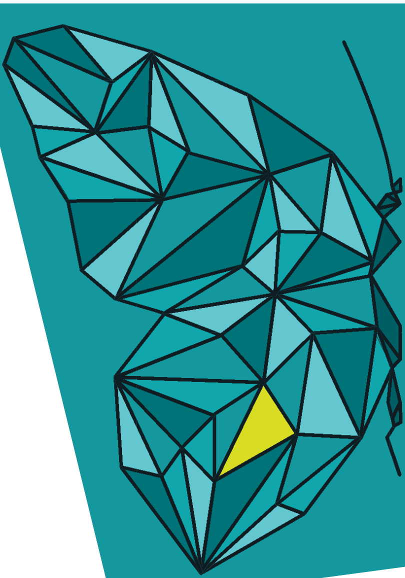

XXI EUROPEAN CONGRESS OF LEPIDOPTEROLOGY

BOOK OF ABSTRACTS

VENUES

Università degli Studi del Molise
- Aula Magna

Dipartimento Agricoltura, Ambiente, Alimenti
- Room A
- Room B

PROGRAMME

ORAL PRESENTATIONS

MONDAY, 3 JUNE 2019

University of Molise - Aula Magna

14.30 - 19.00 REGISTRATION DESK
REGISTRATION OF PARTICIPANTS

16.00 - 17.30 Welcoming words by Organizers
Welcoming words by Authorities
Welcoming words by the Italian Entomological Society - President
Welcoming words by the Societas Europaea Lepidopterologica - President

17.30 - 19.00 KEY NOTE PRESENTATIONS

Alpine microlepidoptera: diversity and survival strategies in a harsh environment
Jürg Schmid
Chemical communication between moths, plants and microbes
Peter Witzgall

19.00 - 20.00 A WELCOME DRINK

TUESDAY, 4 JUNE 2019

University of Molise - Department of Agricultural, Environmental and Food Sciences
Parallel Sessions

ROOM A

Symposium: Evolutionary history of Lepidoptera. Chair: Jadranka Rota

9.00 - 9.40 Key Note: Manually curated data: the next step in Lepidoptera phylogenomics?
Niklas Wahlberg, Carlos Peña, Christopher Wheat, Jadranka Rota, Maria Heikkilä, Lauri Kaila, Victoria Twort
9.40 - 10.00 Advancing Lepidoptera phylogenetics: sequencing hundreds of genes from hundred-year-old museum material
Marianne Espeland, Elsa Call, Lars Dietz, Christoph Meyer
10.00 - 10.20 Diversification of butterflies and moths from the time of the dinosaurs to the present day: a supertree approach
Andrea Chiocchio

10.20 - 11.00 Coffee break

11.00 - 11.20	**Estimating the age of Lepidoptera with fossils meeting strict selection criteria – preliminary results** Maria Heikkilä
11.20 - 11.40	**The relationship between wing pattern and venation, from Micropterigidae to Macroheterocera** Sandra R. Schachat
11.40 -12.00	**Diversification of Nymphalidae butterflies: insights from a species-level phylogeny** Nicolas Chazot, Niklas Wahlberg, Tobias Hartman
12.00 - 12.20	**Diversification dynamics in metalmark moths (Choreutidae): did long-distance dispersals lead to higher diversification rates?** Jadranka Rota
12.20 - 12.40	**Placing the mysterious *Whalleyana* with museomics** Victoria Twort, Joël Minet, Chris Wheat and Niklas Wahlberg
12.40 - 14.00	**Lunch break and POSTER SESSION**
14.00 - 14.20	**Towards a stable global Noctuidae taxonomy** Kevin Keegan, Reza Zahiri, Jadranka Rota, Paul Goldstein, Chris Schmidt, Niklas Wahlberg, Alberto Zilli, Don Lafontaine, David L. Wagner
14.20 - 14.40	**A comprehensive molecular phylogeny of Geometridae (Lepidoptera) with a focus on enigmatic small subfamilies** Leidys Murillo-Ramos, Gunnar Brehm, Pasi Sihvonen, Axel Hausmann, Sille Holm, Hamid Ghanavi, Erki Õunap, Andro Truuverk, Hermann Staude, Egbert Friedrich, Toomas Tammaru, Niklas Wahlberg
14.40 - 15.00	**Biogeography and diversification dynamics of the moth family Geometridae (Lepidoptera)** Hamid Reza Ghanavi, Nicholas Chazot, Isabel Sanmartín, Leidys Murillo-Ramos, Sebastián Duchêne, Pasi Sihvonen, Gunnar Brehm, Niklas Wahlberg
15.00 - 15.20	**Phylogeny of Pericopina (Lepidoptera: Erebidae, Arctiinae, Arctiini) and relocation of some misplaced genera** Simeão de Souza Moraes, Marcelo Duarte
15.20 - 15.50	**Coffee break**
15.50 - 16.10	**In and out of America: ecological and species diversity in Holarctic giant silkmoths suggests unusual dispersal, defying the dogma of a purely Asian origin** Daniel Rubinoff, Camiel Doorenweerd
16.10 - 16.30	**Phylogenetic placement of the skipper genus *Malaza* (Hesperiidae) from Madagascar is illuminated by recovery of a mitogenome from the 140-year-old holotype of *Trapezites fastuosus* Mabille, 1884** David C. Lees, Jing Zhang, Jinhui Shen, Qian Cong, Blanca Huertas, Geoff Martin, Nick V Grishin
16.30 - 16.50	**A phylogenetic framework for *Schinia* flower moths (Noctuidae: Heliothinae)** B. Christian Schmidt, Reza Zahiri
16.50 - 17.10	**The decline of European butterflies: an evolutionary approach** Nicolas Chazot, Alexandre Antonelli

17.10 – 17.30	To bee or not to bee: morphological and behavioural comparison of two new species of bee and wasp mimicking clearwing moths from Malaysia Marta Skowron Volponi, Paolo Volponi
17.30 – 17.50	Developing online observation platforms and portals for moth recording Jurriën van Deijk
17.50 – 18.10	Phylogeny and systematics of Syntomini (Erebidae: Arctiinae) Łukasz Przybyłowicz, David C. Lees, Mauricio M. Zenker, Niklas Wahlberg

ROOM B

General Session

9.40 - 10.00	Size-related life-history traits in geometrid moths: a comparison of a temperate and a tropical community Sille Holm, Juhan Javoiš, Ants Kaasik, Erki Õunap, Robert B. Davis, Freerk Molleman, Heikki Roininen, Toomas Tammaru
10.00 - 10.20	An evolutionary approach to peppered moth (*Biston betularia*) in southern Scandinavia Bafraw Karimi
10.20 - 11.00	Coffee break
11.00 - 11.20	Tribe Perizomini – a taxonomists' trash bin (Lepidoptera, Geometridae, Larentiinae) Erki Õunap
11.20 - 11.40	A double-edged sword: unrecognized cryptic diversity and the taxonomic impediment in the hyperdiverse genus of moths (Lepidoptera: Geometridae) Simeão de Souza Moraes, Leidys Murillo-Ramos, Patrícia Avelino Machado, Hamid Reza Ghanavi, Luiza Magaldi, Karina Lucas Silva-Brandão, Massuo Jorge Kato, André Victor Lucci Freitas, Niklas Wahlberg
11.40 - 12.00	The enigma of *Triphosa taochata* Lederer, 1870 (Lepidoptera: Geometridae: Larentiinae) clarified with morphological methods and DNA barcoding Dominic Wanke, Axel Hausmann, Hossein Rajaei
12.00 - 12.20	The monograph series *The Geometrid Moths of Europe* is now completed Hossein Rajaei, Pasi Sihvonen, Axel Hausmann, Peder Skou
12.20 - 12.40	Review of the Lecithoceridae (Gelechioidea) in Afrotropical Region Jun-Mo Koo, Kyu-Tek Park
12.40 - 14.00	Lunch break and POSTER SESSION
14.00 - 14.20	Synopsis of the tribe Gnorimoschemini (Lepidoptera: Gelechiidae), with a special approach to the Central American and northern South American fauna Patricia Esther Corro-Chang

14.20 - 14.40 Yponomeutidae and ultrasound
Liam O'Reilly, David Agassiz

14.40 - 15.00 Where do the intermediates of fritillary butterflies come from: testing the hypothesis of homoploid hybrid speciation in *Melitaea didyma – M. persea – M. acentria* species complex
Elena Pazhenkova, Vladimir Lukhtanov

15.00 - 15.20 Mito-nuclear discordance in *Colias* butterflies (Lepidoptera, Pieridae): the role of interspecific hybridization and *Wolbachia* infection
Nazar Shapoval, Galina Kuftina, Roman Yakovlev, Anatoly Krupitsky

15.20 - 15.50 Coffee break

15.50 - 16.10 The origin and genetic structure of *Lymantria dispar* in Europe
Michal Rindoš, Reza Zahiri, Alexander Schintlmeistr

16.10 - 16.30 A detailed study of a gynandromorph Lep-Leviathan (Saturniidae)
David Adamski, Diana Marques

16.30 - 16.50 New data on the effectiveness of the sex attractants from the series 'EFETOV-2' for the males of Procridinae species (Zygaenidae): results of field observations in Italy
Konstantin A. Efetov, Gerhard M. Tarmann, Elena E. Kucherenko

16.50 - 17.10 Genomic evidence suggests *Mesapamea remmi* is an imaginary moth species (Lepidoptera: Noctuidae)
Pasi Sihvonen, Kyung Min Lee, Karl-Erik Lundsten, Marko Mutanen

17.10 - 17.30 Vertical stratification structure of a temperate forest caterpillar community in eastern North America
Carlo L. Seifert, Greg P.A. Lamarre, Martin Volf, Leonardo R. Jorge, Scott E. Miller, David L. Wagner, Vojtech Novotny

17.30- 17.50 Mapping the Lepidoptera of Germany: First results
Axel Steiner, Matthias Nuss, Robert Trusch

19.30 - 23.30 CONGRESS DINNER (LA PIANA DEI MULINI – www.lapianadeimulini.it)

WEDNESDAY, 5 JUNE 2019

University of Molise - Department of Agricultural, Environmental and Food Sciences
Parallel Sessions

ROOM A

Symposium: Chemical ecology and multitrophic interactions. Chair: Pasquale Trematerra

9.40 - 10.00 Deception strategies in butterfly social parasites of ants
Francesca Barbero, Luca Pietro Casacci, Simona Bonelli, Emilio Balletto

10.00 - 10.20 Attraction of Zygaenidae and some other Lepidoptera by the sex attractants from the series 'EFETOV-2' in the Crimea
Konstantin A. Efetov, Elena E. Kucherenko

10.20 - 11.00 Coffee break

11.00 - 11.20 Long-term trends in spring caterpillar biomass available to birds in Hungarian oak forests
Csaba Gáspár, László Gimesi, Csaba Béla Eötvös, Anikó Hirka, György Csóka

11.20 - 11.40 Zygaenids do not lie – the fatal impact of wind-transported pesticides on biodiversity
Gerhard M. Tarmann

11.40 - 12.00 *Cydia fagiglandana* sex attractants history: from identification to field application
Antonio De Cristofaro, Sonia Ganassi, Carmela Di Domenico, Dalila Di Criscio, Massimo Mancini, Francesco Parisi, Giacinto Salvatore Germinara, Giuseppe Rotundo

12.00 - 12.20 Management of *Thaumetopoea pityocampa* in recreational areas: Mating-Disruption and Mass-Trapping
Marco Colacci, Pasquale Trematerra

12.20 - 13.30 Lunch break and POSTER SESSION

ROOM B

Symposium: Lepidoptera – Plant interactions. Chair: Carlos Lopez-Vaamonde

9.00 - 9.40 Key-note: Evolution of active pollination and mutualism in *Epicephala* (Gracillariidae)
Atsushi Kawakita

9.40 - 10.00 Evolution of gall-induction and host-plant associations in Phyllanthaceae-feeding *Caloptilia* (Lepidoptera: Gracillariidae)
Antoine Guiguet, Issei Ohshima, Atsushi Kawakita, Astrid Cruaud, Jean-Yves Rasplus, David Hembry, Min Wang, David Giron, Carlos Lopez - Vaamonde

10.00 - 10.20 Historical herbaria to study past distribution and invasion history of phyllophagous insects
Natalia Kirichenko, Evgeniy Akulov, Nikita Babichev, Carlos Lopez-Vaamonde

10.20 - 11.00 Coffee break

11.00 - 11.20 The *Salix* feeding species of *Stigmella* in Europe: almost as difficult to separate as their hosts (Lepidoptera: Nepticulidae)
Erik J. van Nieukerken, Tobias Hartman

11.20 - 11.40 Building a database of Lepidoptera – host – parasitoid associations recorded for the Afrotropical region, results and preliminary analyses
Hermann Staude

11.40 - 12.00 Nocturnal moth-based pollen transport networks at UK farmland ponds
Richard E. Walton, Jan Axmacher, Carl D. Sayer, Helen Bennion.

12.00 - 12.20 Butterfly extinctions
Emilio Balletto, Francesca Barbero, Simona Bonelli, Luca Pietro Casacci, Cristiana Cerrato, Leonardo Dapporto, David Lees

12.20 - 13.30 Lunch break and POSTER SESSION

14.30 - 19.30 CONGRESS FIELD TRIP (CAMPITELLO MATESE)

THURSDAY, 6 JUNE 2019

University of Molise - Department of Agricultural, Environmental and Food Sciences
Parallel Sessions

ROOM A

Symposium: Diversity of Italian Lepidoptera. Chair: Alberto Zilli

9.00 - 9.40 Key-note: how long are 3 kilometres for a butterfly? Ecological constraints and functional traits explain high genetic differentiation between Sicily and the Italian Peninsula
Stefano Scalercio, Alessandro Cini, Mattia Menchetti, Raluca Vodă, Simona Bonelli, Adele Bordoni, Luca Pietro Casacci, Vlad Dincă, Emilio Balletto, Roger Vila, Leonardo Dapporto

9.40 - 10.00	Cryptic species within mimetic complexes: the Italian *Syntomis* moths between divergence and pattern constraints (Lepidoptera: Erebidae) Andrea Chiocchio, Paola Arduino, Rossella Cianchi, Luciano Bullini, Alberto Zilli
10.00 - 10.20	The study of Lepidoptera of Bergamo district (Lombardy, Northern Italy, Bergamo Province): a biodiversity still largely unknown Giovanni Marchese, Melania Massaro
10.20 - 11.00	Coffee break
11.00 - 11.20	New discoveries and a revised view on the Zygaenidae fauna of Italy Gerhard M. Tarmann, Konstantin A. Efetov
11.20 - 11.40	In search of the evolutionary origin of the endemic Sardinian blue butterfly Valentina Todisco, Andrea Grill
11.40 - 12.00	Molise, a small Italian region with a high Lepidoptera biodiversity value Andrea Sciarretta
12.00 - 12.20	Diversity of macromoth communities in mountain forests of southern Apennines Stefano Scalercio
12.20 - 12.40	In search of the ecological determinants for the exceedingly restricted and most outstanding Italian endemic moth, *Brahmaea (Acanthobrahmaea) europaea* Hartig Renato Spicciarelli
12.40 – 14.00	Lunch break and POSTER SESSION

General Session

14.00 - 14.20	Distribution of butterflies in Estonia as revealed by an active mapping project: patterns, changes and causal factors Anu Tiitsaar, Daniel Valdma, Erki Õunap, Tiit Teder, Jaanus Remm, Toomas Tammaru
14.20 - 14.40	Zygaenidae (Lepidoptera) of the eastern Mediterranean region of Turkey Başak Ulaşlı, Konstantin A. Efetov, Feza Can
14.40 - 15.00	Geometrid moths of the Baikal Region: fauna, DNA barcoding and taxonomy Ilya Makhov
15.00 – 15.20	The spatial and temporal occurrence of marsh fritillary (*Euphydryas aurinia*) in Croatia Toni Koren, Petra Novina, Jelena Babić
15.20 - 15.50	Coffee break
15.50 - 17.30	GENERAL MEETING

ROOM B

Symposium: Collections and digitisation. Chair: Geoff Martin

9.40 – 10.20	Keynote speaker: **The digitisation of Lepidoptera collections** Geoff Martin
10.20 - 11.00	**Coffee break**
11.00 - 11.20	**More about storing Butterflies in Bags** Mónica Cruz, Luc Willemse, Rob de Vos, Max Caspers
11.20 - 11.40	**Introducing the Lepidoptera collections in the Natural History Museum Aarhus: history, challenges and perspectives.** Thomas J. Simonsen
11.40 – 12.00	**Wow, what an insect! Digitalization in teaching and in environmental education** Jani Järvi, Pasi Sihvonen
12.00 - 12.20	**Biologer: an open source platform for gathering species occurrence data in Eastern Europe** Miloš Popović, Toni Koren, Ivona Burić, Ana Golubović, Nenad Živanović
12.20 – 12.40	**A list of the primary type specimens of Lepidoptera in the "Muséum d'histoire naturelle de Genève" Geneva, Switzerland** Bernard Landry, Patrick Schmitz, Corinne Reuteler
12.40 - 14.00	**Lunch break and POSTER SESSION**

General Session. Chair: Thomas J. Simonsen

14.00 – 14.20	**Western Indian Ocean Islands in the view of butterfly zoogeography** Zdeněk Faltýnek Fric, Jatishwor Irunbgam Singh, Meenakshi Irungbam Chib, Michal Rindoš
14.20 - 14.40	**Lower Cretaceous Micropterigidae (Lepidoptera) in Spanish amber** Víctor Sarto i Monteys
14.40 - 15.00	**Monoclonal antibodies to lipophorin of the Zygaenidae as a tool for biomedical research** Konstantin A. Efetov, Ekaterina V. Parshkova
15.00 – 15.20	**Phylogeographic pattern of genetic variation in *Aporia crataegi* (Lepidoptera, Pieridae)** Valentina Todisco, Raluca Vodã, Vazrick Nazari
15.20 - 15.50	**Coffee break**
15.50 - 17.30	**GENERAL MEETING**

CLOSING REMARKS

POSTER PRESENTATIONS

Analysing incomplete faunistic knowledge to estimate future species richness distribution under global warming effects: the Iberian butterflies (Papilionoidea)
Enrique García-Barros, Helena Romo Benito, Juan Pablo Cancela Vallejo, Miguel L. Munguira

The residual wetland in the Mediterranean basin and their importance for the protection of endangered species: biodiversity of Microlepidoptera fauna in the salt marshes of southeastern Sicily
Salvatore Bella

Five years of BMS España: Past, present and future
Cancela JP, García-Barros E, Romo Benito H, Munguira ML

Hawkmoths (Lepidoptera: Sphingidae) of the Caldera de Lubá. Bioko Island (Equatorial Guinea)
Pablo Cobos Suárez, Ignacio Martín Sanz, José Luis Viejo Montesinos

Wing pattern variation in the Alcon blue butterfly in Scandinavia over the last century
Philip H. Folman, Thomas J. Simonsen, Roberta E. Hunt, David R. Nash

Lepidoptera Tortricidae from Calabria (southern Italy)
Lorenzo Goglia, Pasquale Trematerra, Stefano Scalercio, Marco Colacci

Motorway wedges as a space for butteflies – a case study from the Czech republic
Vladimír Hula, Tomáš Kuras, Monika Mazalová

Four pyrales from central Spain: Interesting or unusual data from Madrid: *Bostra obsoletalis* (Mann, 1864), *Synaphe predotalis* (Zerny, 1927), *Hypotia miegi* Ragonot, 1895 and *Asalebria geminella* (Eversmann, 1844)
Gareth Edward King, José Luis Viejo Montesinos

Four crambids from central Spain: Interesting or unusual data from Madrid: *Hyperlais rivasalis* (Vázquez, 1905), *Evergestis istatidalis* (Duponchel, 1833), *Evergestis merceti* Agenjo, 1933 and *Evergestis frumentalis* (L. 1761) (Crambidae: Cybalomiinae, Evergestinae)
Gareth Edward King, José Luis Viejo Montesinos

The southern swallowtail (*Papilio alexanor*) in Croatia: rare or just overlooked?
Toni Koren, Dubravko Dender, Matea Martinović, Mladen Zadravec, Ivona Burić

Order Lepidoptera (the Butterflies and Moths) in Shar Planina Republic of Macedonia
Vladimir Krpach

Synergy of two molecular datasets to refine the phylogeny of Crambidae (Lepidoptera: Pyraloidea)
Théo Léger, Richard Mally, Christoph Neinhuis, Matthias Nuss

How do river groves influence the distribution and conservation of butterflies in the Mediterranean region?
Begoña Martín Costa, José Luis Viejo Montesinos, Manuel Martín Alzás

Past and present: a comparative analysis of the butterfly fauna in the mainland part of Dubrovnik-Neretva County
Matea Martinović, Dubravko Dender, Ana Štih, Mladen Zadravec, Jelena Babić, Toni Koren

A surprising finding concerning the noctuid moth *Phlogophora meticulosa* (Linnaeus, 1758) (Lepidoptera Noctuidae)
Rinaldo Nicoli Aldini

Morphological observations on a gynandromorph of *Maniola jurtina* (Linnaeus, 1758) (Lepidoptera, Nymphalidae, Satyrinae)
Rinaldo Nicoli Aldini

Butterflies as bioindicators of heavy metal contamination: a case study at Terni basin valley (Central Italy)
Matteo Pallottini, Enzo Goretti, Gianandrea La Porta,Chiara Argenti, Chiara Petroselli, Paola Gravina, Roberta Selvaggi, David Cappelletti

Records of Lepidoptera in Habitats Directive from Matese National Park (Southern Apennine, Italy)
Francesco Parisi, Pasquale Buonpane, Massimo Mancini, Antonio De Cristofaro

New records of Lepidoptera in Habitats Directive from Aspromonte National Park (Southern Apennine, Italy)
Francesco Parisi, Alessandro Bruno Biscaccianti, Antonino Siclari, Francesco Manti, Elvira Castiglione, Antonio De Cristofaro

Natural enemies of *Euphydryas aurinia provincialis* (Boisduval, 1828)
Manuela Pinzari, Mario Pinzari, Valerio Sbordoni, Donatella Cesaroni

DNA barcoding of Croatian butterflies – preliminary results
Martina Šašić, Iva Mihoci, Martina Podnar, Mladen Kučinić

Use of Lidar data to define habitat use by common butterflies
Guido Tellini Florenzano, Sandro Piazzini

The current state of Lepidoptera biodiversity in Ethiopia
Tesfu Tujuba, Andrea Sciarretta

New records and an updated checklist of the butterfly fauna (Lepidoptera: *Papilionoidaea* and *Hesperioidea*) of Puglia, South-eastern Italy
Giuseppe Cagnetta, Enrico Altini, Daniela Clemente, Rocco Labadessa, Alessio Vovlas

Butterfly richness and diversity in Mediterranean coastal dunes environment: diversity patterns along a vegetation gradient in South-East Italy
Alessio Vovlas, Enrico Altini, Daniela Clemente, Gianfranco Ciola

A complete time-calibrated multi-gene phylogeny of the European butterflies
Martin Wiemers, Nicolas Chazot, Oliver Schweiger, Christopher W. Wheat, Niklas Wahlberg

85 years of coastal forest succession and its effect on Mediterranean moth communities – a case study
Mirko Wölfling, Britta Uhl, Lara Holynski, Konrad Fiedler

Correcting of the identification of a sugarcane butterfly leaf eater in southwest Iran: *Pelopidas thrax* (Hesperiidae)
Ahlam Zerganipour, Mehdi Esfandiari, Mohammad Mahdi Rabieh

Sexual dimorphism in the wing shape and size of *Pelopidas thrax* (Lepidoptera, Hesperiidae)
Ahlam Zerganipour, Mehdi Esfandiari, Mohammad Mahdi Rabieh

Identification of butterflies of "Insect and Mite Collection of Ahvaz" at Shahid Chamran University of Ahvaz, Iran
Ahlam Zerganipour, Mehdi Esfandiari, Mohammad Mahdi Rabieh

Interpreting butterfly responses to climate change using space-for-time substitution: a case study from two Mediterranean mountains
Konstantina Zografou, Robert J. Wilson, John M. Halley, Vassiliki Kati, Andrea Grill

FRIDAY, 7 JUNE 2019

POMPEII - POST CONGRESS TOUR

ABSTRACTS

ORAL PRESENTATION

MONDAY, 3 JUNE 2019

AULA MAGNA

Alpine microlepidoptera: diversity and survival strategies in a harsh environment

Jürg Schmid
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The past few years have seen an ever increasing number of newly described microlepidoptera species in the Alps. This progress is mostly due to the inscreased use genetic data which has unveiled many cases of so called „cryptic diversity". While these laboratory-based results advance rapidly, our knowledge about the biology of many – even trivial – species is still shockingly poor. Thus, modern textbooks often devote large sections of species descriptions to wing pattern and genital structures, while the section „biology" simply says: „first stages unknown". The aim of the present talk is to give a temptative overview of the altitude-related diversity of alpine microlepidoptera. Photographic documentation of many hitherto unknown first stages will be presented and their host plants will be discussed. Some examples of environment-adapted life-cycles of high altidude micromoths species are demonstrated and finally, the question of the highest altitude level where life for lepidoptera is possible in the Alps, is addressed.

Key words: alpine microlepidoptera, diversity, survival strategies

Chemical communication between moths, plants and microbes

Peter Witzgall

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The air that surrounds us is filled with scents. Plants, microbes and all animals produce and release volatile chemicals that deliver a message and make sense - to all those organisms who can perceive and respond to the incoming signals. Since ambient air contains so many volatiles, specific detection is crucial for chemical communication. Volatiles carrying information must be reliably filtered out against the abounding background: perception of specific volatiles must be sensitive, and should not be overwhelmed by the many other ambient volatiles. In animal olfaction, olfactory receptors (ORs) that are specifically tuned to odorant ligands provide this salient interface between environment and responder. Specificity of ORs varies, with some tuned to single or very few ligands, while others are seemingly are more broadly tuned, unless the true key ligands for these have not yet been found. Olfaction is basic to insect reproductive behaviour, including mating, oviposition and feeding and reflects accordingly also phylogenetic diversification. Knowledge of OR genes provides an experimental handle to identify the odorants that mediate mating, oviposition and feeding. Identifying ORs and their key odorants adds not only to taxonomic studies, but most importantly, it yields new perspectives on insect ecology and evolution.

During my lecture in Campobasso, which I am looking forward to, I will attempt to afford proof for this statement.

Key words: chemical ecology, olfaction, odorant receptors, pheromone, kairomone

Related references

Bengtsson JM et al. 2014. A predicted sex pheromone receptor of codling moth *Cydia pomonella* detects the plant volatile pear ester. Front Ecol Evol 2:33

Borrero-Echeverry F et al. 2018. Plant odour and sex pheromone are integral elements of specific mate recognition in an insect herbivore. Evolution 72:2225-2233

Gonzalez F et al. 2017. Antennal transcriptomes of three tortricid moths reveal putative conserved chemosensory receptors for social and habitat olfactory cues. Sci Rep 7:41829

Walker WB et al. 2016. The chemosensory receptors of codling moth *Cydia pomonella* - expression in larvae and adults. Sci Rep 6:23518

TUESDAY, 4 JUNE 2019

ROOM A

EVOLUTIONARY HISTORY OF LEPIDOPTERA

Manually curated data: the next step in Lepidoptera phylogenomics?

Niklas Wahlberg[1], Carlos Peña[2], Christopher Wheat[3], Jadranka Rota[1], Maria Heikkilä[4], Lauri Kaila[4], Victoria Twort[1,4]

[1]Department of Biology, Lund University, Lund, Sweden; [2]Private address; [3]Department of Zoology, Stockholm University, Stockholm, Sweden; [4]Luomus, Finnish Museum of Natural History, Zoology Unit, University of Helsinki, Finland

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Molecular systematics has gone through a large revolution in the past three decades. In an amazingly short period of time, we have advanced from sequencing a handful of select genes to sequencing whole genomes. We have now reached a stage in the field of molecular systematics where the amount of data is no longer a constraint; rather it is the quality of data that we need to deal with. We explore the idea of manually curating a set of reliably aligned DNA sequences using published transcriptomes of Lepidoptera. We have identified a set of 332 genes from published transcriptomes and genomes of Lepidoptera, which are commonly expressed in sequenced transcriptomes and are unproblematic to align at the amino acid level. These have each been checked manually and together they are highly informative about relationships in Lepidoptera. I will discuss the results and the concept of making such data readily available to researchers in a format that is easy to use.

Key words : phylogenomics, Lepidoptera, Ditrysia relationships

Advancing Lepidoptera phylogenetics: Sequencing hundreds of genes from hundred year old museum material

Marianne Espeland[1], Elsa Call[2], Lars Dietz[1], Christoph Meyer[1]
[1]Zoological Research Museum Alexander Koenig, Bonn, Germany; [2]Department of Biology, Lund University
E-mail address: m.espeland@leibniz.zfmk.de

During the last few years the use of next generation sequencing (NGS) for phylogenetic studies has exploded, and also in Lepidoptera there is an increasing amount of such studies based on transcriptomes, target enrichment methods, RAD sequencing and whole genomes. Most of the hitherto applied approaches require good DNA quality and quantity. Museum collections are repositories for diversity collected during the last 200 or so years, but because of the damage of DNA that occurs over time, efficient use of old museum specimens for phylogenetic studies has been difficult. We here present a target enrichment approach to sequence >1500 loci across Lepidoptera for both new and old material. Using this approach we sequenced >500 loci for 127 year old material and more than 1000 loci for specimens collected during the 1930's and later. Although there is correlation between specimen age and the number of sequenced loci there is large variation in sequencing success likely also related to how the specimen has been treated at the time of collection and stored through time.

Key words: NGS, RAD, DNA, Lepidoptera

Diversification of butterflies and moths from the time of the dinosaurs to the present day: a supertree approach

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Lepidopterans are the second most diverse group of multicellular organisms. Great efforts are currently being made to understand how and when such an extraordinary diversification occurred. We tested a new procedure to study the diversification of such high species-rich groups of living organisms. We combined all the available molecular and fossil data in order to investigate the pattern and the timing of diversification across lepidopterans. We generated a single supertree, made of thousands of species, following a tree grafting procedure which consists of three steps: (1) building a solid backbone tree of all lepidopterans, which is fossil calibrated and includes representative of most superfamilies and families, (2) building a large number of phylogenies of smaller groups that contain all the sequenced species belonging to these groups, (3) grafting and scaling these smaller phylogenies onto the tips of the backbone tree, in order to obtain a time-calibrated supertree. Here we show the procedure and the results elucidating the mode and tempo of diversification for Papilionoidea, comparing our results with the previous published data, and the first time-calibrated phylogeny of Bombycoidea and Lasiocampoidea. Finally, we discuss the implications and perspectives of this approach for future research on the evolutionary history of other high species-rich groups of living organisms.

Key words: Bombycoidea, diversification, fossils, Lasiocampoidea, Lepidoptera, Papilionoidea, phylogenetics

Estimating the age of Lepidoptera with fossils meeting strict selection criteria – preliminary results

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I will present new results by international teams re-examining the identifications of known fossil Lepidoptera. A better understanding of the lepidopteran fossil record is emerging as recent advances in research on the morphology and systematics of many groups help make identifications and phylogenetic placement of the fossils more accurate. However, the results also show that the lepidopteran fossil record includes incorrectly dated specimens, erroneous or unsubstantiated identifications, and even forgeries. Of the few reliably identified fossils, a selection is used to date a phylogenetic tree based on 200 taxa and 332 genes. The results of this analysis shed light on the origin and diversification of lepidopteran lineages.

Key words: fossils, evolutionary history, divergence times

The relationship between wing pattern and venation, from Micropterigidae to Macroheterocera

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In an attempt to designate wing pattern homologies across superfamilies, I have studied the relationship between wing pattern and venation in various lineages of Lepidoptera. Wing patterns typically conform to the predictions of one of two models. Under the first model, the "alternating wing-margin model," each transverse band of color-whether dark or light-straddles exactly one vein along the costal margin of the wing. Under the second model, the "uniform wing-margin model," bands of the same color-whether dark or light-straddle each vein along the costal margin of the wing, with bands of the other color reaching the costa between those veins. Under either model, lack of expression can reduce the transverse bands to spots.

The alternating wing-margin model was first described in Tortricidae, has been found to hold for Micropterigidae, and has been used to identify homologies between butterfly wing patterns (the nymphalid groundplan) and the plesiomorphic wing pattern for crown Lepidoptera. The predictive power of this model was confirmed when it was successfully used to pinpoint the exact location of a previously unknown wing vein in Lepidoptera, Sc_2 (observed in Agathiphagidae). The uniform wing-margin model has been found to hold for most of the microlepidopteran genera examined thus far—in the families Psychidae, Tineidae, and Xyloryctidae—and also for the noctuid subfamily Acronictinae. Wing patterns in Geometridae do not follow the predictions of either model.

Key words: color pattern, evolution, microlepidoptera, morphology, scales

Diversification of Nymphalidae butterflies: insights from a species-level phylogeny

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Nymphalidae are the most diverse family of butterflies with more than 6000 species described. Despite their diversity they are relatively well known and large amounts of DNA sequence data have been produced over the years. We assembled a dataset of 2868 species of Nymphalidae for which one to eleven gene fragments were available. The tree was assembled using a tree grafting procedure and time-calibrated using secondary calibrations from our recent time-calibrated tree of butterflies. In addition, we compiled information about biogeographic distribution of species and we generated a large dataset of body size. We estimated ancestral biogeographic ranges, we estimated the dynamics of speciation and extinction rate through time and across different lineages and investigated whether this dynamic correlates with the biogeographic distribution of lineages and/or with phenotypic evolution. We found in particular that tropical regions show very contrasted patterns of diversification through time. South-East for example was a major source of dispersal events during the early period of diversification and the Neotropics were characterized by low extinction rate. However, we found no relationship between either body size or the rate of body size evolution and speciation or extinction.

Key words: Nymphalidae, diversification rate, historical biogeography, body size.

Diversification dynamics in metalmark moths (Choreutidae): did long-distance dispersals lead to higher diversification rates?

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As lepidopterists we are aware of great variation in species richness among different groups of butterflies and moths, as well as among different areas in the world. Such variation ultimately results from the heterogeneous dynamics of speciation and extinction processes. Yet, which factors – biotic or abiotic – actually explain such dynamics? In our study we explored how colonizing new areas as well as new host plants affects diversification dynamics in metalmark moths (Choreutidae). We first inferred a molecular phylogeny for 256 species of choreutids (ca. 40% of known species) from a dataset of about 8,000 base pairs (10 nuclear and 1 mitochondrial gene) using maximum likelihood. After time-calibrating the tree we estimated a historical biogeography hypothesis with BioGeoBEARS and we also inferred the evolutionary history of host plant use. Then we compared different models of lineage diversification, partitioning the dynamics of speciation/extinction either according to the pattern of historical biogeography or host plant use to assess which factor explains the diversification of metalmark moths the best.

Key words: BioGeoBEARS, Choreutidae, diversification, dispersal, historical biogeography, host plants

Placing the mysterious *Whalleyana* with museomics

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Whalleyana is a genus of moth endemic to Madagascar. Very little is known about the two species that make up this genus, including their phylogenetic placement within Lepidoptera. In order to assess the taxonomic positioning of *Whalleyana*, we utilize whole genome sequencing of *Whalleyana vroni* and four potentially related species. Due to the fact that *Whalleyana vroni* has not been seen in Madagascar since the 1990's, DNA was extracted and sequenced from museum specimens. *De novo* genome assembly resulted in highly fragmented assemblies, however we were able to recover the majority of our 332 genes of interest (manually curated gene set for Lepidoptera). This data was combined with our existing Lepidoptera dataset, encompassing a diverse range of taxa spanning over 200 species. The phylogenetic position of *Whalleyana* based on our phylogenomic analysis will be discussed.

Key words: *Whalleyana*, phylogenomics, museomics

Towards a stable global Noctuidae taxonomy

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The Noctuidae are a cosmopolitan group of approximately 12,000 species in 1,100 genera. A recent paper, focusing on the noctuid subfamily Amphipyrinae, sequenced DNA from 57 genera of amphipyrines and ~120 noctuid genera in total with stunning results: the 57 genera of apmhipyrines were found to belong in ten distinct subfamily-level lineages – with two of these lineages perhaps being new subfamilies. Here, we expand upon that recent study, inferring a phylogeny for ~350 noctuid genera (~1/3 of all described noctuid genera). We placed special emphasis on selecting type-genera for all higher-level taxa in Noctuidae, as well as expanding the focus of our geographic sampling beyond North America and Europe. Our preliminary findings suggest much work remains to reconcile noctuid taxonomy and phylogeny, with many genera in need of reassignment, subfamilies to describe, and even genera with species in separate subfamilies!

Key words phylogenetics, systematics, taxonomy, Noctuidae, moth

A comprehensive molecular phylogeny of Geometridae (Lepidoptera) with a focus on enigmatic small subfamilies

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Our study aims to investigate the relationships of the major lineages within the moth family Geometridae, with a focus on the poorly studied Oenochrominae-Desmobathrinae complex, and to translate some of the results into a coherent subfamilial and tribal level classification for the family. We analyzed a molecular dataset of 1206 Geometridae terminal taxa from all biogeographical regions comprising up to 11 molecular markers that includes one mitochondrial (COI) and 10 protein-coding nuclear gene regions (Wingless, ArgK, MDH, RpS5, GAPDH, IDH, Ca-ATPase, Nex9, EF-1alpha, CAD). The molecular data set was analyzed using maximum likelihood as implemented in IQ-TREE and RAxML. We found high support for the subfamilies Larentiinae, Geometrinae and Ennominae in their traditional scopes. Sterrhinae is monophyletic only if *Ergavia* Walker, *Ametris* Hübner and *Macrotes* Westwood, which are currently placed in Oenochrominae, are formally transferred to Sterrhinae. Desmobathrinae and Oenochrominae are found to be polyphyletic. The concepts of Oenochrominae and Desmobathrinae required major revision and, after appropriate rearrangements, these groups also form monophyletic subfamily-level entities. Oenochrominae *s.str.* as originally conceived by Guenée is phylogenetically distant from *Epidesmia.* The latter is hereby described as the subfamily Epidesmiinae Murillo-Ramos, Sihvonen & Brehm, **subfam. nov.** Epidesmiinae are a lineage of “slender-bodied Oenochrominae” that include the genera *Ecphyas* Turner, *Systatica* Turner, *Adeixis* Warren, *Dichromodes* Guenée, *Phrixocomes* Turner, *Abraxaphantes* Warren, *Epidesmia*

Duncan [& Westwood] and *Phrataria* Walker. Archiearinae are monophyletic if *Dirce* and *Acalyphes* are formally transferred to Ennominae. We also found that many tribes were para- or polyphyletic and therefore propose tens of taxonomic changes at the tribe and subfamily levels. Archaeobalbini **stat. rev.** Viidalepp (Geometrinae) is raised from synonymy with Pseudoterpnini Warren to tribal rank. Chlorodontoperini Murillo-Ramos, Sihvonen & Brehm, **trib. nov.** and Drepanogynini Murillo-Ramos, Sihvonen & Brehm, **trib. nov.** are described as new tribes in Geometrinae and Ennominae, respectively.

Key words: Phylogeny, new subfamily, moths, Epidesmiinae, taxonomy, loopers

Biogeography and diversification dynamics of the moth family Geometridae (Lepidoptera)

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Highly diverse groups offer a great opportunity to study the processes which have shaped their diversity. Within Lepidoptera, moths of the family Geometridae present one of these very diverse groups which is distributed all around the globe. Based on the recent work of Murillo-Ramos et al. where the most complete phylogeny of the group was obtained, here we present a first study on the diversification dynamics and biogeographic processes which have shaped the actual diversity and distribution ranges of this family. In the absence of reliable fossils for the group, using secondary calibration points available from the literature, we constructed a time calibrated phylogeny using BEAST2 software. This first dated tree was further used as the base for our macroevolutionary and biogeographic analyses. In order to study branch-specific diversification patterns BAMM was used. The accuracy of this software has been highly debated in the recent years. Therefore, a different implementation of branch-specific diversification model in RevBayes was also used to be able to compare the results. The overall picture of diversification in the family present a quasi-constant speciation rate with the exception of few more recent independent groups which appears to have a sudden threefold increase in their speciation rates. Extinction rates do not seem to vary at all in the whole tree. In order to evaluate the historical biogeography of the group, a time-stratified biogeographical analysis was performed using RevBayes. The biogeographic analysis of the geometrid moth family illustrates numerous interesting dispersal and expansion events and elucidates the important role of Neotropic and Australia in the early history of this group.

Key words: Diversification, Biogeography, Geometridae, Lepidoptera

Phylogeny of Pericopina (Lepidoptera: Erebidae, Arctiinae, Arctiini) and relocation of some misplaced genera

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Pericopina (Lepidoptera: Erebidae, Arctiinae, Arctiini) are distributed exclusively in the Neotropical region and until recently the subtribe comprised 37 genera. Studies on the taxonomy and systematics of this group are scarce, and the last phylogenetic study available placed some Afro-Indo-Malayan genera among the Neotropical Pericopina. Through a survey of adult morphological characters we analyzed the phylogenetic relationships in Pericopina with the inclusion of *Nyctemera* Hübner and other Afro-Indo-Malayan genera as putative members of this subtribe. In addition, we tested the monophyly of *Dysschema*, a key-genus for understanding the evolutionary patterns related to the extreme sexual dimorphism and polymorphism in Pericopina. A cladistic analysis based on 164 morphological characters did not corroborate the monophyly of Pericopina: *Xenosoma* Felder is the only genus among the Neotroprical pericopines related to the Afro-Indo-Malayan species; *Scearctia* Hering is closelly related to the Lithosiini and *Pteroodes* Butler shows some morphological affinities with Phaegopterina. These genera are enrolled in supra-generic groups with which they share phylogenetic affinities. *Dysschema* was also not supported according its present taxonomic composition.

Key words: pericopines, morphology, neotropical, *Dysschema*

In and out of America: ecological and species diversity in Holarctic giant silkmoths suggests unusual dispersal, defying the dogma of a purely Asian origin

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There is growing evidence that the North Atlantic Land Bridge may have had a significant, underappreciated, role in structuring Northern Hemisphere biodiversity. Understanding the biogeography of less vagile animals with specific habitat requirements could provide fine-scale information about the duration and environmental conditions of both the North Atlantic Land Bridge and the Bering Land Bridge. *Saturnia* giant silkmoths have a relictual distribution from the Neogene, with species and subgenera endemic to sub-regions across nearly the entire Northern Hemisphere.

We sequenced six nuclear and mitochondrial genes totaling 4,674 base pairs from representatives of all subgenera, and augmented this with publicly available COI sequences to build a dataset covering 34 *Saturnia* species--about half of the described species, including every region where they occur. Datasets were subjected to phylogenetic, molecular dating and biogeographic analyses.

We found that adding a 'Jump' parameter to a Dispersal-Extinction-Cladogenesis (DEC) model results in contradictory biogeographic inferences, with the Jump dispersal model being more biologically plausible for *Saturnia*. In contrast to previous assumptions, we found that *Saturnia* has a much earlier origin in North America, with a secondary colonization of Europe, most simply explained by a relatively recent (19.6–11.7 Ma ago) transit across the North Atlantic Land Bridge, and subsequent dispersal across all of Eurasia. Without Jump dispersal, *Saturnia* biogeography requires complex patterns of in-situ extinction and recolonization followed by bursts of dispersal and speciation.

While DEC+J models usually fit data better than DEC models, they cannot be directly compared. However, in cases where jump dispersal is a reasonable assumption, the +J parameter may be appropriate. Allowing Jump dispersal in *Saturnia* moth biogeography invokes far fewer assumptions and suggests the use of both Beringia and the North Atlantic Land bridge; the importance of the latter for other groups may be underestimated.

Key words: Beringia, North Atlantic Land Bridge, *Saturnia*, *Calosaturnia*, *Rinaca*, *Eudia*, *Agapema*, *Neoris*, *Perisomena*, Saturniidae

Phylogenetic placement of the skipper genus *Malaza* (Hesperiidae) from Madagascar is illuminated by recovery of a mitogenome from the 140 year old holotype of *Trapezites fastuosus* Mabille, 1884

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The genus *Malaza* (Hesperiidae) has three described species, all endemic to the mainland of Madagascar. One of them, with lavishly coloured underside wings, *M. fastuosus*, has not been reported in the wild for nearly 50 years. We used a single foreleg of the (at least) 140 year-old holotype specimen of *Trapezites fastuosus* Mabille, 1884 from the collection of the Natural History Museum London without destruction of external morphology to extract DNA and assemble a complete mitogenome from next generation sequencing reads. Phylogenetic analysis of available skipper mitogenomes places *Malaza* towards the base of Hesperiidae, closer to Heteropterinae than to Hesperiinae. Available mitogenomes of these groups have monocot-feeding caterpillars, although the biology of *Malaza* remains elusive. It appears to be a member of an evolutionarily highly distinct ancient skipper lineage, morphologically with several unusual features (e.g. hairy eyes and loss of a tubular vein M_2 in the hindwing).

Key words: Madagascar, Hesperiidae, phylogeny, *Malaza*, next generation sequencing

A phylogenetic framework for *Schinia* flower moths (Noctuidae: Heliothinae)

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The genus *Schinia* is one of the most diverse among the Noctuidae, and their evolutionary success is associated with a diversification of hostplant-specialist feeding strategies across the Asteraceae and other plant families. Most species have a highly specialized ecology closely tied to the host plant, where adult flight coincides with flowering phenology, adult and larval phenotypes that are cryptic on the host plant, and specialized reproductive morphology to permit insertion of eggs into particular plant tissue. The extreme variation in adult wing pattern, coupled with conserved internal morphology, has previously made it difficult to hypothesize relationships within *Schinia* and related genera. We present a molecular phylogenetic framework for the genus, and examine patterns of hostplant shifts and concomitant morphological adaptations.

Key words: Noctuidae, Heliothinae, molecular

The decline of European butterflies: an evolutionary approach

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As many other organisms, populations of butterflies in Europe are declining as the result of the major global changes. Several attempts have already been made at different scales to identify the ecological factors explaining why some species are coping better than others with these changes. However, this has rarely been done within an evolutionary framework. Here, we combined published datasets of body size, range size, voltinism and dispersal capacity with ecological niche information and population trends across European butterflies and analyzed them using a new complete phylogeny. For three dimensions of the ecological niche – climatic, habitat, trophic (host-plants) – we estimated the rate of niche evolution and niche breadth. We tested for correlations between traits and ecological niche components while considering phylogenetic relationships and we tested which factors significantly explain why some species are declining. We found that slower habitat evolution and less generations per year tend to increase the risk of declining. However, we also identified a high sensitivity to the datasets used and the definition of endangered species.

Key words: European butterflies, population trends, ecological niche, phylogeny

To bee or not to bee: morphological and behavioural comparison of two new species of bee and wasp mimicking clearwing moths from Malaysia

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Clearwing moths (Lepidoptera: Sesiidae) are a classic example of Batesian mimicry, being non-toxic lepidopterans that imitate species that display defence mechanisms, i.e. members of the order Hymenoptera – bees and wasps. Two new species of clearwing moths, *Heterosphecia pahangensis* Skowron, 2015 and *Pyrophleps ellawi* Skowron Volponi, 2017, have been described from lowland dipterocarp primary rainforests of Peninsular Malaysia. Although they occur in the same habitat and both belong to the Osminiini tribe, they can be immediately distinguished in the field, for *H. pahangensis* is a bee mimic, and *P. ellawi* is a potter wasp mimic. *H. pahangensis*' has a bee-like posture and appearance, bright bands on the abdomen and tufts of hair-like scales on the hind legs, in some individuals with bright yellow patches which most probably imitate bees' *corbicula*. On the other hand, *P. ellawi* has a slender, dark blue body, long legs and hind leg tufts that are hidden under the wings in the sesiid's typical resting position (and thus unlike the pollen-laden hind legs of bees). The hind legs of both species are non-functional in terms of locomotion: the moths seem to use them as a mimicry feature only and, occasionally in *H. pahangensis*, to chase off conspecifics from puddling spots. *H. pahangensis* was the first species of clearwing moth reported to mud-puddle (the process of sucking up liquids from moist substrate), providing insight into a novel aspect of Sesiidae ecology. A number of Oriental species were later observed puddling, including *P. ellawi*. Interestingly, *H. pahangensis* and *P. ellawi* puddling on the same river bank would be immediately distinguishable from each other also in flight – the bee mimic flies in a rugged, zigzag trajectory, in a similar manner to a bee, whereas the wasp mimic has a faster, more regular flight, traces larger curves and is very difficult to tell apart in flight from potter wasps co-occurring in the same area. Thus, their mimicry includes not only morphological aspects, but behaviour as well. The original species descriptions published in Zootaxa and ZooKeys both include supplementary videos showing unique footage of the moths' behaviour in their natural habitat and additional material has been recently recorded.

Keywords: clearwing moth, Batesian mimicry, Sesiidae, new species, behaviour, Malaysia

Developing online observation platforms and portals for moth recording

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For more than two centuries, lepidopterists have been collecting moths in the Netherlands. Besides professionals, a growing number of volunteers are getting involved. This creates many opportunities for citizen science projects. The specimens are not only collected for private collections, but especially photographs are taken to document recorded species. In order to use these observations for scientific purposes the data are entered into several online observation portals. Where validation in the past used to be by checking collection material, nowadays it is increasingly based on photographic evidence. I will present an overview of the validation procedure to obtain reliable records and will discuss the potential advantages of disseminating this information by facilitating open access. Eventually, these data can be used to assess biodiversity changes in relation to moths.

Key words: Moths, Online observations, Open access, Validation

Phylogeny and systematics of Syntomini (Erebidae: Arctiinae).

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The Old World tribe Syntomini is the most neglected of the three major groups of the subfamily Arctiinae (Noctuoidea: Erebidae). In none of the previous morpho-genetic studies was Syntomini sampled adequately enough to provide information about the tribe's systematic diversity and relationships above species level. As such data are of crucial importance for a comprehensive understanding of arctiine diversity and evolution, we have investigated the relationships of the major lineages of Syntomini based on up to eight mitochondrial and nuclear genes and 91 species representing 39 genera. We cover most of the known genera and major geographic regions, including, for the first time, Madagascar, where there is a significant syntomine radiation. We find that the thyretines in particular, which are restricted to the Afrotropical region, are paraphyletic. As a result we propose to treat Thyretini as an artificial assemblage and synonymise it under Syntomini. All but one of the Madagascan radiation of syntomines comprise a monophylum, the exception being the monobasic genus *Fletcherinia* Griveaud which is related to at least one African member of *Ceryx* Wallengren. Also surprising from a biogeographic point of view is that the genus *Dysauxes* Hübner, which includes the European Handmaiden moth, turns out to be nested within the Madagascan radiation. Our study also makes clear that much more detailed studies are needed to revise not only *Ceryx* and *Amata* Fabricius from Asia and Africa but the Afrotropical syntomine genera, many of which do not form clades in our phylogenetic reconstruction, and to further inventory the diversity that is present in the Afrotropics.

Key words: Thyretina, Madagascar radiation, *Dysauxes*

TUESDAY, 4 JUNE 2019

ROOM B

GENERAL SESSION

Size-related life-history traits in geometrid moths: a comparison of a temperate and a tropical community

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Comparative studies on insect life histories are facilitated by the increasing availability of reliable phylogenies but are hampered by the scarcity of comparable data. Fortunately, there are morphological proxies of life-history traits of ecological relevance that can be recorded from preserved insect specimens. Body and egg sizes are straightforward examples, but there are also ecologically informative morphometric indices available, like those indicative of the position of a species on the continuum from capital to income breeding. We present the results of a phylogenetically informed analysis comparing the values of life-history traits for a sample of tropical geometrid moth species to a selection of species representing a temperate habitat. Tropical moths were on average larger than temperate ones. Tropical moths also had somewhat lower relative abdomen masses than temperate ones. This indicates that the tropical rather than the temperate moths tend to use an income (rather than capital) breeding strategy. However, we found no difference in a related index of pro-ovigeny. Nevertheless, the differences in studied traits were relatively low between the two regions compared. This allows us to conclude that the world may not be so different for a tropical and a temperate moth after all (Ecological Entomology, in press).

Key words: income breeding, capital breeding, body size, egg size, phylogenetic comparative methods, Bayesian inference

An evolutionary approach to Peppered Moth (*Biston betularia*) in southern Scandinavia

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Peppered moth (*Biston Betularia)* is a classical schoolbook case exemplifying natural selection. The species was dominated by a light colour morph, namely *f. typica,* during the first half of the 19th century. By the 20th century, the light form had decreased dramatically. In its place was the much darker form – *f. carbonaria*. The explanation for this shift in abundances was increased soot emissions from industries, settling on tree trunks. The formerly conspicuous *f. carbonaria* was now camouflaged, while f. *typica* was easy to spot by predators. Since the beginning of the 20th century, soot emission has decreased dramatically. One would therefore assume that *f. typica* is once more the dominant form of peppered moth. Studies have shown that colour can be affected by temperature as well; Higher temperatures sometimes result in lighter individuals. In addition, Bergmann's rule predicts that as temperature increases, body size decreases. Body size and wing colour are two focal points of this ongoing bachelors' thesis. The aim of this study is to look at specimens from the 50's-80's as well as from 2018 and compare colour and size in and between populations in southern Scandinavia. Of interest is also whether changes in these two traits are correlated as well as if changes can be linked to pollution and global warming.

Key words: peppered moth, biston betularia, polymorphism, natural selection, pollutants, global warming

Tribe Perizomini – a taxonomists' trash bin (Lepidoptera, Geometridae, Larentiinae)

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According to the current system of Geometridae, the tribe Perizomini have a cosmopolitan distribution and comprise more than 180 described species. We found the tribe to be polyphyletic. In particular, molecular phylogenetic analysis based on mitochondrial and nuclear loci reveals that the genus *Martania* does not belong to Perizomini. Moreover, all species of *Perizoma* sampled from regions other than Palaearctics do not belong to this genus but are scattered throughout the phylogeny of Larentiinae. The results of a molecular phylogenetic analysis are supported by morphological examination of the key taxa.

Key words: Perizomini, molecular phylogenetic analysis

A double-edged sword: unrecognized cryptic diversity and the taxonomic impediment in the hyperdiverse genus of moths (Lepidoptera: Geometridae)

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The genus *Eois* Hübner (Geometridae: Larentiinae) comprises 254 valid species. As a megadiverse genus, *Eois* potentially includes many undescribed cryptic species and embodies a problematic taxonomic scenario. The actual diversity of *Eois* is greatly underestimated and the Neotropical fauna is poorly known. In this paper we compare three species delimitation methods: ABGD, bPTP, and mPTP to highlight the hidden diversity within a subset of *Eois* species. Our results point to an increase of between 37% and 185% in the species number. Within some *Eois* species complexes the hypothesis of cryptic diversity is corroborated by morphological traits. For these complex we provide a preliminary taxonomic assessment. Additionally, for some species complexes, we found no congruence among the three methods, which indicates the importance of species and locality sampling as well as the previous alpha taxonomic knowledge in avoiding biased results. Moreover, we stress the importance of the species discovery approach – in an integrative taxonomy sense – using morphological attributes and life history to corroborate molecular analysis.

Key words: species delimitation, integrative taxonomy, neotropical, *Eois*

The enigma of *Triphosa taochata* Lederer, 1870 (Lepidoptera: Geometridae: Larentiinae) clarified with morphological methods and DNA barcoding

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Triphosa taochata was described based on a small syntype series and regarded as bona species for nearly the last 150 years by most authors. However, this species was dubious for many lepidopterists, who worked on the fauna of the western Palearctic region. During the recent taxonomic revision of the genus *Triphosa* Stephens, 1829 in the Middle East and Central Asia, the syntype series of this species (consisting of two male and two female specimens, deposited in Staudinger´s collection, Museum für Naturkunde Berlin) was dissected for the first time. Although all syntypes had the characteristic *Triphosa* wing pattern, the males showed genitalia similarities to *Hydria cervinalis* (Scopoli, 1763), whereas the females were *Triphosa* like. Based on morphological examination and DNA barcoding of numerous specimens from Turkey, Caucasus and Iran, the diagnostic characters of this species have been clarified and its genitalia pattern identified. These results allowed us to designate the lectotype of this species, which could be DNA barcoded, too. Additionally, two new species from the Middle East were discovered.

Key words: *Hydria*, lectotype designation, Triphosini

The monograph series *The Geometrid Moths of Europe* is now completed

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The monograph series *The Geometrid Moths of Europe* was initiated in 1994 with the objective of providing a modern taxonomic revision on the entire European fauna, including taxonomy, rich illustrations on adults, genitalia and diagnostic characters to allow reliable species identification, and to summarise distribution and biology. Altogether five volumes have been published until 2015 (Hausmann 2001, Mironov 2003, Hausmann 2004, Hausmann & Viidalepp 2012, Skou & Sihvonen 2015) and DNA barcodes have been provided for nearly all species (only eleven species are missing currently). The sixth and concluding volume will be presented in SEL meeting in Campobasso, Italy (2019). Volume 6 focuses on Gnophini and Boarmiini and it is the largest book in the series with over 900 pages, 30 colour plates, 131 genitalia plates, and it includes phylogenetic information based on molecules, a systematic, annotated checklist with synonyms for the entire Geometridae fauna of Europe (999 species) and adjacent regions. We will provide a brief history of the project, its authors, and share our experience for what is needed to carry out such monumental work, altogether including 3652 pages, and covering 10% of the European Lepidoptera and close to 1% of the European insect fauna. We will furthermore discuss the importance of such work in the context of current taxonomy and biodiversity crises.

Key words: Geometridae, Europe, taxonomic revision.

Review of the Lecithoceridae (Gelechioidea) in Afrotropical Region

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The family Lecithoceridae (Gelechioidea) is one of the highly diverse groups of Microlepidoptera with more than 1,260 known species worldwide (Park, 2018), but it has been poorly known with just more than 100 known species in Afrotropical Region (*Afromoths*, compiled by De Prins & De Prins, 2018). For review of the family in the region, we re-examined these types and their related specimens which are deposited in various museums including RMCA (Tervuren, Belgium) and TMSA (Pretoria, Africa), and found many of species were erroneously misplaced in their generic status or even the family. In a preliminary study, four new genera and more than 60 new species were or are being described, based on loan material provided by various workers worldwide which were collected since the early of 1900'. For identification of new species, COI barcode sequences were also obtained and provided.On the other hand, the family Lecithoceridae has been defined by the apomorphies of having the antenna being longer than the forewing and the gnathos always directed downward or reduced, however, we found that many African species have their antennae shorter than the forewing.

Key words: Lepidoptera, Gelechioidea, Lecithoceridae, Afrotropical, new genera, new species

Synopsis of the tribe Gnorimoschemini (Lepidoptera: Gelechiidae), with a special approach to the Central American and northern South American fauna

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The tribe Gnorimoschemini includes an important group of micro moths, which stand out by their tiny size around 10 mm and their importance for different ecosystems. Immatures af species such as *Keiferia lycopersicella*, *Phthorimaea operculella*, *Tecia solanivora*, *Tuta absoluta,* and the complex *Symmetrischema tangolias* are responsible for large losses in Solanaceae crops worldwide; while other species could function as biological indicators in fragile ecosystems. With important gaps in the knowledge of their life histories, few larvae described especially from the Neotropics, few specialists in the world, and around 4,700 species described for the whole tribe and thousands of others still remain unnamed, the lack of concise literature that allows the specific diagnosis make the group attractive for systematics studies, including functional morphology, phylogenetics and the application of molecular markers to entangle cryptic complexes within the group. The present work aims to show advances in studies based on the type material deposited in collections worldwide, and illustrate morphological aspects that allow the association at the generic and specific level of these insects. It highlights a total of 21 genera and at least 210 species with new records for the Neotropics. While the greater knowledge and reference collections for the group are concentrated in North America and Europe. The occasion is used to promote the development of collections in our region that allow advances in the knowledge of the group.

Key words: tuber moth, systematics, functional morphology, homology, phylogenetics

Yponomeutidae and ultrasound

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At the last SEL Congress DA posed the question "Do *Yponomeuta* spp. sing?" on account of structures noticed in the hyaline patch of the hindwing. LO and colleagues have explored this and measured the strength and frequency of ultrasound produced and noted when it was emitted.

Tests showed no facility for hearing in *Yponomeuta* and whenever they fly the sound is produced, of a frequency similar to that used by bats. Whilst ultrasound production is well known in macrolepidoptera, such as Arctiinae, it has seldom been reported in microlepidoptera. In macros, it is generated by muscles attached to the regions of thin cuticle on the body, but in *Yponomeuta* the sound is produced by buckling of the wing.

It is argued that this is acoustic aposematism, due to similarities with arctiine sounds, and it is likely that *Yponomeuta* are distasteful or poisonous.

Key words: Yponomeutidae, ultrasound, sign, production

Where do the intermediates of fritillary butterflies come from: testing the hypothesis of homoploid hybrid speciation in *Melitaea didyma – M. persea – M. acentria* species complex

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Resent whole-genome and multilocus studies shows that speciation via interspecific hybridization is widespread in nature. In the butterfly genus *Melitaea* (Lepidoptera, Nymphalidae) a high number of individuals and populations are known that are intermediate in male genitalia morphology. These intermediated have been were hypothesized to be a result of ancient or ongoing interspecific hybridization. Recently described species *M. acentria* from Israel demonstrates intermediate morphological characters between *M. persea* and *M. didyma*. Analysis of DNA barcodes reveals two mitochondrial haplotypes within the *M. acentria* population, one of which is species-specific and another one is similar to those found in *M. persea*. This allows us to hypothesize that *M. acentria* has a hybrid origin.

We performed whole-genome resequencing of M. acentria and its presumptive ancestors to check this hypothesis. Analysis of genome-wide SNPs have not revealed any footprints of ancient hybridization between *M. didyma* and *M. persea*. At the same time, we found traits of sporadic hybridization between sympatric population of *M. didyma* and *M. acentria*. Despite a possible mitochondrial introgression between *M. persea* and *M. acentria*, there was a lack of significant difference in genomes of *M. acentria* with different mitochondrial haplotypes.

The financial support for this study was provided by the grant 19-14-00202 from the Russian Science Foundation to the Zoological Institute of the Russian Academy of Sciences and by the RFBR grant 18-04-00263a.

Key words: hybridization, speciation, Melitaea, whole-genome sequencing

Mito-nuclear discordance in *Colias* butterflies (Lepidoptera, Pieridae): the role of interspecific hybridization and *Wolbachia* infection.

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Discordance between "phylogenetic entities" revealed by mitochondrial\nuclear genes and "traditional species" recognized on the basis of morphological characters, ecological traits and distribution is a quite common phenomenon in modern taxonomic and evolutionary studies. However, the factors determining such discrepancies have received little attention despite its obvious significance for taxonomy and evolution. During the complex investigation of the Palaearctic Lepidoptera we have studied cases of incongruence between molecular markers and morphological characters for a number of taxa of the genus *Colias* (Lepidoptera: Pieridae) on a base of approach uniting analysis of multilocus molecular data and methods of population genetics. The most striking example of mito-nuclear discordance was found in the taxonomically well-studied species - Moorland clouded yellow (*Colias palaeno*). We used six gene regions (mitochondrial COI, and nuclear CAD, EF-1a, GADPH, RPS5, and wingless) to analyze the genetic structure of this species. Analysis of the COI gene revealed the presence of five highly diverged mitochondrial lineages (the genetic distance ranged from 1,5% to 9%). In contrast to this, we have found that *Colias palaeno* is genetically homogenous with respect to studied nuclear genes. Thus, the discovered mitochondrial lineages did not correspond neither to the phenotypic traits, nor to the clustering of nuclear genes. Simultaneously, haplotypes similar to *Colias palaeno* were found in other *Colias* species, suggesting that some of detected lineages may have appeared as a result of interspecific hybridization and mitochondrial introgression. Additionally, we found that the mitochondrial clades are strongly associated with two different *Wolbachia* strains, supporting the hypothesis that the mito-nuclear discordance resulted from selection on the mitochondrial genome due to selective sweeps by *Wolbachia* strains. We conclude that *Wolbachia* infection and mitochondrial introgression has played a key role in the evolution of mitochondrial genomes of *Colias palaeno*. The financial support for this study was provided by the grants from the Russian Foundation for Basic Research No. 18-34-00756, 17-04-00828, 17-04-00754. The work was conducted within the framework of the state task No. 6.2884.2017/4.6 Ministry of Education and Science of Russian Federation.

Key words: Lepidoptera, phylogeography, Wolbachia infection, mitochondrial introgression

The origin and genetic structure of *Lymantria dispar* in Europe

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The Gypsy Moth (*Lymantria dispar* L.) is considered as one of the most destructive forest pests in the Holarctic Region. It is a classic example of an invasive polyphagous species introduced from Palearctic to Nearctic decades ago through human activities. The detrimental ecological impacts of *L. dispar* control programs are considerable, particularly through decline in native non-target species. Indigenous populations of *L. dispar* are found throughout Europe, northern Africa and Asia. Although considerable researches have been devoted to exploring genetic structure of Gypsy Moths, rather less attention has been paid to understanding the natural history of this economic pest species. We examined 218 individuals collected through the Holarctic Region and they were sequenced for two mitochondrial (COI, CYT-b) and three nuclear (EF-1α, RpS5, wingless) markers. Our results showed that Europe was colonised through Russia during Calabrian stage of Pleistocene Epoch. We recovered also high genetic diversity and confirmed Europe as the source of primary invasion to the Nearctic Region.

Key words: Gypsy Moth, Erebidae, Lymantriinae, phylogeography, Palaearctic Region

The study was supported by: Genomics Applications Partnership Program (GAPP 6102), Genome Canada, Genome British Columbia, Genome Quebec, the Canadian Forest Service (Genomics Research and Development Initiative, GRDI), the Canadian Food Inspection Agency and the University of Southern Bohemia (GA JU 038/2019/P).

A detailed study of a gynandromorph lep-leviathan (Saturniidae)

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A cross between two Lep-Leviathans, *Citheronia regalis* from northeastern US and *C. splendens* from southwestern US, produced many F1 hybrid progeny and a single gynandromorph specimen. The gynandromorph was recognized during the last instar as significant bilateral differences were observed, including color, length and numbers of barbules on the scoli, and setal positions on the head capsule and anal plate. No differences in size, shape, or numbers of crochets were observed on any adjacent prolegs. Pupal differences include only positions of male and female gonopores. The adult exhibits a much larger female "*regalis*" side compared to a smaller male "*splendens*" side. Gynandromorphic differences from all life-stages, except the egg, are documented using photography, colorized chaetotaxal maps, and ZBrush 3-D sculpting software in video format. Gynandromorphic features are sex-linked due to an irregular distribution of genes from both sexes during early mitotic division.

Key words: gametogenesis, immature stages, mitosis, Saturniidae

New data on the effectiveness of the sex attractants from the series 'EFETOV-2' for the males of Procridinae species (Zygaenidae): results of field observations in Italy

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Three sex attractants EFETOV-2, EFETOV-S-2 and EFETOV-S-S-2 synthesized in the Crimean Federal University were tested in field observations undertaken in Italy for four years from 2015 to 2018. Rubber caps with the attractants were fixed on cardboard rectangles, labelled and attached to twigs of the bushes or clothes on the researcher as he slowly crossed the biotope. Attracted specimens were collected by netting them near the lure. Sometimes Delta plastic sticky traps with the baits were also used. The males of three genera of Procridinae were attracted to the lures from the series 'EFETOV-2': *Rhagades* Wallengren, 1863 (one species), *Adscita* Retzius, 1783 (five species), and *Jordanita* Verity, 1946 (three species). The sex attractants for one species, viz. *Adscita* (*Adscita*) *italica* (Alberti, 1937), were found for the first time. The males of this species were caught by the sticky trap with EFETOV-2 and in addition came to the lures with EFETOV-S-S-2 and EFETOV-S-2. All three variants of the attractants were effective for one more species *A.* (*Tarmannita*) *mannii* (Lederer, 1853). However, other Procridinae species demonstrated a strong preference for only one type of attractant. For example, the most abundant species *Jordanita* (*Solaniterna*) *subsolana* (Staudinger, 1862) (with more than 400 attracted specimens) reacted only to the lures with EFETOV-S-2 while the males of *Rhagades* (*Rhagades*) *pruni* ([Denis & Schiffermüller], 1775) were attracted only to the baits with EFETOV-S-S-2.

Key words: Zygaenidae, Procridinae, Italy, sex attractants, lures, monitoring.

Genomic evidence suggests *Mesapamea remmi* is an imaginary moth species (Lepidoptera: Noctuidae)

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Taxonomic status of the noctuid moth *Mesapamea remmi* (Lepidoptera) has remained controversial since its description in 1985. Based on morphology, it has been considered a valid species or a hybrid between *M. secalis* and *M. didyma*. We studied the case by mitochondrial COI gene, seven nuclear genes and by genomic tools with a data of >9 000 loci and >1 500 000 base pairs across the genome. Our analyses showed that genomic data does not support hybrid hypothesis and that *M. remmi* is not separated genetically from *M. secalis*, while they both are clearly distinct from *M. didyma*. Reproductive organs of *M. remmi* males are distinct and diagnosable, whereas females are teratological. These data support the view that *M. remmi* is not a valid species and we consider *M. remmi* Rezbanyai-Reser, 1985 to be a junior synonym of *M. secalis* (Linnaeus, 1758). We demonstrate that genomic approaches provide an efficient way to address various difficult and long-standing taxonomic issues, in this case over-splitting of species.

Key words: ddRAD sequencing, taxonomic status, synonym

Vertical stratification structure of a temperate forest caterpillar community in eastern North America

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Vertical niche partitioning might be one of the main driving forces explaining the high insect diversity of forest ecosystems. However, the forest's vertical dimension is comparatively understudied, especially in temperate forests. In this study, we investigated the vertical structure of an arboreal caterpillar community in eastern North America. Within a 0.2-ha forest stand, all deciduous trees ≥ 5 cm DBH were felled and systematically searched for caterpillars. Sampled caterpillars were assigned to a specific stratum (i.e., understory, midstory or canopy) depending on their vertical position and classified into feeding guilds as either exposed feeders (external feeders) or concealed feeders (i.e., leaf rollers, leaf tiers, webbers). In total, 3,892 caterpillars representing 215 species of butterflies and moths were collected and identified using an integrative taxonomy approach (caterpillar morphology and DNA barcoding). While stratum had no effect on caterpillar density, feeding guild composition changed significantly with concealed caterpillars becoming the dominant guild in the canopy. Species richness and diversity was found to be highest in the understory and midstory and declined strongly in the canopy. Family and species composition changed considerably among the strata; understory and canopy showed the lowest similarity. Furthermore, families of 'Microlepidoptera', especially Despressariidae, dominated the canopy, while families of Noctuoidea and Geometroidea were found to be prevalent in the understory. Food web analyses further revealed that network specialization increased towards the canopy, caused by an increase in the specialization of the caterpillar community. In summary, our study revealed a pronounced stratification structure of a temperate forest caterpillar community unveiling a distinctly different assemblage of the canopy stratum.

Key words: caterpillar density, diversity, feeding guild, forest canopy, specialization

Mapping the Lepidoptera of Germany: First results

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The website www.lepidoptera.de attempts to bring together all available digital data on the historical and recent distribution of the Lepidoptera of Germany. The data are collected from regional databases in the 16 federal states of Germany and from various lepidopterist's personal databases. A tool for the direct online input of records is also provided.

The procedures ensuring quality control (i.e. guarding against misidentifications) include the cooperation of regional experts who are responsible for checking and releasing – or blocking – those records submitted via the online tool.

As of April 2019 a total of 4.9 million datasets were included in the database. The regional coverage is not yet complete but it is already possible to visualise major changes in the distribution of many taxa: a number of species have become extinct either locally or in the entire country, many species are becoming increasingly rarer, and a few of the less specialised species can still expand their area of distribution.

The project is sponsored by the Bundesamt für Naturschutz (Federal Agency for Nature Conservation).

Key words: mapping, distribution, Germany, decline, expansion

WEDNESDAY, 5 JUNE 2019

ROOM A

CHEMICAL ECOLOGY AND MULTITROPHIC INTERACTIONS

Deception strategies in butterfly social parasites of ants

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Much of the ecological success of ants is due to their social organization, maintained by a complex communication system. Chemical, acoustic and visual signals coordinate a large number of individuals in the collective decision-making process and determine the plasticity of the colony in responding rapidly to biotic and abiotic variations. Due to the presence of trophic resources in a protected environment, nests attract many organisms that have evolved strategies to elude the colony defences. Amazing examples of strict coevolutionary dynamics, host manipulation, chemical and acoustic mimicry have been described in *Maculinea* butterflies. These butterflies are obligate social parasite of *Myrmica* ants. After a brief phytophagous period, the larvae complete their development and pupate in the ant nest. *Maculinea* immature instars spend 11-23 months inside the nests, preying on the ant brood (predatory species) or being fed by throphallaxis (cuckoo species). The parasite's ability to corrupt the host communication code is necessary for it to be retrieved and "adopted" by foraging workers and to achieve a high social status in the colony hierarchy, as observed in the cuckoo species, allowing full acceptance in the nest and the exploitation of the colony resources.

With a special focus on the chemical ecology of distinct Italian populations, some of the most recent findings of our research will be presented to clarify the evolutionary significance of vibroacoustic and chemical cues in the context of multimodal interspecific communication.

Key words communication, vibroacoustic signals, cuticular hydrocarbons, myrmecophily

Attraction of Zygaenidae and some other Lepidoptera by the sex attractants from the series 'EFETOV-2' in the Crimea

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During 2014–2017 the sex attractants from the series 'EFETOV-2' were used in field screening tests in the Crimea. The chemical structure of these substances (esters of 2-dodecenoic acid and enantiomers of 2-butanol) is very similar to the structure of the known natural sex pheromones of Procridinae (Zygaenidae). Delta sticky traps with the attractive baits were applied in various biotopes. Sometimes we merely placed the lures on the ground in the habitat. Seven target species were attracted: *Theresimima ampellophaga* (Bayle-Barelle, 1808), *Rhagades* (*Rhagades*) *pruni* ([Denis & Schiffermüller], 1775), *Adscita* (*Adscita*) *geryon* (Hübner, 1813), *Jordanita* (*Tremewania*) *notata* (Zeller, 1847), *J.* (*J.*) *graeca* (Jordan, 1907), *J.* (*J.*) *globulariae* (Hübner, 1793), and *J.* (*Solaniterna*) *subsolana* (Staudinger, 1862). *Th. ampellophaga* was found on the Mountain Agarmysh due to the sex attractant-based monitoring. It is the most northern record of this species in the Crimea outside the hitherto known distribution on the Southern coast of the peninsula. The males of *Th. ampellophaga* were captured by sticky trap with attractant EFETOV-S-2 almost 2 km from the nearest vineyards. Thus, the sex attractants from the series 'EFETOV-2' can be successfully used for the detection of Procridinae populations (even with low density) in different regions. In addition two other Lepidoptera species were attracted by the lures. *Argyresthia semifusca* (Haworth, 1828) (Yponomeutidae) was found in the traps with EFETOV-S-S-2, and *Dolicharthria stigmosalis* (Herrich-Schäffer, 1848) (Crambidae) was caught by the traps with EFETOV-S-2. The sex attractant for *D. stigmosalis* was discovered for the first time.

Key words: Zygaenidae, Procridinae, Crimea, sex attractants, traps, lures, monitoring

Long-term trends in spring caterpillar biomass available to birds in Hungarian oak forests

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Numerous recent studies report an alarming decrease in diversity, biomass or abundance of insects in various habitats. Such studies are hampered by the scarcity of suitable long-term data. We used data from The Hungarian Forestry Light Trap Network (operating from the 1st of March until the 31st of December on a daily basis) to test whether the spring caterpillar biomass showed any long term (20-55 years) trends in oak-dominated forests. Light trap catching data of selected night-active macrolepidopteran species (suitable bird food in larval stage) from 7 different locations were used for the indirect estimation of the relative caterpillar biomass. The volume of caterpillars belonging to different species was calculated using the average length and diameter of the fully grown larva. These values were multiplied with the abundance of the given species and then summed for years and locations. These values were considered as potential relative spring caterpillar biomass at a given location in a given year. The time series analysed showed strong year-to-year fluctuations, but no uniform trends. Considering the last 2-3 decades almost all traps showed an increasing trend. Based on the climate change's indirect effects further increase can be predicted in spring caterpillar biomass as major food source of insectivorous birds. So the food availability in long term will likely not influence the birds' breeding success negatively in the Hungarian oak dominated forests.

Key words: oak forests, spring caterpillar abundance, insectivorous birds, long term trends, light traps

Zygaenids do not lie – the fatal impact of wind-transported pesticides on biodiversity

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During a project on the biodiversity of meadows in Alto Adige/Südtirol in the Italian Alps in the late 1990's it was recognised for the first time that the Zygaenidae had disappeared in many habitats where earlier they had been common. However, butterflies and other Lepidoptera were still present. Further research confirmed that Zygaenidae must be extremely sensitive to air contamination by pesticides and can possibly be used to discover unseen poison in the air even if a habitat seems to be perfectly in order. The reason why these insects are so sensitive to pesticides is not yet known. Nevertheless, it is now well documented that Zygaenidae disappear when pesticides are wind-transported into their habitats, even in very small amounts. From 2015–2018 a special survey took place in Mals/Malles to study whether the populations are in good condition, whether they have become rare and are now in critical condition or whether they have already disappeared from their former habitats. The results confirmed again that zygaenids have disappeared from Alpine valleys especially those with apple monocultures with heavy pesticide use, not only close to the apple orchards but also on far distant slopes where thermic winds have transported the poison into the environment. From 23 zygaenid species known from the province Alto Adige/Südtirol, five have disappeared in the last 40 years. A recent study on the territory of Mals/Malles published by the Environmental Institute in Munich (Germany) in 2018, where poisons in the air were analysed with modern technology, perfectly confirms the results obtained by observations of zygaenids. Up to 600 metres above the bottom of the valley, where apple orchards are sprayed, various poisonous substances in the air could be found and wind transport into the mountains was confirmed.

Key words: Zygaenids, pesticides, biodiversity

Cydia fagiglandana sex attractants history: from identification to field application

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The beech moth, *Cydia fagiglandana* (Zeller) (Lepidoptera, Tortricidae), is one of the main pest insect of chestnut fruits. First report on its sex attractants dates to 1984 by field trapping tests. Later on, laboratory and field studies highlighted that the main components of the beech moth sex pheromone are *E*8*E*10-12:Ac and *E*8*E*10-12:OH. During the last decades these compounds have been widely used as monitoring tool for *C. fagiglandana*. Currently, pheromone-based techniques are considered the most promising control strategies of the beech moth and our recent investigations have led to the registration of a pheromone-based commercial product for field application. During the last years, the efficacy of the pheromone dispenser Ecodian CT™ (Isagro S.p.A.), a wire made up of a cellulose core covered by Mater-Bi® (Novamont S.p.A.), containing the synthetic sex attractants *E*8*E*10-12:Ac and *E*8*E*10-12:OH), was evaluated. Field tests were conducted in three chestnut areas of the Campania region. In each area, field trials were carried out in at least two hectares' chestnut groves. Males beech moth trap catches and larval damages on chestnut fruits were significantly lower compared to the untreated control areas.

Key words: beech moth, chestnut fruit, *E*8*E*10-12:Ac, *E*8*E*10-12:OH, biotechnical control

Management of *Thaumetopoea pityocampa* in recreational areas: Mating-Disruption and Mass-Trapping

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Our research activities are aimed at the development of innovative technologies for pest management of *Thaumetopoea pityocampa* adult population using pheromone Mating-Disruption (MD) and Mass-Trapping (MT) in a pine woodland recreational area (located in central-south Italy) growing *Pinus halepensis*.

Mating-Disruption method. During 2015 and 2016 two plots composed of one hectare each were identified. Pheromones for MD of *T. pityocampa* males [20±0.5 g of active ingredient (*13Z*)-13-hexadecen-11-yn-1-yl acetate (pityolure) were used] were applied to an experimental plot; the other plot was without MD and considered as control-plot. Approximately 600 infested trees were present in both plots. MD showed a high effectiveness. In 2015 and 2016 the number of males monitored by pheromone traps and number of nests present in the plot with MD were lower than the males and the nests recorded in the control-plot without pheromones. MD applied in recreational areas is a control method that can be also applied in private gardens, public parks, in urban and semi-urban areas.

Mass-Trapping method. During 2016-2018 two plots composed of one hectare each were identified. 10 G-traps baited with pityolure were placed in the experimental Mass-Trapping plot (MT-plot); the other plot was used as a control plot (C-plot). The *T. pityocampa* male population was monitored using the 2 central traps in the MT-plot and 2 traps positioned in the C-plot. In addition, the winter nests build by overwintering larvae on pine trees were counted. After 2 years of MT, the number of adults trapped by the monitoring traps decreased in the MT-plot, but not in the C-plot, whereas the number of nests decreased in both plots. According to our results, the MT method is able to reduce *T. pityocampa* infestations. This pheromone method can be applied in combination with other control systems in the context of Integrated Pest Management in recreational areas.

Key words: Pine processionary moth, pheromones, Mass-Trapping, Mating-Disruption, pest management

WEDNESDAY, 5 JUNE 2019

ROOM B

LEPIDOPTERA – PLANT INTERACTIONS

Evolution of active pollination and mutualism in *Epicephala* (Gracillariidae)

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Lepidopteran insects are generally parasites of plants and rarely benefit their hosts. However, some seed-parasitic moths have evolved to actively pollinate their host plants to ensure food (seeds) for the hatching larvae, and consequently became the sole pollinators their hosts. The yucca–yucca moth association is the best-known example, but ecologically analogous mutualisms continue to be discovered. I will present the natural history of the recently found pollination mutualism between Phyllanthaceae trees/shrubs and *Epicephala* moths (Gracillariidae). In the Old World tropics, roughly 500 species of Phyllanthaceae are pollinated by specialized *Epicephala* seed parasites that lay eggs in flowers and whose larvae feed on the developing seeds. Remarkably, the ovipositing moths actively collect pollen on male flowers with their proboscises and use it to pollinate female flowers. A hatched moth larva usually destroys only a fraction of the seeds produced in each fruit, leaving others viable for plant reproduction. In most cases, each Phyllanthaceae species has its own pollinator *Epicephala* species, and this high specificity is mediated by floral scent, which the pollinators use to locate host flowers in the dark. Phylogenetic analysis of plants and moths suggest that *Epicephala* pollination evolved at least five times independently in Phyllanthaceae, after the origin of pollination behavior in *Epicephala* 25 million years ago. I will present results of our recent studies addressing various ecological and evolutionary aspects of this mutualism, such as mechanism of mutualism stability, pollen dispersal distances, evolution of non-pollinators, and transoceanic dispersal.

Key words: Asia, *Epicephala*, Gracillariidae, obligate pollination mutualism, Phyllanthaceae, seed parasite, tropics

Evolution of gall-induction and host-plant associations in Phyllanthaceae-feeding *Caloptilia* (Lepidoptera: Gracillariidae)

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Gall-induction has repeatedly evolved in different groups of insects. However, most lineages of gall-inducers contain a reduced number of species. Therefore, it is difficult to assess whether gall-induction should be considered as an evolutionary dead-end or a key innovation that contributes to evolutionary success. Insect groups that include species either capable or not capable of inducing galls are good models to infer the transition of feeding habit. They can also be used to study whether the evolution of gall-induction can lead to adaptive radiation. In our study, we focused on species of the *Caloptilia* genus (Lepidoptera: Gracillariidae) associated with Phyllanthaceae and that currently comprises a single species of gall-inducer. However, previous works have suggested the existence of multiple undescribed gall-inducing species of *Caloptilia*, which may suggest the existence of an overlooked adaptive radiation of gall-inducing moths. We sampled nine species of *Caloptilia* associated with *Glochidion* (Phyllanthaceae) and inferred phylogenies from five genes commonly used in insect phylogeny as well as Ultra Conserved Elements (UCEs). Both datasets showed that gall-inducers form a well-supported monophyletic group, but the deeper nodes were only resolved in the UCE tree. The UCE phylogeny also strongly supported the monophyly of *Caloptilia* species associated with Phyllanthaceae and *Glochidion*. Our analysis recovered the monophyletic gall-inducers in a derived position within the clade of species associated with *Glochidion*. Two of the three gall-inducers share the same host species sympatrically with non-gall-inducing species, suggesting that gall-induction appeared only once, most likely from a non-galling species developing on *Glochidion*. Therefore, gall induction could be a key innovation that would have opened up a new ecological niche for *Caloptilia* associated with *Glochidion*. The inferred topologies also uncover the series of gall structure evolution, from opened to completely closed structures.

Key words: *Glochidion*, gall, leaf miner, leaf roller phylogeny, Ultra-Conserved Elements

Historical herbaria to study past distribution and invasion history of phyllophagous insects

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Historical herbarium collections are important sources of information about past distribution of endophagous arthropod pests, such as leaf miners and gallers. Their larvae and pupae concealed in herbarised plant tissues can be effectively used in invasive ecology studies. Here we focus on the lime leafminer, *Phyllonorycter issikii* (Kumata, 1963) (Lepidoptera: Gracillariidae), an invasive micromoth in the Palearctic, to study its past distribution and clarify invasion history based on data extracted from historical herbaria. We performed an extensive survey of *Tilia* in the world biggest herbarium collections to find early evidence of the recent presence of *Ph. issikii* in the western Palearctic (presumable invaded range) comparing to the eastern Palearctic (presumable native range). No mines on *Tilia* leaves were recorded in Europe before late 20th century supporting *Ph. issikii* recent invasion. In contrast, dozens of mines were recorded in East Asia dated back to 19th century, before the insect was formally described. Typical *Phyllonorycter* mines were especially abundant in the Russian Far East but also present in Japan, South Korea, and China. In fact, *Ph. issikii* was not known in China before our study. According to one-century-old herbarium specimens, *Tilia*-feeding *Phyllonorycter* is present in seven Chinese provinces. *Phyllonorycter* mines were also revealed on leaves of *Tilia americana* collected in the USA and Canada in the 19th and 20th centuries, that were likely made by the local leafminer, *Ph. lucetiella* (Clemens, 1859). *Ph. issikii* willingly attack leaves of this lime species in botanical gardens in Russia. However so far no records of *Ph. issikii* have been known from the Nearctic. Archival larvae and pupae sampled from herbaria are being currently analyzed genetically in order to confirm species identity and find further details on *Ph. issikii* invasion in Palearctic.

This study was supported by the Russian Foundation for Basic Research (grant No. 19-04-01029).

Key words: invasive micromoth, past range, historical herbaria

The *Salix* feeding species of *Stigmella* in Europe: almost as difficult to separate as their hosts (Lepidoptera: Nepticulidae)

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The European leafmining *Stigmella* species feeding on *Salix*, with the exception of the unrelated *Stigmella nivenburgensis* and *S. pallidiciliella*, form a cluster of around 15 sibling species that are hard to differentiate with anything but DNA barcoding. The complex comprises the widespread Holarctic *Stigmella salicis, S. vimineticola, S. arbusculae* and 7 or 8 previously unrecognised species (some temporarily indicated with cluster numbers), for which one older synonym is available. The group also includes a few species that are better diagnosed, but also have been partly confused in the past: *S. obliquella*, *S. zelleriella* and *S. benanderella*. Male genitalia can be recognised by a combination of traditional morphometrics, geometric morphometrics of uncus and gnathos and some discrete characters such as the number or shape of cornuti. Female genitalia differ in apophysis length and presence or absence of spines in the spermathecal duct, with a connection between ovipositor length and egg position: short on leaf upperside, long on leaf underside, with some exceptions. Also *S. myrtillella*, feeding on *Vaccinium* species, belongs to the complex; we report here the first finding of larvae of this species on *Salix daphnoides* in the Alps. Three species are widespread in Europe: *S. salicis*, (absent from the south) and feeding on "sallows" (= *Salix caprea*, *Salix cinerea*, *Salix aurita* and relatives), and clusters 2 and 3. Cluster 2 is almost monophagous on *Salix caprea* and has easily recognizable leafmines, cluster 3 has a very wide host range, and eggs are deposited on the leaf upperside; cocoons are often spun on twigs above the water. There is one boreo-alpine species, *S. arbusculae*¸ one Central-South European species, *S. vimineticola*, specialised on *Salix eleagnos* and a number of species feeding on sallows and restricted to south-western Europe (clusters 5 and 6) and species only occurring respectively on the Iberian Peninsula, the Tyrrhenian Islands and Sicily. The latter group, except cluster 6, is completely vicariant with *S. salicis*. Despite the morphological similarity, most of these species have originated between 4 and 12 million years ago, the most recent splits being between Nearctic and Palaearctic taxa.

Key words: DNA barcodes, cryptic species, leafmines, hostplants

Building a database of Lepidoptera – host – parasitoid associations recorded for the Afrotropical region, results and preliminary analyses

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In 2012 the authors' database on Afrotropical Lepidoptera – plant associations (including all published records to date) provided such associations for less than 7% of the Lepidoptera species diversity in southern Africa. Only a handful Lepidoptera – parasitoid associations were recorded. This paucity of information led to the formation of LepsocAfrica's successful Citizen Science project, the Caterpillar Rearing Group (CRG). The database now provides Lepidoptera – host associations for 13.6% of the southern African Lepidoptera fauna, effectively doubling, in seven years, the available information which was accumulated in over a century. Over 600 Lepidoptera – parasitoid associations have now been recorded. In order to enhance the analytical value and accuracy of the database, the development of fields to include an up to date phylogeny of organisms at all three trophic levels is ongoing. This includes the development of fields to include ecological and biogeographical information as well as fields evaluating accuracy levels. A preliminary high-level analysis of the data is presented and some examples of new insights already resulting from the data are shown. An appeal is made for enhanced collaboration between the CRG and similar organisations covering Lepidoptera – host – parasitoid associations in other world faunistic regions.

Key words Afrotropical Region, Lepidoptera, caterpillar, early-stages, host-associations, parasitoids, database, citizen science project

Nocturnal moth-based pollen transport networks at UK farmland ponds

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Plant-pollinator relationships form an important part of ecosystem functioning in agricultural landscapes. The majority of recent pollinator network studies have focused on bees and, to a lesser extent, on hoverflies and butterflies. In contrast, pollen transport networks linked to nocturnal settling macro-moths remain largely unknown. With moth species richness and abundance experiencing severe declines across Europe, and especially within agricultural landscapes, the persistent knowledge gaps regarding scale and sources of nocturnal moth pollen transport in intensive agricultural landscapes is highly problematic. Using farmland pond systems adjoining arable fields in North Norfolk, UK as a case study, we surveyed insect-pollinated flowering plant, nocturnal moth and diurnal pollinator communities in 2016 and 2017. Moth species were captured using light traps and subsequently searched for pollen on their bodies. Nearly half of all moth specimens carried pollen, and their network contained more pollinator species than the local diurnal pollinator networks. Nocturnal moths also pollinated several plant species where we observed no diurnal species visits. Additionally, important network-level metrics were more favourable in moth-pollen networks. This research establishes settling moth communities as having unique pollen transport networks in agricultural landscapes, highlighting their great contribution to pollen transport. This study strongly indicates that nocturnal settling moth species can provide key ecosystem services in agriculture via pollination, and that moths warrant urgent inclusion in future pollinator studies.

Key words: pollen transport, moth pollinators, agricultural landscape, semi-natural habitat

Butterfly extinctions

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Only three butterflies are officially listed as globally 'Extinct' in the IUCN Red List, out of 697 animal species known for having disappeared in historical times. However, information on insular faunas and species/area relationships suggest that extinctions were more numerous in the past than is currently possible to observe. While the butterfly faunas of the islands more distant from mainland are predictably 'under-saturated' and the opposite is observed for those located close inshore, other, generally ecological, factors come into play. Indications are that the more specialised species tend to become increasingly isolated because of habitat fragmentation, so that the more strongly anthropic or particularly windy islands tend to be colonised by opportunistic species. However, untangling the effects of human agency from those of natural processes is frequently difficult. At regional level, only one 'species' (*Pieris wollastoni*) is likely to have become extinct in Europe (Madeira), while another (*Lycaena helle*) may have disappeared from Italy. Discussion on more local extinctions will be restricted to Italian cases. Seen in perspective, the continuing trend will probably favour the generalist, broad ranging, often migratory and multivoltine species, while most of the others will tend to disappear.

Key words: island biogeography, species/area relationships, over- and under-saturated insular faunas, local extinctions

THURSDAY, 6 JUNE 2019

ROOM A

DIVERSITY OF ITALIAN LEPIDOPTERA GENERAL SESSION

How long are 3 kilometres for a butterfly? Ecological constraints and functional traits explain high genetic differentiation between Sicily and the Italian Peninsula

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Butterfly populations of Mediterranean islands often show contrasting mtDNA lineages, even on islands that were connected to the mainland during glacial maxima. Understanding the mechanisms establishing genetic diversification and maintaining the boundaries between lineages requires comparative phylogeographic studies relating genetic structure, functional traits and dispersal constraints. We analysed the mitochondrial COI gene of butterflies occurring around the narrow Messina strait (3km wide) separating Sicily from the Italian Peninsula (1394 sequences). A total of 655 specimens represented 84 species out of 90 recorded in Sicily (Sicily barcoding dataset-SBD). Among them, 81 species have also been sequenced for the southern Italian Peninsula (Zoogeographic Dataset-ZD, 1361 specimens) and 72 met the minimum sampling requirement to model genetic differentiation against geographic location and species traits (Comparative Dataset-CD, 1297 specimens). More than a third of the species showed completely segregated haplogroups across the strait and 32 of 84 species in the SBD (38.1%) were Sicilian endemic haplogroups. By comparing the ZD with 5049 specimens from the entire Palearctic region, we found that one quarter of Sicilian populations (and 37.0% of endemic lineages) had their closest relatives in distant areas, instead of the neighbouring Italian Peninsula. Based on the CD dataset we found that the populations occurring on the two sides of the Messina strait revealed the strongest genetic contrasts in the study area. For each species of this dataset, we also evaluated several functional traits and ecological constraints to dispersal. Phylogenetic regressions showed that haplotype diversity is related to an intrinsic phenological trait (the length of the flight period), while indices of spatial differentiation were explained by both intrinsic traits (wingspan and trophic generalism) and contemporary local constraints (winds experienced at the strait and climatic costs of dispersal). We found that a relatively narrow sea strait (3km wide) can largely impede dispersal of butterfly matrilines. Because of unfavourable winds during flight periods, populations of less dispersive Sicilian butterflies tended to differentiate in endemic variants or to maintain relict populations. Understanding these phenomena required the integration of DNA sequences, species traits and physical constraints for an entire community at continental scale.

Key words butterflies, COI differentiation, environmental constraints, dispersal, functional traits, Messina strait

Cryptic species within mimetic complexes: the Italian *Syntomis* moths between divergence and pattern constraints (Lepidoptera: Erebidae)

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The day-flying moth genus *Syntomis* comprises several similarly-looking taxa involved in Müllerian mimicry rings. These moths are therefore at a crossroad between independent evolutionary divergence and constraints limiting their phenotypic diversification because of their mimetic relationships. Different set of characters (e.g., genetic/genomic, physiological/metabolic, phenotypic, behavioural etc.) are thus likely to show signals, which reflect their own interplay with the various evolutionary forces that is in turn affected by the allopatric/sympatric occurrences of populations of these moths and other co-mimics in nature. Resolving the still controversial systematic relationships among various taxa/populations of *Syntomis* is therefore a prerequisite for any further assessment on the evolutionary diversification of these moths. In this study, we analysed a number of Western Palearctic taxa, focusing on the '*Syntomis*-rich' Italian fauna, via a multi-locus genetic approach which combined mitochondrial and nuclear molecular markers, together with traditional morphological analyses of species delimitations and time-based phylogenetic reconstructions. The results showed incongruence among current species and subspecies delimitations. Both mitochondrial and nuclear markers suggested the presence of four, well-distinct genetic groupings. The genetic distance and the time of divergence between the Italian subspecies *S. kruegeri kruegeri* and the Balkan subspecies *S. kruegeri marjana* is the same as that found between *S. phegea* and *S. ragazzii*, which are well-distinct, sympatrically occurring species. These divergences were estimated to have taken place during the Early Pleistocene, which coincided with major changes in climate and vegetation in the Western Palearctic, and may have boosted geographic separation and ecological vicariance. Our results highlight major gaps in knowledge on these moths and call for detailed assessment of cryptic diversity in complexes of mimetic species, also in temperate regions.

Key words: cryptic biodiversity, Italian peninsula, Müllerian mimicry, *Syntomis*, species delimitation

The study of Lepidoptera of Bergamo district (Lombardy, Northern Italy, Bergamo Province): a biodiversity still largely unknown

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The Bergamo district, in the center of Lombardy region, occupies a varied geomorphologically territory with mountain systems, hilly area and flat land. Bergamo Alps and surroundigs are considered a biodiversity hotspot, more then 147 endemic Invertebrates species are known and many researchers have contributed to highlight the uniqueness of the wildlife composition. Attention has been dedicated in recent time to the Lepidoptera component to achieve a more comprehensive overview on fauna of the area. As a result of these research efforts new data are presented on the distribution of several noteworthy species of macro- and microlepidoptera in the Bergamo territory. Specialized taxa like *Micropterix gaudiella* Zeller & Huemer, 2015, *Catoptria orobiella* Huemer & Tarmann, 1994, *Scythris arerai* Huemer, 2000, *Sattleria karsholti* Huemer & Hebert, 2011 are endemic species with a limited distribution within a restricted area of the Bergamo Prealps (Arera Valley) and western the Alps. They are known from a very few localities and in this study we present new unpublished data. A reviewed distribution in Italy on the basis of original records are reported for *Typhonia ciliaris* (Ochsenheimer, 1810) *Leptopterix turatii* (Hartig, 1936), *Callisto coffeella* (Zetterstedt, 1839) *Catoptria luctiferella* ssp. *meridialpina* Burmann, 1975, *Catharia simplonialis* (Heydenreich, 1851) *Metaxmeste phrygialis* (Hübner, 1796) and *Epiblema grandaevana* (Lienig & Zeller, 1846)—species found mainly on the highest peaks of the Alps as well as in Scandinavia, in the northern Asia and on the isolated limestone massifs, such as Bergamo Prealps, part of few entities that have a separate arctic-alpine range. Whereas, widely distributed species in Europe and Asia such as *Korscheltellus lupulinus* (Linnaeus,1758), *Korscheltellus fusconebulosus* (de Geer,1778), *Sabra harpagula* (Esper, 1786), *Pheosia gnoma* (Fabricius, 1777) and *Diaphora sordida* (Hübner, 1803), are rare in the studied area, localized and reported with one or two specimens with the exception of *Pharmacis carna* (Denis & Schiffermüller, 1775) sampled in a conspicuous number of specimens. The Bergamo district seem to have received insufficient attention from lepidopterists, the survey of recent years confirm this. The presence of *Glacies bentelii perlinii* Turati, 1914 is reported for the first time as well as *Glacies alpinata* (Scopoli, 1763), which was recorded in the district with only a single specimen present in a historical collection. All this suggests that there is still a lot of work to do especially for Microlepidoptera, so far an undercollected fauna due to the objective difficulties involved in their

study. A preliminary work to determine the Pterophoridae specimens has resulted in encouraging results, *Capperia celeusi* (Frey, 1886), *Merrifieldia leucodactyla* (Denis & Schiffermüller, 1775) *Pselnophorus heterodactyla* (Muller, 1764) and *Platyptilia nemoralis* Zeller, 1841 are recorded for the first time in Lombardy. It is expected that after revisions of still insufficiently studied families and organizing surveys aimed at deepening the knowledge will increase the level of Lepidoptera diversity in the Bergamo district.

Key words: Lepidoptera, Bergamo district, new reports

New discoveries and a revised view on the Zygaenidae fauna of Italy

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Forty five species of Zygaenidae are currently known from Italy where reference material has been examined and the determination confirmed. One species, *Jordanita algirica* (Rothschild, 1917), needs confirmation because the examined historical specimens from Sicily are the only reference material that is available and no other records are known. Two species, *Zygaena nevadensis* Rambur, 1858, and *Z. angelicae* Ochsenheimer, 1808, have been found only recently on Italian territory. The earlier published data on *Z. nevadensis* have been proved to be erroneous and this species was newly discovered on La Sila in Calabria. The hybrids of *Z. angelicae* and *Z. transalpina* (Esper, 1780) have been found near the border between Italy and Slovenia and at least few 5-spotted specimens with '*Z. angelicae*' habitus were observed. The records of *Adscita albanica* (Naufock, 1926) have turned out to be the newly described *A. dujardini* Efetov & Tarmann, 2014, which replaces *A. albanica* in France, Italy, Switzerland and Slovenia whereas *A. albanica* is restricted to the Balkans, Ukraine and Russia. Moreover, the distribution borders of *Adscita alpina*, *A. italica* and *A. statices* have been studied and hybrids of *A. alpina* and *A. statices* and *A. alpina* and *A. italica* have been found. Although the rich Italian fauna of Zygaenidae with three endemic species may seem to be fully investigated (based on the number of publications on Italian species), a lot of questions about their origin, distribution, biology and ecology remain still open. New data about recently discovered and possibly disappeared populations, hybrid zones between species and subspecies, interesting distribution patterns and the impact of DNA results on the taxonomy and biogeography of the Italian zygaenid fauna are discussed.

Key words: Zygaenidae fauna, Italy, forty five species, distribution, hybrid zones

In search of the evolutionary origin of the endemic Sardinian blue butterfly

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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 are trying to reconstruct the evolutionary history of the Sardinian blue butterfly, *P. barbagiae* de Prins and van der Poorten 1982, using the variable region of the COI mitochondrial gene (659bp) and four nuclear markers (28S rRNA, wingless, Internal Transcribed Spacer 2 and Elongation Factor 1α). The species is distributionally 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 158 specimens, including 11 individuals of *P. barbagiae*, representing seven species out of ten described in the genus from widely distributed sites throughout the western Palaearctic region.

Maximum Likelihood and Bayesian inference analyses confirmed the monophyly of the genus *Pseudophilotes* and clearly supported the closer affinity of *P. barbagiae* to the species assemblage of *P. baton*, *P. vicrama* and *P. panoptes* as opposed to *P. abencerragus*. The Sardinian endemic *P. barbagiae* turned out to be a young endemic, but clearly with European instead of North African origin and evolved through allopatric isolation on the island of Sardinia only about 0.74 Mya.

Key words: endemic Sardinian, *Pseudophilotes*

Molise, a small Italian region with high Lepidoptera biodiversity value

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Molise Region, located between the Adriatic Sea and the regions of Abruzzo, Latium, Campania and Apulia, represents the second smallest Italian region, with a total area of 4,437 km^2 and an altitude ranging from 0 m/asl on the Adriatic coast to 2,241 m/asl of Monte La Meta. From a geomorphological point of view, the Molise territory is divided into two differentiated sectors: one eastern, consisting of hills sloping towards the sea, the other western, characterized by imposing carbonate massifs, in which the highest altitudes are reached. Despite being a region with modest territorial development, due to its geo-climatic peculiarities, Molise has a high floristic diversity and hosts a wide range of habitats. However, it is the least investigated Italian region as regards the fauna of the invertebrates. Here, an updated overview of the Macrolepidoptera biodiversity known in the Molise Region is reported. Although the first records of butterflies and moths for Molise date back to the first decades of the nineteenth century by the Neapolitan naturalist Oronzo Gabriele Costa, for a long time the regional territory was much neglected. Most of the current knowledge has been gathered by field explorations carried out over the past thirty years. Currently, the Macrolepidoptera fauna of Molise has a total of 967 species, only partially reported in the scientific literature. This presentation illustrates the Macrolepidoptera species found in biotopes located in coastal areas, wetlands, inland hills and in the Matese, Mainarde and Alto Molise mountain ranges.

Key words: Macrolepidoptera, Italy, biodiversity

Diversity of macromoth communities in mountain forests of southern Apennines

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Over the last years, we studied the diversity of macromoth communities in seven of the most representative mountain forest types of Calabria, southern Apennines, Italy. Investigated forests are characterized by *Acer* sp. pl., *Fagus sylvatica*, *Castanea sativa*, *Alnus glutinosa*, *Pinus nigra calabrica*, and *Abies alba*. The extensive and standardized field effort we applied allowed us to depict the structure of moth communities and to link them to the management of forests. Each forest type displays a peculiar moth community, in most cases dominated by species trophically linked to the dominant tree. Endemic species, such as *Ptilophora variabilis*, *Isturgia spodiaria*, *I. messapiaria*, *Hydriomena sanfilensis*, *Solitanea mariae*, and *Xanthorhoe vidanoi*, strongly characterize these communities from a biogeographic viewpoint. Among most the interesting findings, we can report *Acasis appensata*, *Perizoma lugdunaria*, *Nebula senectaria* from Geometridae, *Cymbalophora rivularis* and *Orectis proboscidata* from Erebidae. These studies allowed us to estimate that moth diversity of southern Apennines is far from being well known as the range of several species was extended southward, species new to science were recurrently described and the taxonomic position of others was often revalued in part based on molecular analyses. In next years we expect that forested ecosystems of Apennines will increase its importance as biodiversity hotspot at continental scale for the presence of an increasingly number of endemic species. In fact, the populations of some species (for example *Drymonia dodonaea*, *D. querna*, *Isturgia spodiaria*, but many others) showed a great divergence in the COI mitochondrial gene utilized in barcoding analyses from those of Central Europe suggesting further taxonomic studies.

Key words: Lepidoptera, Italy, biodiversity

In search of the ecological determinants for the exceedingly restricted and most outstanding Italian endemic moth, *Brahmaea (Acanthobrahmaea) europaea* Hartig

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Brahmaea (Acanthobrahmaea) europaea Hartig, 1963, is an Italian endemic exhibiting an exceedingly restricted geographic distribution. In 1971, a nature reserve was established to protect this species, the Riserva Naturale di "Grotticelle" (Basilicata Region). Subsequently, the Reserve was annexed to the Special Area of Conservation (SAC) of "Grotticelle di Monticchio". In 1997, for the first time, a group of *B. (A.) europaea* caterpillars was found in nature. During research conducted in 2013-2014, an egg cluster of *B. europaea* was observed for the first time, and other groups of larvae were found inside the Reserve. Palatability tests allowed to assess *Fraxinus angustifolia* subsp. *oxycarpa*, *Ligustrum vulgare* and *Phillyrea latifolia* (Oleaceae) as the host plants of the moth among those present in the Reserve. From spring 2015 to spring 2017, new bioethological observations on *B. europaea* were conducted, and surveys aimed at mapping the distribution of its host plants in the overall SAC were also undertaken. During 2016 and 2017, other egg clusters and groups of larvae were found, which enabled to detail several aspects of the egg-laying and larval behaviour until pupation. In addition, a map of the local Habitat 91B0, "Thermophilous *Fraxinus angustifolia* woods", has been outlined. Recently, prolonged diapause by pupae of *B. europaea* kept in the laboratory has been documented. In spring 2018, four adults successfully emerged from two years old pupae. In this communication, considering its extremely restricted range and poor knowledge about its ecological requirements, the conservation status of *B. europaea* is summarized and the options to increase the extension and connectivity of the environmental patches that actually or can potentially host Bramea populations are briefly evaluated.

Key words: *Brahmaea europaea*, Italy

Distribution of butterflies in Estonia as revealed by an active mapping project: patterns, changes and causal factors

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Distribution of butterflies was mapped throughout the territory of Estonia in 2016-2017. In more than 1200 sites, systematically pre-selected using a repeatable algorithm, butterflies were counted in the course of three phenologically targeted rounds of visits. In total, over 180,000 individuals representing 97 butterfly species were recorded. We compared the resulting distribution maps with historical records. We conclude that, on the time scale of a century, the changes in the Estonian butterfly fauna have been moderate. For about 75% of the species, no conclusive evidence of a change in distribution or abundance could be inferred. Of the rest, there are more butterfly species with a positive than a negative trend in abundance or distribution. Some but not all of these changes can plausibly be associated with the ongoing climate change. An observation of conservation concern is the decline of several dry meadow specialists. Dozens of landscape-level parameters were inferred for each site from original observations and topographic databases. We are going to present preliminary results on determinants of butterfly species richness in Estonia.

Keywords: butterflies, Papilionoidea, distribution, faunistics, climate change, landscape ecology, species richness

Zygaenidae (Lepidoptera) of the Eastern Mediterranean Region of Turkey

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The Zygaenidae fauna of the Eastern Mediterranean Region (Provinces: Adana, Mersin, Hatay, Kahramanmaraş, and Osmaniye) of Turkey was studied by using attractant traps as well as by netting specimens in 2017–2018. Zygaenidae species from four genera were found: *Theresimima* Strand, 1917 (1 species), *Adscita* Retzius, 1783 (1 species), *Jordanita* Verity, 1946 (3 species), and *Zygaena* Fabricius, 1775 (10 species). The sex attractants for the Procridinae had been produced in the Crimean Federal University and were esters of 2-dodecenoic acid and isomers of 2-butanol: EFETOV-2 (racemic mixture of *R*- and *S*-enantiomers), EFETOV-S-2 (*R*-enantiomer) and EFETOV-S-S-2 (*S*-enantiomer). Fifteen Procridinae and Zygaeninae species were collected and identified as *Theresimima ampellophaga* (Bayle-Barelle, 1808), *Adscita* (*Adscita*) *obscura* (Zeller, 1847), *Jordanita* (*Tremewania*) *notata* (Zeller, 1847), *J.* (*Praviela*) *anatolica* (Naufock, 1929), *J.* (*Solaniterna*) *subsolana* (Staudinger, 1862) (Procridinae), *Zygaena* (*Mesembrynus*) *minos* ([Denis & Schiffermüller], 1775), *Z.* (*M.*) *diaphana* Staudinger, 1887, *Z.* (*M.*) *purpuralis* (Brünnich, 1763), *Z.* (*M.*) *graslini* Lederer, 1855, *Z.* (*M.*) *punctum* Ochsenheimer, 1808, *Z.* (*Agrumenia*) *olivieri* Boisduval, 1828, *Z.* (*A.*) *carniolica* (Scopoli, 1763), *Z.* (*A.*) *viciae* ([Denis & Schiffermüller], 1775), *Z.* (*A.*) *loti* ([Denis & Schiffermüller], 1775), and *Z.* (*Zygaena*) *filipendulae* (Linnaeus, 1758) (Zygaeninae).

Key words: Zygaenidae, attractant, Eastern Mediterranean Region, Turkey

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Geometrid moths of the Baikal Region: fauna, DNA barcoding and taxonomy

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Many groups of organisms appear to be so large and complicated that their diversity, distribution and structure are not estimated yet. One of these groups is geometrid moths, the second largest family of lepidopterans, containing at least 23000 described species. Our study is devoted to this remarkable taxon and covers a poorly known Russian territory – the wide area of Siberia adjacent to the Lake Baikal. First we studied the literary data accumulated from the middle of the XIX century up to now: about 50 sources in total. The milestones in the history of the investigation of Geometridae in the territory of Baikal Siberia were indicated. Furthermore, we have revised and redefined the part of the materials collected during this period ourselves. At the moment, we consider the ideas about the Geometridae fauna in the Baikal region to be rather fragmentary for several reasons: (1) the lack of specialists, (2) the absence of keys for the family, (3) the most part of territory is hard to get access to. The northern areas of the region such as Yerbogachenskaya Plain, Patomskoye Highlands, Severobaikalskoye Highlands and Stanovoye Highlands, Vitimskoye Plateau and Prilenskoye Plateau remain extremely poorly studied. In order to reveal the fauna fully we summarized the numerous specimens collected by the author over ten years and the collections of the following institutes: the Zoological Institute, Russian Academy of Sciences (Saint Petersburg), the Department of Biology and Soil sciences, Irkutsk State University (Irkutsk), the Institute of General and Experimental Biology (Ulan-Ude) and the Institute of Animal Systematics and Ecology, Siberian Branch of Russian Academy of Sciences (Novosibirsk). Also, several private collections were revised. As a result, several species were found in the region for the first time: 32 new species records for the Irkutsk Oblast and 13 new records for the Republic of Buryatia. The presence of 22 doubtful species in the South Baikal region was also confirmed. Two potentially new species from the genera *Entephria* and *Acasis* were found. The female genital structures of the rare Baikal–Far Eastern species, *Scardostrenia reticulata* Sterneck, 1928, were described and figured for the first time. The faunal list was updated to contain 350 species from 145 genera and 5 subfamilies. Originally illustrated keys for Archiearinae, Geometrinae subfamilies and several separate genera from Ennominae, Sterrhinae and Larentiinae (in total, 140 species from 52 genera) were composed.

We applied molecular-genetic methods to create a library of DNA barcodes. The barcodes of 112 species (a third of the fauna of the region) were obtained. When processing a part of them, it appeared that some taxa, previously considered as widespread Euro-Siberian species, were in fact their Eastern-Palaearctic vicariants, for instance the pair *Rheumaptera cervinalis* Sc. – *Rh. neocervinalis* Inoue. Besides, a molecular analysis based on COI marker showed potential species synonymies in the genera *Hemistola* and *Charissa*. In the first case when considering a group of *Hemistola chrysoprasaria* Esper., *H. zimmermanni* Hedem., *H. intermedia* Djak., *H. veneta* Butl. We expected *H. zimmermanni* and *H. veneta* to be merely a colour form of one species, and *H. intermedia* to be a subspecies of *H. zimmermanni*. In the second case *Charissa macguffini* Smiles, *Ch. benepunctaria* Wehrli and *Ch. subsplendidaria* Wehrli should be treated as polymorphisms of *Ch. turfosaria* Wehrli. Thus, DNA barcoding as a tool demonstrates an ability to detect cryptic species and focus efforts on problem taxa. In conclusion it should be noted that the spectrum of unresolved problems remains quite wide: like unfinished faunistic inventorying or questions of systematics and phylogeography.

Key words: Geometridae, Siberia, fauna, DNA barcoding

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The spatial and temporal occurrence of marsh fritillary (*Euphydryas aurinia*) in Croatia

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The marsh fritillary (*Euphydryas aurinia*) is one of the most colorful and easily recognizable fritillaries in Croatia. It is protected under the law in Croatia and is listed under EU Habitats and Species Directive (Annex II and IV). Accordingly, a monitoring plan should be developed and implemented for reporting the species status and population trends in the country. However, most of the knowledge about its distribution is based on historical literature covering only some parts of the country. Especially lacking are the records from the Mediterranean biogeographical region due to the lack of recent systematic surveys. In order to update the knowledge about its spatial and temporal distribution, and facilitate further surveys and conservation activities, we analyzed the historical and current records and potential threats across all three biogeographical regions of Croatia. In the literature, only 76 species-records were found, from all three biogeographical regions, with the records from the Mediterranean region being the scarcest. Our recent survey confirmed almost all the historical records and recorded this species in 130 new localities across all three regions. The most important additions are from the overlooked Mediterranean region where we managed to record numerous populations across the central and southern Dalmatian hinterland. The most notable records are from southernmost part of Dalmatia, on Mt. Snježnica, which are isolated from other populations in Croatia but are most probably connected to the ones in Bosnia & Herzegovina. In general, two population ecotypes are known from the country; wetland populations inhabiting damp grasslands, mostly in the continental biogeographical region and the dry grassland populations inhabiting dry grasslands that have an abundance of plants growing on lime-rich soil, occurring mostly in the alpine and Mediterranean biogeographical region. Accordingly, the observed threats also differ with respect to the region and habitat type. In the continental regions, the populations are usually isolated with limited possibility of dispersal due to the distances between suitable habitats. Habitat destruction and changes in the water regimes are the most notable threats in the region. Some of the recorded populations are extremely small, and most probably prone to local extinctions. In the alpine and Mediterranean regions, the populations are usually larger, occurring in larger habitat patches (mainly extensive mountain pastures and grasslands). In such area, natural succession caused by the decline of extensive grazing is the main threat.

Key words: distribution, ecological network, Habitats Directive, Annex II, Annex IV

TUESDAY, 6 JUNE 2019

ROOM B

COLLECTION AND DIGITISATION PLATFORMS

GENERAL SESSION

The digitisation of Lepidoptera collections

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Digitisation of Lepidoptera specimens from collections has been taking place for at least 20 years and records of digitised specimens available online are now in the millions. Based on my own personal views and experiences working at the NHMUK, London, where I have been involved in digitisation projects totally some 750,000 specimens, I will be looking at a brief history of digitisation, digitisation workflows, data validation, as well as the impact the generated data have on the research community/other stakeholders and what the future may hold. As considerable investment in specimen digitisation has been made by the NHMUK and other museums/institutes worldwide I will also examine the impact on the collections staff, collections and the actual specimens.

Key words: digitisation, Lepidoptera, workflows, data, collections

More about storing butterflies in bags

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At the SEL meeting in 2017, Naturalis Biodiversity Center, Leiden, the Netherlands, presented a new workflow to make the data of its large collection of butterflies stored in paper bags available to science. The new workflow, developed in 2015-2016, carried out by volunteers, consists of digitizing and imaging butterflies and restoring them in acid-free glassine bags. It proved to be more efficient in terms of time, money and space requirements than the traditional method of mounting all specimens. In early 2017, 16,500 papered Papilionidae had been processed at Naturalis. By the end of 2018, an additional 70,000 papered butterflies from all major families of Rhopalocera had been processed. To optimize storage, the workflow was adjusted to allow for differently sized butterflies. For Papilionidae a pilot study was carried out using image recognition to provide on-the-fly identifications. Results of the pilot study are discussed in the context of pros and cons and the general applicability. Out of some 80,000 processed butterflies, 12,000 have been identified by specialists based on their images. Results are exemplified including details of butterflies requiring mounting. Some examples of day-to-day issues and challenges are discussed with the method chosen to tackle these. Finally, plans for future developments are highlighted.

Key words: image recognition, papered butterflies, glassine envelopes, efficient storage, volunteers, workflow

Introducing the Lepidoptera collections in the Natural History Museum Aarhus: history, challenges and perspectives.

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To most lepidopterists ‘public Lepidoptera collections’ and ‘Denmark’ equals the Natural History Museum of Denmark (ZMUC) in Copenhagen. While ZMUC with its more than 2 million specimens and tradition for outstanding research indeed is the major natural history museum in Denmark, it is not the only one. The Natural History Museum Aarhus (NHMA) was founded in 1911, and is an independent, self-governing institution supported by the Ministry of Culture and Sports, and the city-council of Aarhus (the second largest Danish city). While NHMA’s collections are considerably smaller than those of ZMUC, the Lepidoptera collections are still substantial and dating back more than a century, with strong focus on Scandinavia and Greenland. As such the museum is an extremely valuable, but underutilised resource for especially faunistic and biodiversity studies focused on northern Europe and Greenland. Here I will give an overview of the Museum’s collections, history and current activities with focus on digitisation initatives, as well as outlining prospects and challenges for the future.

Key words: Regional collections, Natural History Museum Aarhus, digitisation, Specify

Wow, what an insect! Digitalization in teaching and in environmental education

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Insects and insect identification are elemental parts in various sectors in modern societies ranging from identification of adverse alien and pest species, to understanding the role of beneficial pollinators, and to the need to identify insects at various hierarchical levels from order to species. Here, we present a case study from university context, demonstrating how physical, collection-based teaching material aimed for biology students can be supplemented with digital teaching material, and how this material allows new pedagogical techniques to be used. We produced one high-resolution digital plate for each 26 insect orders found in northern Europe, including Lepidoptera, which summarise their diagnostic characters and allows easy identification at order-level. We demonstrate the benefits of digital teaching material, how it can be used in teaching, environmental education, identification and in popularizing insects. We also share our experiences how much resources and time are needed to produce digital material, and which kind of equipment and technical set-ups proved functional.

Key words: Digitalization, insect, teaching, environmental education

Biologer: an open source platform for gathering species occurrence data in Eastern Europe

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In recent years biodiversity science and nature conservation has a lot to thank to Citizen Science projects, which helped to involve more people. The projects resulted in significant increase of available data on biodiversity and allowed researchers access to large novel datasets. In parallel, there was ongoing development of various biodiversity software used to collect, store and even analyze these data, but mostly limited to central and northern Europe. The slow pace progress of Citizen Science in eastern Europe is related to limited number of experts and projects, while the existing software and the data are closed and owned by researchers, institutions or organizations. Having this in mind we developed Biologer, an online platform licensed as open source software. Biologer was designed a user-friendly online interface for entering occurrence data accompanied by a simple android application used to collect data from the field surveys. It is created from user's perspective, allowing researchers and nature enthusiast to choose how they prefer to share the data with others, with strong encouragement towards open data and open source software. Biologer was created in 2018. So far two regional communities were established, in Serbia (biologer.org) and Croatia (biologer.hr). In Serbia, the platform has been fully operational from the beginning of 2018, used by about 200 people who collected over 45.000 data. The Croatian database has been operational from the beginning of 2019 and has enlisted about 40 users which collected 5.600 data. We encourage the previous and future visitors to these countries who collect data about Lepidoptera to participate in this project and help us collect additional information about the biodiversity of Eastern Europe. Although the software is only collecting occurrence data from the field, further development will make possible to enter data from the literature, personal and museum collections and transects. It is also possible to create new Biologer communities in the region, extend the taxonomic scope of the project and create a unique taxonomic database to be used by all Biologer communities.

Key words: Biologer communities, platform, Eastern Europe

A list of the primary type specimens of Lepidoptera in the "Muséum d'histoire naturelle de Genève" Geneva, Switzerland

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A list of 437 primary type specimens found to have been deposited in the "Muséum d'histoire naturelle de Genève" Geneva (MHNG), to date (13.v.2019), is presented. Thirty-seven families of Lepidoptera are represented by primary type specimens, the most diversified being the Noctuidae (96), Pyralidae *sensu lato* (82), and Erebidae (41). Sixty-seven of the names (15.3%) for which these 437 primary types form the basis are now synonyms, 105 (24.0%) are used in other combinations, and 265 (60.6%) remain as in the original combinations. Sixty-seven authors were responsible for the descriptions of the corresponding taxa, the most prolific being Joseph de Joannis (1864-1932; 56 taxa), Jacques Plante (1920-2003; 54 taxa), and Bernard Landry (1962-; 50 taxa). The oldest taxa for which the MHNG holds type specimens were described by Achille Guenée (1809-1880) in 1872. The most prolific decades in terms of taxonomic descriptions for which the primary types are deposited in the MHNG are the 1920s, with 80 taxa and the 1990s with 74 taxa, followed by the 1930s with 61 taxa. The Afrotropical region, with 40.3% of the taxa and the Palearctic region with 27.7% are the best represented, followed by the Neotropical (23.8%), the Oriental (7.3%), and the Australasian (0.9%) regions; none of the MHNG primary types are from the Nearctic region.

Key words: type specimens, Lepidoptera, Muséum, Genève

Western Indian Ocean Islands in the view of butterfly zoogeography

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Islands, contrary to the majority of inland areas, form discrete units well defined geographically, with distinct boundaries and with well measurable distance. The numbers of species inhabiting islands are much lower than on continents and thus it is much easier to explore the whole fauna within a reasonable time. We investigated biogeographic patterns of butterflies inhabiting the islands scattered in the western part of the Indian Ocean, the study is based on both published records and our own data. The butterfly fauna of the Western Indian Ocean Islands is composed predominantly of butterflies originating from Africa and/or species widespread in Afro-Oriental region. The fraction of endemic species is small but significant, with the exception is Madagascar with an incredibly rich endemic fauna. The species numbers on the islands follow the equilibrium island biogeography model cf. MacArthur & Wilson – the species numbers are positive with island area and negative with distance from Africa. On the other hand, the number of endemic species is correlated with island age. The endemic species did not have time to develop on young islands.

Keywords: Ecology, evolution, island biogeography

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Lower Cretaceous Micropterigidae (Lepidoptera) in Spanish amber

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Paleoentomological research on Spanish amber began in 1995 when abundant and diverse bioinclusions were found in amber excavated from the Sierra de Cantabria (in northern Spain). The fossil lepidopterans discovered (26 thus far) came from the outcrops of Peñacerrada I (Moraza, Burgos) (22), and El Soplao (Rábago, Cantabria) (4), which were located in the north of the Iberian Plate during the Cretaceous, in the east margin of the Basque-Cantabrian Basin. The outcrops are Upper Albian in age (*ca.* 105 Ma), and the amber is associated with coal from plant material deposited in deltaic environments. Among the arthropods, the lepidopteran record is rather humble; so far, only 22 moths have been found in Peñacerrada I (1.22%), and four in El Soplao (0.73%). El Soplao specimens are jaw-moths of the family Micropterigidae, and one of these might be *Micropterix* Hübner, 1825, found in a piece of amber that also includes (likely) Schizaeaceae fern spores; the other three might be *Sabatinca* Walker, 1863, but their wing venations are obscured by debris and will require further study. Peñacerrada I specimens include 21 micropterigids, likely conspecific, which we have included in the genus *Sabatinca*. The 22nd specimen seems to be a Glossatan Tineoidea, although its assignation is uncertain since its head and thorax are lacking. Their descriptions are still pending. Micropterigids include pre-angiosperm moths and are considered the most primitive extant lineage of Lepidoptera, remaining essentially unchanged since the Early Cretaceous and containing currently about 21 living genera / 260 species. The earliest indisputable fossil micropterigid, perfectly preserved in Barremian Lebanese amber, is datable to about 130 Ma; followed later by the Spanish specimens (*ca.* 105 Ma), and then those of Myanmar (Cenomanian in age, *ca.* 99 Ma). Extant larval micropterigids are dependent mainly on liverworts, and then as adults on fern spores or (in a few cases) angiosperm pollen. The palynological fossil record of the Basque-Cantabrian Basin suggests that the resin was produced in subtropical forests which developed under a seasonal wet-dry climate and were inhabited by ferns, gymnosperms (the conifers that dominated this forest, mainly araucariaceans and cheirolepidiaceans) and early angiosperms.

Key words: Micropterigidae, Sabatinca, Micropterix, Lower Cretaceous, fossil amber, Spain

Monoclonal antibodies to lipophorin of the Zygaenidae as a tool for biomedical research

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The first author has previously shown the effectiveness of using of some insect proteins and peptides together with monoclonal antibodies (MABs) specific to them for the solution of some biomedical problems. For example, MABs to melittin (a peptide from *Apis mellifera* venom) were used in model experiments with human proteins. We suggested that lipophorin (amphiphilic lipoglycochromoprotein) from Lepidoptera haemolymph would be the perspective molecule for biological and medical research. Different components of this complex protein provide its ability to interact with different polar and nonpolar substances. Due to the presence of carotenoids lipophorin has a yellow colour and can be identified either visually or by spectrophotometric analysis. In our laboratory using hybridoma technique we created four hybridomas producing MABs to lipophorin of *Adscita* (*Adscita*) *geryon* (Hübner, 1813) (Zygaenidae, Procridinae). These MABs were used for comparing their interaction with lipophorins of the representatives of different Procridinae genera (viz. *Theresimima*, *Rhagades*, *Adscita* and *Jordanita*) by enzyme-linked immunosorbent assay (ELISA). Phylogenetic trees were constructed after processing the numerical data with the help of computer programs NJ TREE and TDROW. Some of MABs showed broad specificity and the ability to recognize lipophorin of some other families of Lepidoptera. We consider that human immunoglobulins G (IgG) are able to interact non-specifically with the amphiphilic metabolites which blood concentration increases at malignant tumours. We have shown that IgG can also non-specifically interact with amphiphilic molecules obtained from insects. So the latter substances can be used as model molecules for the investigation of IgG in pathology. For the study of interactions of human IgG with lipophorin of Zygaenidae we used anti-lipophorin MABs and anti-IgG MABs earlier obtained in our laboratory. We have elaborated our own scheme of ELISA and compared the interaction of lipophorin with IgG from the blood serum of healthy persons and patients with different malignant tumours. It has been found that the majority of studied IgG from the blood serum of the patients with oncological pathology interact with lipophorin reliably more strongly than IgG of healthy people. Thus, monoclonal antibodies to lipophorin are an efficient tool for a wide frame of biomedical research.

Key words: lipophorin, Zygaenidae, hybridoma technique, monoclonal antibodies, malignant tumours, human immunoglobulins

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Phylogeographic pattern of genetic variation in *Aporia crataegi* (Lepidoptera, Pieridae)

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The black-veined white, *Aporia crataegi* (1758), is regarded as the most widespread and common species in the genus *Aporia*, occurring from northwestern Africa, throughout most Europe, to Asia. It is considered a species of Least Concern in the European Red List of Butterflies, even though in several parts of Europe it started to significantly decline or even go extinct, such as in Britain from where it has been extinct since the 1920s.

In order to assess the phylogeographic pattern of the species and to investigate if the current taxonomic entities match this pattern, we analyzed 197 specimens from across the range of *A. crataegi* using the mtDNA cytochrome oxidase (COI) barcoding region.

In contrast to the elevated number of subspecies currently recognized under *A. crataegi* (25, *sensu* Della Bruna *et al.* 2004), our analyses revealed that the mitogenomic structure of this species is shallow and weak. Beside a main group, consisting of two well-supported haplogroups (one distributed from Spain to China and the other in the Italian Peninsula and Spain), four distinct lineages were identified in Iran, Sicily, North Africa and Japan. The present haplotypes distribution pattern in Europe is consistent with an expansion of the species from Mediterranean refuges after the last Pleistocene glaciation. An estimation of the expansion times will be conducted.

Key words: *Aporia crataegi*, DNA barcode, phylogeography

ABSTRACTS

POSTER PRESENTATIONS

Analysing incomplete faunistic knowledge to estimate future species richness distribution under global warming effects: the Iberian butterflies (Papilionoidea)

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Although butterfly distributions are well worked out at a broad grid size across most of Europe, the coverage of exhaustive faunistic information (dense prospective effort at high geographic resolution) remains moderate or low throughout most areas in south-European countries. This hampers statistical analyses of the richness and its geographic distribution, which in turn complicates extrapolations of future climate scenarios to estimate the potential changes in species richness. Using updated occurrence data on the Iberian (mainland Spanish and Portuguese) Papilionoidea we determined the 50 x 50 km grid size as the most reasonable balance between geographic accuracy and completeness. We then estimated the observed and expected present species richness at that geographic resolution. Present richness was then modelled on the basis of climate and physiographic variables using the expected values; weighted regressions were applied to reflect the uncertainty related to completeness. The results were used for extrapolation of a future climate scenario (2070) and these expectations were compared to the present data. Not surprisingly, either temperature or precipitation (or both) explain a significant proportion of the variance of present species richness. As a consequence any extrapolations of species numbers to a future climate scenario tend to be negative across all of the area.

Key words: Faunistic, richness, global warming, Iberian butterflies

The residual wetland in the Mediterranean basin and their importance for the protection of endangered species: biodiversity of Microlepidoptera fauna in the salt marshes of southeastern Sicily

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The Mediterranean salt marshes are generally located near the sheltered shores of the basin. Recent researches highlighted a dramatic decline of these ecosystems surfaces that caused their fragmentation and the damage of the habitats. Nowadays the salt marshes are strongly reduced as a consequence of the geomorphological evolution linked to climatic change and to human activities. Disturbance *via* overgrazing, pollution, tourism and other forms of coastal development are serious threats to such places, which are in need of urgent and strict protection. Recently in many mediterranean regions these delicates ecosystems have been declared as protected areas aiming to guarantee the protection of the biodiversity, which is adapted to these environmentally unique areas. A case in point is the Lepidoptera community of salt marshes, which is strongly influenced by the Mediterranean climate and the above mentioned factors. Researches on salt marsh habitats are rather fragmentary and thus information on species diversity are limited. The objective of the research was the improvement of the knowledge of the insects in the Pantano Longarini marsh. This area (SCI ITA090003) is located in southeastern Sicily (36°42′ N, 15°01′ E; 2 m a.s.l.) between the Syracuse and Raguse provinces on the south edge of the Hyblean calcareous plateau. The great natural importance of this protected area (1,358 ha) is due to its considerable environmental diversity (dunal complexes, rocky coasts, salt marshes, garrigues, streams, etc.). The research was carried out over two years (2015-2017), based on monthly observations. Moths were attracted to light (160 W mercury vapour lamp). The survey resulted in a total of 253 species of macromoths and 118 of micromoths being collected. The microlepidoptera species belonged to the following sixteen families: Alucitidae (1 sp.), Autostichidae (1 sp.), Choreutidae (1 sp.), Coleophoridae (11 spp.), Cosmopterigidae (1 sp.), Crambidae (8 spp.), Depressariidae (2 spp.), Elachistidae (2 spp.), Gelechiidae (24 spp.), Plutellidae (1 sp.), Pterolonchidae (1 sp.), Pterophoridae (13 spp.), Psychidae (2 spp.), Pyralidae (33 spp.), Tineidae (2 spp.), and Tortricidae (15 spp.). Among them some taxa are reported as new records in Europe, and/or in Italy. This study significantly increases the knowledge on the Lepidopterofauna of Sicily, updating data on rare and highly endangered species. These unique environments have been only partially investigated and entomological researches are in progress.

Key words: salt marshs, microlepidoptera, Sicily

Five years of BMS España: Past, present and future

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The Spanish Butterfly Monitoring Scheme, BMS España, started in 2014 as an assessment tool for the butterflies of Spain and its habitats. The network had 60 transects in 2015 after the first year of the scheme. In these five years, BMS España has gradually increased its number of volunteers and transects, with new itineraries along the Iberian Peninsula, Baleares and Canary Islands. In 2019, the network has reached a total of 240 volunteers and 160 transects.

In this study, we present a summary of the results of the first five years of the project, the achievements made and the future objectives. A total of 202.000 butterflies of 190 species (a 81% of the Iberian species) have been recorded. In the future, it is expected that the coverage of BMS España increases, reaching new provinces and recording new species and populations for the network.

Key words: Butterfly monitoring, network, Spain

Hawkmoths (Lepidoptera: Sphingidae) of the Caldera de Lubá. Bioko Island (Equatorial Guinea)

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Located in the south of Bioko Island, the volcanic Caldera of Lubá represents the only sample of the monsoon forests in Equatorial Guinea. Declared Scientific Reserve in 1997, the first records about its Lepidoptera diversity were obtained during the scientific expeditions carried out by the Polytechnic University of Madrid in the years 2005 and 2007 (Martín, 2015a, 2015b, 2016; Martín & Cobos, 2010, 2014, 2015, 2016a, 2016b; Martín, I., Cobos, P. & Rodríguez de Rivera, O., 2011). Both expeditions were done with correspondence to the Spanish Investigation, Development and Innovation (I+d+i) National Plan: CGL2005-23762-E and CGL2006-27110-E/BOS. In the present piece of work, the first results of the hawkmoths are showed. Of the 546 specimens of Lepidoptera collected on both expeditions, 299 are moths and 45 belong to the Sphingidae family. Among the total 14 species, referred for the first time to the inside of the Caldera of Lubá, another five of them mean the first quotes in the Island of Bioko: *Centroctena rutherfordi, Daphnis nerii, Nephele funebris, Temnora nephele, Temnora scitula* (Macroglossinae) and *Andriasa contraria* (Smerinthinae), one mean the first quotes in Equatorial Guinea: *Temnora zantus apiciplaga* (Macroglossinae).

Key words: Afromoths, Sphingidae, hawkmoths, Caldera Lubá, Bioko, Equatorial Guinea

Wing pattern variation in the Alcon blue butterfly in Scandinavia over the last century

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In 1964, Svend Kaaber carried out a large-scale survey of the morphology of the Alcon blue butterfly in southern Scandinavia, where he found clines in wing patterns, which he interpreted as evidence of two species interbreeding in the area. The specimens used in this study are still available, together with additional specimens collected in the region over the last 50 years. We digitally photographed the upper and lower surfaces of over 1000 specimens under standard lighting conditions, and used modern image analysis techniques to repeat and go beyond his analysis. Here we present the initial results of this image analysis, which confirms many of the geographical patterns that Kaaber found, but where we have also examined temporal changes in wing patterns.

Key words: *Phengaris (Maculinea) alcon*, image analysis, geographical variation

Lepidoptera Tortricidae from Calabria (southern Italy)

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The tortricid Lepidoptera from the Calabria territory (southern Italy) have received sporadic attention by both Italian and foreign entomologists. In the present research, a tortricid list as updated and complete as possible for Calabria is reported. For this purpose, in addition to our specimens collected from 2013 to 2018, we included in the list the species found by P. Trematerra in the course of previous entomological researches in that region. The localities visited were especially in the northern and central part of the Calabrian territory, such as the Pollino Massif, Sila Mountains and the bordering areas from sea level up to 1500 m abov sea level. Our specimens were caught mainly by light at night-time and by butterfly net during day-time. The material was identified morphologically through examination of wing pattern and genitalia. 181Tortricidae were recorded, the most diverse subfamily is Olethreutinae with 102 taxa, followed by Tortricinae with 75, and the Chlidanotinae with four. Fifty-nine species are recorded for the first time in Calabria. Of particular interest are 23 species that have the southern limit of their distribution the Calabria territory. A biogeographic study of Tortricidae in Calabria, using chorological analysis, was carried out. This study show that the taxa with a Cosmopolitan (1.10%) or a Subcosmopolitan (2.21%) distribution are few; more than 59% of the taxa have a wider Palaearctic distribution. On the other hand, much fewer have a European (18.78%), Mediterranean (6.63%) or Endemic (2.21%) distribution. The endemic species are represented by *Archicnephasia hartigi* Razowski, 1983, *Cnephasia zangheriana* Trematerra, 1991, *Cochylimorpha scalerciana* Trematerra, 2019, and *Isotrias martelliana* Trematerra, 1990. A limited number of specimens belonging to taxa potentially harmful to agricultural and forest plants were recorded in Calabria, this suggest that these areas may in good health and maintains a high degree of naturalness.

Key words: Tortricidae, fauna, Calabria, southern Italy

Motorway wedges as a space for butteflies – a case study from the Czech republic

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Motorway wedges have great potential for the survival of butterfly populations. The edges of the roads represent potentially suitable habitats for the occurrence and development of species and the function of migratory corridors in the spread of individuals in the landscape. The margins are wide enough, often with appropriate exposure and blocked succession. In addition, all of these parameters have a large amount variability. The habitats along the roads populate various kinds of butterflies mainly linked to forest-free habitats. At 10 selected sites (with an area of 1000 m^2) along the motorways (in the whole Czech Republic) we have registered so far 49 species of butterflies, including species of conservation importance as *Carcharodus alceae, Spialia sertorius, Zerynthia polyxena, Colias alfacariensis, Glaucopsyche alexis, Polyommatus bellargus, Plebejus argus, Polyommatus coridon, P. thersites* or *Lycaena dispar*. A key moment for species survival on road bodies (= habitat suitability) is, in particular, the nature of the vegetation that is on slopes of the roads. Therefore, within our activities, we are focus on the specification and production of a suitable forb and grass seed mixture that would be applicable for greening slopes of roads, the so-called butterfly blend. Whole the preparation process began with the evaluation of potential food plants for butterflies, continued with seeding of nectaring plants and their production for market (in 4 places across the Czech Republic). Among the species of plants used the "butterfly seed mixture" are mainly *Cichorium intybus, Origanum vulgare, Centaurea stoebe, C. oxylepsi, Salvia pratensis, S. nemorosa, Potentila argentea, Inula salicina* and *Rumex acetosella*. The species were chosen with respect to the number of flowers, cultivation possibility and ease of maintenance. The mixture formed was experimentally sowing 3 areas (Hradec Králové, Příbram, České Budějovice - CZ); these the area hosts a higher number of species and individuals than conventionally sown. Despite these positives, however, we encounter a major difficulty. It's regionality of seeds. So based on the necessary of regionality we have solve it via preparation of several seed grass-forb mixtures for different regions of Czech Republic.

Key words: butterflies, motorway wedges, grass-forbs seed mixtures

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Four pyrales from central Spain: Interesting or unusual data from Madrid: *Bostra obsoletalis* (Mann, 1864), *Synaphe predotalis* (Zerny, 1927), *Hypotia miegi* Ragonot, 1895 and *Asalebria geminella* (Eversmann, 1844).

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Data were gathered on four poorly-known pyrales from Madrid (Central Spain): Pyralidae: Pyralinae: *Bostra obsoletalis* (Mann, 1864), *Synaphe predotalis* (Zerny, 1927), *Hypotia miegi* Ragonot, 1895 and Phycitinae: *Asalebria geminella* (Eversmann, 1844). Label data were examined of 39 specimens (four species) collected 2000-2018. These preliminary results suggest important biodiversity even in the centre of Europe’s capital cities.

The Pyraloidea is one of the largest superfamilies within the Lepidoptera (Heppner, 1991) with 914 recognised European species (Nuss *et al.*, 2014). The Mediterranean Basin is an important source of biodiversity as many species are associated with sub-desertic or eremic environments (especially in the Pyralinae and Phycitinae) or with botanic families with a focus on the Mediterranean as is the case with the Brassicaceae and the Crambid subfamily the Evergestinae (Munroe & Solis, 1999; Goater, 2005). The Iberian Pyraloidea fauna is relatively poorly-known despite their numerical importance: 505 taxa (García Barros *et al.*, 2015).

Specimens in the collection of the first author (Col. GEK) were examined and data compiled in an *ad hoc* manner on those taxa thought to be of faunistic interest. Material had been taken in the field with an entomological net since 2000 especially in the sub-desertic areas of Madrid province of the Tagus valley (Ciempozuelos, 600m; N40°09'09.1; W003°36'27.1).

Key words: Pyralidae, Pyralinae, Phycitinae, Madrid, central Spain, disturbed habitats

Four crambids from central Spain: Interesting or unusual data from Madrid: *Hyperlais rivasalis* (Vázquez, 1905), *Evergestis istatidalis* (Duponchel, 1833), *Evergestis merceti* Agenjo, 1933 and *Evergestis frumentalis* (L. 1761) (Crambidae: Cybalomiinae, Evergestinae).

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Data were put together for four poorly-known Crambids species from Madrid (Central Spain): Cybalomiinae: *Hyperlais rivasalis* (Vázquez, 1905); Evergestinae: *Evergestis istatidalis* (Duponchel, 1833), *E. merceti* Agenjo, 1933 and *E. frumentalis* (L., 1761), associated with eremic or disturbed habitats, even in the streets of Madrid (two species). Label data were examined for 121 specimens (four species) collected 2000-2018. These results suggest important biodiversity even in the centre of Europe’s capitals.

The Pyraloidea is one of the largest superfamilies within the Lepidoptera (Heppner, 1991) with 914 recognised European species (Nuss *et al.*, 2014). The Mediterranean Basin is an important source of biodiversity as many species are associated with sub-desertic or eremic environments (especially in the Pyralinae and Phycitinae) or associate with botanic families with a focus on the Mediterranean as is the case with Brassicaceae and the crambid subfamily the Evergestinae (Munroe & Solis, 1999; Goater, 2005). The Iberian Pyraloidea fauna is relatively poorly-known despite their numerical importance: 505 taxa (García Barros *et al.*, 2015).

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Key words: Crambidae, Cybalomiinae, Evergestinae, Madrid, Central Spain, Disturbed habitats

The southern swallowtail (*Papilio alexanor*) in Croatia: rare or just overlooked?

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The southern swallowtail (*Papilio alexanor*) is one of the most enigmatic butterfly species in Croatia. Historical observations of the species stretch from the end of 19th century until the middle of the 20th century, but until recently, the status and the current distribution of this species in Croatia was completely unknown. Many field trips were done in order to confirm its presence at the historical locations during the last decade, but without any success. Following the rediscovery of several historical populations in the Dalmatian costal area in 2014, we conducted a more targeted survey of this species in most of its historical range in central and southern Dalmatia. This included extended time periods, selection of appropriate habitats and search for its hostplants. As a result, we managed to confirm the species in many of its historical sites, as well as record it in many new localities and habitats. Both the adults and caterpillars were surveyed, and *Opopanax chironium* was confirmed as the only known hostplant in Croatia. New data about its habitat, flight period and abundance have been collected. Our observations shows that *P. alexanor* is present in the submediterranean hilly and montane coastal areas of Croatia, from Omiš, Biokovo and Kozjak, across the hinterland of Dubrovnik-Neretva County to Snježnica Mt. in the south. While favorable weather conditions that could proliferate the expansion of populations may be the reason of the significant increase of new observations, the lack of previous records is most likely the result of its short flight period, high habitat fidelity and a lack of targeted field surveys. While its status as a vulnerable species is justified due to the still limited distribution, the populations are most probably stable. However, in order to confirm this, targeted monitoring should be done across the species' range in the country. Most of the species' habitat, especially steep southern-facing cliffs, are not easily accessible, and not prone to succession. Regardless, the main threat to its survival is the destruction of favorable road edges and slopes on which *O. chironium* grows in abundance, as well as potential illegal collecting. The southern swallowtail is a strictly protected species in Croatia, and the collecting of adults or other life stages is prohibited by law.

Key words: Lepidoptera, Papilionidae, distribution, Habitats Directive, Annex IV

Order Lepidoptera (the Butterflies and Moths) in Shar Planina Republic of Macedonia

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The order Lepidoptera (butterflies and moths) are the best studied insect species in Macedonia represented by 2.640 species. On the basis of desk-top analysis, and our complementary research on field trips carried out on the Shar Mountain, we recorded a total of 961 taxa. The best known are the Butterflies (Lepidoptera, Rhopalocera), represented by 217 species, of which 176 taxa are registered on the mountain range of Shar Planina, which is 81.1% of the total number of species known for Macedonia. They belong to 6 families: Hesperiidae is represented by 19 species, Papilionidae 6 species, Pieridae 18 species, Riodinidae 1 species, Lycaenidae 52 species, Nymphalidae 80 species. 784 species of night active Lepidoptera (moths) have been recorded on the Sharr Mountain. There are 187 taxa from the Geometridae, the second in number are Noctuidae with 175 species, then Erebidae with 64 taxa, Pyralidae 61 species, Crambidae 52 species, Tortricidae 51, Gelechiidae 25 species, Zygaenidae 21 taxa, Oecophoridae 17, Sesiidae 16, Notodontidae 15, Coleophoridae 13, and Pterophoridae 10, Tineidae 9, Yponomeutidae, Sphingidae and Lasiocampidae with 8 species, Psychidae 6, Drepenidae and Plutellidae with 4 species, Saturniidae, Nolidae and Cossiidae with 3 species, Gracillariidae, Scythrididae, Elachistidae, Cosmopterigidae, Adelidae and Nepticulidae with 2 species, the following families are represented by one species: Aegyrestiidae, Blastobasidae, Carposinidae, Choreutidae, Euteridae, Lecithoceridae, Limacodidae, Opostegidae, and Thyrididae. Significantly for Lepidoptera is that they are among the indicators used to determine the quality of the habitat. There is a high degree of endemism in the records. But there are also species that are of particular importance as target species and species protected by international conventions: BERN; BON; IUCN; CITES. Based on the numerous presence of such species of certain habitats, the level of biodiversity is estimated and the habitat is revalidated.

Key words: butterflies and moths, Sharr Mountain, Macedonia

Synergy of two molecular datasets to refine the phylogeny of Crambidae (Lepidoptera: Pyraloidea)

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Crambidae form one dichotomy of the Pyraloidea (“snouth moths”), and with over 10’000 species described, they comprise about two third of their diversity. They can be best separated from their sister-group, the Pyralidae, by the morphology of the adult tympanal organs and the larvae. We present the first molecular phylogeny of Crambidae including all subfamilies currently recognized in the group. We make use of molecular data available from two previous major studies and published transcriptomes or genomes, compiling ten genes totalling 11247 bp. Up to eight genes are sequenced for thirty-nine additional taxa, with Catharinae, Cybalomiinae and Linostinae sampled for the first time. Maximum Likelihood and Bayesian Analyses recover topologies mostly agreeing with that of Regier et al. (2012), with several groupings showing better support. Catharinae and Cybalomiinae are recovered in a clade Glaphyriinae + Odontinae. Linostinae are assigned either to the latter clade, or to the “CAMMSS clade” sensu Regier et al. (2012). Lathrotelinae are recovered monophyletic and sister to the Musotiminae in the Bayesian analysis. The position of Hoploscopini as sister to ((Crambinae + Erupini) + (Scopariinae + Heliothelinae)) render Heliothelinae paraphyletic and prompts the elevation of Hoploscopini to subfamily level as Hoploscopinae **stat. n.** Strong support is obtained for the Heliothelinae s. str. as sister to the Scopariinae. Evolution of host plant preferences are discussed.

Key words: molecular, phylogeny, Crambidae

How do river groves influence the distribution and conservation of butterflies in the Mediterranean region?

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In the Iberian Peninsula there remains a great diversity of water systems, and riverbanks are an example of such. Riverbanks maintain high water content throughout the year, providing a high degree of humidity in the soil and thereby enabling the development of characteristic vegetation: the riparian forest, in contrast to adjacent drier areas.

Butterfly communities present in four river groves were studied for two years with three transects per river, each set up in differing vegetation, density and degree of conservation. Additionally, butterflies taxa in a parallel strip per site were sampled.

Results show that there are not only hygrophilous species present (generally restricted to riparian forest) but that also many others that might usually be taken external to riparian forest, but that during the summer are to be found in such areas due to conditions of hydro-deficit. For this reason, the degree of conservation of river groves can be seen as being an important factor regarding faunistic biodiversity.

Key words: Butterflies, Papilionoidea, riparian forests, conservation, Mediterranean climate

Past and present: a comparative analysis of the butterfly fauna in the mainland part of Dubrovnik-Neretva County

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Dubrovnik-Neretva County is a small Croatian region stretching between Bosnia & Herzegovina and Montenegro, along the coastal part of southeastern Dalmatia. Historically it was one of the most often visited areas by many leading entomologists of the 19th and 20th centuries. Aside from the historical records, new surveys of butterfly diversity of this area were almost non-existent. This represents a challenge for effective local management of protected species. During the last decade, we visited the area repeatedly to gather recent data about the butterfly diversity. In order to show how much the knowledge about the butterfly fauna in the mainland part of Dubrovnik-Neretva County improved in the last decade, historical observations from the litterature were compared with recent observations. A total of 43 published references contained 680 records of 99 different butterfly species, some of which were probably erroneous. All historical records were georefferenced, in order to compare the spatial distribution of historical and newly gathered data. A grid containing 33 10x10 km squares was used for the comparison. Three main centres of research were revealed in the County: Neretva river delta, Pelješac peninsula and the surroundings of Dubrovnik city. During the last decade, we have gathered more than 7500 species records for the area. In total we recorded 112 species, of which 28 new species for the first time. The previously known distribution in Croatia for species like *Euphydryas aurinia*, *Parnassius mnemosynae*, *Papilio alexanor*, *Muschampia proto* and *Kirinia roxelana* has been greatly expanded. With a surface area of only 1.781 km² Dubrovnik-Neretva County is one of the smallest counties in Croatia. While its surface area is slightly more than 3% of the territory of Croatia, it contains 64% species of the Croatian butterfly fauna. In the future surveys, additional species may be recorded, but no large increase in the number is expected. Out of 127 species living in the County, 11 species are categorized as nearly threatened (NT) at the European level, 113 have conservation status of least concerned (LC), while for one species category is data deficient (DD). Habitat degradation, succession and a decrease of extensive livestock grazing are recognized as the highest threats for butterflies in the area.

Key words: Southern Croatia, Lepidoptera, diversity, conservation status

A surprising finding concerning the noctuid moth *Phlogophora meticulosa* (Linnaeus, 1758) (Lepidoptera Noctuidae)

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The Angle Shades moth, *Phlogophora meticulosa* (Linnaeus, 1758) (Noctuidae), is a migratory species which is widespread in Europe, western and central Asia and north Africa; it is known throughout Italy, including on the two major islands. Sometimes it is also a crop pest. This contribution points out a very singular finding regarding this insect. On the evening of 20.05.2013, at Piacenza (northern Italy) on the campus of the Università Cattolica del Sacro Cuore, on the outside surface of a building, a specimen of *Ph. meticulosa* resting on the wall near an artificial light was collected by the author. The specimen at first sight had, at the tip of its abdomen, a rather showy, pendulous extension of an unclear nature. Examination in the laboratory showed that it was a male whose genital armature was holding another similar male armature, almost devoid of the typical covering of hairs and scales and, so to speak, 'torn' from another male abdomen. Also the tip of the abdomen of the specimen with this singular abdominal appendix was partially devoid of the covering of hairs and scales which normally characterizes the males of this species including on genital armature, so that all these structures were well in evidence. The specimen at the time of capture appeared hardly or not at all reactive: it was probably dying if not already dead but if the latter, it had died recently, because it was clinging to the wall with its legs and resting near an attractive light source, and under laboratory examination and subsequent preparation still retained some elasticity in the joints. A microscopic preparation and examination of the tip of the abdomen was set up. The two male genital armatures were similar and conspecific. The coupling between them was by means of the uncus of the male specimen collected, which was holding the right valve of the other armature tightly; this torn armature was therefore placed almost transversely with respect to the other and did not show other kinds of connections with the abdomen of the entire specimen, connections which would have suggested a teratological case. In all likelihood it belonged to another male specimen, from which it had been torn. How should this curious finding be interpreted? A teratological case is to be excluded (the duplication of ectodermal genital structures in a single specimen - male or female - is a known but very rare monstrosity among insects of some orders; in these cases the two 'twin' structures are generally close together, side by side with each other, and, obviously, both connected with the abdomen). By way of hypothesis, the phenomenon may be the consequence of an attempt to mate with a female by two males attracted almost simultaneously by the same female pheromone, with subsequent 'conflict' and accidental mechanical coupling of the uncus of the first to a valva of the second, which then attempting to free itself from the grip and fly away may have ‘lost’ its armature. It is not to be excluded that predation e.g. by an insectivorous bird on one of the two hooked males is the real cause of this strange situation. The author would be interested in hearing any other opinions on this matter. Is anyone aware of similar observations? Does the hypothesis formulated here seem likely? Thanks to anyone who might kindly provide some comments.

Key words: Angle Shades moth, males, genital armature, mating, unusual observation

Morphological observations on a gynandromorph of *Maniola jurtina* (Linnaeus, 1758) (Lepidoptera, Nymphalidae, Satyrinae)

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Gynandromorphism is a teratological condition consisting in the simultaneous presence of both male and female phenotypic characteristics, with a clear demarcation between one and the other, in the same individual of an animal species with separate sexes. To whatever degree, it is always a rather uncommon phenomenon; in the class of insects it is fairly widespread. The major or minor frequency at which this anomaly has been reported for different taxa of insects also derives from the presence (or lack thereof), in the different species, of more or less marked sexual dimorphism. For the Lepidoptera, in which in a relatively large number of taxa (mainly in Papilionoidea) a sometimes very pronounced sexual dichromatism is present and evident above all in the colouring of the two pairs of wings, over time many gynandromorph specimens have been reported (e.g. in Lycaenidae, Nymphalidae, Pieridae, Papilionidae, etc.). The case presented here concerns a specimen of the Meadow Brown butterfly, *Manjola jurtina* (Linnaeus, 1758) (Nymphalidae Satyrinae). The salient morpho-chromatic characteristics are illustrated, including the conformation of the final abdominal segments and the ectodermal genital structures, examined after clarification. Reports of gynandromorphs of Lepidoptera species presenting sexual dichromatism are often limited to the illustration of the habitus of the whole insect, without examination of genital morphology. *M. jurtina* has a wide distribution in the Palearctic region: it is common throughout almost all Europe and in the Mediterranean basin, from sea level up to about 2000 m, and it is found in Anatolia, Iran, Iraq, Kazakhstan, the Urals and western Siberia. It is a univoltine species, which flies between late May and September, with a more or less long period of flight, characterized by proterandry; in the southernmost part of its range it has a prolonged aestivation. It frequents flowery meadows and pastures, grassy glades with bushes, forest edges, gardens and parks. The host plants of the larvae are spontaneous Poaceae. The specimen of the present report has right wings with the typical female colouring, therefore with a striking orange area on the upper surface of the forewing, which stands out against the general brown colour of the fore- and hindwing, while on the upper surface of the left wings the brown colour dominates uniformly. Similarly, on both sides the lower surface has the less striking chromatic differences that distinguish,

respectively, the two sexes. The shape and size of the four wings (right forewing 22 mm long, left forewing 21 mm) are rather similar on both sides. Overall, the relatively small specimen size is closer to the average male size of this species than to the slightly larger female. The antennae on the two sides are similar. The final abdominal segments in the still intact specimen, dry preserved, do not show dissymmetries or other anomalies of any kind; an initial examination of the preparation of the tip of the abdomen highlights female structures both on the right side and on the left side. The specimen was field-collected at Buguggiate (northern Italy: Lombardy: province of Varese) on 20.07.1990.

Key words: wood nymphs, Meadow Brown butterfly, gynandromorphism, morphology, genitalia

Butterflies as bioindicators of heavy metal contamination: a case study at Terni basin valley (Central Italy)

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The present work aimed at evaluating the use of butterflies as novel bioindicators for atmospheric contamination. The study was focused on the Terni basin valley (Central Italy) a current hot-spot for environmental studies, due to the heavy load of pollutants by industrial activities and to the orographic conditions that favor air stagnation and pollutants accumulation. The goal of the study was to evaluate the environmental contamination through the use of butterflies in relation to the distance of the catching site from the productive pole of the city of Terni. The monitoring campaign was carried out at 9 sampling sites (from 133 to 967 m a.s.l.), investigated between June and September 2014, along a transect centered on the city (NW-SE axis, 21 km long). Heavy metal bioaccumulation levels (Cd, Cr, Ni, Zn, Cu, Pb, Co, V, Mn) were analyzed in 470 butterfly specimens belonging to five species: *Coenonympha pamphilus*, *Lasiommata megera*, *Polyommatus icarus*, *Pieris napi*, and *Pieris rapae*. At each site, we chose a random sample throughout the sampling period corresponding to a dry weight of about 100 mg (in two replicates) for each species. The analysis highlighted a bioaccumulation increase of Ni, Vu, Zn, and Mn in all the five butterfly species in the sites close to the metallurgical plant, while Cr showed this trend only in two species, namely *C. pamphilus* and *L. megera*. Cd, Pb, V, and Co were almost always below the lowest detectable level in all the butterflies. These results suggested species-specific bioaccumulation in relation to the heavy metals most associated to the emissions by the metallurgical activities, highlighting how butterflies can be used to detect the heavy metal contamination related to the anthropic activity in a territory.

Key words: Butterflies, bioindicators, metal contamination, Terni, Italy

Records of Lepidoptera in Habitats Directive from Matese National Park (Southern Apennine, Italy)

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The recent establishment of the Matese National Park has increased the interest in the species included in the EU "Habitat Directive" (92/43/EEC). The Matese Massif is located between Campania and Molise Regions. It covers an area of about 1,440 km^2 and has a maximum altitude of 2,050 m represented by Mt. Miletto. It is one of the most extensive mountain chains within the southern Apennines (Italy). The area is almost entirely encompassed within three Sites of Community Importance (SCI, European Commission Habitats Directive), which are: "Matese Casertano", "Pendici meridionali del Monte Mutria" and "La Gallinola-Monte Miletto-Monti del Matese"; and, additionally, within two Special Protection Areas (SPA) ("Matese" and "Le Mortine"). The vegetation of Matese is similar in its general characteristics to that of other mountain ranges of the Central and Southern Apennines, with several belts which succeed each other uphill. Unfortunately, the knowledge of the entomological fauna and in particular of the threatened species of the area is still very poor. This contribution collects preliminary data on the macrolepidoptera fauna included in the Habitats Directive based on both literature records and unpublished results of research carried out by the authors in several localities within the mountain chain. The results show the presence of 6 species (Rhopalocera): *Euphydryas provincialis* (Boisduval, [1828]), *Maculinea arion* (Linnaeus, 1758), *Melanargia arge* (Sulzer, 1776), *Parnassius mnemosyne* (Linnaeus, 1758), *Zerynthia cassandra* Geyer, 1828 and two species of Heterocera: *Euplagia quadripunctaria* (Poda, 1761), *Proserpinus proserpina* (Pallas, 1772) included in the Habitats Directive. Insects, especially Lepidoptera, are excellent bioindicators and play an extremely important role in natural ecosystems. The presence of species included in the Habitats Directive confirms the importance of the Mountain massif, now a National Park, regarding the conservation of threatened species.

Key words: Matese National Park, Mountain Massif, Rhopalocera, Heterocera

New records of Lepidoptera in Habitats Directive from Aspromonte National Park (Southern Apennine, Italy)

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Aspromonte National Park extends for 642 km^2 in the extreme southern offshoot of the Apennine chain, to protect a mountainous complex of remarkable biogeographical interest, which still maintains vast, well-preserved and structurally evolved forest areas. Knowledge on the insect population of Aspromonte National Park is very poor, especially with regard to the Lepidoptera. In accordance with the directives of the National Biodiversity Strategy, a research program was implemented in 2015 that aims to study the distribution, ecology and role of the species included in the annexes of the Habitats Directive (92/43/EEC) for the conservation of ecosystems. It's aim is also to characterize the biogeographical and conservation significance of the protected area within the main mountainous groups of the southern Apennines and, more generally, of the entire Italian peninsula. In 2018, preliminary explorations were carried out to define the monitoring areas of the northern sector, of the Tyrrhenian and Ionian slopes and in the central sector of the National Park. The results confirm the presence of four species included in the EU "Habitat Directive": *Parnassius apollo* (Linnaeus, 1758), *Parnassius mnemosyne* (Linnaeus, 1758), *Zerynthia cassandra* Geyer, 1828 and *Euplagia quadripunctaria* (Poda, 1761). The search for *Papilio alexanor* Esper, 1800 took place mainly in the locations indicated by the last discovery dating back to 1980 (San Luca d'Aspromonte). Despite the presence of suitable habitats and foodplants, it was not possible to report new results. The search for *Eriogaster catax* (Linnaeus, 1758) was concentrated on sites that showed adequate vegetation characteristics. The research did not lead to the reporting of adult individuals. The obtained results increase the knowledge of the macrolepidoptera in the Habitats Directive of this important massif of the southern Apennine. We also believe that the study of the distribution of individual species has an important predictive role and provides detailed data on habitat quality.

Key words: Aspromonte National Park, Apennine, Lepidoptera, Habitats Directive

Natural enemies of *Euphydryas aurinia provincialis* (Boisduval, 1828)

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Euphydryas aurinia (Rottemburg, 1775) is one of the most seriously threatened European butterflies, suffering a severe decline in most countries. Although there are several studies on its ecology and biology, the factors affecting its mortality and the role of natural enemies on its population dynamics are yet not fully known.

Larval survival plays a key role in establishing butterfly population size and distribution range; thus, knowing the sources and variation in larval mortality is essential to understand and predict population dynamics. The larval mortality of *E. aurinia* is mainly attributed to abiotic factors, parasitoids and predators.

In this paper, we present new data on natural enemies of caterpillars of a population of *Euphydryas aurinia* spp. *provincialis* in Central Italy. In the study area, females oviposit on several plants, including *Gentiana cruciata,* and caterpillars live in a communal silken web at I-III larval instar.

During July-August, we photographed in the field and/or collected on sight any potential predator that visited the larval webs on gentians. We visited the larval webs during day-light and every 2-3 hours per day along the same transect path; this was marked by numbered flags, located at each of the host plants. For each visitor observed, we recorded the date and time of the observation and took notes on prey-predator interaction.

Various arthropods, from spiders to insects, have been recorded frequenting the larval web of *E. aurinia.* Among insects, the greatest number of observations was on hymenopterans and dipterans. Of these, females of the tachinid *Erycia furibunda* stayed at butterfly larval webs to parasite the I-III instar larvae. They visited a single larval group repeatedly through time, acting as a potential and substantial mortality factor for our endangered study species.

Key words: butterfly, larvae, predators, parasitoids

DNA barcoding of Croatian butterflies – preliminary results

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In 2017 we started a 4-year project of DNA barcoding of Croatian biodiversity (CroBarFauna) funded by the Croatian Science Foundation with primary goal to study the amount and geographic distribution of the genetic diversity of selected groups of Croatian fauna using DNA barcoding methodology, flagging species for further taxonomic, phylogenetic and phylogeographic studies. The aim for the Lepidoptera group is to provide the DNA barcode library of 198 species of Croatian butterflies. In the last decades, our work has been attempted to collect and create a national database of distribution records in Croatia to publish the national checklist and the red list of butterflies. Today it is clear that collecting has been sporadic and uneven making our work in finding certain species hard. Until now, we managed to barcode 298 specimens belonging to 123 species. A few taxa share DNA barcodes and within few species we found higher intraspecific divergences. While majority of butterflies can be easily recognised using morphological features, identifying some taxa is still challenging and DNA barcoding is helping the right identification thus gathering distribution data and helping in developing conservation plans for about 25% of Croatia's butterfly fauna considered of conservation concern. Establishment of national database of genetic biodiversity will contribute to the global level and enriching international data basis (BOLD and GenBank) with DNA barcodes of not yet represented taxa and taxa from this underrepresented geographic region.

Key words: butterflies, Croatia, DNA barcoding

Use of Lidar data to define habitat use by common butterflies

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Lidar (Light Detection and Ranging) data is a powerful tool to describe the vegetation structure, including small structures, like gaps in the forest. These features are of paramount importance for butterflies, giving them flowery grassland 'islands' within a forested landscape. Within the Foreste Casentinesi National Park, the Tuscany Region ownership (Arezzo Province) extends over 7615 hectares, almost all covered by woodland. In this area we had the opportunity to carry out a Lidar survey, with a 1 m^2 resolution. Butterfly data were collected by visual identification over three years (2016-2018). Every observation was located (<5 m accuracy), recording also date and time of each sighting. GAM (Generalized Additive Models) models were built for species or species complexes with at least 25 observations in the study period. We have considered date, time and grassland extent, measured as the % of grassland habitat, i.e. having a CHM (Canopy Height Model) Lidar data less than 0.5 m, as GAM covariates, comparing species data with surveyed area in a binomial fashion. To avoid unbalancing problems, we compared species sightings with equal numbers of sites, randomly selected from the sample, repeating the sampling 1000 times. Models were fitted according to the minimization of AICc (corrected AIC), leaving those covariates that reduced AICc values. It was possible to analyse data from 11 butterfly species or species complexes (*Pieris brassicae, Melanargia galathea, Lasiommata maera, Hipparchia hermione/H. fagi, Pararge aegeria, Aporia crataegi, Lasiommata megera, Argynnis paphia, Coenonympha arcania, Ochlodes sylvanus, Pieris napi*). Date and time of the sighting are the most important GAM factors for all species, allowing us to define the species' phenology. Lidar grassland data have an important effect, too, leading to appreciable reductions in AICc model values. All species but one show the positive effect of grassland cover, though with species-specific relationships, from forest-edge to genuine grassland butterflies.

Key words: Lidar, GAM models, forested landscape

The current state of Lepidoptera biodiversity in Ethiopia

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Ethiopia, among the largest countries in African continent, is located in the horn of Africa and has a very diverse topography: from 20 mountain peaks above 4000 meters to the second-lowest point on earth, the Danakil Depression that lies 120 m below sea level. Because of vast highlands being isolated by the surrounding dry lowlands, Ethiopia is among the mega-biodiverse countries in Africa and the degree of endemism in its flora and fauna is very high. Despite the rich heritage of biological diversity and many diverse ecosystems, the conservation of its habitats have received scant attention and the country is experiencing rapid biodiversity loss. Widespread clearcutting of forest and conversion into agroforests, farmland or human settlements represent the major threats to the Ethiopian biodiversity in general and Lepidoptera in particular. Here we intend to present the current knowledge of Ethiopian Lepidoptera and give some insights into the expected biodiversity of this major insect order in the country. The review is based on all pertinent published scientific papers from older up to 2018. In addition, records from relevant online databases were also included. According to the obtained results, 2,322 Lepidoptera taxa, belonging to 48 families, have been documented, including 598 endemic species or subspecies. The current state of knowledge of the Ethiopian butterflies and moths relative to their potential appear to be particularly low, when compared to other African countries. Some recent contributions, based on reviews focusing on Ethiopian species of the family Geometridae, will be presented. The results suggested that the estimate for the entire order of Lepidoptera in Ethiopia will be more than 10,000 species, of which a considerable number are new to science. Though still being far from complete, this work provides a significant baseline data for undertaking effective conservation actions and underlines the extreme importance of further researches on Lepidoptera in the horn of Africa.

Key words: Africa, checklist, Endemic species, Geometridae

New records and an updated checklist of the butterfly fauna (Lepidoptera: *Papilionoidaea* and *Hesperioidea*) of Puglia, South-eastern Italy

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An updated checklist of Rhopalocera occurring in the Apulian region, in the south-eastern part of Italian peninsula, is presented with their current status. The surveys were carried out from 2007 to 2018, and 109 butterfly species from 6 families, including several confirmations of historical published records, have been recorded. Among these, threatened species such as *Zerynthia cassandra*, *Melanargia arge*, *Euphydryas aurinia* should be mentioned. In this work new localities and confirmations for *Lycaena alciphron* on Gargano promontory and *Danaus chrysippus* were registered. Including all the published records, mainly in 'grey' literature, the total number of butterfly species recorded in Apulia rise to 120, which equates to 40% of the total Italian and approximately 24% of the total European butterfly fauna. A revised checklist represents a starting point for further research, provides a foundation for future butterfly conservation actions and implies that more research is needed, in order to increase the general knowledge of those insects in South Italy.

Key words: Cheklist, Puglia, Rhopalocera

Butterfly richness and diversity in Mediterranean coastal dunes environment: diversity patterns along a vegetation gradient in South-East Italy

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The butterfly assemblages of coastal ecosystems in the "Dune Costiere" Regional Park in Apulia, South Italy, were studied to evaluate the ecological value of Mediterranean coastal dune environment. Five different habitat types were investigated bi-weekly from April to September 2018, in order to assess the abundance, species richness and diversity of butterflies: Backdunes (EC Habitat 2250*), Grey Dunes with garigue vegetation (EC Habitat 6220*), Prairie with Grassy Heat, Woodland in a calcareous gorge and a Reconstructed Shrubland Area in an abandoned quarry. A total of 3886 individuals, belonging to 39 butterfly species and five families, were recorded during the sampling period. *Melanargia arge* and *Zerynthia cassandra* are the most important species occurring in the area. Both are Italian endemic species: *M. arge* is listed in Annexes II and IV of the "Habitat Directive" and probably is associated with *Stipa austroitalica*; *Z. cassandra* which was recently split from *Z. polyxena (*Annex IV). Another important species present is *Thymelicus acteon*, listed as near threatened (NT) in IUCN European Red List of Butterflies. The highest Shannon index value (H=2.50) and the highest number of species (N=28) were found in Reconstructed Shrubland habitat. Woodland was the habitat with the lowest Shannons' index value (H=2.05) and with less biodiversity of butterflies (22 different species, as Grey Dunes). The assemblages were also compared with multivariate method. The results of several diversity indexes suggests that the presence of *Stipa austroitalica* in Grey Dunes plays an important ecological role in dunal succession and can promote the persistence of species of conservation importance.

Key words: Butterfly conservation, Coastal dunes, Lepidoptera Rhopalocera, *Melanargia arge, Zerynthia cassandra*

A complete time-calibrated multi-gene phylogeny of the European butterflies

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With the aim of supporting ecological analyses in butterflies, the third most species-rich superfamily of Lepidoptera, we present the first time-calibrated phylogeny of all 496 extant butterfly species in Europe, including 18 narrow endemics for which no public DNA sequences had been available previously. It is based on a concatenated alignment of the mitochondrial gene COI and up to 11 nuclear gene fragments, using Bayesian inference of phylogeny. To avoid region-specific sampling bias the European tree is grafted on a global genus-level backbone butterfly phylogeny. In addition to the consensus tree which is shown here, we will provide the posterior distribution of trees and the full concatenated alignment in an upcoming publication for further analyses.

Key words: Phylogeny; time tree; European Butterflies

85 years of coastal forest succession and its effect on Mediterranean moth communities – a case study.

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Traditional extensive land-use practices contributed to the highly diverse landscapes being home of thousands of species, rendering the Mediterranean today one of the global biodiversity hotspots. However, land-use change, especially intensification and abandonment are today a major problem for biodiversity conservation. Pineta san Vitale, a forest nature reserve near Ravenna (NE Italy) was for centuries used for wood and pine nut production. Cattle grazing below the pine trees held the understory open. Over time, these extensive practices got unprofitable and were partly abandoned. In 1988, forest use finally ceased because of new conservation laws. As a result, massive changes in vegetation occurred, with more dense forest replacing formerly open habitats. We studied how these changes have altered moth communities over time. We compared historic collections (1933-1976: 107 species; and 1977-1996: 157 species) with own samples (1997-2002: 174 species; and 2011+2012: 187 species); 300 moth species in total. Over the last 85 years, total moth richness did not decay and may even have increased.

Yet, species composition has changed profoundly. The proportion of generalist species increased from 20 to 33%, whereas the fractions of woodland and open habitat species decreased by roughly 10 percentage points. Locally lost species were on average larger than those that persisted over time or were only observed in recent decades. We attribute these changes to the progress of secondary succession and to the isolation of the reserve from other near-natural areas. Generalist species are likely better adapted to pass through anthropogenically exploited landscapes and colonize isolated forests, while habitat specialists might not be capable of this to the same extent. We conclude that succession has contributed to an increase of total moth species richness, but isolation favors the immigration of generalist species, resulting in a decadal shift in species composition.

Key words: biodiversity, conservation biology, generalists, habitat specialists, Italy, Lepidoptera, long-term changes, moth diversity, insect community

Correcting of the identification of a sugarcane butterfly leaf eater in southwest Iran: *Pelopidas thrax* (Hesperiidae)

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In recent decades, sugarcane plantations have been developed in vast areas of Khuzestan province, southwest Iran. New pests have been arisen after development of sugarcane farms and the most important ones belong to Lepidoptera. Changing natural ecosystems to monocultural agroecosystems, such as development of sugarcane plantations in Khuzestan, may result in pests outbreak or shift of a species from wild host plants to cultivated ones due to loss in biodiversity. Therefore, a permanent monitoring of the entomofauna is necessary. In this regard, we reexamined a butterfly leaf roller species which has previously recorded as *Parnara* sp. according to literature. Green larvae of this species feed on sugarcane leaves and roll them by their white silks. Specimens of this butterfly were collected from sugarcane fields of Khuzestan province. Further materials were also studied from neighboring areas in Khuzestan such as Ahvaz, Khorramshahr, Mollasani, Shushtar, Dezful, Shush and Lali regions. We examined wing patterns and genitalia, and also utilized DNA barcoding by means of standard primers (LepF1 & LepR1) for species identification. Results revealed that it is actually *Pelopidas thrax* (Hübner, 1821), despite of its similar habitus to members of the genus *Parnara*. It is also known as millet skipper and occurs from southern Europe and eastern Mediterranean islands to North Africa, Middle East, India and Pakistan. It feeds on a *Saccharum* species in Oman as well. It has at least two generations in Khuzestan and is frequently seen on shrub verbenas and reed species. Information on its biology will be reviewed here.

Key words: Lepidoptera, *taxonomy, identification, sugarcane, Khuzestan*

Sexual dimorphism in the wing shape and size of *Pelopidas thrax* (Lepidoptera, Hesperiidae)

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Sexual dimorphism is an especially common form of intraspecific variation in the Lepidoptera. Sexual dimorphism may arise as size dimorphism, shape dimorphism or by the dependence of shape in relation to size. In this research, sexual wing dimorphism of *Pelopidas thrax* (Hübner, 1821) was studied by geometric morphometrics. This species occurs in southwest Iran and its larvae sometimes feed on sugarcane leaves and roll them by their white silks. Required specimens were collected by a collecting net in Ahvaz city and adjacent areas in Khuzestan province, southwest Iran, during September-October 2017. In order to investigate sexual dimorphism in the wing shape and size, right forewings of 40 males and 40 females as well as right hindwings of 39 males and 39 females were photographed after removing scales. We digitized 18 fixed landmarks in forewings and 14 fixed landmarks in hindwings to capture configuration of shape and size, using geometric morphometrics. Consensus configuration, relative warp analysis and centroid size were calculated by TPS series softwares. Thirty two shape variables in forewings and twenty four in hindwings were obtained through relative warps analysis by tpsRelw and limits of shape variation were determined for males and females. Sexual dimorphism were observed in size and shape of for- and hindwings of *P. thrax* and graphically illustrated. Multivariate statistics by geomorph package in R confirmed significant differences in shape of forewing ($F=42.10$, $p= 1\times10^{-4}$) and hindwing ($F=114.90$, $p= 1\times10^{-4}$) between sexes. T-test on centroid size of both wings showed greater values in females than males, which visualized by boxplots. Multivariate regressions of shape coordinates on centroid size were all significant (except one) in fore- and hindwings of males and females and revealed allometry which explained between 0.8% to 19.6% of shape variance in each case. Significant shape differences between wings of males and females were still remain after removing allometric effects. The analysis demonstrated different allometric patterns for sexes in both fore- and hindwings.

Key words: morphology, natural selection, intraspecific variation

Identification of butterflies of "Insect and Mite Collection of Ahvaz" at Shahid Chamran University of Ahvaz, Iran

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Butterflies with about 18000 species are one of the best known groups of insects and include five families in Iran. Foreign collectors have been studied butterflies of Iran since many years ago, because of geographic attractiveness of this country for insect faunal studies. In the present work, we studied butterflies of "Insect and Mite Collection of Ahvaz" located at Department of Plant Protection, Shahid Chamran University of Ahvaz which dates back to 50 years ago. As a result, 82 species and subspecies belonging to Papilionidae (5 species), Hesperiidae (11 species), Lycanidae (15 species), Pieridae (16 species and a subspecies) and Nymphalidae (33 species and a subspecies) were identified from 21 different Iranian provinces. Among them, 21 taxa were new provincial records for provinces of Khuzestan (9 records), Ilam (4 records), Isfahan and Yazd (2 records each), Lorestan, Bushehr, Khorasan-e Razavi and Kohgiluyeh-va Boyerahmad (1 record each). Our results indicate that despite of well-known information about butterflies in Iran, their local and provincial distribution maps may be further complete through more investigations to achieve more explicit species diversity in each area.

Key words: Lepidoptera, Insect collection, Khuzestan, Iran

Interpreting butterfly responses to climate change using space-for-time substitution: a case study from two Mediterranean mountains

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Inferring species' responses to climate change in the absence of long-term time series data is a challenge, but can be achieved by substituting space for time. For example, thermal elevational gradients represent suitable proxies to study phenological responses to warming. We used butterfly data from two Mediterranean mountains to test whether mean dates of appearance of communities and individual species show a delay with increasing elevation, and an accompanying shortening in the duration of flight periods. We found a 16-day delay in the mean date of appearance per kilometre increase in elevation for butterfly communities overall, and an average 23-day shift for 29 selected species, alongside average summer temperature lapse rates of 3 °C per km. At higher elevations there was a shortening of the flight period for the community of eight days per km, with a nine day average decline per km for individual species. Rates of phenological delay differed between the two mountain ranges, although this did not seem to result from the respective temperature lapse rates. These results suggest that climate warming could lead to advanced and lengthened flight periods for Mediterranean mountain butterfly communities. However, although univoltine species largely showed the expected response of delayed and shortened flight periods at higher elevations, multivoltine species showed less consistent patterns. Hence, whilst projections of overall community responses to climate change may benefit from space-for-time substitutions, understanding species-specific responses to local features of habitat and climate may be needed to accurately predict the effects of climate change on phenology.

Key words: developmental delay, elevational gradient, emergence time, flight period, changing climate, voltinism

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